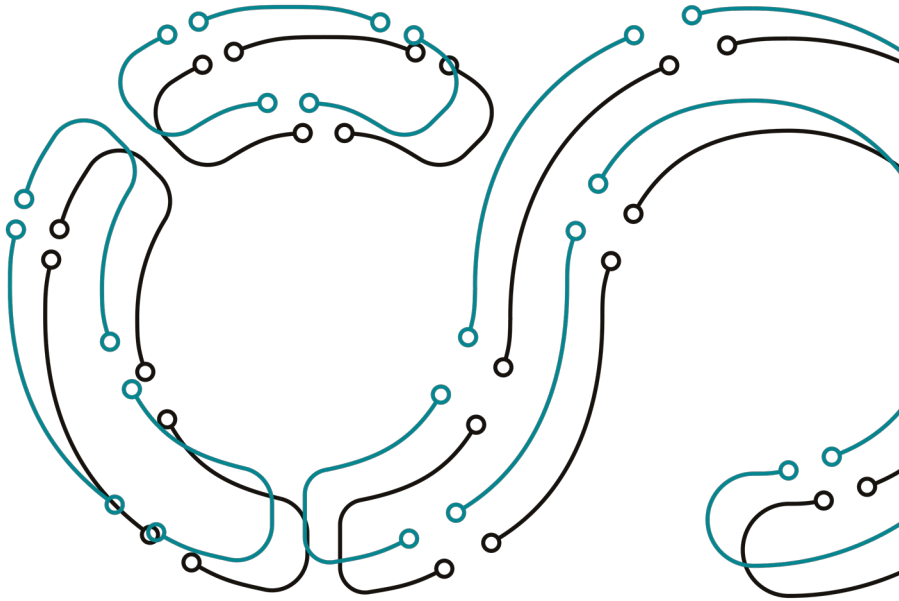
Connecting users, data, and services

EOSC Symposium 2026 / 14-16 October / Florence

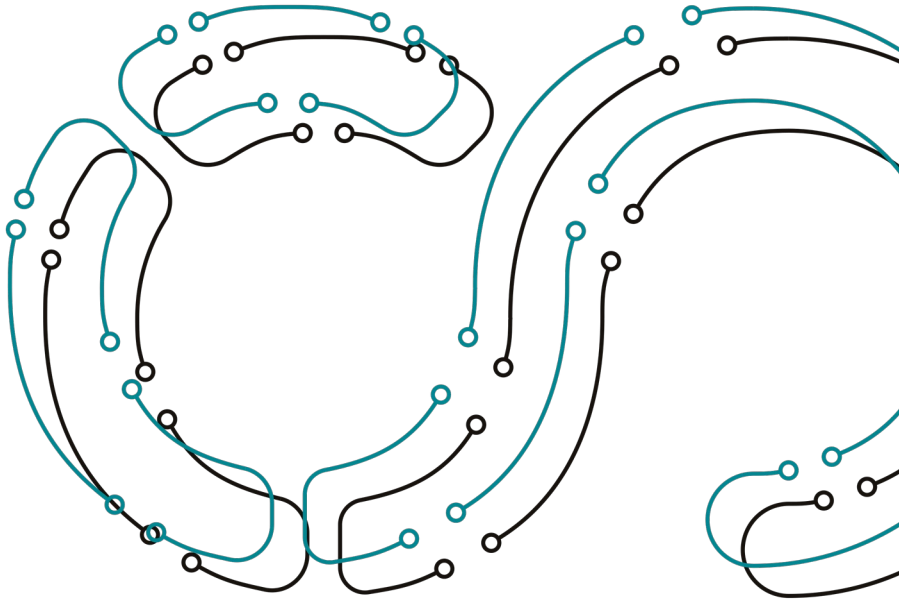


Under the patronage of MUR COMUNE DI FIRENZE

EOSC GRAVITY Funded by the European Union

Federated Workflows Using Galaxy

Wolfgang Maier, University of Freiburg



Galaxy in a nutshell

a platform that:

- provides graphical, OS-independent, controlled access to compute infrastructure

- connects to repositories and registries of all sorts

- features a tool and workflow execution engine

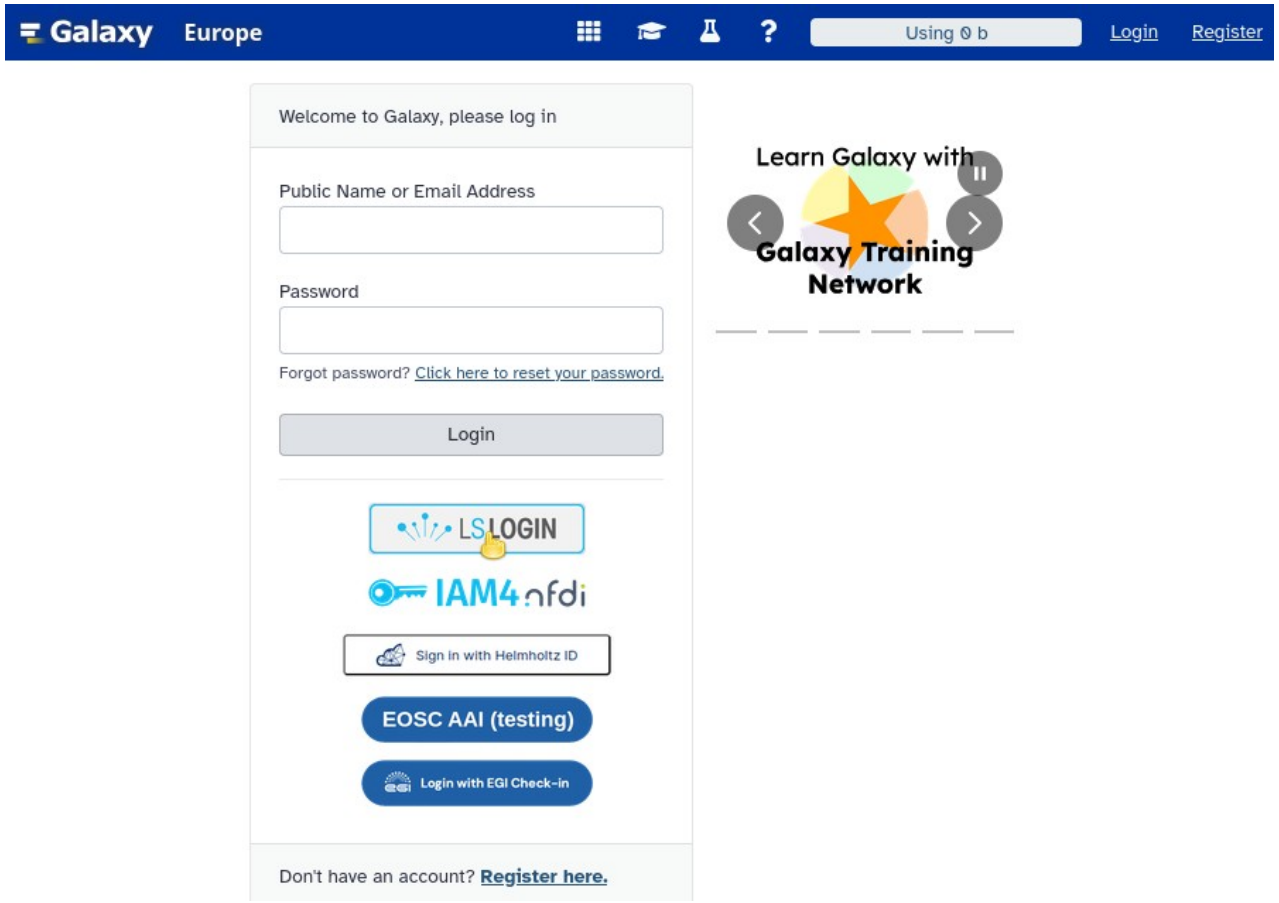


Showcase:

Real-world Avian Influenza genomic analysis bridging WorkflowHub, Galaxy and Zenodo

Step 1:

Logging in to Galaxy



at **usegalaxy.eu/login/**

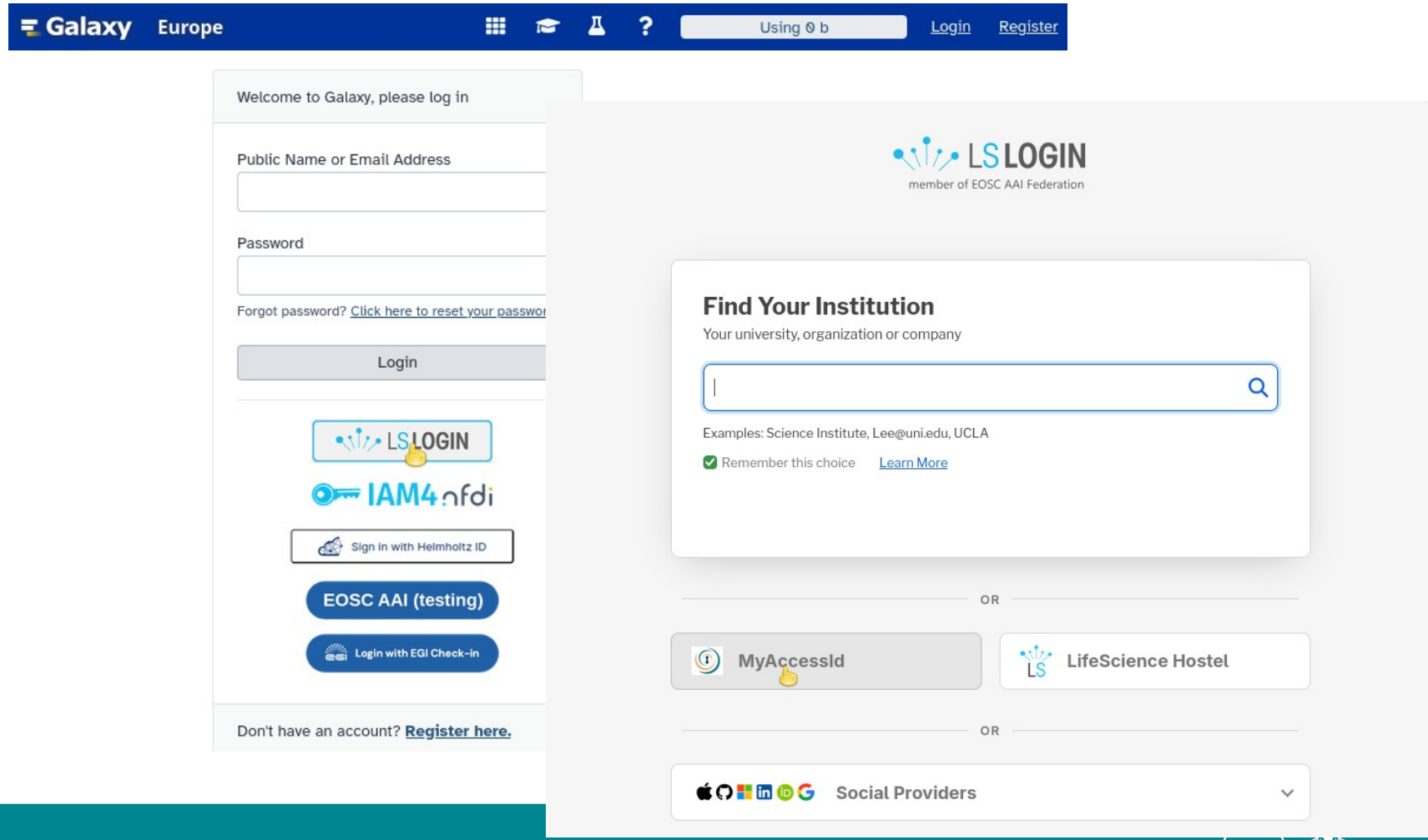
via LSLogin and MyAccessID

Galaxy EUROPE

elixir Recommended Interoperability Resources

Step 1:

Logging in to Galaxy



at **usegalaxy.eu/login/**

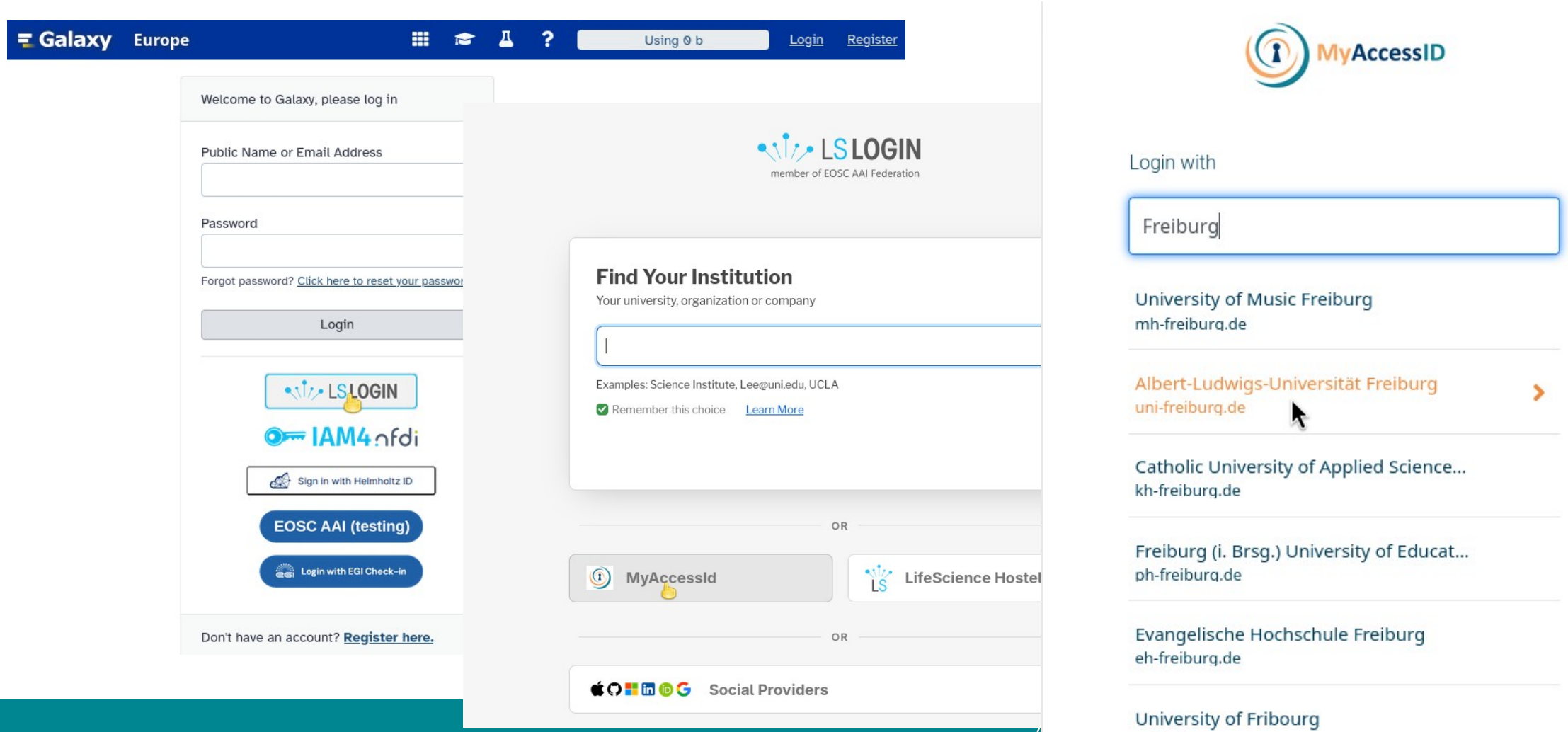
via LSLogin and MyAccessID

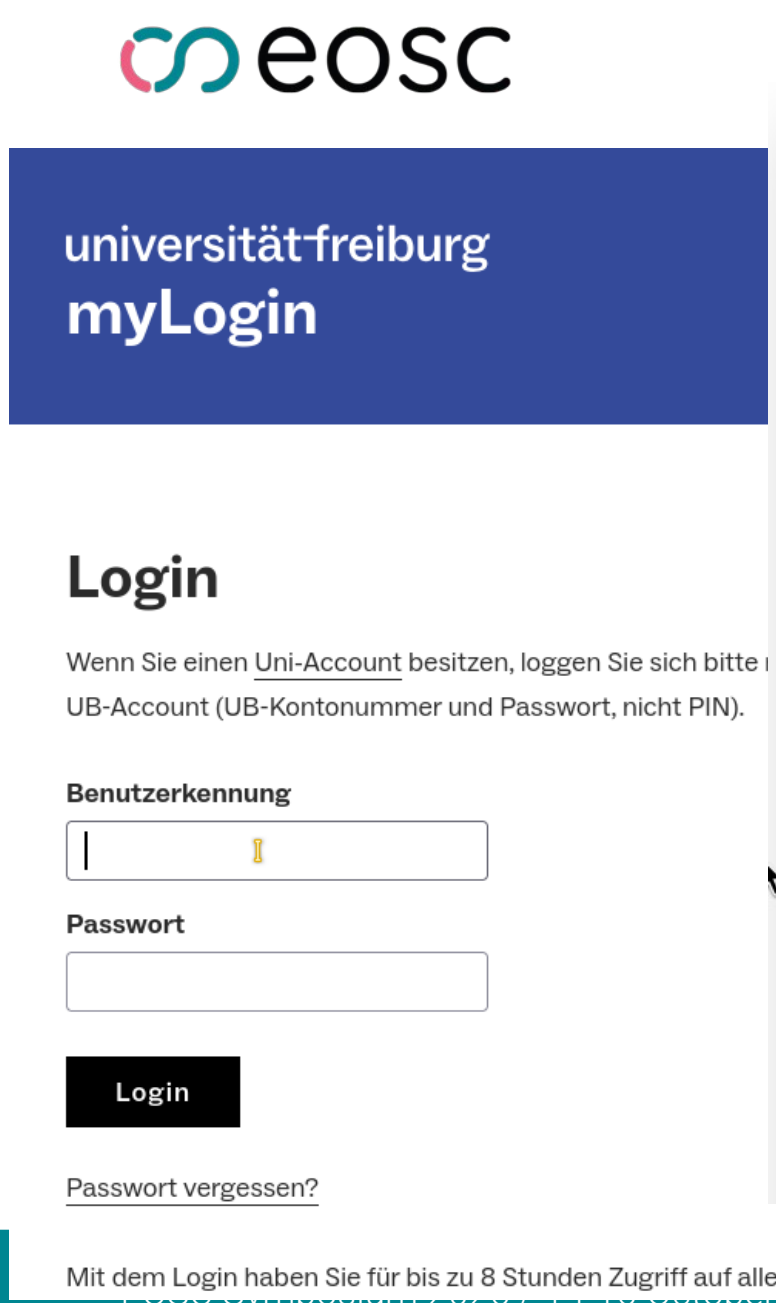
Galaxy EUROPE

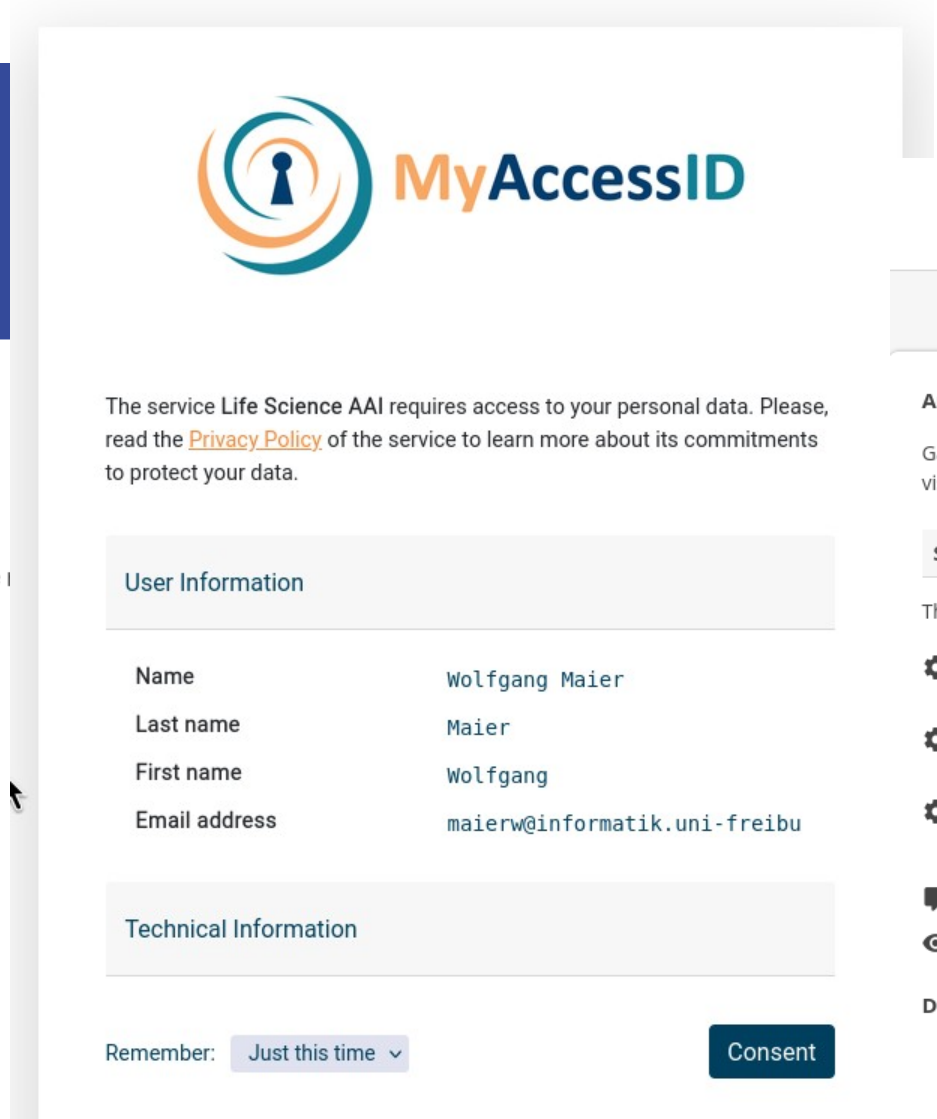
elixir Recommended Interoperability Resources

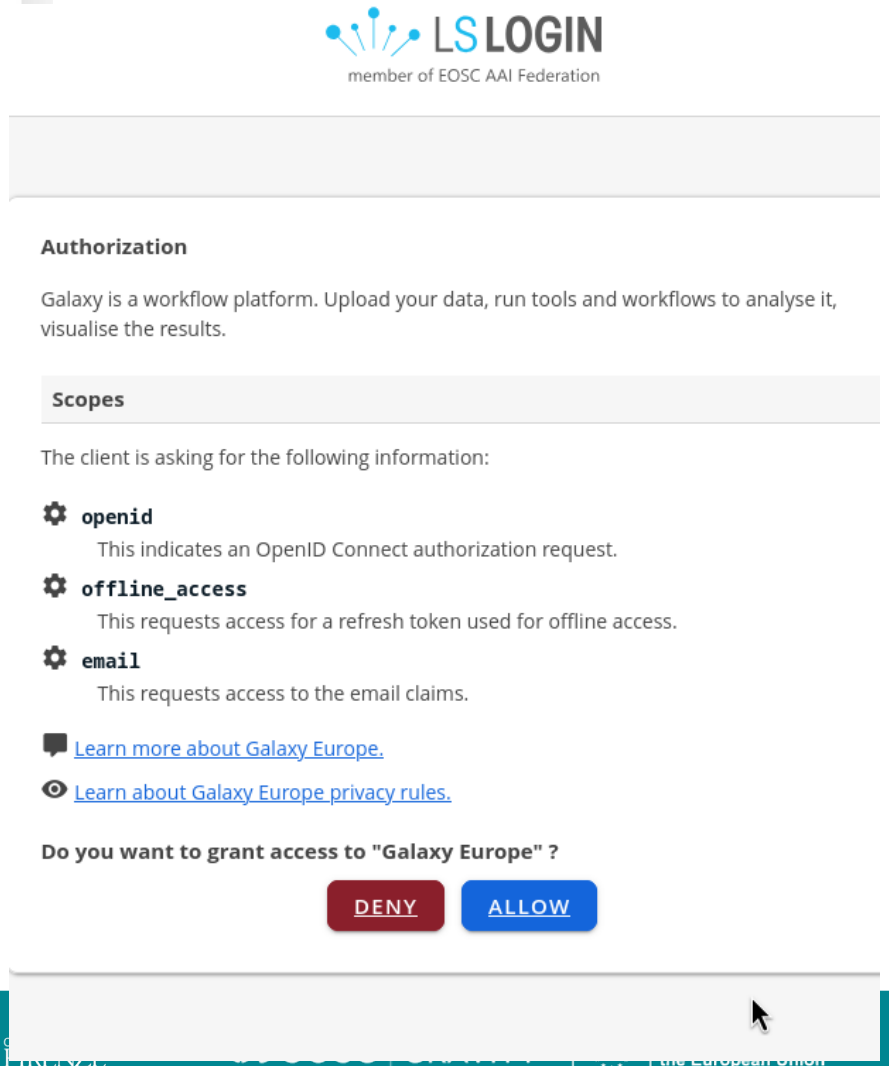
Step 1:

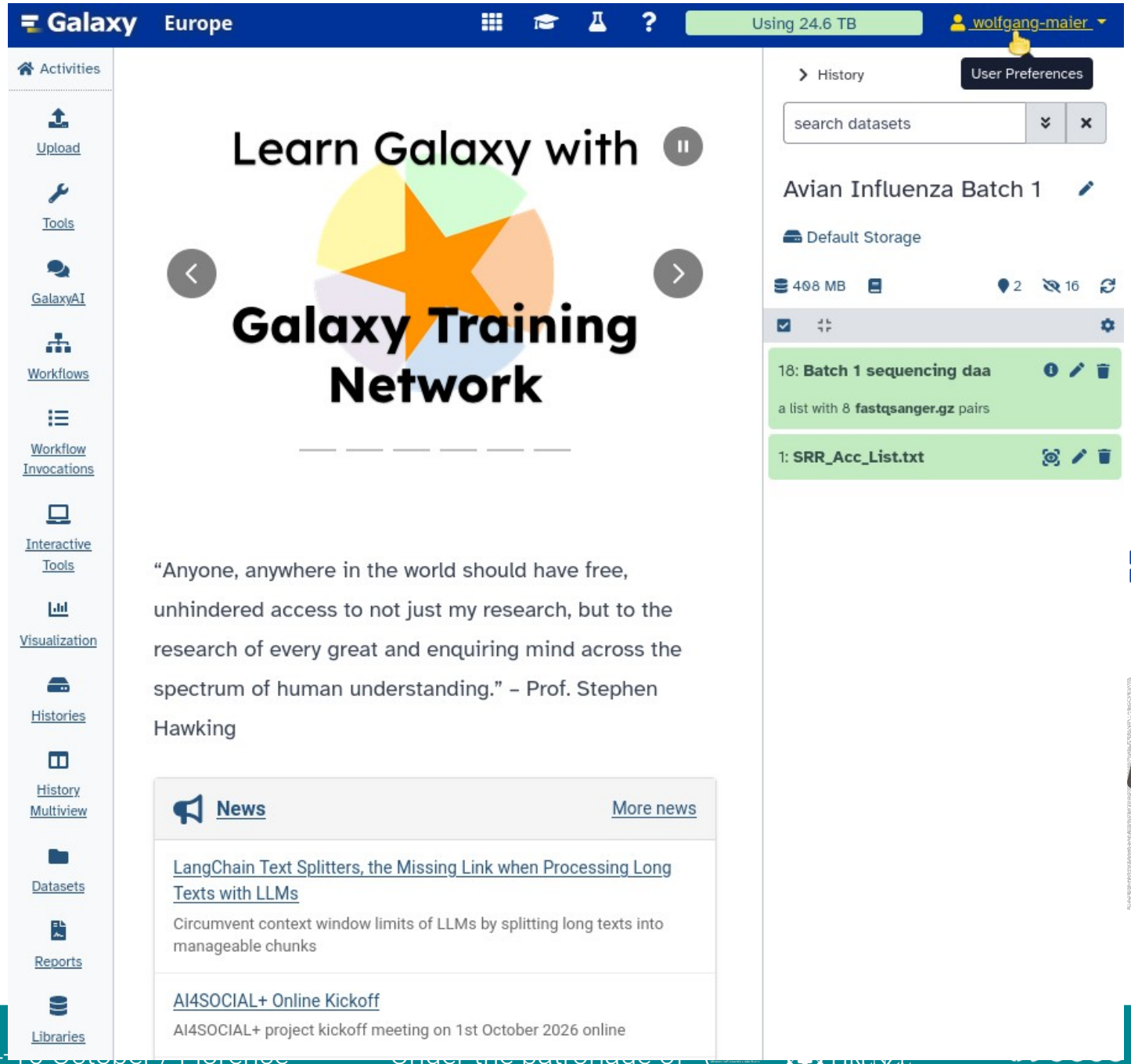
Logging in to Galaxy




universität freiburg
myLogin
Login
Wenn Sie einen Uni-Account besitzen, loggen Sie sich bitte
UB-Account (UB-Kontonummer und Passwort, nicht PIN).
Benutzerkennung
Passwort
Login
Passwort vergessen?
Mit dem Login haben Sie für bis zu 8 Stunden Zugriff auf alle An

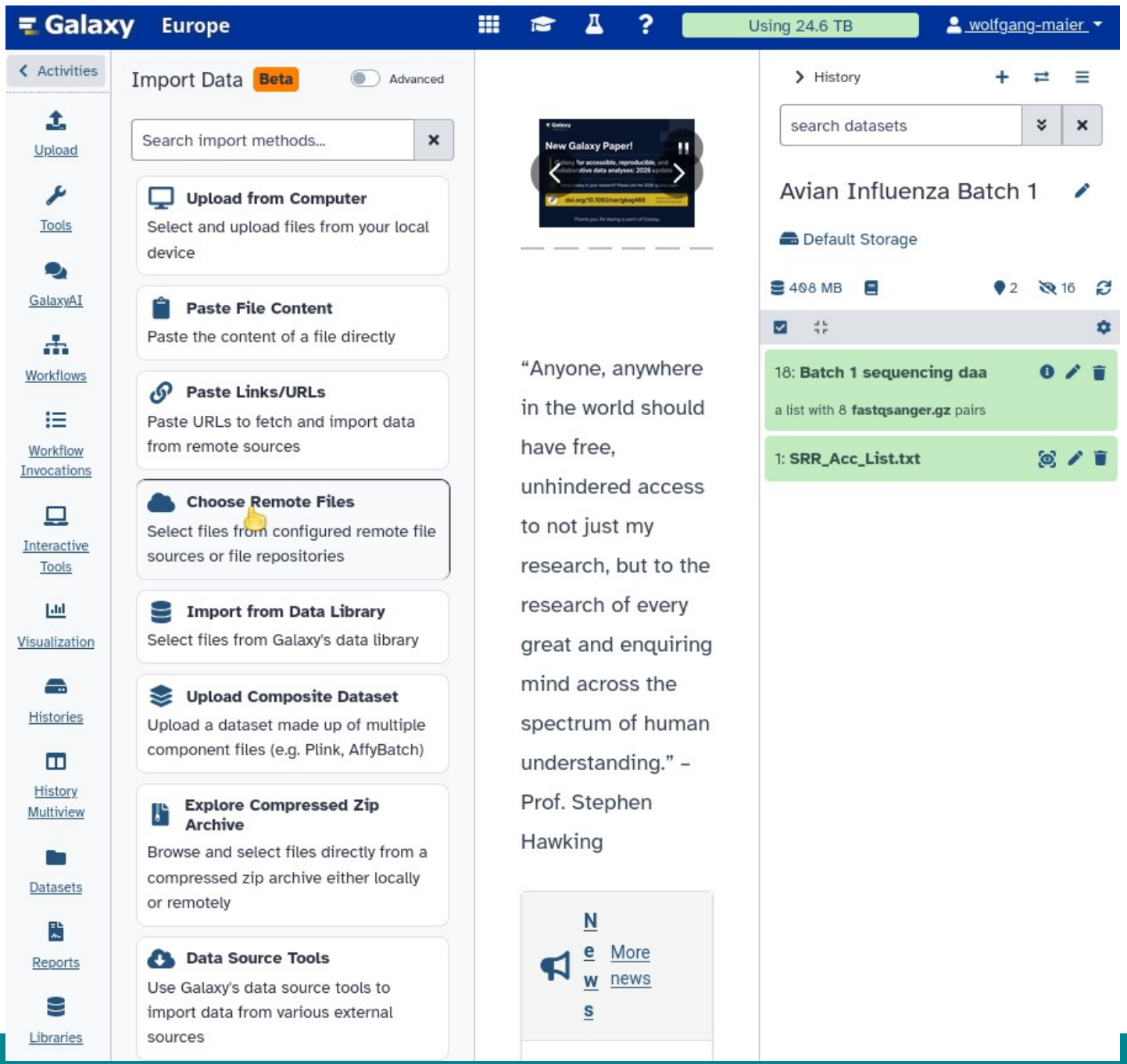

MyAccessID
The service Life Science AAI requires access to your personal data. Please, read the Privacy Policy of the service to learn more about its commitments to protect your data.
User Information
Name Wolfgang Maier
Last name Maier
First name Wolfgang
Email address maierw@informatik.uni-freibu
Technical Information
Remember: Just this time
Consent


LS LOGIN
member of EOSC AAI Federation
Authorization
Galaxy is a workflow platform. Upload your data, run tools and workflows to analyse it, visualise the results.
Scopes
The client is asking for the following information:
openid
This indicates an OpenID Connect authorization request.
offline_access
This requests access for a refresh token used for offline access.
email
This requests access to the email claims.
Learn more about Galaxy Europe.
Learn about Galaxy Europe privacy rules.
Do you want to grant access to "Galaxy Europe" ?
DENY
ALLOW



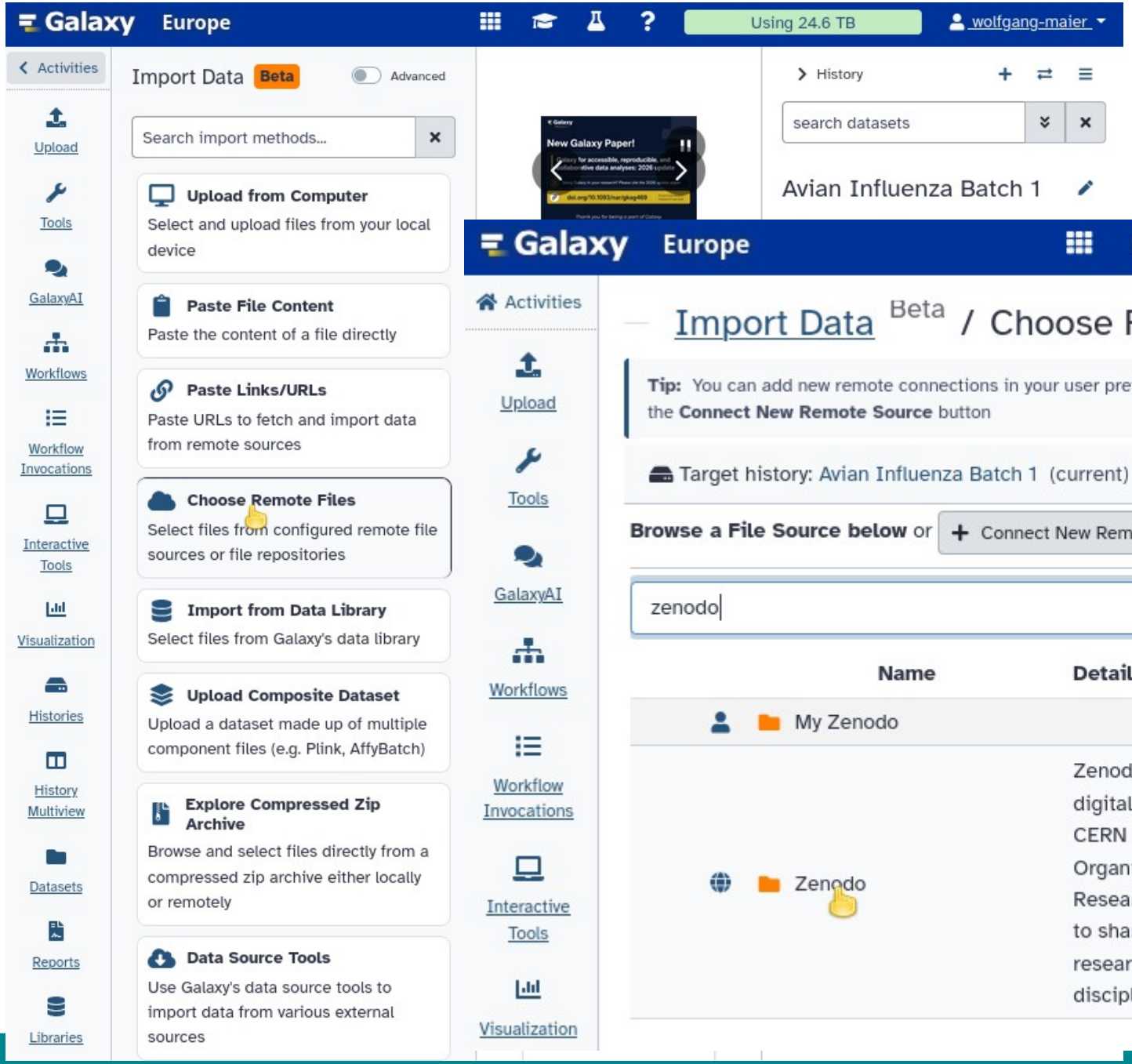
Galaxy EUROPE

elixir Recommended Interoperability Resources



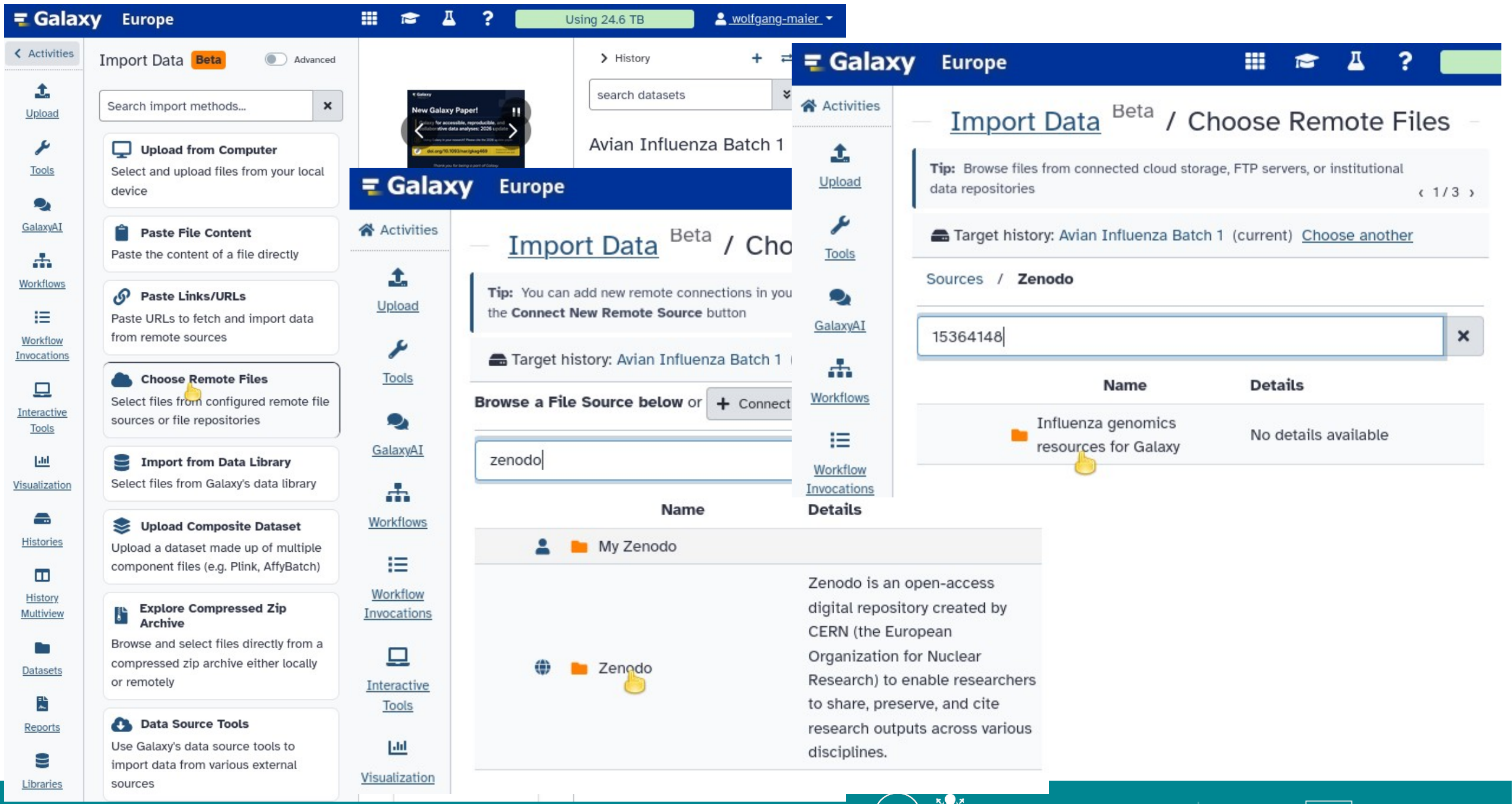
Step 2:

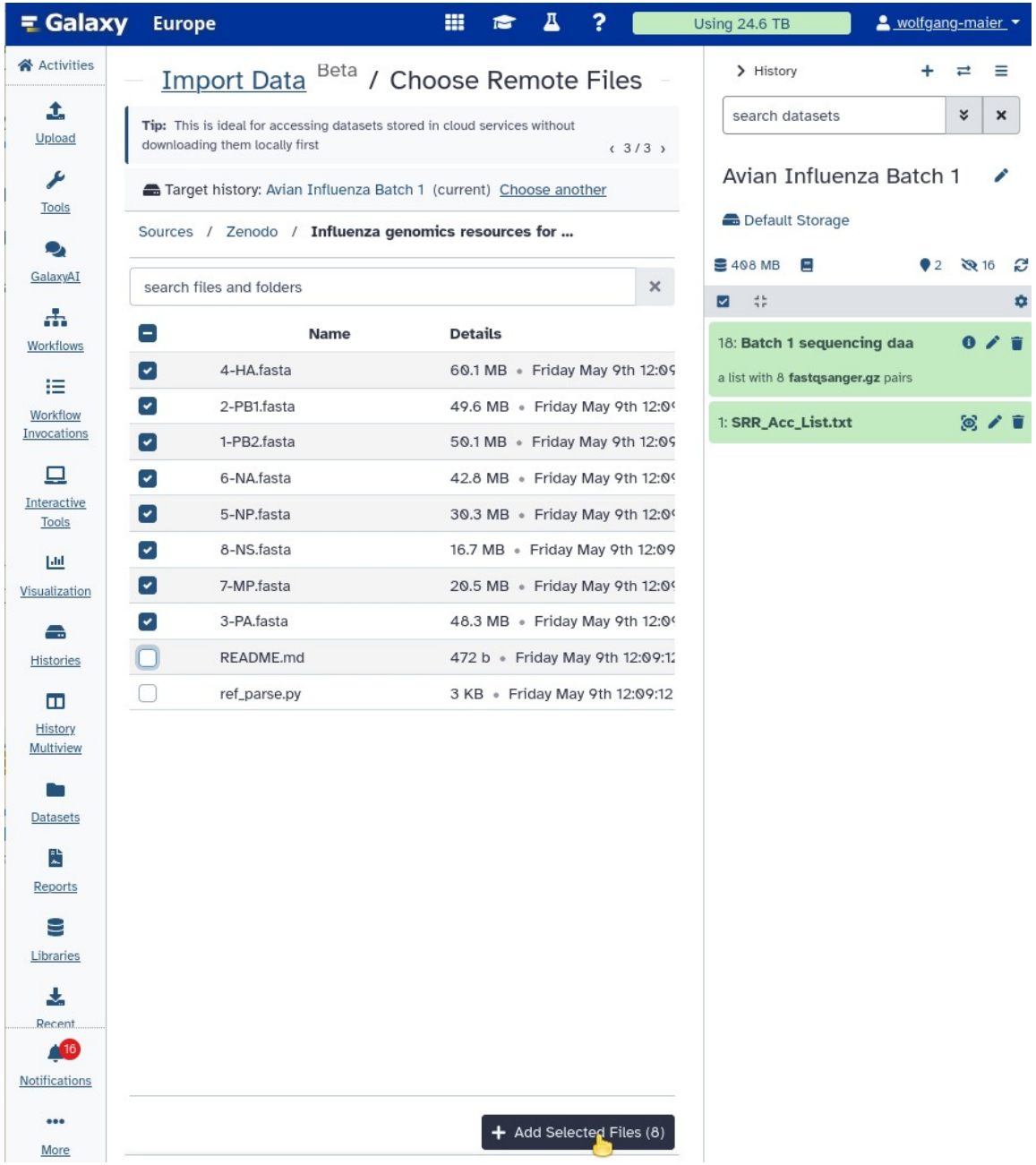
Get required reference data from Zenodo



Step 2:

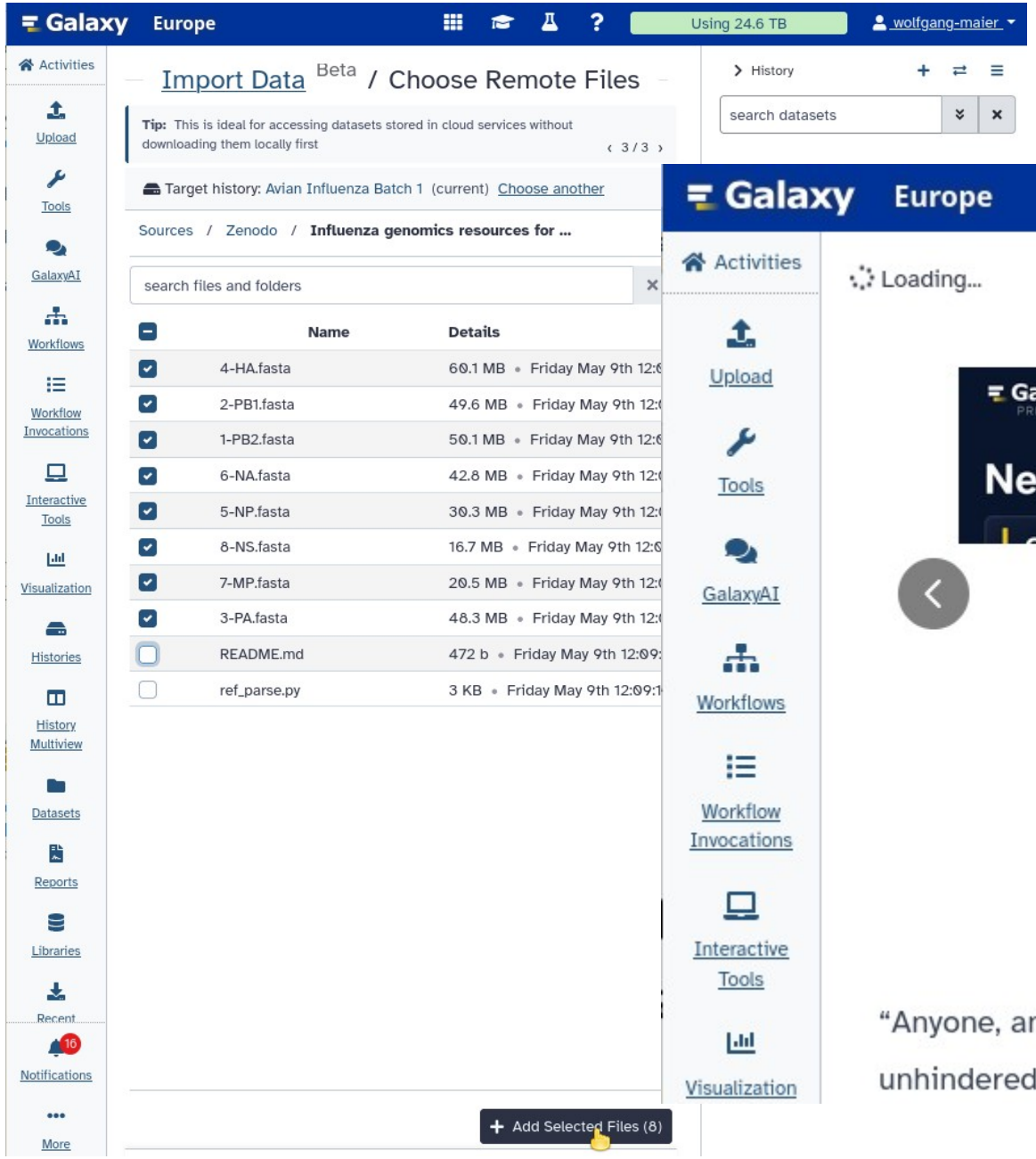
equired reference data from Zenodo

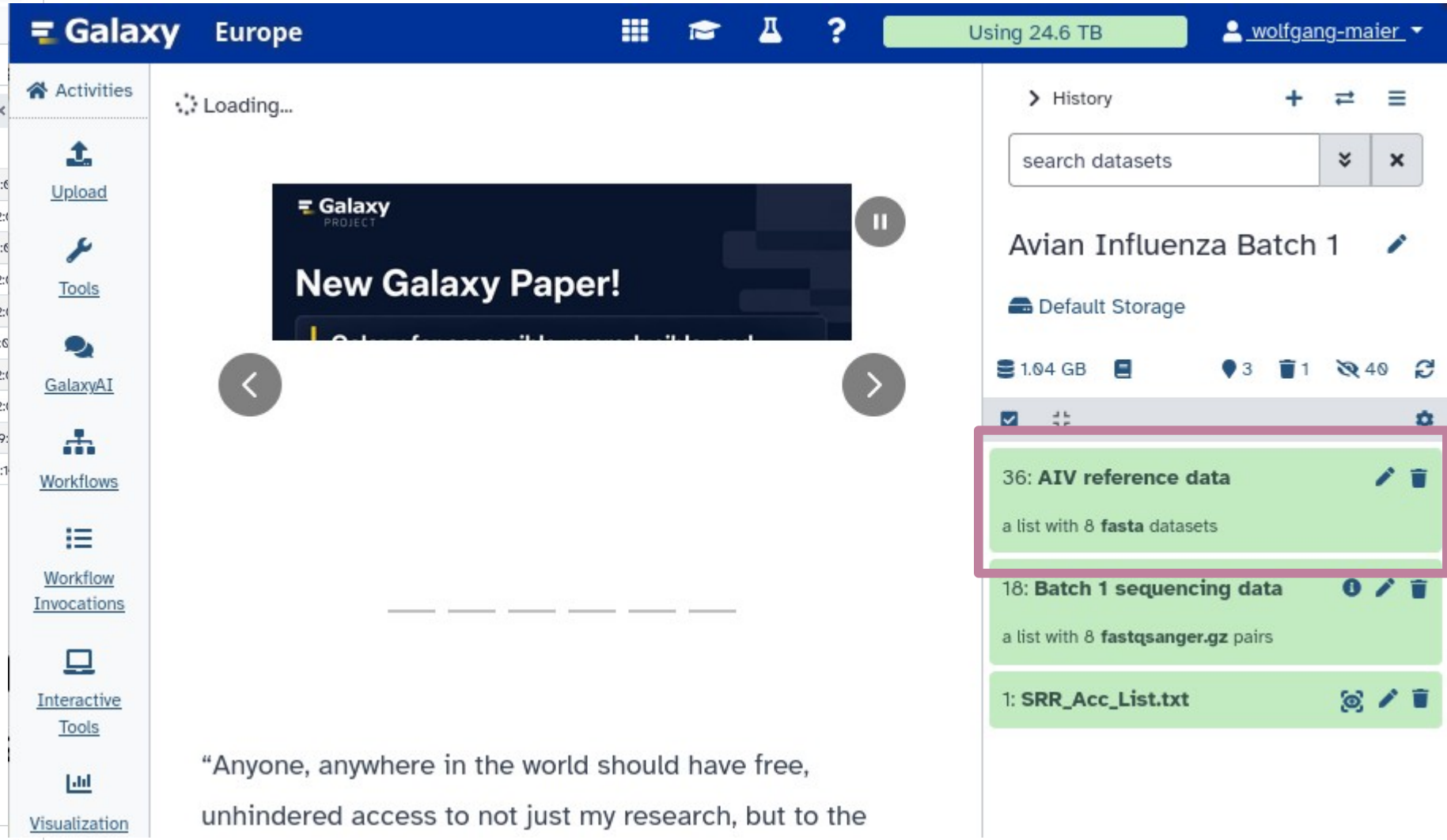

Galaxy Europe
Using 24.6 TB
wolfgang-maier
Activities
Import Data Beta
Advanced
Search import methods...
Upload from Computer
Select and upload files from your local device
Paste File Content
Paste the content of a file directly
Paste Links/URLs
Paste URLs to fetch and import data from remote sources
Choose Remote Files
Select files from configured remote file sources or file repositories
Import from Data Library
Select files from Galaxy's data library
Upload Composite Dataset
Upload a dataset made up of multiple component files (e.g. Plink, AffyBatch)
Explore Compressed Zip Archive
Browse and select files directly from a compressed zip archive either locally or remotely
Data Source Tools
Use Galaxy's data source tools to import data from various external sources
Upload
Tools
GalaxyAI
Workflows
Workflow Invocations
Interactive Tools
Visualization
Histories
History Multiview
Datasets
Reports
Libraries
New Galaxy Paper!
History
search datasets
Avian Influenza Batch 1
Galaxy Europe
Activities
Import Data Beta / Cho
Tip: You can add new remote connections in you the Connect New Remote Source button
Target history: Avian Influenza Batch 1
Browse a File Source below or + Connect
zenodo
Name
Details
My Zenodo
Zenodo
Zenodo is an open-access digital repository created by CERN (the European Organization for Nuclear Research) to enable researchers to share, preserve, and cite research outputs across various disciplines.
Galaxy Europe
Activities
Import Data Beta / Choose Remote Files
Tip: Browse files from connected cloud storage, FTP servers, or institutional data repositories
‹ 1 / 3 ›
Target history: Avian Influenza Batch 1 (current) Choose another
Sources / Zenodo
15364148
Name
Details
Influenza genomics resources for Galaxy
No details available



Step 2:

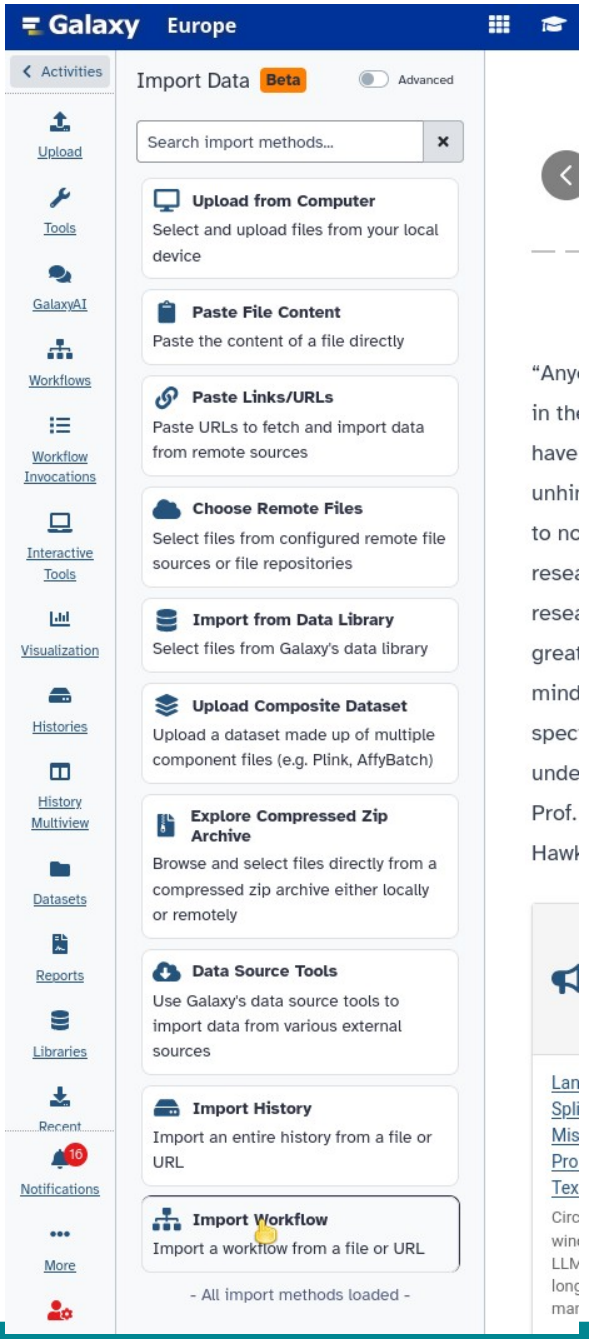
Get required reference data from Zenodo


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Activities
Upload
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GalaxyAI
Workflows
Workflow Invocations
Interactive Tools
Visualization
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History Multiview
Datasets
Reports
Libraries
Recent
Notifications
More
Import Data Beta / Choose Remote Files
Tip: This is ideal for accessing datasets stored in cloud services without downloading them locally first
‹ 3 / 3 ›
Target history: Avian Influenza Batch 1 (current) Choose another
Sources / Zenodo / Influenza genomics resources for ...
search files and folders
Name
Details
4-HA.fasta 60.1 MB • Friday May 9th 12:
2-PB1.fasta 49.6 MB • Friday May 9th 12:
1-PB2.fasta 50.1 MB • Friday May 9th 12:
6-NA.fasta 42.8 MB • Friday May 9th 12:
5-NP.fasta 30.3 MB • Friday May 9th 12:
8-NS.fasta 16.7 MB • Friday May 9th 12:
7-MP.fasta 20.5 MB • Friday May 9th 12:
3-PA.fasta 48.3 MB • Friday May 9th 12:
README.md 472 b • Friday May 9th 12:09:
ref_parse.py 3 KB • Friday May 9th 12:09:1
+ Add Selected Files (8)
History
search datasets


Galaxy Europe
Using 24.6 TB
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Activities
Upload
Tools
GalaxyAI
Workflows
Workflow Invocations
Interactive Tools
Visualization
Loading...
Galaxy PROJECT
New Galaxy Paper!
"Anyone, anywhere in the world should have free, unhindered access to not just my research, but to the
History
search datasets
Avian Influenza Batch 1
Default Storage
1.04 GB
3
1
40
36: AIV reference data
a list with 8 fasta datasets
18: Batch 1 sequencing data
a list with 8 fastqsanger.gz pairs
1: SRR_Acc_List.txt

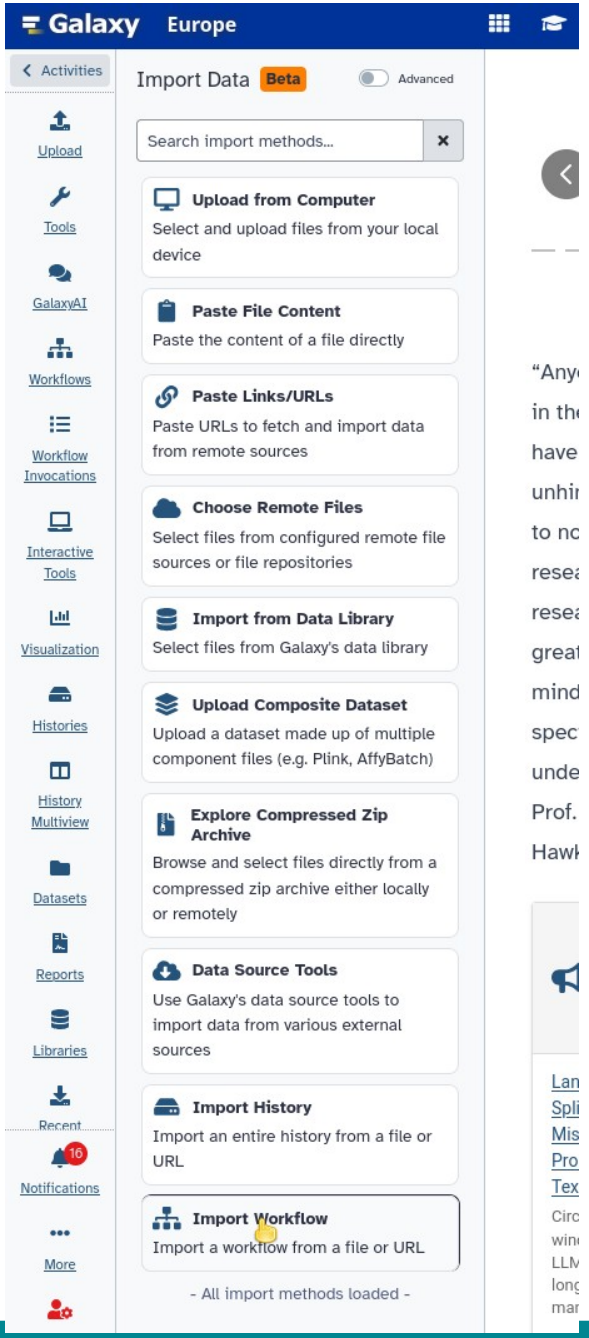
Step 3:

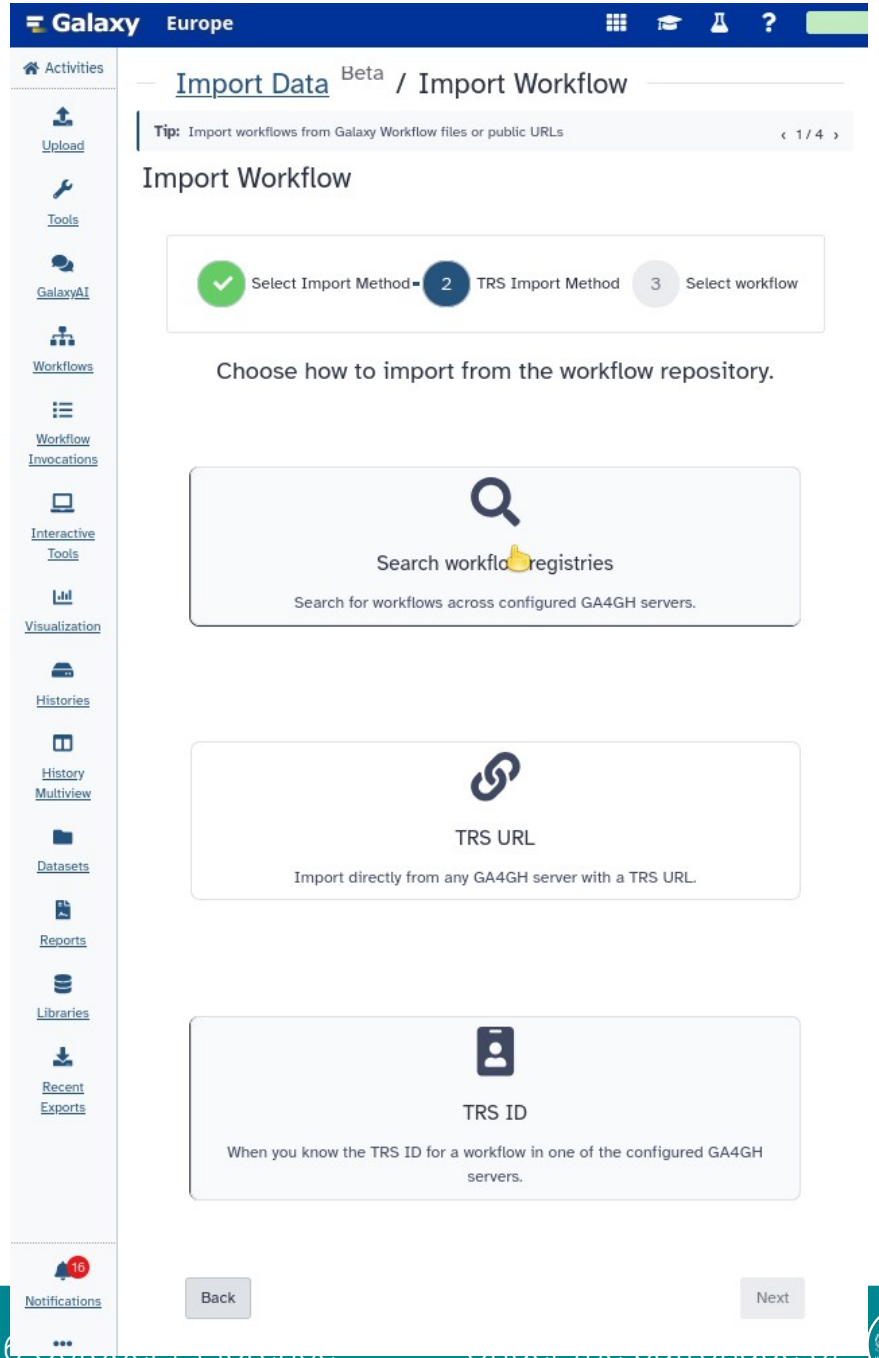
Getting an analysis workflow from WorkflowHub



Step 3:

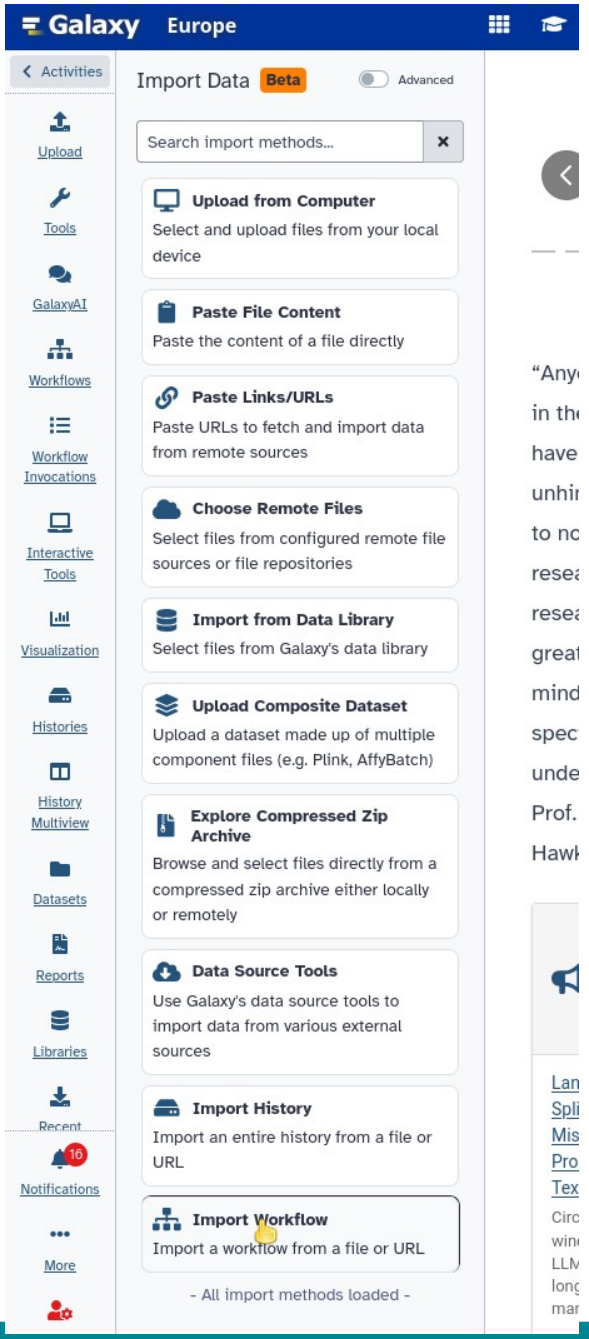
Getting an analysis workflow from WorkflowHub

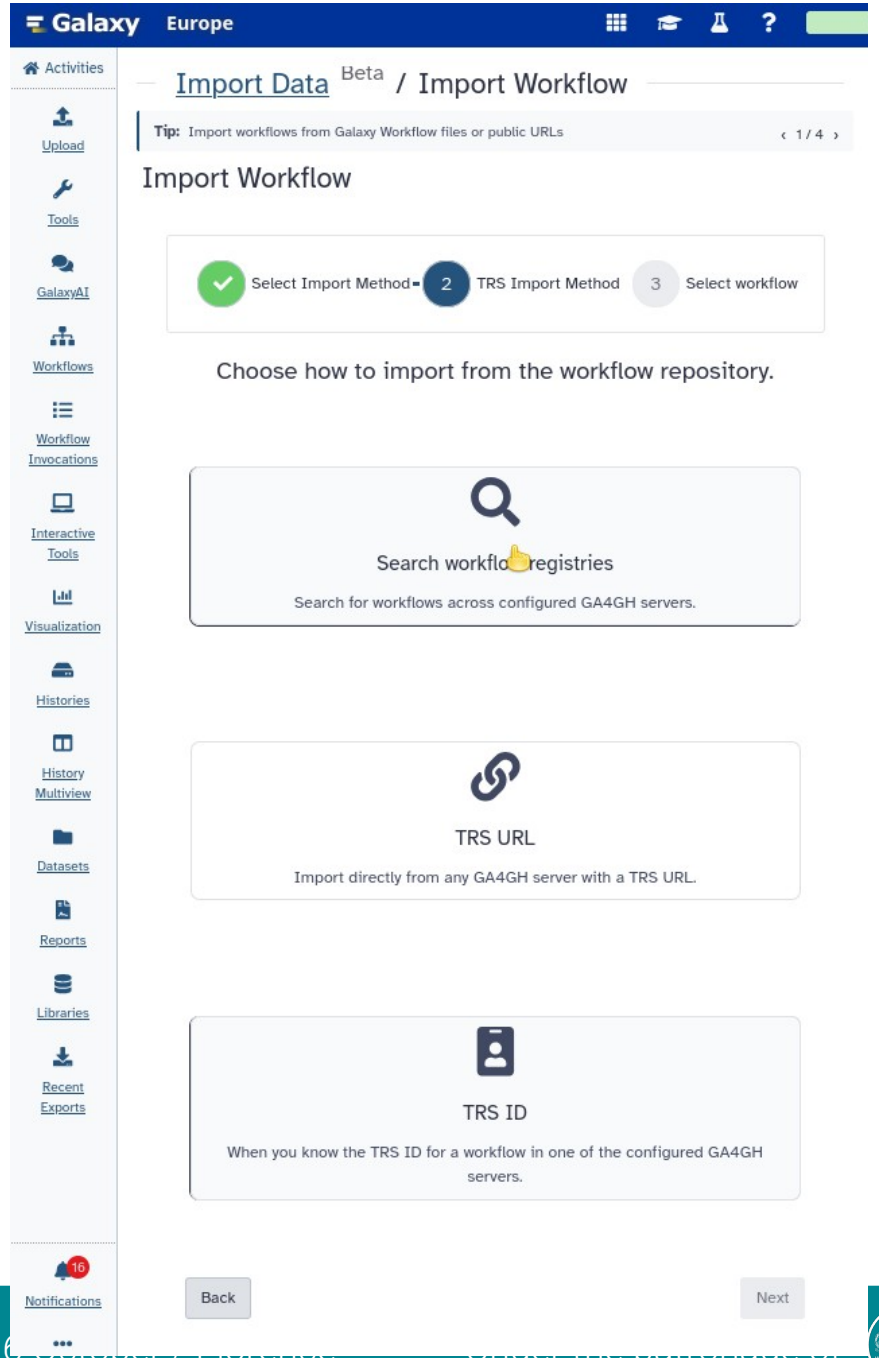


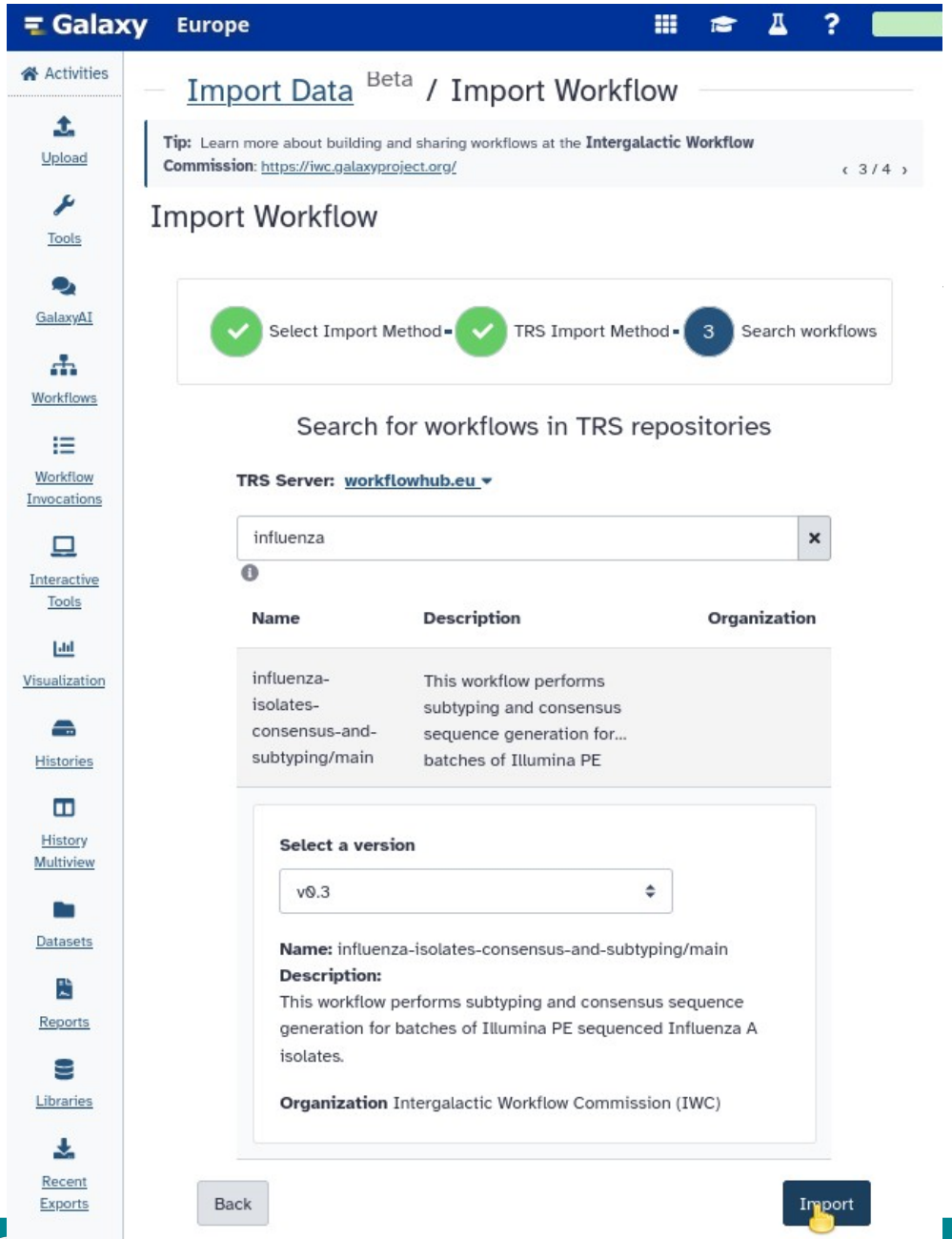


Step 3:

Getting an analysis workflow from WorkflowHub

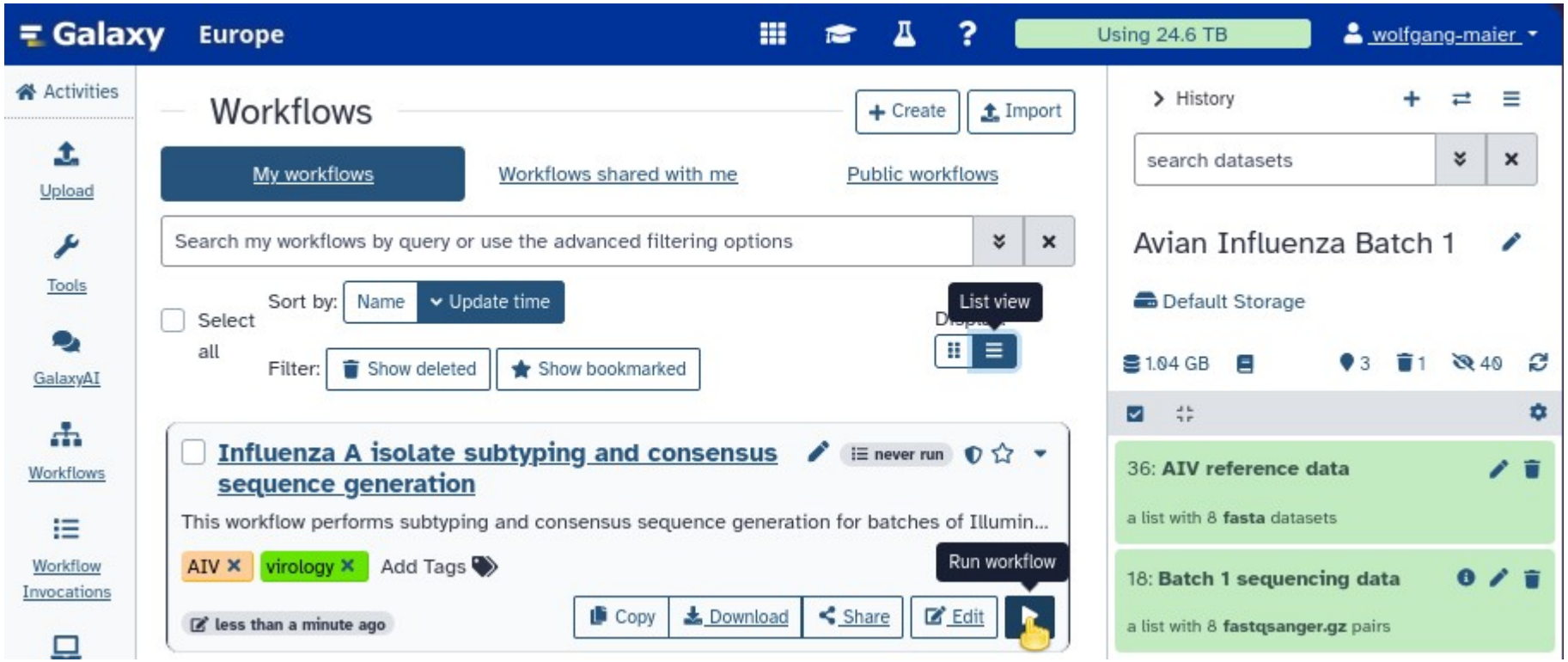

Galaxy Europe
Activities
Import Data Beta
Advanced
Search import methods...
Upload from Computer
Select and upload files from your local device
Paste File Content
Paste the content of a file directly
Paste Links/URLs
Paste URLs to fetch and import data from remote sources
Choose Remote Files
Select files from configured remote file sources or file repositories
Import from Data Library
Select files from Galaxy's data library
Upload Composite Dataset
Upload a dataset made up of multiple component files (e.g. Plink, AffyBatch)
Explore Compressed Zip Archive
Browse and select files directly from a compressed zip archive either locally or remotely
Data Source Tools
Use Galaxy's data source tools to import data from various external sources
Import History
Import an entire history from a file or URL
Import Workflow
Import a workflow from a file or URL
- All import methods loaded -
Upload
Tools
GalaxyAI
Workflows
Workflow Invocations
Interactive Tools
Visualization
Histories
History Multiview
Datasets
Reports
Libraries
Recent
Notifications
More


Galaxy Europe
Activities
Import Data Beta / Import Workflow
Tip: Import workflows from Galaxy Workflow files or public URLs
‹ 1 / 4 ›
Import Workflow
Select Import Method
2 TRS Import Method
3 Select workflow
Choose how to import from the workflow repository.
Search workflow registries
Search for workflows across configured GA4GH servers.
TRS URL
Import directly from any GA4GH server with a TRS URL.
TRS ID
When you know the TRS ID for a workflow in one of the configured GA4GH servers.
Back
Next
Upload
Tools
GalaxyAI
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Workflow Invocations
Interactive Tools
Visualization
Histories
History Multiview
Datasets
Reports
Libraries
Recent Exports
Notifications


Galaxy Europe
Activities
Import Data Beta / Import Workflow
Tip: Learn more about building and sharing workflows at the Intergalactic Workflow Commission: https://iwc.galaxyproject.org/
‹ 3 / 4 ›
Import Workflow
Select Import Method
TRS Import Method
3 Search workflows
Search for workflows in TRS repositories
TRS Server: workflowhub.eu
influenza
Name
Description
Organization
influenza-isolates-consensus-and-subtyping/main
This workflow performs subtyping and consensus sequence generation for... batches of Illumina PE
Select a version
v0.3
Name: influenza-isolates-consensus-and-subtyping/main
Description:
This workflow performs subtyping and consensus sequence generation for batches of Illumina PE sequenced Influenza A isolates.
Organization Intergalactic Workflow Commission (IWC)
Back
Import
Upload
Tools
GalaxyAI
Workflows
Workflow Invocations
Interactive Tools
Visualization
Histories
History Multiview
Datasets
Reports
Libraries
Recent Exports

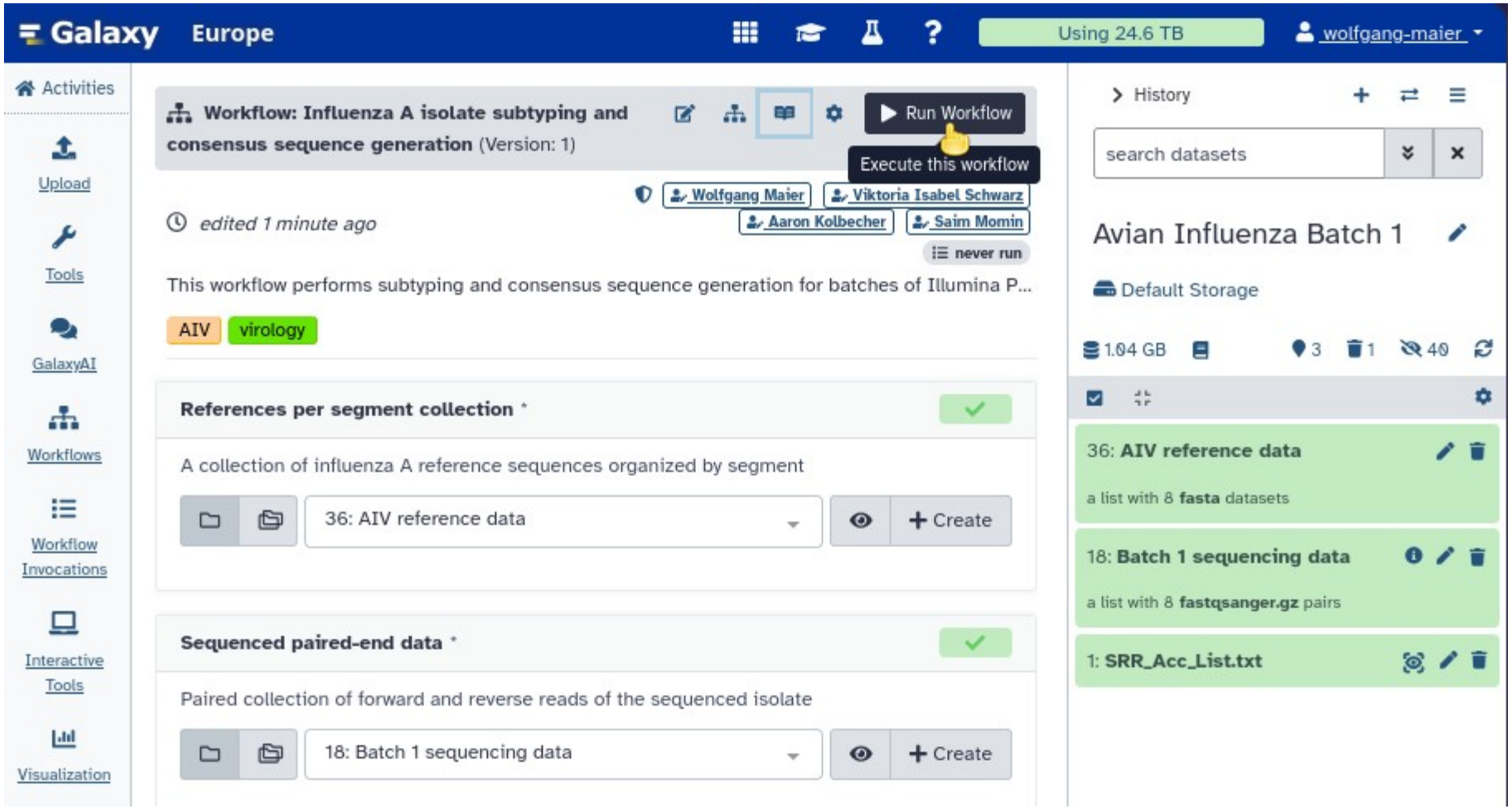
Step 4:

Performing the analysis

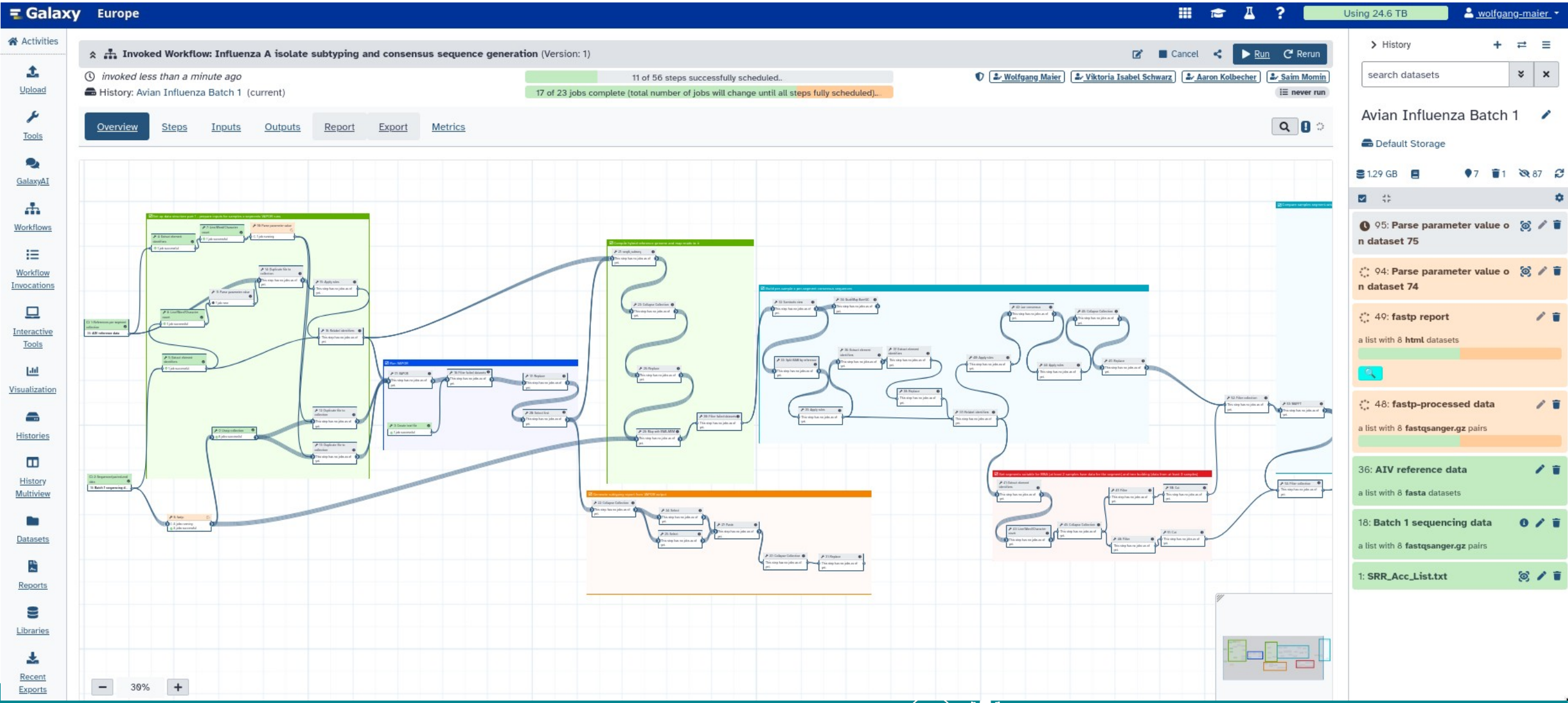


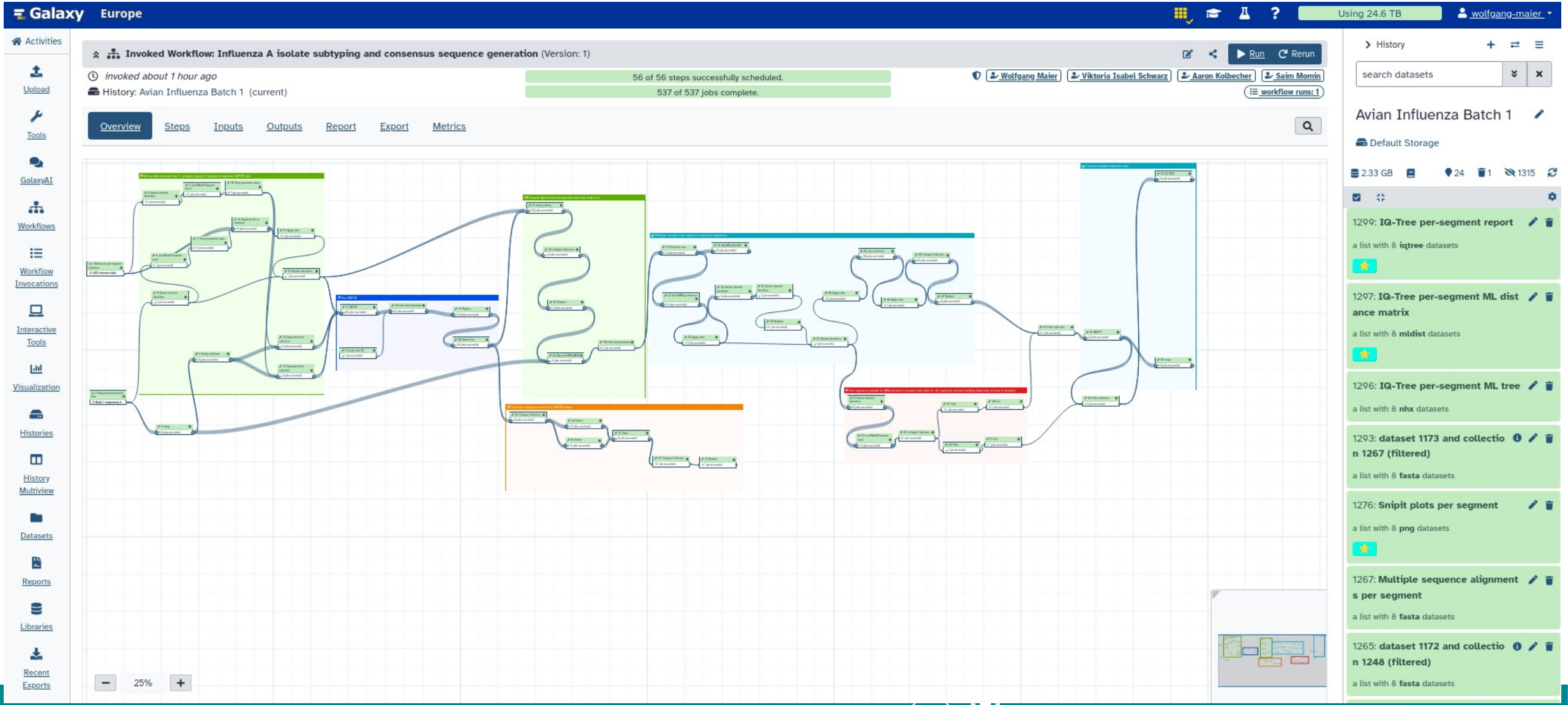
Step 4:

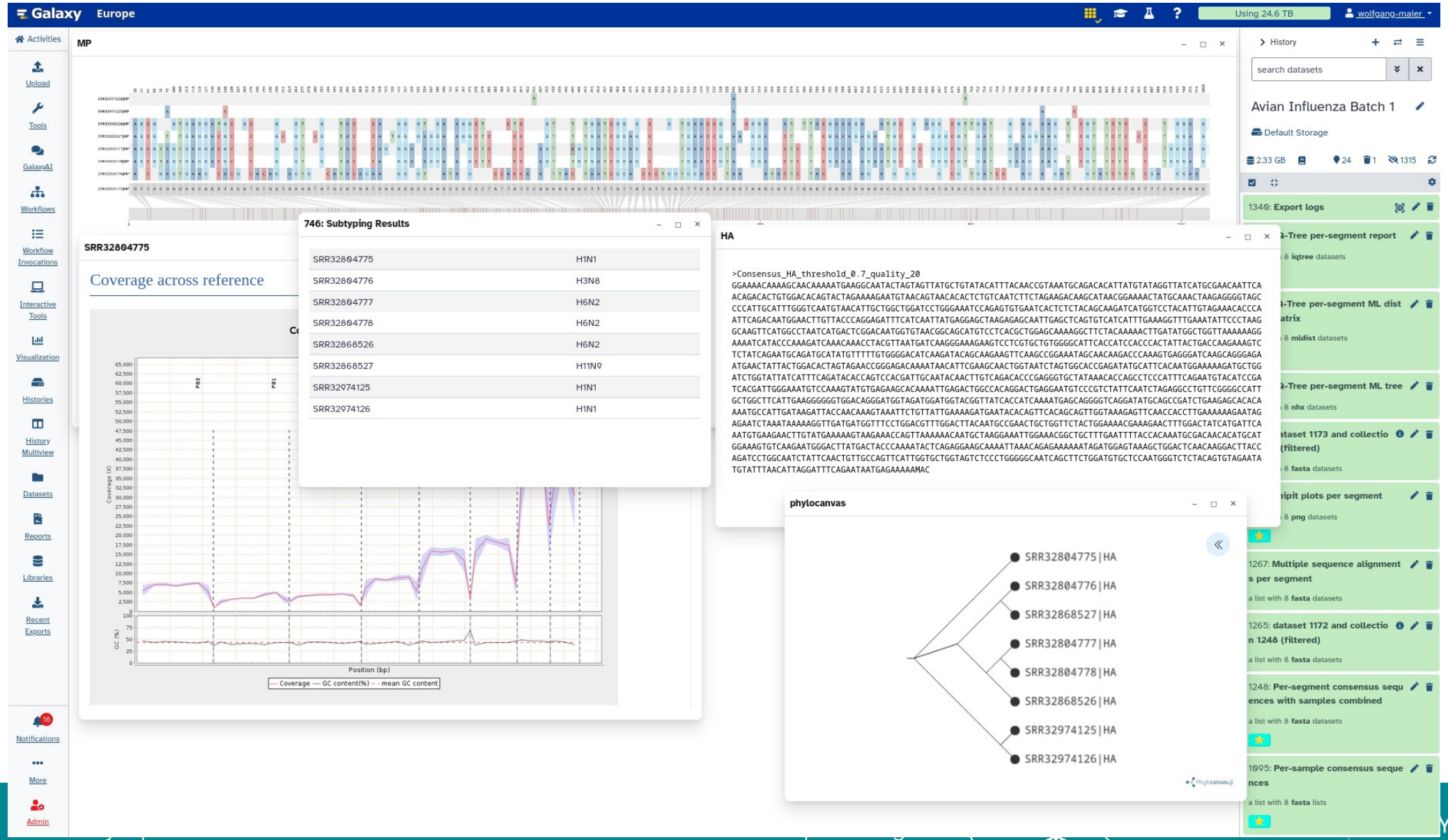
Performing the analysis



Relax and let Galaxy's workflow engine do the hard work for you

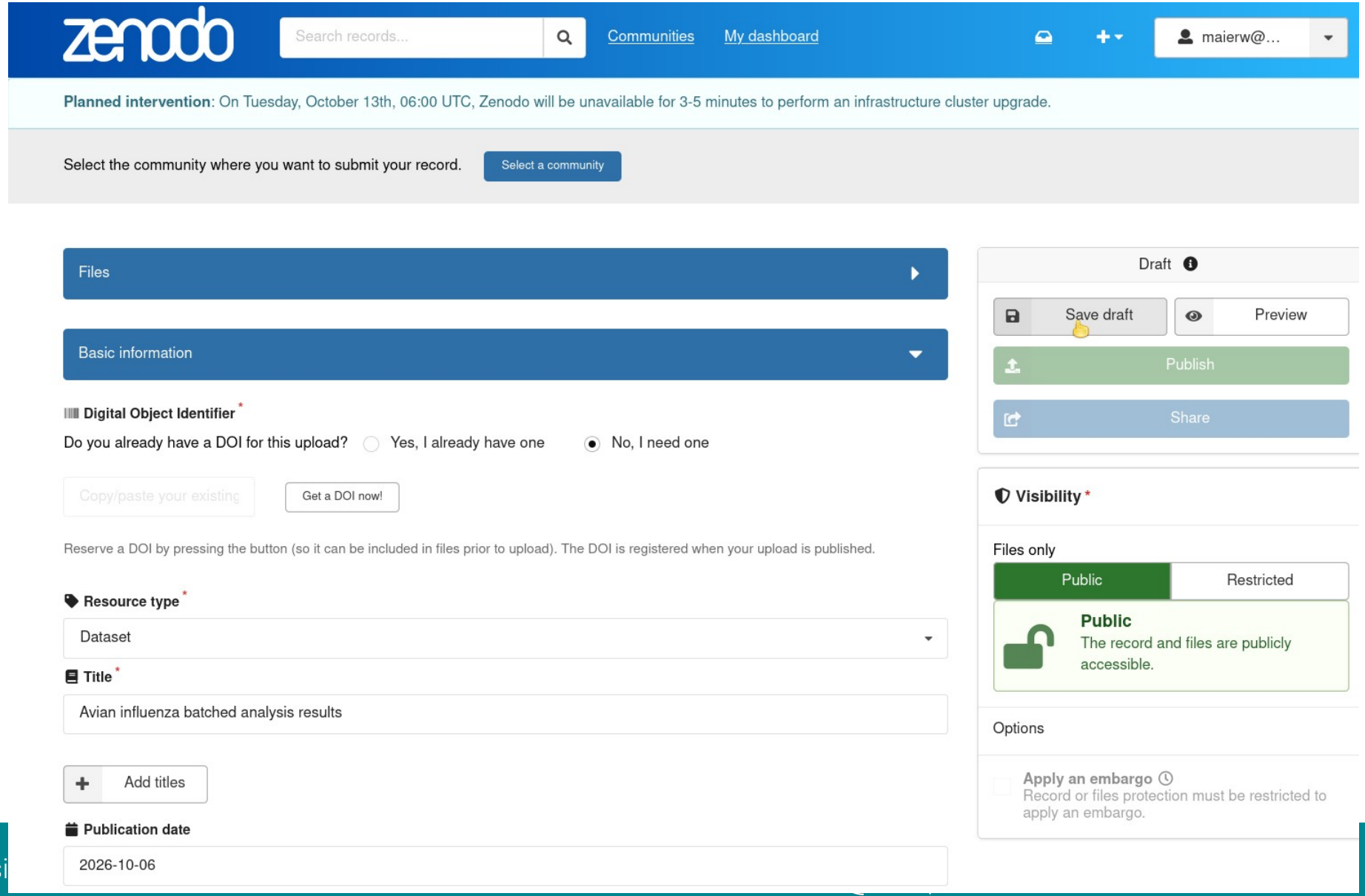



Galaxy Europe
Using 24.6 TB
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Activities
Upload
Tools
GalaxyAI
Workflows
Workflow Invocations
Interactive Tools
Visualization
Histories
History Multiview
Datasets
Reports
Libraries
Recent Exports
Invoked Workflow: Influenza A isolate subtyping and consensus sequence generation (Version: 1)
Run
Rerun
invoked about 1 hour ago
History: Avian Influenza Batch 1 (current)
56 of 56 steps successfully scheduled.
537 of 537 jobs complete.
Wolfgang Maier
Viktoria Isabel Schwarz
Aaron Kolbecher
Saim Momin
workflow runs: 1
Overview
Steps
Inputs
Outputs
Report
Export
Metrics
25%
History
search datasets
Avian Influenza Batch 1
Default Storage
2.33 GB
24
1
1315
1299: IQ-Tree per-segment report
a list with 8 iqtree datasets
1297: IQ-Tree per-segment ML distance matrix
a list with 8 mldist datasets
1296: IQ-Tree per-segment ML tree
a list with 8 nhx datasets
1293: dataset 1173 and collection 1267 (filtered)
a list with 8 fasta datasets
1276: Snipit plots per segment
a list with 8 png datasets
1267: Multiple sequence alignments per segment
a list with 8 fasta datasets
1265: dataset 1172 and collection 1248 (filtered)
a list with 8 fasta datasets

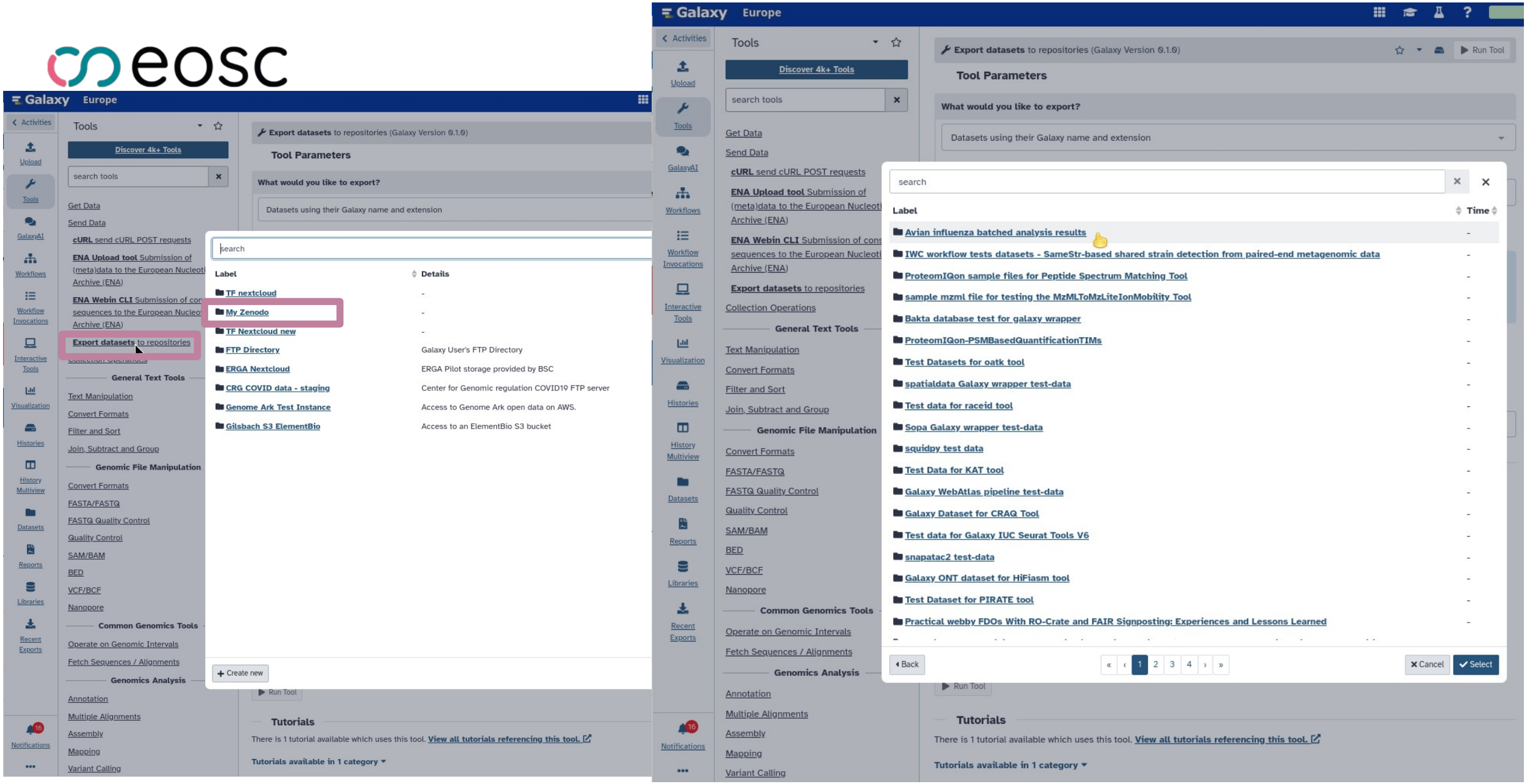


Funded by the European Union

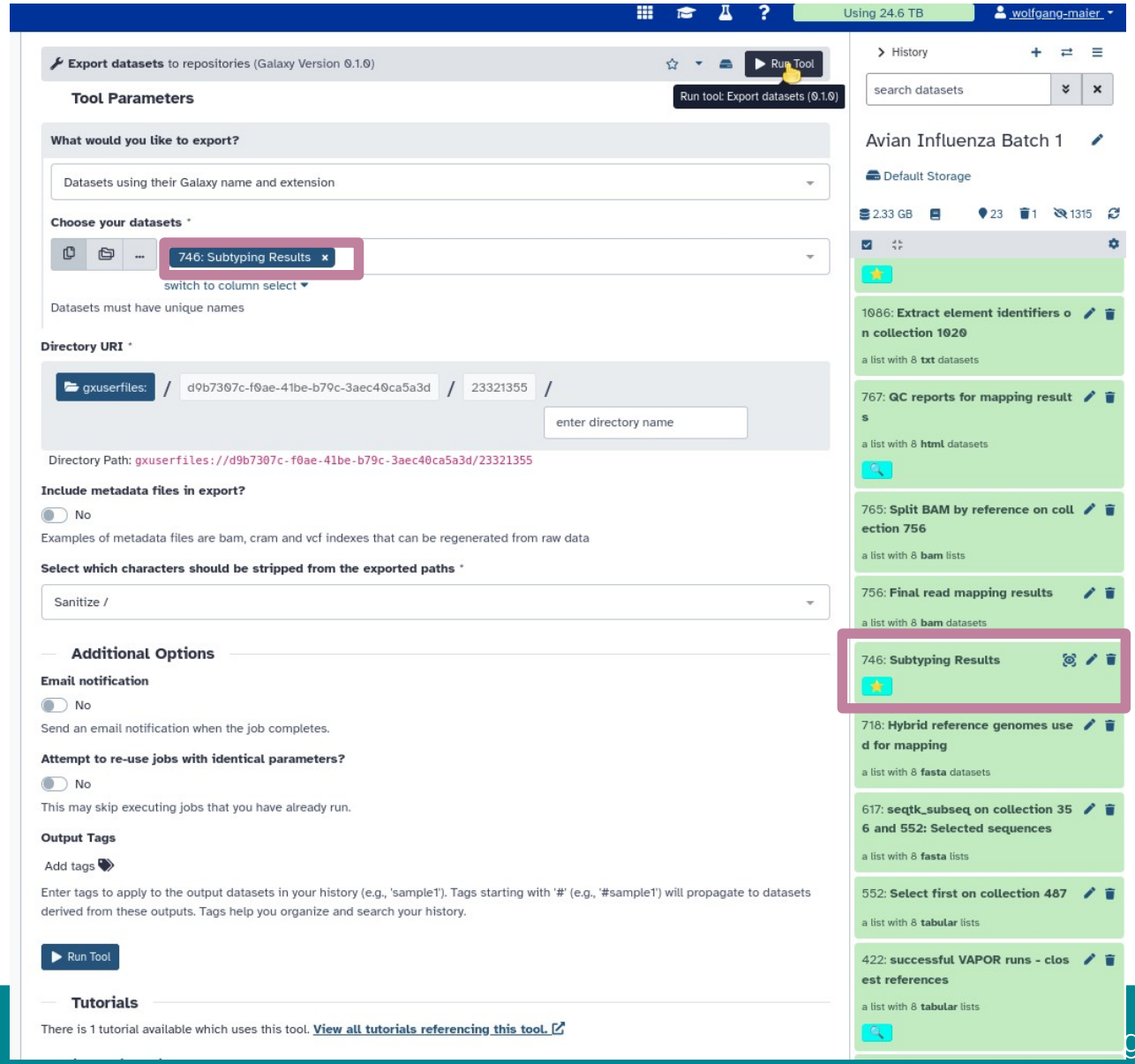
Step 5: Exporting analysis artifacts

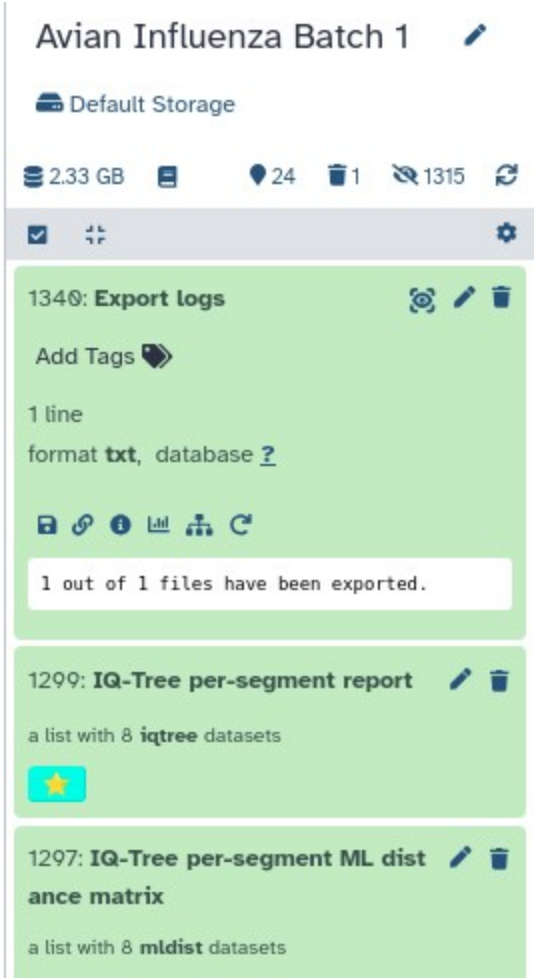


Funded by the European Union

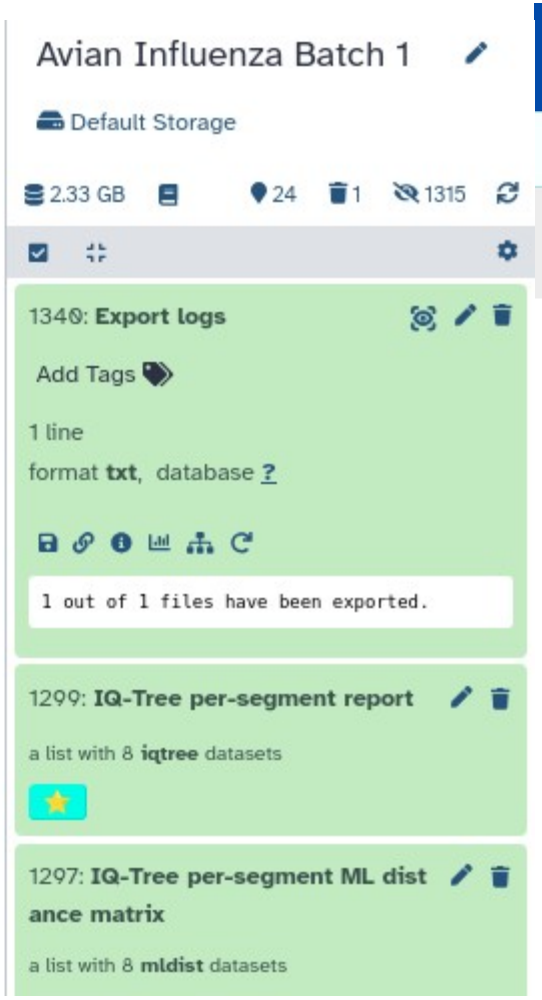

Galaxy Europe
Activities
Tools
Discover 4k+ Tools
search tools
Get Data
Send Data
cURL send cURL POST requests
ENA Upload tool Submission of (meta)data to the European Nucleotide Archive (ENA)
ENA Webin CLI Submission of consequences to the European Nucleotide Archive (ENA)
Export datasets to repositories
Collection Operations
General Text Tools
Text Manipulation
Convert Formats
Filter and Sort
Join, Subtract and Group
Genomic File Manipulation
Convert Formats
FASTA/FASTQ
FASTQ Quality Control
Quality Control
SAM/BAM
BED
VCF/BCF
Nanopore
Common Genomics Tools
Operate on Genomic Intervals
Fetch Sequences / Alignments
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Notifications
Export datasets to repositories (Galaxy Version 0.1.0)
Run Tool
Tool Parameters
What would you like to export?
Datasets using their Galaxy name and extension
search
Label
Details
TF nextcloud
My Zenodo
TF Nextcloud new
FTP Directory
Galaxy User's FTP Directory
ERGA Nextcloud
ERGA Pilot storage provided by BSC
CRG COVID data - staging
Center for Genomic regulation COVID19 FTP server
Genome Ark Test Instance
Access to Genome Ark open data on AWS.
Gilsbach S3 ElementBio
Access to an ElementBio S3 bucket
Create new
Time
Avian influenza batched analysis results
IWC workflow tests datasets - SameStr-based shared strain detection from paired-end metagenomic data
ProteomIQon sample files for Peptide Spectrum Matching Tool
sample mzml file for testing the MzMLToMzLiteIonMobility Tool
Bakta database test for galaxy wrapper
ProteomIQon-PSMBasedQuantificationTIMs
Test Datasets for oatk tool
spatialdata Galaxy wrapper test-data
Test data for raceid tool
Sopa Galaxy wrapper test-data
squidpy test data
Test Data for KAT tool
Galaxy WebAtlas pipeline test-data
Galaxy Dataset for CRAQ Tool
Test data for Galaxy IUC Seurat Tools V6
snapatac2 test-data
Galaxy ONT dataset for HiFiasm tool
Test Dataset for PIRATE tool
Practical webby FDOs With RO-Crate and FAIR Signposting: Experiences and Lessons Learned
Back
1 2 3 4
Cancel
Select
Tutorials
There is 1 tutorial available which uses this tool. View all tutorials referencing this tool.
Tutorials available in 1 category

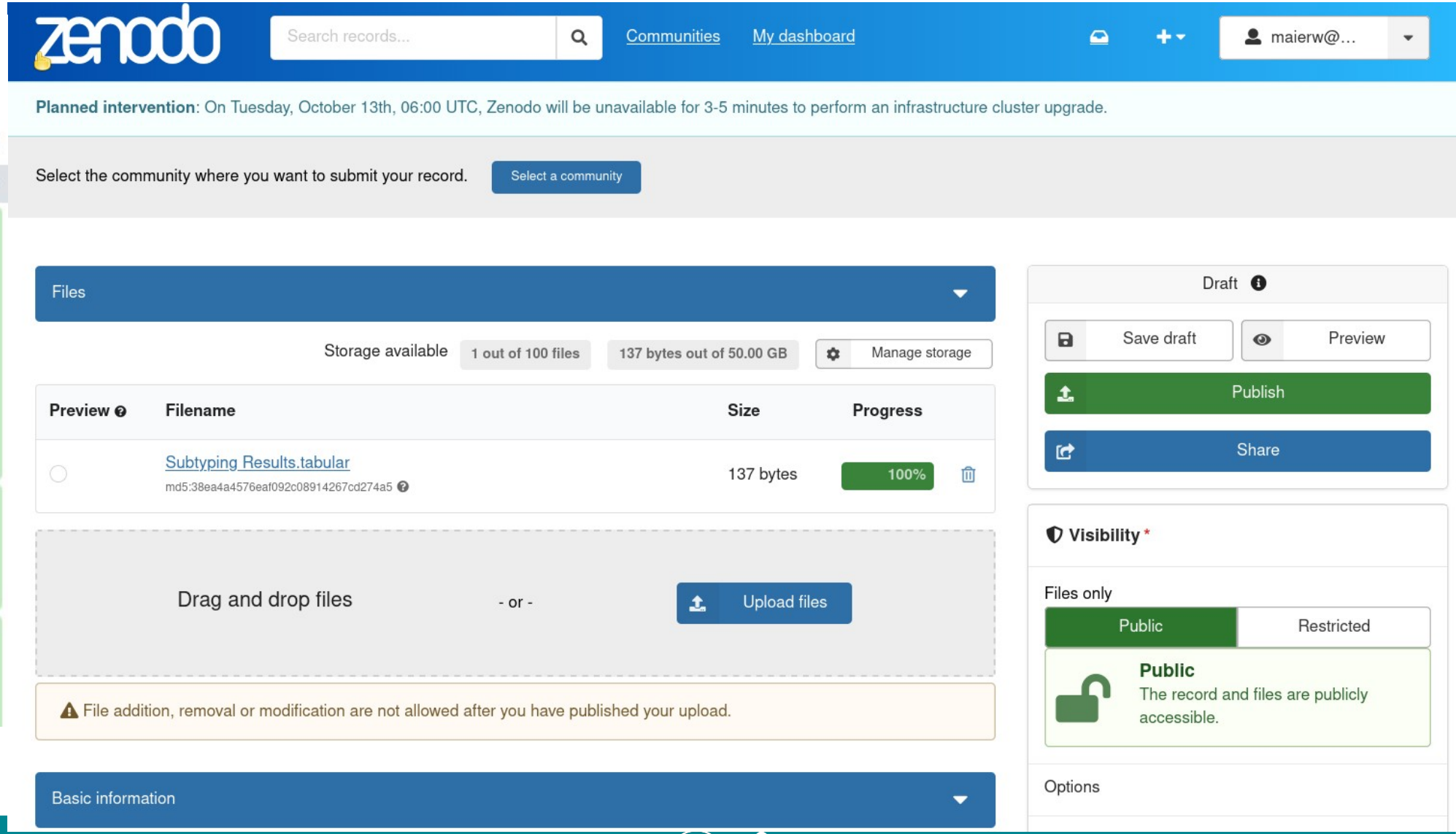
Step 5: Exporting analysis artifacts



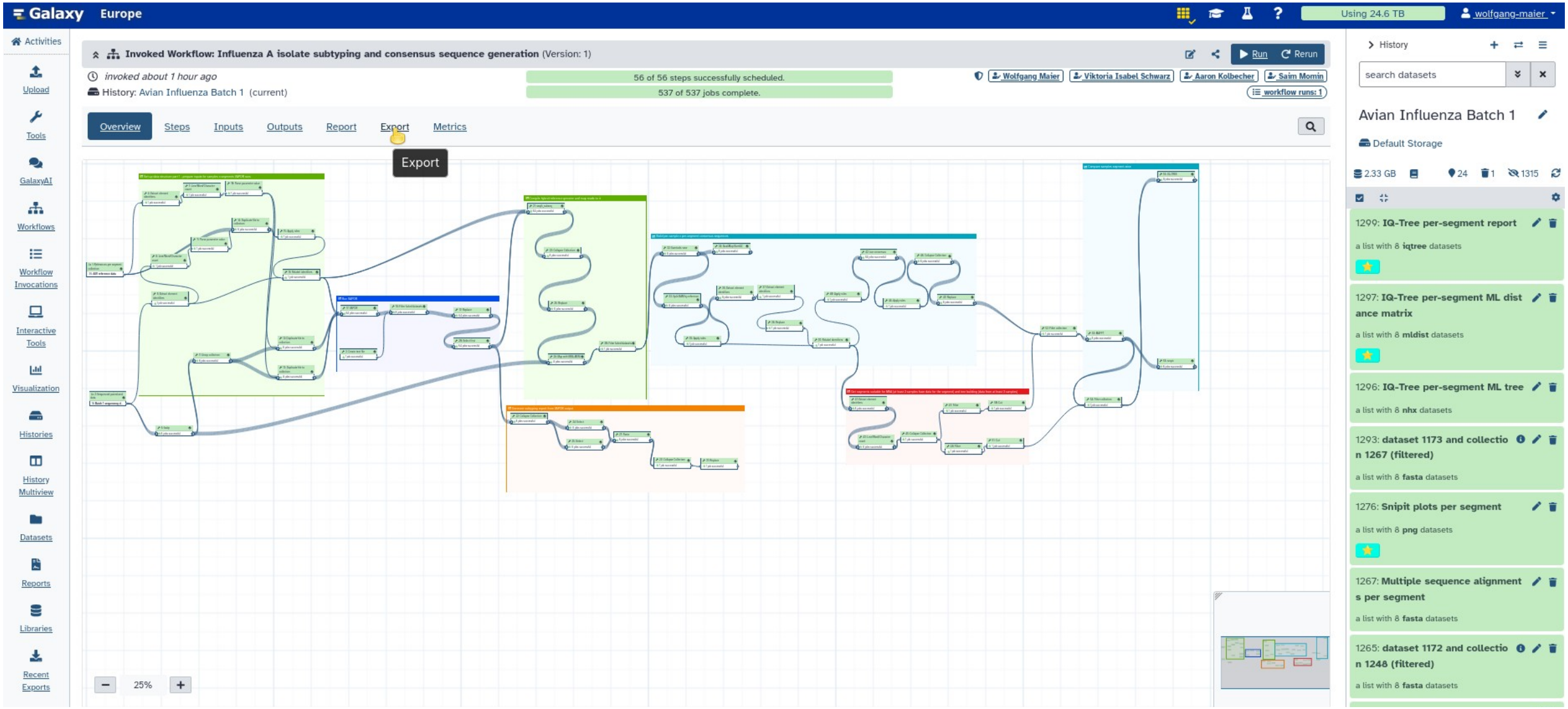


Step 5: Exporting analysis artifacts

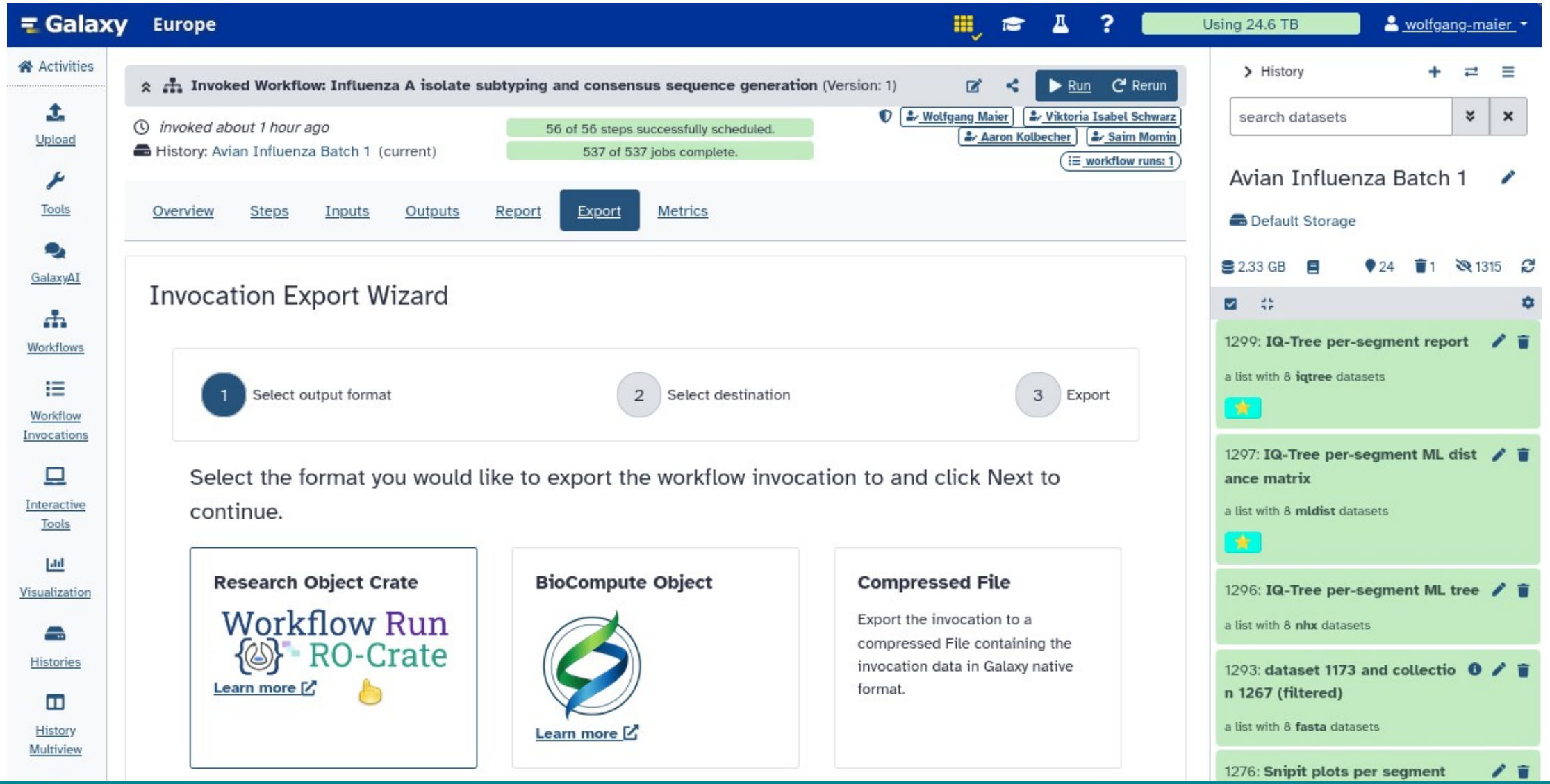




Step 5: Exporting analysis artifacts



Step 5: Exporting analysis artifacts



Step 5: Exporting analysis artifacts



User Preferences / My Repositories / Create New

Select file source option to create new sources. These options are configured by your Galaxy adm

Search file source option

Onedata

If you have an Onedata account, you can use this repository to import and export your data directly from and to Onedat
The minimal supported Onezone version is 21.02.4. More information on Onedata can be found on Onedata's website.

Amazon Web Services Private Bucket

Setup access to a private AWS bucket using a secret access key.

Amazon Web Services Public Bucket

Setup anonymous access to a public AWS bucket.

Azure Blob Storage

Setup access to your Azure Blob Storage.

B2DROP by BSC

B2DROP is a Nextcloud to sync and share your research data provided by BSC.

B2DROP by EUDAT

B2DROP is a Nextcloud to sync and share your research data provided by EUDAT.

Dataverse

The Dataverse Project is an open-source web application for sharing, preserving, citing, exploring, and analyzing resear
enables institutions and researchers to host and manage datasets with rich metadata and persistent identifiers. This co
allows you to connect Galaxy to a Dataverse instance of your choice.
Note: Your **registered email address** will be used to create datasets in Dataverse.

Dropbox

Connect to your Dropbox account to download and upload files.

eLabFTW

eLabFTW is a free and open source electronic lab notebook from Deltablot. It can keep track of experiments, e
from a research lab. Each lab can either host their own installation or go for Deltablot's hosted solution. Here yo
eLabFTW instance of your choice.

FTP Server

Setup connections to FTP and FTPS servers to download and upload files. Enable TLS to secure the connectior

Google Drive

Configure your Google Drive account to accept file uploads. Only files uploaded by this Galaxy instance can be

Hugging Face Hub

Hugging Face Hub is a platform for sharing machine learning models and datasets. Using this plugin you can c
Face Hub to access public or private machine learning models repositories.

InvenioRDM

InvenioRDM is a research data management platform that allows you to store, share, and publish research data
Invenio framework and is designed to be highly customizable. Here, you can connect to an InvenioRDM instanc

OMERO

Connect to an **OMERO** server to browse and import images stored there. You can connect to the Image Data R
own OMERO server instance. When connecting to **IDR**, you can use the public credentials (username: "**public**",

RSpace

RSpace is an electronic lab notebook (ELN) designed for documenting, managing and sharing scientific data. T
configuration allows you to connect to an RSpace instance of your choice.

S3 Compatible repositories with Credentials

The APIs used to connect to Amazon's S3 (Simple Storage Service) have become something of an unofficial st
storage across a variety of vendors and services. Many vendors offer storage APIs compatible with S3. Here, yo
based repository as long as you have the relevant credentials.

WebDAV (e.g. Nextcloud, Owncloud, Opencloud)

Zenodo

Zenodo is an open-access repository for research data, software, publications, and other digital artifacts. It is developed and maintained by CERN and funded by the European Commission as part of the OpenAIRE project. Zenodo provides a free platform for researchers to share and preserve their work, ensuring long-term access and reproducibility. Zenodo is widely used by researchers, institutions, and organizations to share scientific knowledge and comply with open-access mandates from funding agencies.

Select

OneDrive

Connect to your full Microsoft OneDrive. You will be asked to grant Galaxy permission to access files across your OneDrive, not just the Galaxy app folder.

Select

OneDrive

Connect to the Galaxy folder in your Microsoft OneDrive. Galaxy will only access its own app folder, not the rest of your OneDrive.

Select

IIIF Manifest

Browse and import image canvases from an IIIF (International Image Interoperability Framework) Presentation API manifest. IIIF is a framework used by museums, libraries, and archives to deliver high-quality digital images of cultural heritage materials through a standardized API. You can find public IIIF resources at https://iiif.io/guides/finding_resources/.
The images imported from the IIIF manifest will be added to your Galaxy history as new datasets, allowing you to analyze and work with them using Galaxy's tools and workflows.

Select

ARC

Connect to a DataHub/GitLab instance using arcfs-fsspec.

Select

Common Crawl

Common Crawl is an open repository of web crawl data containing petabytes of web pages collected since 2008.
Use this plugin to browse archived crawl releases and navigate to individual WARC, WET, or WAT files that can be imported into Galaxy histories.

Select

CKAN

CKAN is an open-source data portal platform for managing and sharing datasets. This configuration allows you to connect Galaxy to a CKAN instance of your choice.

Select

eosc

36 months (started last week) to:

TRACK SMARTER	Make energy use visible, measurable and FAIR
TRANSFER LESS	Move only the necessary data
STORE LESS	Optimise storage footprints with storage classes and modern file formats
COMPUTE LESS	Reduce redundant processing and allocate right-sized resources
DRIVE CHANGE	Raise awareness and drive adoption into European research infrastructures



funded by the EU

ESG4Stars

ESG****

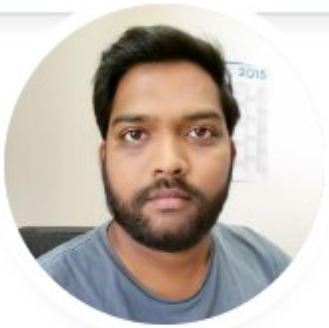
Sustainable Scientific Workflows for Research Infrastructures

PROJECT PARTNERS

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The Galaxy Europe team at this meeting



Pavankumar Videm



Wolfgang Maier

Find us at the booths of the EOSC Nodes: *Germany* or *Life Sciences Connect*

Contact details at: galaxyproject.org/eu/people