



usegalaxy.no and connection to NeLS



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ELIXIR Norway, Norwegian e-infrastructure for Life Sciences and usegalaxy.no

usegalaxy.no – The national Galaxy server

Web-based platform

Provide bioinformatic tools and workflows

Open to all Norwegian users and collaborators

Enable accessible, reproducible, and transparent computational biomedical research

Directly connected to the NeLS storage

The screenshot displays the UseGalaxy.no web interface. At the top, there's a navigation bar with links for Workflow, Visualize, Shared Data, Help, User, and various system icons. The main content area features a "Welcome to UseGalaxy.no" message from ELIXIR Norway. It includes a brief introduction to Galaxy, a "Quick Start Guide" link, and information about disk usage. Below this is a "Tools and Workflows" section with a "Contact Support" button. The left sidebar contains a detailed tree-view catalog of bioinformatics tools categorized by function: Tools, Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS (Text Manipulation, 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 Alignments/Sequences), GENOMICS ANALYSIS (Annotation, Apollo, Assembly, Epigenetics, Genome Editing, Genome Diversity, Mapping, Motif Tools, Multiple Alignments). At the bottom of the page, there are logos for partner institutions: University of Bergen, University of Oslo, NTNU, Norwegian University of Life Sciences, and UiT The Arctic University of Norway. A footer note states "galaxy version: 21.09". On the right side, there's a "History" panel showing an empty history and a "Tweets from @elixirnorway" feed with one tweet from ELIXIR Norway.



usegalaxy.no – The basics

Important features:

Tools menu with ~2000 tools sorted in sections

Current disk usage
(default is 200 GB total personal disk space)

Status of compute backend

Quick start guide

Contact support

Help and guides

The screenshot illustrates the usegalaxy.no web interface with several key components highlighted by red boxes:

- Tools menu (left):** A sidebar containing a search bar, an "Upload Data" button, and a list of tool categories. The "GENERAL TEXT TOOLS" section is currently selected.
- Main window (center):** The main content area displays the "Welcome to UseGalaxy.no" page. It includes a brief introduction to Galaxy, current disk usage information, and links to the Quick Start Guide and Help Desk. Below this is a "Tools and Workflows" section with a "Contact Support" button.
- History panel (right):** A panel titled "History" showing an "Unnamed history" section which is currently empty. It includes a note: "This history is empty. You can load your own data or get data from an external source".

Below the main content, there are logos for partner institutions: University of Bergen, University of Oslo, NTNU, Norwegian University of Life Sciences, and UiT The Arctic University of Norway. The footer also shows the galaxy version: 21.09.

Tools menu

Main menu

History

Main window



Your account and saved data

Account settings and saved data such as saved histories and visualizations

Histories other users have shared with you

Log of analysis workflows you have run

The screenshot shows the Galaxy Norway web interface. At the top, there is a navigation bar with links for Workflow, Visualize, Shared Data, Help, and User. The User link is highlighted with a red box and an orange arrow points from the text "Home" to it. Below the navigation bar, the main content area displays a welcome message for "Welcome to UseGalaxy.no". On the left, there is a sidebar with a "Tools" section containing various genomic analysis tools categorized under GENERAL TEXT TOOLS, GENOMIC FILE MANIPULATION, and COMMON GENOMICS TOOLS. The "User" menu is open, showing options like Logout, Datasets, Histories, Histories shared with me, Pages, Workflow Invocations, Visualizations, and Active InteractiveTools. To the right of the main content, there is a "History" panel showing an empty history with a message: "This history is empty. You can load your own data or get data from an external source". The bottom right corner features the ELIXIR logo.



Support and tutorials

Contact ELIXIR Norway helpdesk for support

Access to Galaxy wiki, and Galaxy Project tutorials/videos

Interactive Galaxy “tour”

The screenshot shows the Galaxy Norway web interface. At the top, there's a navigation bar with links for Home, Workflow, Visualize, Shared Data, Help, User, and various icons. A red box highlights the 'Help' dropdown menu. An orange arrow points from the text 'Recent updates' to this red box. Below the navigation bar, the main content area has a sidebar on the left listing various genomic tools and analysis methods. The main panel displays the 'Welcome to UseGalaxy.no' page, which includes a brief introduction to Galaxy, a 'Quick Start Guide' button, and sections for Support, Search, Mailing Lists, Videos, Wiki, How to Cite Galaxy, Interactive Tours, Introduction to Galaxy, Galaxy Version: 21.09, and Terms and Conditions. On the right side, there's a history panel showing a recent tweet from the @elixirnorway account and a message from the Universitetet i Oslo.



Shared data

Data shared by other users or ELIXIR-NO with all users of usegalaxy.no

For example, workflows and complete histories

You can import shared data to your user

The screenshot shows the Galaxy Norway web interface. At the top, there is a navigation bar with links for Home, Workflow, Visualize, Shared Data (which is highlighted with a red box), Help, User, and various icons. Below the navigation bar, there is a sidebar with a search bar and several categories: Tools, Get Data, Collection Operations, GENERAL TEXT TOOLS, GENOMIC FILE MANAGERS, FASTA/FASTQ, FASTQ Quality Control, Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore, COMMON GENOMICS, and GENOMICS ANALYSIS. The main content area displays the "Welcome to UseGalaxy.nc" page, which includes information about Galaxy, a "Quick Start Guide", and links to Data Libraries, Histories, Workflows, Visualizations, and Pages. To the right, there is a "Tweets from @elixirnorway" feed and a "History" panel.

Links to Galaxy Project training

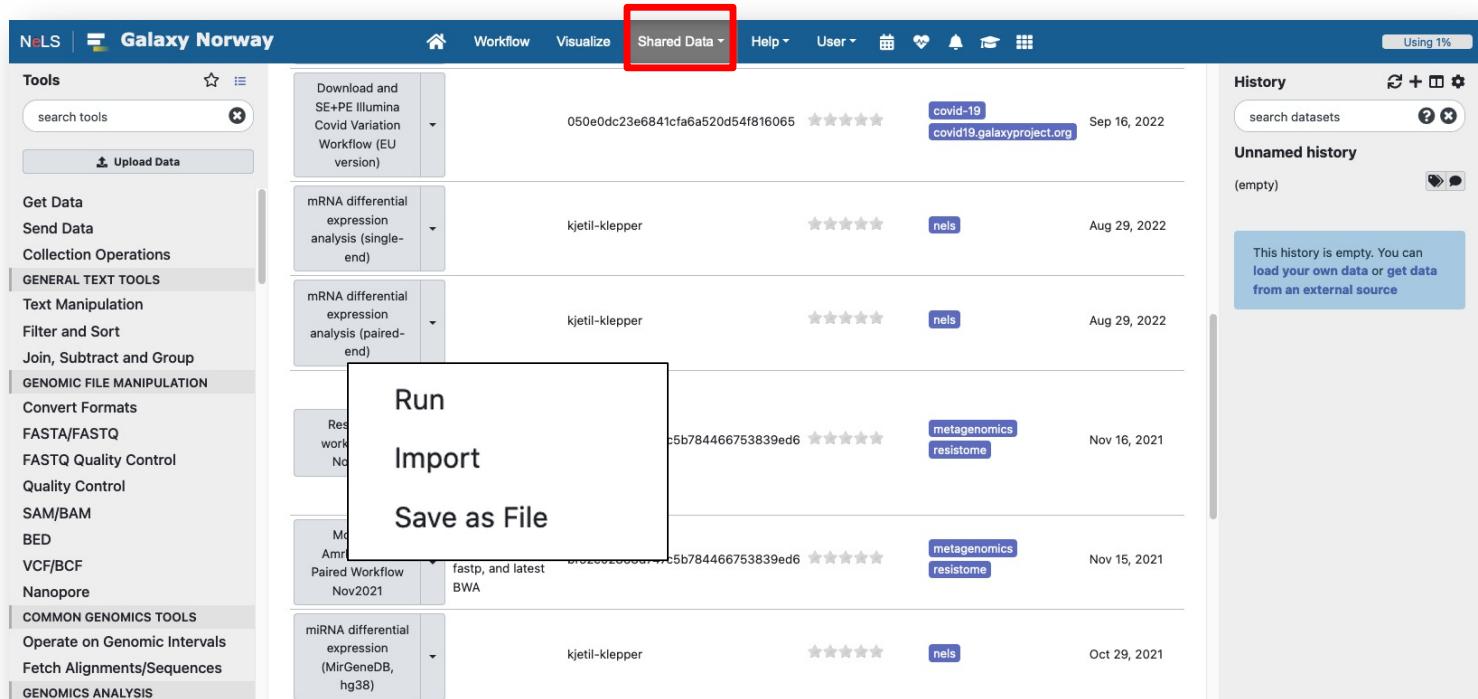


Shared data: workflows

List of all workflows that are shared with all usegalaxy.no users

You can import shared data to your own user

By selecting any workflow you can run data analysis, import into your user or save it on another computer



The screenshot shows the Galaxy Norway web interface. At the top, there is a navigation bar with links for Home, Workflow, Visualize, Shared Data (which is highlighted with a red box), Help, User, and other system icons. Below the navigation bar is a sidebar containing various tool categories: Tools, Get Data, Collection Operations, GENERAL TEXT TOOLS, GENOMIC FILE MANIPULATION, COMMON GENOMICS TOOLS, and GENOMICS ANALYSIS. The main area displays a list of shared workflows. Each workflow entry includes a title, author, rating, tags, and a timestamp. A modal window titled "Run", "Import", and "Save as File" is overlaid on the list, indicating an action is being performed on one of the workflows.

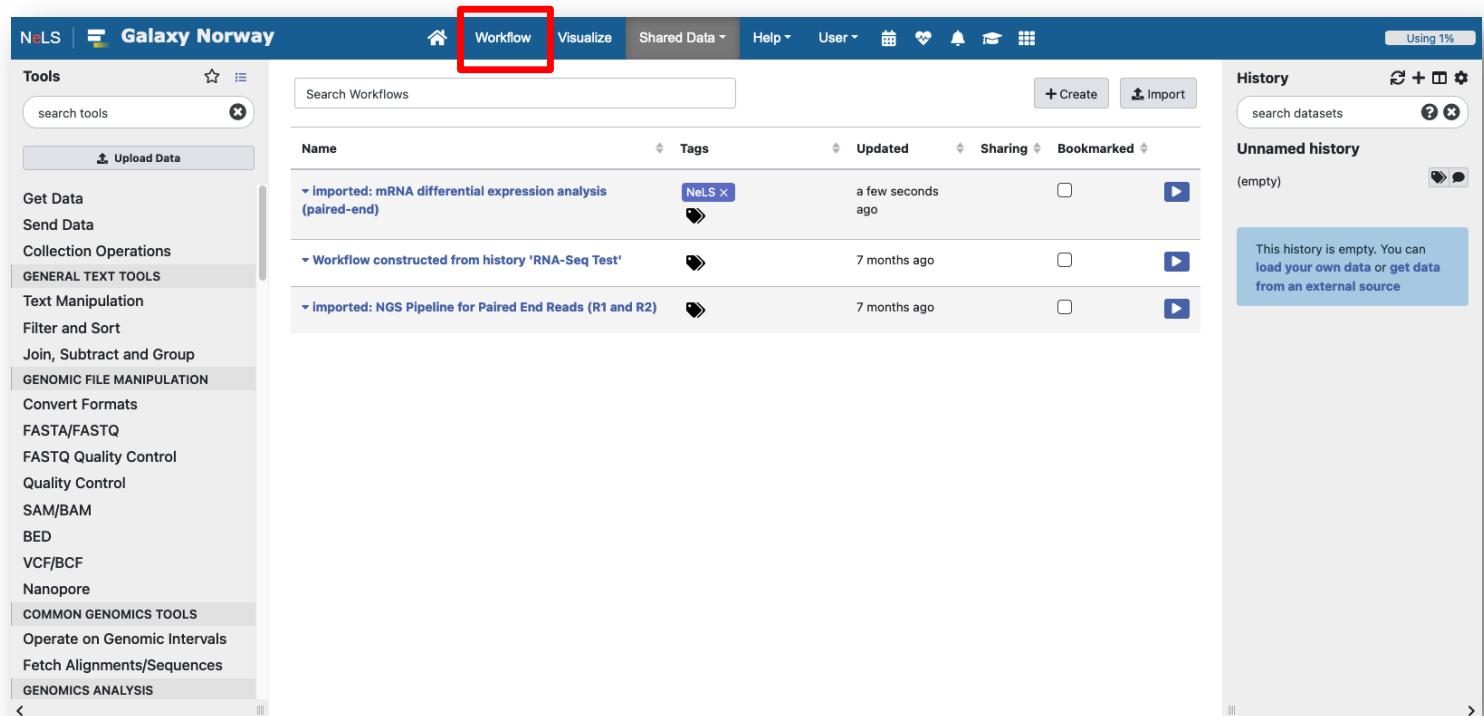
Workflow Title	Author	Rating	Tags	Date
Download and SE+PE Illumina Covid Variation Workflow (EU version)	050e0dc23e6841cfa6a520d54f816065	★★★★★	covid-19 covid19.galaxyproject.org	Sep 16, 2022
mRNA differential expression analysis (single-end)	kjetil-klepper	★★★★★	nels	Aug 29, 2022
mRNA differential expression analysis (paired-end)	kjetil-klepper	★★★★★	nels	Aug 29, 2022
Res work No	5b784466753839ed6	★★★★★	metagenomics resistome	Nov 16, 2021
Paired Workflow Nov2021	fastp, and latest BWA	★★★★★	metagenomics resistome	Nov 15, 2021
miRNA differential expression (MirGeneDB, hg38)	kjetil-klepper	★★★★★	nels	Oct 29, 2021



Workflows

Your own workflows.
These are the imported
or the workflows you
have made yourself

You can create new
workflows here



The screenshot shows the Galaxy Norway web interface. The top navigation bar includes links for NeLS, Galaxy Norway, Home, Workflow (which is highlighted with a red box), Visualize, Shared Data, Help, User, and various system icons. On the left, a sidebar titled 'Tools' lists categories like Tools, Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS, GENOMIC FILE MANIPULATION, COMMON GENOMICS TOOLS, and GENOMICS ANALYSIS. The main content area displays a table of workflows. The table has columns for Name, Tags, Updated, Sharing, and Bookmarked. Three workflows are listed:

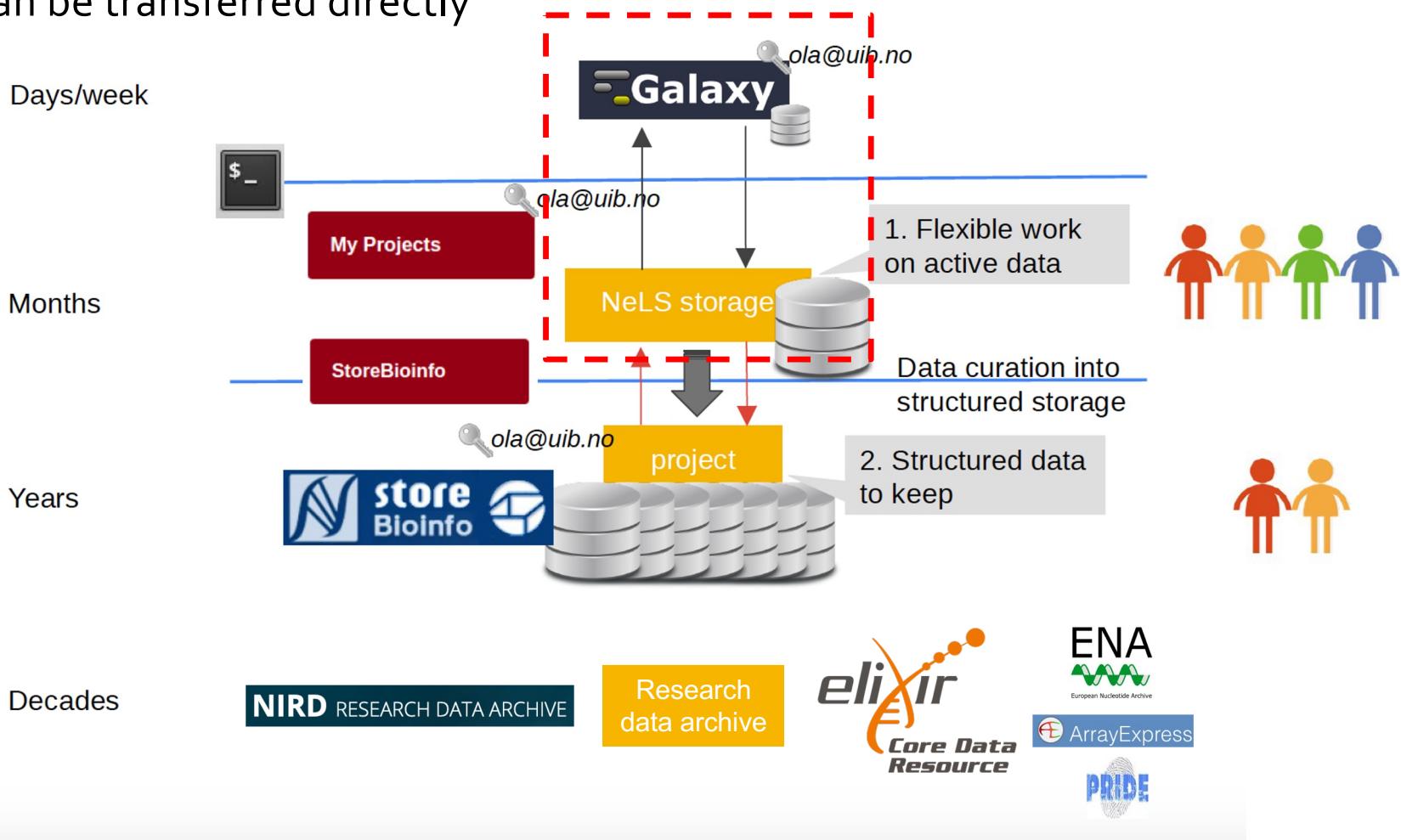
Name	Tags	Updated	Sharing	Bookmarked
imported: mRNA differential expression analysis (paired-end)	NeLS	a few seconds ago	<input type="checkbox"/>	
Workflow constructed from history 'RNA-Seq Test'		7 months ago	<input type="checkbox"/>	
Imported: NGS Pipeline for Paired End Reads (R1 and R2)		7 months ago	<input type="checkbox"/>	

To the right, there's a 'History' panel showing an 'Unnamed history' section which is currently empty. A message in the history panel says: 'This history is empty. You can load your own data or get data from an external source'.



Usegalaxy.no is connected to NeLS

Data can be transferred directly



Importing data from your computer

Drag and drop, or
browse and select file

Alternatively, paste URL
for data available on the
web

Specify datatype if you
know (e.g. Fasta)

The screenshot shows the Galaxy Norway web interface. On the left, a sidebar titled 'Tools' lists various bioinformatics tools categorized under 'GENERAL TEXT TOOLS', 'GENOMIC FILE MANIPULATION', 'COMMON GENOMICS TOOLS', and 'GENOMICS ANALYSIS'. Two red arrows point to the 'Upload Data' button and the 'Send Data' link. The main content area displays the 'Welcome to UseGalaxy.no' page, which includes a brief introduction to Galaxy, usage tips, and disk usage information. On the right, a 'History' panel shows a single entry for 'norway' with a tweet from 'elixirnorway'. A message at the bottom of the history panel encourages users to load their own data or get data from an external source.

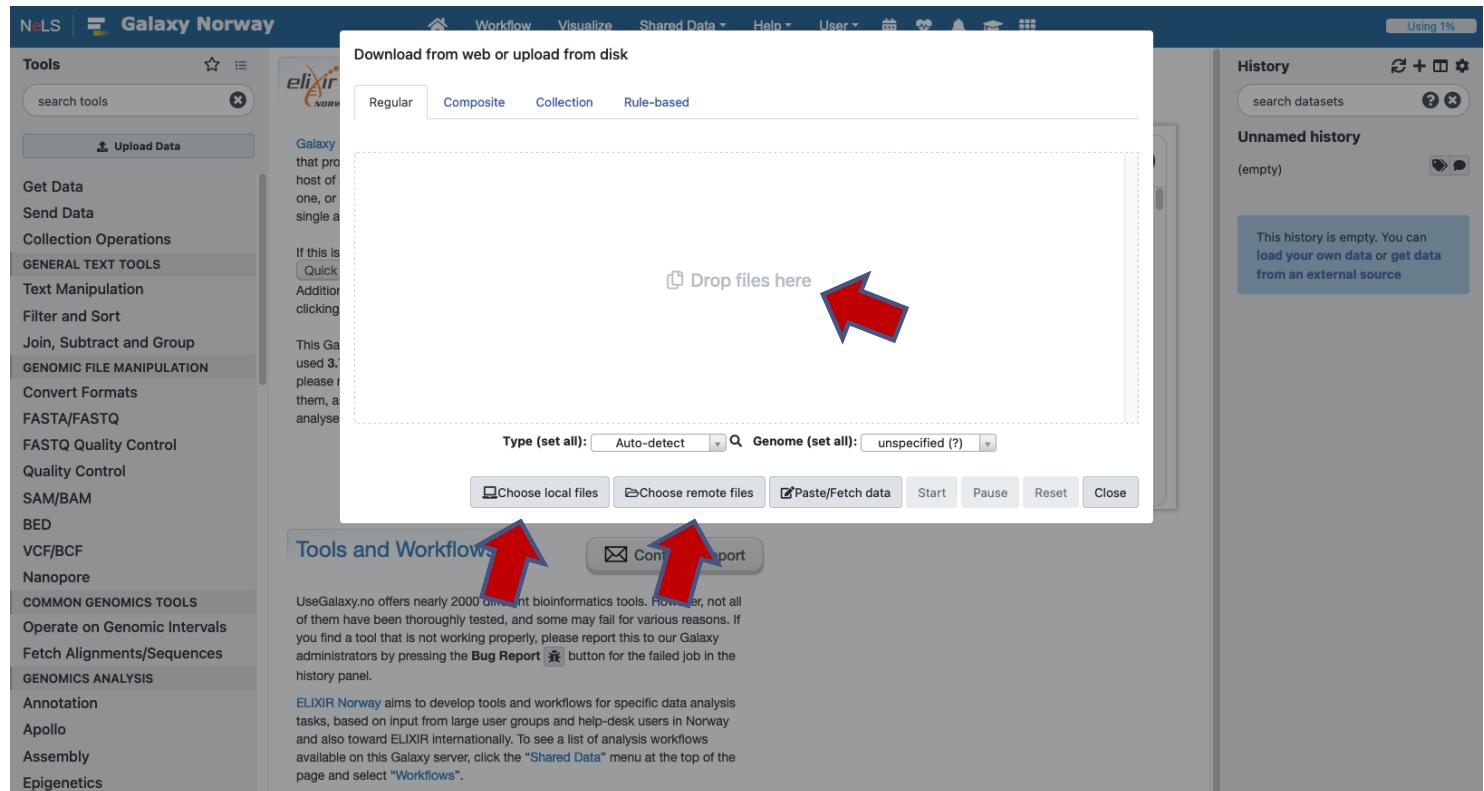


Importing data from your computer

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Specify datatype if you
know (e.g. fasta)

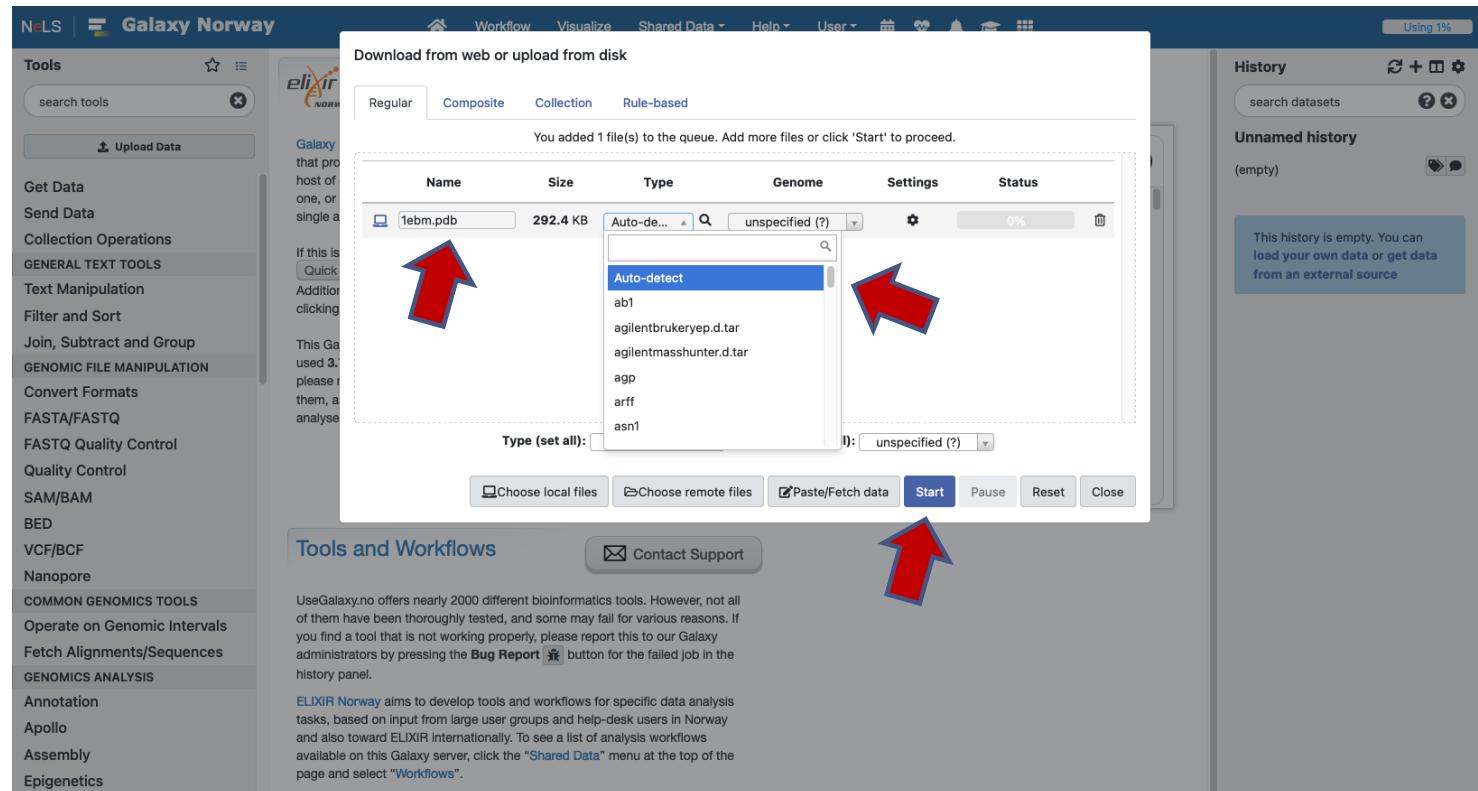


Importing data from your computer

Drag and drop, or
browse and select file

Alternatively, paste url
for data available on the
web

Specify datatype if you
know (e.g. fasta)



Visualize

Various tools for visualizing data in your history

The screenshot shows the Galaxy Norway web interface. At the top, there is a navigation bar with links for Home, Workflow, Visualize (which is highlighted with a red box), Shared Data, Help, User, and various system icons. On the left, a sidebar titled 'Tools' lists several categories: Tools (with a search bar and 'Upload Data' button), Get Data, Send Data, Collection Operations, GENERAL TEXT TOOLS (Text Manipulation, 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 Alignments/Sequences), and GENOMICS ANALYSIS (Annotation, Apollo, Assembly, Epigenetics, Genome Editing). The 'Visualize' section contains a list of visualization tools with their descriptions and icons: Trackster (Fast, interactive visualization for large, NGS/HTS datasets using only a web browser), Audio player (Audio player), Bar Horizontal (NVD3) (Renders a horizontal bar diagram using NVD3 hosted at <http://www.nvd3.org>), Bar Horizontal Stacked (NVD3) (Renders a stacked horizontal bar diagram using NVD3 hosted at <http://www.nvd3.org>), Bar Stacked (NVD3) (Renders a scatter plot using NVD3 hosted at <http://www.nvd3.org>), Bar diagram (NVD3) (Renders a regular bar diagram using NVD3 hosted at <http://www.nvd3.org>), Bar diagram (jqPlot) (Renders a bar diagram using jqPlot hosted at <http://www.jqplot.com>), Box plot (jqPlot) (Processes tabular data using R and renders a box plot using jqPlot hosted at <http://www.jqplot.com>), and CSG Viewer (Constructive Solid Geometry (CSG) viewer). On the right, there is a 'History' panel showing an unnamed history with one dataset: '1: 1ebm.pdb'. The bottom right corner features the ELIXIR logo.



Visualize

Various tools for visualizing data in your history

The screenshot shows the Galaxy Norway web interface. The top navigation bar includes links for NELS, Galaxy Norway, Workflow, Visualize (which is highlighted with a red box), Shared Data, Help, User, and various system icons. On the left, a sidebar titled 'Tools' lists categories like General Text Tools, Genomic File Manipulation, and Common Genomics Tools. In the center, a 3D ribbon model of a protein structure is displayed, composed of grey and purple segments. To the right, the 'History' panel shows an unnamed history containing one dataset named '1: 1ebm.pdb'.



Importing data from NeLS

Import data from
Personal or Project
folders in NeLS

The screenshot shows the Galaxy Norway web interface. On the left, a sidebar titled 'Tools' lists various genomic analysis tools under categories like 'GENERAL TEXT TOOLS', 'GENOMIC FILE MANIPULATION', and 'COMMON GENOMICS TOOLS'. Two red arrows point to the 'Upload Data' button at the top of the sidebar and the 'Send Data' link in the 'Get Data' section. The main content area features a 'Welcome to usegalaxy.no' banner with the ELIXIR NORWAY logo. Below it, there's a 'Tweets' feed from the ELIXIR Norway account (@elixirnorway) with two tweets about the Oslo NorMIC imaging node and the start of a new period. A blue callout box highlights the 'NeLS Storage tools' section, which explains the configuration of NeLS Storage as a remote file source and provides instructions for using the new data transfer tools.



Importing data from NeLS

Galaxy Norway

Using 0%

History

Unnamed history
(empty)

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

Download from web or upload from disk

Regular Composite Collection Rule-based

Drop files here

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

Choose local files Choose remote files Paste/Fetch data Start Pause Reset Close

Get Data Send Data Collection Operations GENERAL TEXT TOOLS Text Manipulation 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 Alignments/Sequences GENOMICS ANALYSIS Annotation Apollo Assembly Epigenetics

The NeLS storage system has been integrated with Galaxy. This means that you can now upload files directly to NeLS storage from within Galaxy. This is done by using the "Get files from NeLS storage" and "Send files to NeLS storage" tools. These tools have been removed and replaced with new functionality. Learn how to use the new data transfer tools here.

If you don't have a NeLS Storage account already, you must first visit the [NeLS Portal](#) to create one automatically.

Tools and Workflows Contact Support

ELIXIR Norway aims to develop tools and workflows for specific data analysis tasks, based on input from large user groups and help-desk users in Norway

NeLS Portal to create one automatically.'"/>

Importing data from NeLS

The screenshot shows the Galaxy Norway web interface. On the left, there's a sidebar with various tools and data management options. A red arrow points to the 'Download from' dropdown menu, which is open and displays a list of storage options. The list includes:

Label	Details
■ NeLS Storage	Your personal folder in NeLS Storage
■ NeLS Storage Projects	Your projects folder in NeLS Storage
■ Configurable SSH storage	configure access in user preferences
■ Dropbox	Dropbox files (configure access in user preferences)
■ OwnCloud	External OwnCloud files (configure access in user preferences)
■ EBI FTP server	European Bioinformatic Institute FTP server
■ NCBI FTP server	NCBI FTP server
■ ENSEMBL FTP server	ENSEMBL FTP server
■ Genome Ark	Access to Genome Ark open data on AWS.
■ 1000 Genomes	Access to the 1000 Genomes Project with human genetic variation, including SNPs, structural variants, and their haplotype context.
■ The Cancer Genome Atlas	Access to the Cancer Genome Atlas (TCGA)
■ COVID-19 Data Lake	A centralized repository of up-to-date and curated datasets on or

At the bottom of the dialog box, there are 'Cancel' and 'Ok' buttons. The main Galaxy interface background shows a history panel with an empty history named 'Unnamed history'.



Importing data from NeLS

The screenshot shows the Galaxy Norway web interface. On the left, there's a sidebar with various tools and sections like 'Tools', 'Get Data', 'Send Data', etc. A red arrow points to a dropdown menu labeled 'Regular' in the 'Download from NeLS' section. The main area displays a list of datasets from NeLS storage:

Label	Time
Elixir_workshops	-
NTNU_Bjoras_Chromatin_Dynamics_2021	-
Ulo-Test-Project	-
UIO_Dahl_Chromatin_2018	-
Rinholm_group_DoNotUseYetPlease	-
OUS_Alseeth_BaseModificationsHTS_A_1_2018	-
UiB_Stokke_DeepSeaQuence_2021	-

At the bottom of the dialog, there's a note about removed functionality and a link to learn how to use new data transfer tools.



Importing data from NeLS

The screenshot shows the Galaxy Norway web interface. On the left, there's a sidebar with various tools and categories like 'Get Data', 'Send Data', and 'Collection Operations'. The main area has tabs for 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. A central 'History' panel shows an 'Unnamed history' with a message: 'This history is empty. You can load your own data or get data from an external source'. A prominent 'Download from NeLS' dialog box is open in the center. It contains a search bar and a table with columns for 'Label' and 'Time'. Several files are listed, including 'elixir-nels-galaxy-wsJune2019.pptx', multiple fastq files for LNCaP and RWPE cell lines, and a Microsoft Word document. Most of these files have checkboxes next to them, and several are checked. A red arrow points to the 'OK' button at the bottom right of the dialog box.



Importing data from NeLS

The screenshot shows the Galaxy Norway interface. On the left, a sidebar lists various tools and data types. In the center, a modal window titled "Download from web or upload from disk" displays a list of 12 uploaded files. At the bottom of this list is a dropdown menu for selecting a reference genome. A red arrow points to the "Genome (set all)" dropdown, which is currently set to "unspecified (?)." Below the dropdown is a list of available genomes, with "Human Dec. 2013 (GRCh38/hg38) (hg38)" highlighted in blue.

Name	Size	Type	Genome	Status
RWPE_rep1_1.fasta	90.5 MB	Auto-de...	unspecified (?)	0%
LNCaP_rep1_1.fastq	196.2 MB	Auto-de...	unspecified (?)	0%
LNCaP_rep1_2.fastq	196.2 MB	Auto-de...	unspecified (?)	0%
LNCaP_rep2_1.fastq	173.2 MB	Auto-de...	unspecified (?)	0%
LNCaP_rep2_2.fastq	173.2 MB	Auto-de...	unspecified (?)	0%
LNCaP_rep3_1.fastq	200.5 MB	Auto-de...	unspecified (?)	0%

Specify datatype if you know (e.g. fastqsanger)

If your data is aligned reads or will be aligned to a genome, specify this reference genome



Importing data from NeLS

Galaxy Norway

Download from web or upload from disk

Regular Composite Collection Rule-based

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

Name	Size	Type	Genome	Settings	Status
RWPE_rep1_1.fasta	90.5 MB	Auto-de...	Human Dec. 20...	...	0%
LNCaP_rep1_1.fastq	196.2 MB	Auto-de...	Human Dec. 20...	...	0%
LNCaP_rep1_2.fastc	196.2 MB	Auto-de...	Human Dec. 20...	...	0%
LNCaP_rep2_1.fastq	173.2 MB	Auto-de...	Human Dec. 20...	...	0%
LNCaP_rep2_2.fastq	13.2 MB	Auto-de...	Human Dec. 20...	...	0%
LNCaP_rep3_1.fastq	1.2 MB	Auto-de...	Human Dec. 20...	...	0%

Type (set all): Auto-detect Q Genome (set all): Human Dec. 20...

Choose local file fastqillumina.bz2 fastqillumina.gz fastqsanger

Fetch data Start Pause Reset Close

History search datasets

Unnamed history (empty)

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

Tools search tools Upload Data

Get Data Send Data Collection Operations

GENERAL TEXT TOOLS

Text Manipulation 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 Alignments/Sequences

GENOMICS ANALYSIS Annotation Apollo Assembly

Tools and Workflows Contact Support

ELIXIR Norway aims to develop tools and workflows for specific data analysis



Importing data from NeLS

Galaxy Norway

Using 0%

History

unnamed history

(empty)

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

Download from web or upload from disk

Regular Composite Collection Rule-based

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

Name	Size	Type	Genome	Settings	Status
RWPE_rep1_1.fastq	90.5 MB	fastqsa...	Human Dec. 20...	0%	
LNCaP_rep1_1.fastq	196.2 MB	fastqsa...	Human Dec. 20...	0%	
LNCaP_rep1_2.fastq	196.2 MB	fastqsa...	Human Dec. 20...	0%	
LNCaP_rep2_1.fastq	173.2 MB	fastqsa...	Human Dec. 20...	0%	
LNCaP_rep2_2.fastq	173.2 MB	fastqsa...	Human Dec. 20...	0%	
LNCaP_rep3_1.fastq	200.5 MB	fastqsa...	Human Dec. 20...	0%	

Type (set all): fastqsanger Q Genome (set all): Human Dec. 20...

Choose local files Choose remote files Paste/Fetch data Start Pause Reset Close

The NeLS storage system is now integrated directly into the Galaxy interface, allowing users to upload and download data between UseGalaxy.no and NeLS. As a consequence, the old "Get files from NeLS storage" and "Send files to NeLS storage" tools have been removed and replaced with new functionality. Learn how to use the new data transfer tools here.

(If you don't have a NeLS Storage account already, you must first visit the NeLS Portal to create one automatically.)

Tools and Workflows Contact Support

ELIXIR Norway aims to develop tools and workflows for specific data analysis tasks, based on input from large user groups and help-desk users in Norway and also toward ELIXIR internationally. To see a list of analysis workflows



Importing data from NeLS

Galaxy Norway

Workflow Visualize Shared Data Help User

Using 0%

History

search datasets

Unnamed history

12 shown

(empty)

12: RWPE_rep3_2.fast
11: RWPE_rep3_1.fast
10: RWPE_rep2_2.fast
9: RWPE_rep2_1.fastq
8: RWPE_rep1_2.fastq
7: LNCaP_rep3_2.fast
6: LNCaP_rep3_1.fast
5: LNCaP_rep2_2.fast
4: LNCaP_rep2_1.fast
3: LNCaP_rep1_2.fast
2: LNCaP_rep1_1.fastq
1: RWPE_rep1_1.fastq

Download from web or upload from disk

Regular Composite Collection Rule-based

Name Size Type Genome Settings Status

RWPE_rep1_1.fastq 90.5 MB fastqsa... Human Dec. 20... 100% ✓
LNCaP_rep1_1.fastq 196.2 MB fastqsa... Human Dec. 20... 100% ✓
LNCaP_rep1_2.fastq 196.2 MB fastqsa... Human Dec. 20... 100% ✓
LNCaP_rep2_1.fastq 173.2 MB fastqsa... Human Dec. 20... 100% ✓
LNCaP_rep2_2.fastq 173.2 MB fastqsa... Human Dec. 20... 100% ✓
LNCaP_rep3_1.fastq 200.5 MB fastqsa... Human Dec. 20... 100% ✓
LNCaP_rep3_2.fastq 200.5 MB fastqsa... Human Dec. 20... 100% ✓

Type (set all): fastqsanger Q Genome (set all): Human Dec. 20...

Choose local files Choose remote files Paste/Fetch data Start Pause Reset Close

The NeLS storage system has been replaced by the new NeLS storage system between UseGalaxy.no and NeLS. As a consequence, the old "Get files from NeLS storage" and "Send files to NeLS storage" tools have been removed and replaced with new functionality. Learn how to use the new data transfer tools here.

If you don't have a NeLS Storage account already, you must first visit the NeLS Portal to create one automatically.

Tools and Workflows Contact Support

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Importing data from NeLS & Histories

New datasets:

- either uploaded to Galaxy
- or generated by running a tool

New datasets are added to top of the user's current history (with a number)

Histories represent a chronological record of all the steps you have performed in your analysis

Every dataset in a history includes complete information about how that dataset was created, for instance which tool was used to produce the data and the specific parameter settings that tool was run with

The screenshot shows the UseGalaxy interface. On the left, a sidebar titled 'Tools' lists various genomic analysis tools. A blue box highlights the 'NeLS Storage tools' section, which contains text about the configuration of NeLS Storage and instructions for using new data transfer tools. In the center, there is a 'Welcome to usegalaxy.no' message and a 'Tweets' feed from the ELIXIR Norway Twitter account. On the right, a 'History' panel shows a list of datasets in an 'Unnamed history' session, each with edit and delete icons.

Makes it possible to trace the provenance and evolution of each dataset through time, and it also enables automatic extraction of workflows from a history to reproduce the complete analysis or apply the same processing steps to other datasets.

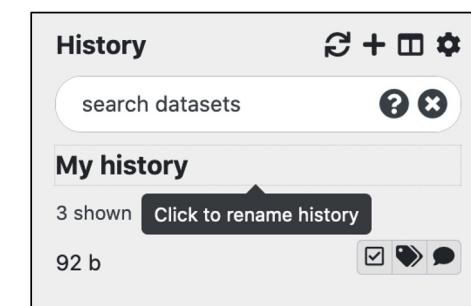
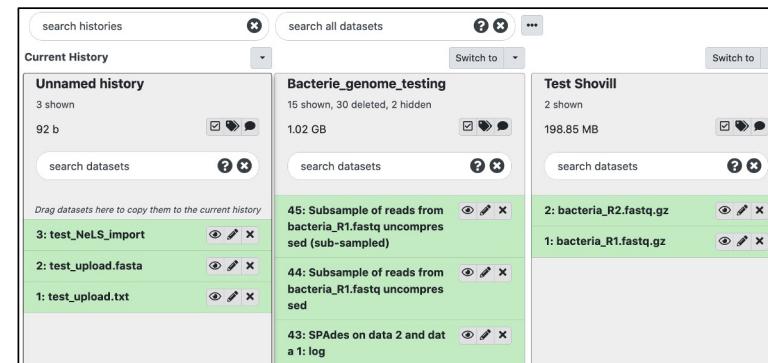
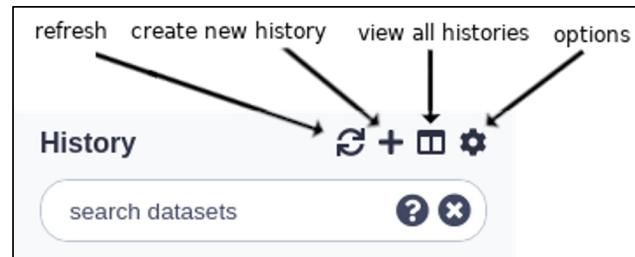


Use galaxy histories to organise data

You can make as many histories as you want and switch between them

Typically, you can have one history for each project or analysis

You can rename your histories, all must have unique names (Press enter to save the name)



A dataset is equivalent to file(s)

In Galaxy the term dataset are the inputs and outputs of each step in an analysis project

Datasets also can be a collection of files, or a list of files

Datasets can have different states

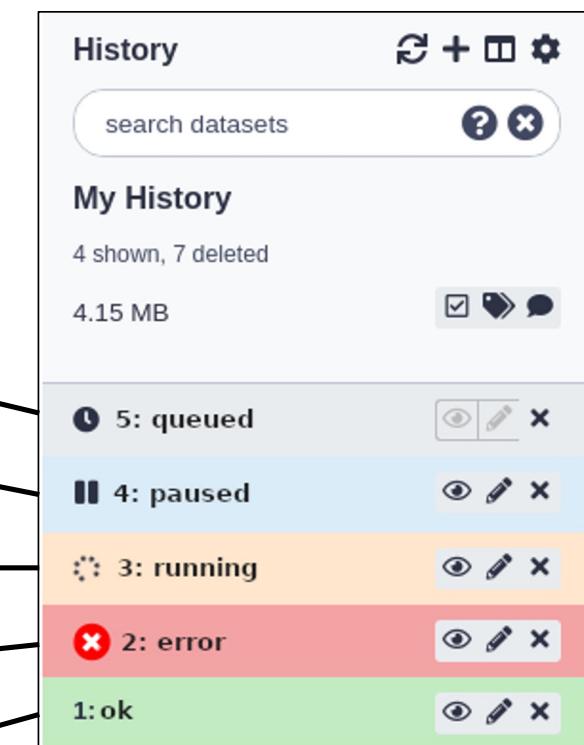
Job has not yet started but will create this dataset

Paused jobs can be resumed but will create this dataset

Job is running but will create this dataset

The job failed with an error

The job completed successfully



Operations and information on datasets

Multiple operations can be performed on each dataset

View dataset by clicking on the filename

Change format (datatype) of dataset

Extensive information for each dataset in the history

For example, version of the tool and reference genome used in an analysis

The screenshot illustrates the Galaxy web interface for managing datasets. On the left, a list of datasets is shown:

- 3: test_NeLS_import
- 2: test_upload.fasta
- 1: test_upload.txt

Below the list, detailed information for dataset 1 is provided:

- 1 line
- format: txt, database: ?
- uploaded txt file
- Download links (txt, fasta, csfasta, fasta.gz)
- Test file

Three arrows point from labels on the left to specific UI elements:

- A bracket labeled "Data description" points to the "format" and "database" information.
- An arrow labeled "Download data" points to the download links.
- An arrow labeled "Detailed information" points to the "Test file" button.

At the top right, there are three buttons: "View data", "Edit attributes", and "Delete data". Arrows point from these labels to their respective icons. To the right of the list is a modal window titled "Edit dataset attributes" showing a dropdown menu with "fasta" selected.

Dataset Information:

- Number: 1
- Name: test_upload.txt
- Created: Sat Jan 23 21:05:25 2021 (UTC)
- Filesize: 10 bytes
- Dbkey: ?
- Format: txt

Job Information:

- Galaxy Tool ID: upload1
- Galaxy Tool Version: 1.1.7



Delete and permanently delete datasets

Deleting a dataset (and histories) is equal to hiding the data, or putting it in the trash bin

It is possible to recover deleted datasets

Permanently deleting (purging) datasets (and histories) will free up disk space and cannot be recovered

My history
4 shown,
92 b

6: My list a list with 2 items	X
3: test_NeLS_import	<input type="button" value="eye"/> <input type="button" value="edit"/> X
2: test_upload.fasta	<input type="button" value="eye"/> <input type="button" value="edit"/> X
1: test_upload.txt	<input type="button" value="eye"/> <input type="button" value="edit"/> X

Delete

My history
6 shown, hide deleted
92 b

6: My list a list with 2 items	X
3: test_NeLS_import	<input type="button" value="eye"/> <input type="button" value="edit"/> X
2: test_upload.fasta	<input type="button" value="eye"/> <input type="button" value="edit"/> X
⚠ This dataset has been deleted Undelete it Permanently remove it from disk	
1: test_upload.txt	<input type="button" value="eye"/> <input type="button" value="edit"/> X



Galaxy sharing data

An efficient method
for sharing analysis
with collaborators

Good practice to get
support from the
Helpdesk

The screenshot shows the Galaxy Norway web interface. On the left, a sidebar lists various tools and operations. In the center, a main panel displays a history titled 'imported from archive: My first history'. It includes options to make the history accessible or publicly available. A URL is provided for sharing. On the right, a vertical sidebar titled 'History Actions' contains several options: Copy, Share or Publish (which is highlighted with a red box), Show Structure, Extract Workflow, Set Permissions, Make Private, and Resume Paused Jobs. Below this, sections for 'Dataset Actions', 'Downloads', and 'Nels storage' are listed. A red circle highlights the 'More Options' icon at the top right of the main panel.

NeLS | Galaxy Norway

Tools

- search tools
- Upload Data

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

- Text Manipulation
- Filter and Sort
- Join, Subtract and Group

GENOMIC FILE MANIPULATION

- Convert Formats
- FASTA/FASTQ
- FASTQ Quality Control
- Quality Control

Workflow Visualize Shared Data Help User

Share or Publish History `imported from archive: My first history`

Make History accessible

Make History publicly available in Published Histories

This History is currently accessible via link.
Anyone can view and import this History by visiting the following URL:

url: <https://usegalaxy.no/u/91eaa2a9ab5b4bf99f4968b8e4e94e76/h/imported-from-archive-my-first-history>

Share History with Individual Users

History Actions

- Copy
- Share or Publish
- Show Structure
- Extract Workflow
- Set Permissions
- Make Private
- Resume Paused Jobs

Dataset Actions

- Copy Datasets
- Collapse Expanded Datasets
- Unhide Hidden Datasets
- Delete Hidden Datasets
- Purge Deleted Datasets

Downloads

- Export Tool Citations
- Export History to File

Nels storage

- Export History
- Import History

Exporting data

**IMPORTANT: usegalaxy.no
is not meant for storage**

Please move your data when
your data analysis is done

You can export a complete
history including datasets to
a file on your local system or
to NeLS

NeLS

Galaxy Interaction

You are at : » Home / Personal / WS2019B

Name	Size
HandsOn_NeLS_Galaxy.txt	67 bytes
sample1_R1.fastq.gz	12.9 MB
sample1_R2.fastq.gz	13.8 MB

Use current folder

Using 16%

History Actions

- Copy
- Share or Publish
- Show Structure
- Extract Workflow
- Set Permissions
- Make Private
- Resume Paused Jobs

Dataset Actions

- Copy Datasets
- Collapse Expanded Datasets
- Unhide Hidden Datasets
- Delete Hidden Datasets
- Purge Deleted Datasets

Downloads

- Export Tool Citations
- Export History to File

Nels storage

- Export History
- Import History

