



usegalaxy.no and connection to NeLS

Given by who

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 user and collaborators

Enable accessible, reproducible, and transparent computational biomedical research

Directly connected to the NeLS storage

NeLS | **Galaxy Norway** | Analyze Data | Workflow | Visualize | Shared Data | Help | User | Using 16%

Tools | search tools

Get Data
Send Data
Collection Operations
Lift-Over
Text Manipulation
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
Operate on Genomic Intervals
Statistics
Graph/Display Data
Phenotype Association
Interactive Tools
Mapping
SAM/BAM
Annotation
Assembly
Imaging
ChemicalToolBox

Welcome to usegalaxy.no

Galaxy is a web-based platform for data intensive life science research that provides users with a unified, easy-to-use graphical interface to a host of different analysis tools. These tools can be run interactively, one by one, or combined into multi-step workflows that can be executed as a single analysis.

If this is your first time using Galaxy, you might want to have a look at this [Quick Start Guide](#). Additional documentation and tutorials on using Galaxy can be found [here](#).

This Galaxy server has limitations on disc usage, and you have currently used **34.0 GB** of your total quota of **200.0 GB**. To free up disc space, please move your files to the NeLS Storage after you are finished with them. If you require a larger disc quota, contact the [Help Desk](#).

Galaxy version upgrade

UseGalaxy.no has now been upgraded to version 20.09. New features include the ability to upload data directly from the tool form and support for multimedia files. Visit [this page](#) for more information.

Tweets by @eliximorway

ELIXIR Norway @eliximorway
Few spots left on the @swcarpentry course from ELIXIR Norway and @DigitalLiv for PhD candidates & researchers [korbinib.github.io/2021-02-01-DLN...](#)
Jan 19, 2021

Katharina Lauer @lauerkatharina
Starting on 20 Jan, a series of 6 webinars will demonstrate that #openscience is key for responding to #COVID19 and public health crises
[bit.ly/38VpdpS](#)

History | search datasets | Unnamed history (empty) | This history is empty. You can load your own data or get data from an external source



usegalaxy.no – The basics

Important features:

Tool menu with ~2000 tools sorted in sections

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

Server alerts

Quick start guide

Contact support

Q&A forum

Main menu

The screenshot shows the main menu of usegalaxy.no. At the top is a navigation bar with 'NeLS Galaxy Norway' and various menu items like 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. On the left is a 'Tools' sidebar with a search bar and a list of tool categories: Get Data, Send Data, Collection Operations, Lift-Over, Text Manipulation, Convert Formats, Filter and Sort, Join, Subtract and Group, Fetch Alignments/Sequences, Operate on Genomic Intervals, Statistics, Graph/Display Data, Phenotype Association, Interactive Tools, Mapping, SAM/BAM, Annotation, Assembly, Imaging, and ChemicalToolBox. The main window contains a 'Welcome to usegalaxy.no' message, a 'Tweets' section by @eliximorway, and a 'Galaxy version upgrade' notification. On the right is a 'History' sidebar with a search bar and a message indicating that the history is empty and suggesting to load data from an external source.

Tool menu

Main window

History

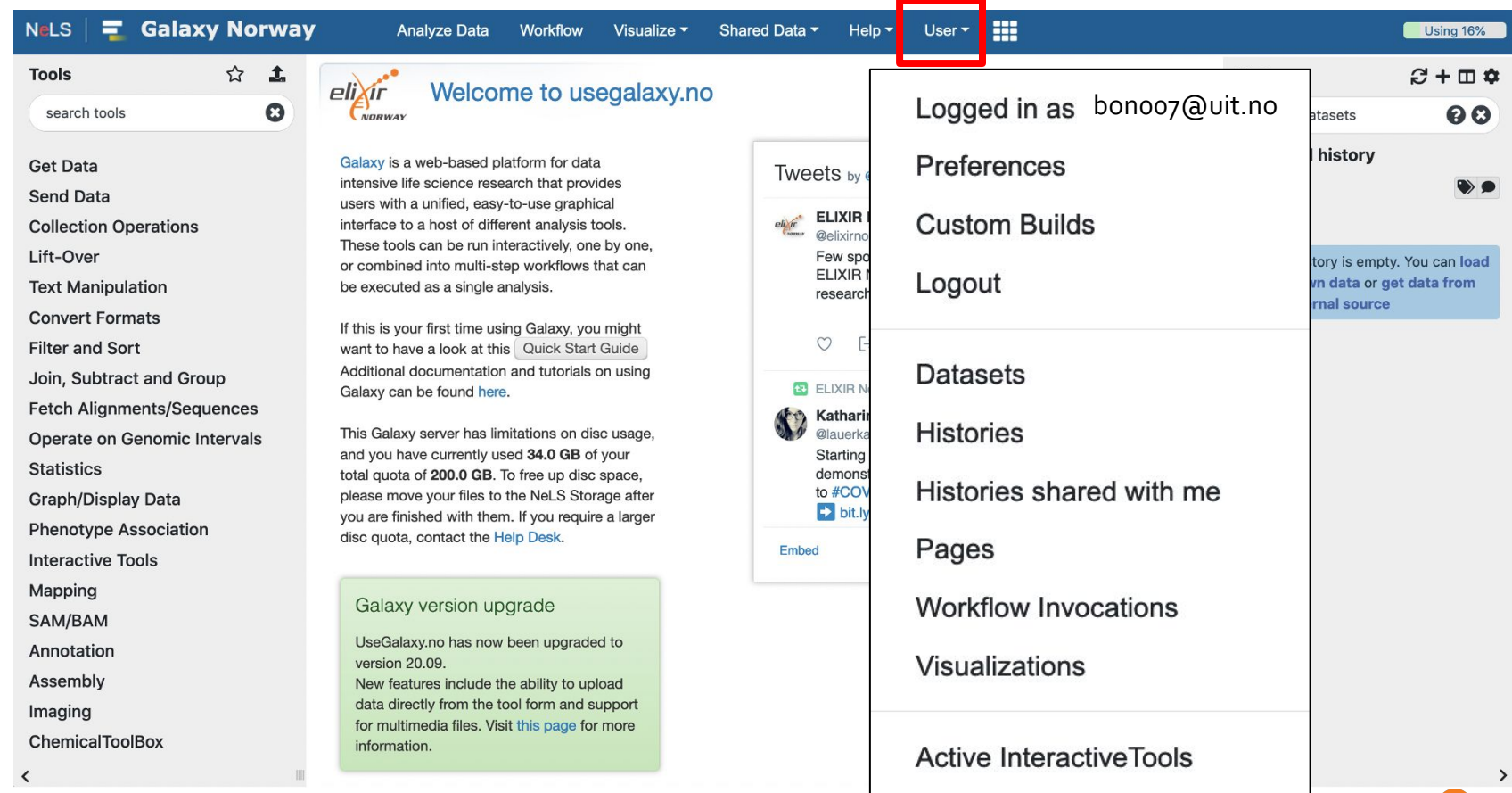


Your account and saved data

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. The top navigation bar includes 'NeLS', 'Galaxy Norway', and several menu items: 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The 'User' menu is highlighted with a red box and is open, displaying a list of options: 'Logged in as bon007@uit.no', 'Preferences', 'Custom Builds', 'Logout', 'Datasets', 'Histories', 'Histories shared with me', 'Pages', 'Workflow Invocations', 'Visualizations', and 'Active InteractiveTools'. The main content area features a 'Welcome to usegalaxy.no' message, a 'Quick Start Guide' link, and a 'Galaxy version upgrade' notification. A left sidebar contains a 'Tools' section with a search bar and a list of tool categories. A right sidebar shows a 'history' section with a message: 'History is empty. You can load data or get data from external source'.

Support and tutorials

Contact ELIXIR
Norway helpdesk for
support

Access to Galaxy wiki,
and tutorials

The screenshot shows the Galaxy Norway web interface. The top navigation bar includes 'NeLS', 'Galaxy Norway', and several menu items: 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The 'Help' menu is highlighted with a red box and is open, displaying a list of options: 'Support', 'Search', 'Mailing Lists', 'Videos', 'Wiki', 'How to Cite Galaxy', 'Interactive Tours', and 'Terms and Conditions'. The main content area features a 'Welcome to usegalaxy.no' message, a 'Tools' sidebar with a search bar and various tool categories, and a 'Galaxy version upgrade' notification box at the bottom. A tweet from ELIXIR Norway is also visible on the right side of the page.



Shared data

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

E.g. workflows and complete histories

You can import shared data to you user

Instructions how to use ELIXIR-NO supported workflows are also here

The screenshot shows the Galaxy Norway web interface. The top navigation bar includes 'NeLS', 'Galaxy Norway', and several menu items: 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data' (highlighted with a red box), 'Help', and 'User'. A dropdown menu for 'Shared Data' is open, listing 'Data Libraries', 'Histories', 'Workflows', 'Visualizations', and 'Pages'. The main content area features a 'Welcome to usegalaxy.no' message, a 'Galaxy version upgrade' notification, and a tweet from Katharina Lauer. The left sidebar contains a 'Tools' section with a search bar and various tool categories. The right sidebar shows a 'History' section with a search bar and a message indicating that the history is empty.

Shared data: workflows

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

You can import shared data to your 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 interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data' (highlighted with a red box), 'Help', and 'User'. The left sidebar contains a 'Tools' section with a search bar and various tool categories. The main content area displays 'Published Workflows' with a search bar and a table of workflow details. The right sidebar shows 'History' and 'Unnamed history' sections.

Name	Annotation	Owner	Community Rating	Community Tags	Last Updated
16S Workflow with Mothur program		kjetil-klepper	★★★★★		Oct 17, 2020
NGS Pipeline for Paired End Reads (R1 and R2)		kjetil-klepper	★★★★★		Oct 17, 2020
miRNA differential expression (miRBase, hg38)		kjetil-klepper	★★★★★	nels	Oct 15, 2020
miRNA differential expression (MirGeneDB, hg38)		kjetil-klepper	★★★★★	nels	Oct 14, 2020
COVID-19: PE Variation		kjetil-klepper	★★★★★	nels	Oct 13, 2020
Pre-process COVID-19 PE collections		kjetil-klepper	★★★★★	nels	Oct 13, 2020
Pre-process COVID-19 PE single sample		kjetil-klepper	★★★★★	nels	Oct 13, 2020

Context menu options:

- Run
- Import
- Save as File

Workflows

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

You can create new workflows here

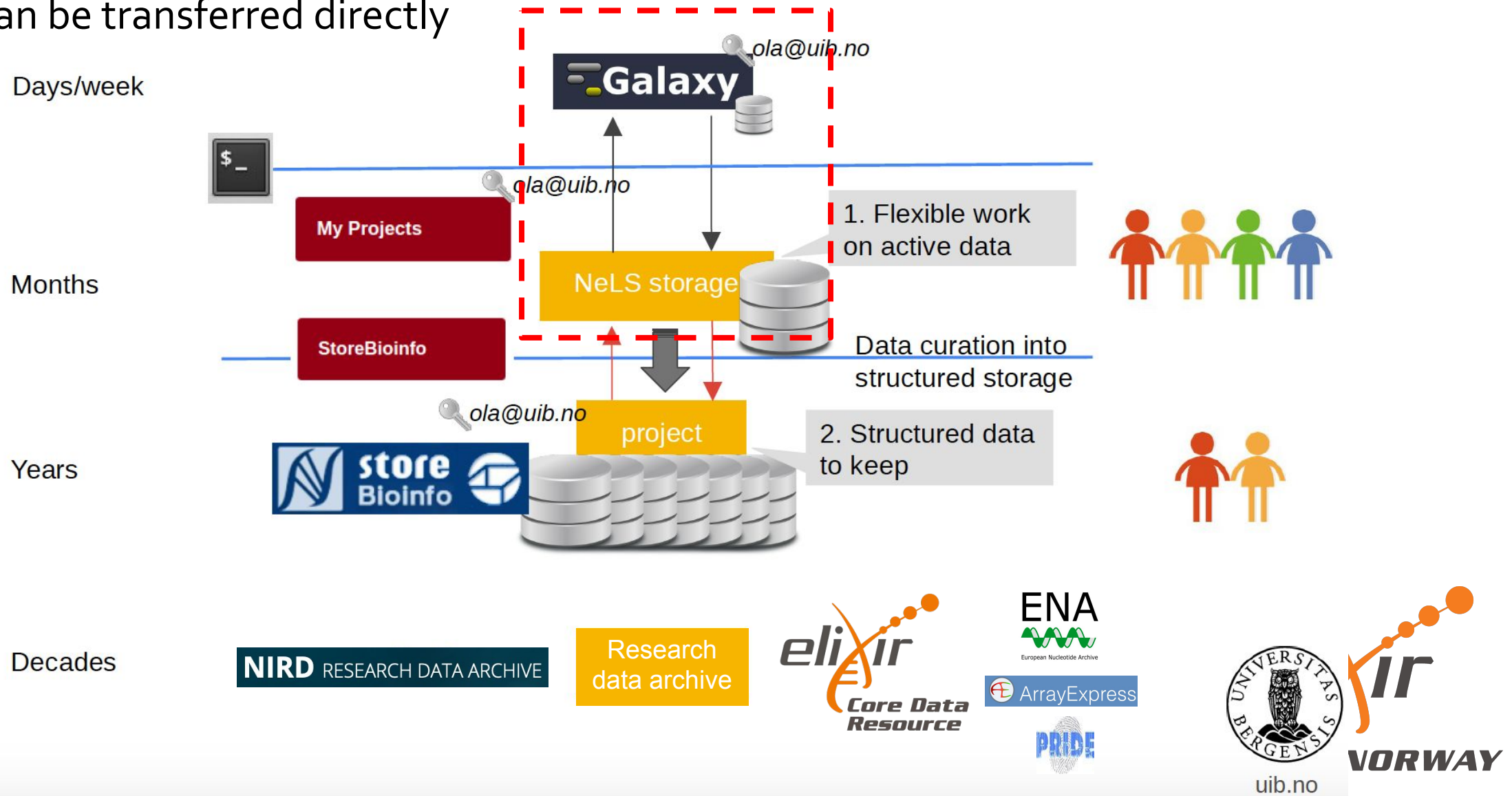
The screenshot displays the Galaxy Norway interface. The top navigation bar includes 'Analyze Data', 'Workflow' (highlighted with a red box), 'Visualize', 'Shared Data', 'Help', and 'User'. The left sidebar lists various tool categories such as 'Get Data', 'Send Data', 'Collection Operations', etc. The main content area shows a 'Search Workflows' input field and a table of workflows. The table has columns for Name, Tags, Updated, Sharing, and Bookmarked. Two workflows are listed:

Name	Tags	Updated	Sharing	Bookmarked
imported: miRNA differential expression (miRBase, hg38)		3 days ago		<input type="checkbox"/>
Taxonomic_profiling_Metaphlan2 Taxonomic annotation and visualization of shotgun metagenomic data	metagenomics	2 months ago		<input type="checkbox"/>

The right sidebar shows a 'History' panel with an empty history and a message: '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)

If your data is aligned
reads, specify the
reference genome
your data was aligned
against

The screenshot shows the Galaxy Norway interface with the 'Download from web or upload from disk' dialog box open. The dialog has tabs for 'Regular', 'Composite', 'Collection', and 'Rule-based'. Below the tabs, it says 'You added 2 file(s) to the queue. Add more files or click 'Start' to proceed.' A table lists the files:

Name	Size	Type	Genome	Settings	Status
test_upload.txt	9 b	txt	----- Additional ...	⚙️	0%
test_upload.fasta	9 b	Auto-de...	----- Additional ...	⚙️	0%

Below the table, there are dropdown menus for 'Type (set all):' (set to 'Auto-detect') and 'Genome (set all):' (set to '----- Additional ...'). The 'Genome' dropdown is highlighted with a red box. A search box for the genome is open, showing 'human' and a list of options: 'Human Apr. 2003 (NCBI33/hg15) (hg15)', 'Human Dec. 2013 (GRCh38/hg38) (hg38)', 'Human Feb. 2009 (GRCh37/hg19) (hg19)', and 'Human July 2003 (NCBI34/hg16) (hg16)'. The 'Human Dec. 2013 (GRCh38/hg38) (hg38)' option is highlighted. At the bottom of the dialog, there are buttons for 'Choose local files', 'Paste/Fetch data', 'Start', 'Select', 'Pause', 'Reset', and 'Close'.

Importing data from your computer

The two imported files will appear as two datasets in your history

The datasets are displayed in the order in which they were created/imported, with the oldest/first shown at the bottom

Galaxy also adds an increasing number in front of the files

The screenshot shows the Galaxy Norway web interface. The top navigation bar includes 'NeLS', 'Galaxy Norway', and various menu items like 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The main content area displays a welcome message from ELIXIR NORWAY, a tweet from @elixirnorway, and a 'Galaxy version upgrade' notification. On the right side, the 'History' panel is visible, showing two datasets: '2: test_upload.fasta' and '1: test_upload.txt'. The '2: test_upload.fasta' dataset is highlighted with a red box.



Importing data from NeLS

Import data from
Personal or Project
folders in NeLS

Redirect to the NeLS
portal (require login)

Files are selectable

The screenshot shows the Galaxy Norway web interface. The top navigation bar includes 'NeLS', 'Galaxy Norway', and various menu items like 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. A 'Tools' sidebar on the left has a search bar and a 'Get Data' button highlighted with a red box. Below it, a list of tools is visible, including 'Get files from NeLS storage'. The main content area displays a 'Welcome to usegalaxy.no' message and a 'History' panel. A 'Galaxy Interaction' window is open, showing a breadcrumb path: 'Home / Projects / ELIXIR_online_course_2021 / intro_usegalaxy'. Below the path is a table with two columns: 'Name' and 'Size'. The table contains one entry: 'test_NeLS_import.txt' with a size of '72 bytes'. A 'Send to Galaxy' button is located at the bottom of the window.

Name	Size
test_NeLS_import.txt	72 bytes

Importing data from NeLS

Redirect back to
usegalaxy.no

Imported data from
NeLS will appear in
your history

Note: the yellow colour
of files as this jobs are
being processed (green
= job complete)

The screenshot shows the Galaxy Norway web interface. The top navigation bar includes 'NeLS', 'Galaxy Norway', and various menu options like 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The 'Tools' sidebar on the left lists various data retrieval tools such as 'Get files from NeLS storage', 'EGA Download Client', and 'NCBI ESummary'. The main content area displays a 'Welcome to usegalaxy.no' message, a tweet from ELIXIR Norway, and a 'Galaxy version upgrade' notification. The 'History' sidebar on the right shows a list of datasets, with the top entry '3: Get files' highlighted in yellow, indicating it is currently being processed. Below it are two completed jobs, '2: test_upload.fasta' and '1: test_upload.txt', both highlighted in green.



Use galaxy histories to organise data

The current history is
"your current work
space"

The history panel
displays datasets in the
order in which they were
created

The screenshot displays the Galaxy Norway web interface. The top navigation bar includes 'NeLS', 'Galaxy Norway', and various menu options like 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The left sidebar contains a 'Tools' section with a search bar and a list of tools under 'Get Data', such as 'EGA Download Client', 'NCBI ESummary', 'NCBI ESearch', 'NCBI EPost', 'NCBI ELink', 'NCBI EInfo', 'NCBI EGQuery', 'NCBI EFetch', 'NCBI ECitMatch', 'IEDB MHC Binding prediction', 'UniProt download proteome as XML or fasta', 'UniProt ID mapping and retrieval', 'Unipept', and 'Download and Generate Pileup'. The main content area features a 'Welcome to usegalaxy.no' message, a 'Tweets by @eliximorway' section, and a 'Galaxy version upgrade' notification. The right sidebar, titled 'History', is highlighted with a red border and shows a search bar, 'Unnamed history' with 3 datasets, and a list of datasets: '3: test_NeLS_import', '2: test_upload.fasta', and '1: test_upload.txt'. Each dataset entry includes an eye icon, an edit icon, and a delete icon.

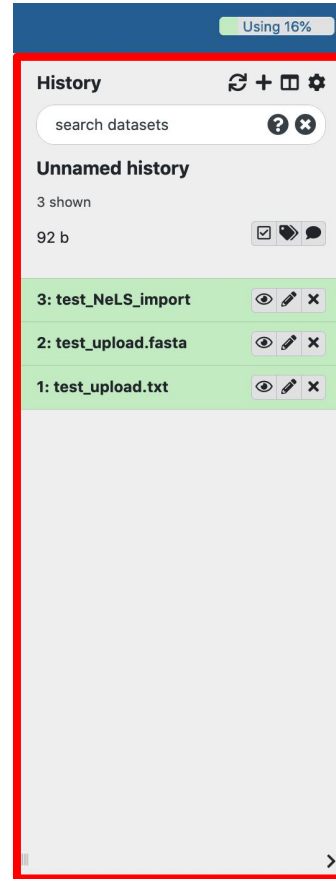
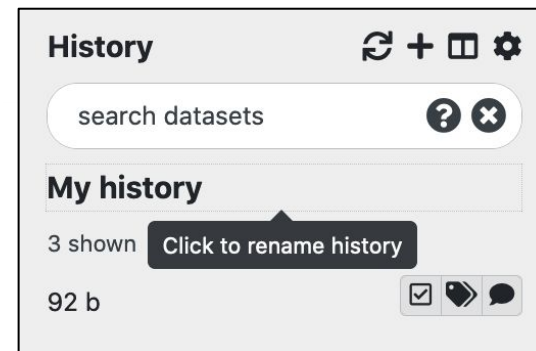
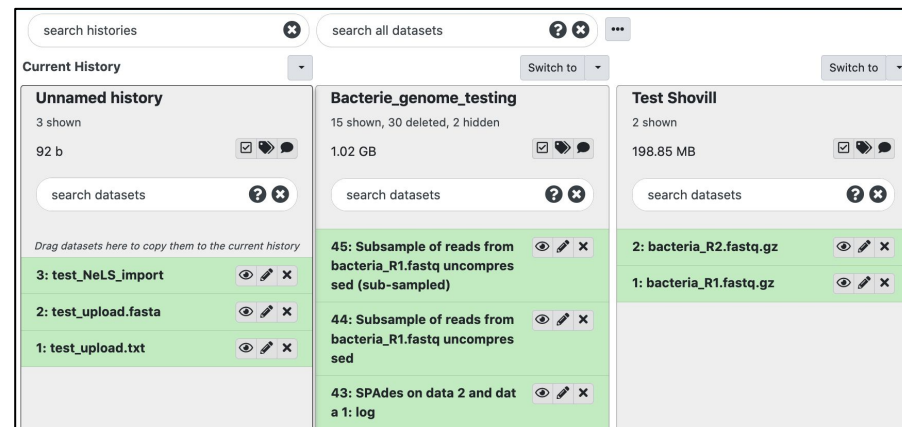


Use galaxy histories to organise data

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)



Datasets 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

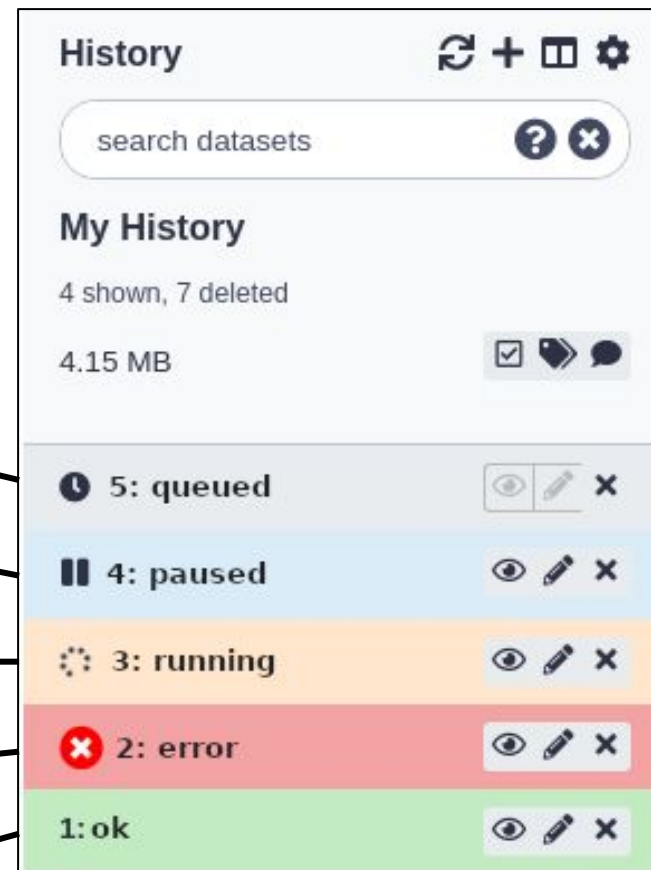
Job has not yet started but will create this dataset

Paused jobs can be resumed but will create this dataset

Job is running but will create this dataset

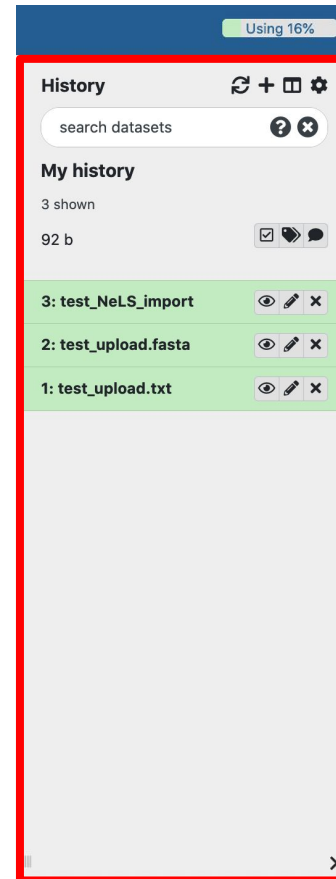
The job failed with an error

The job completed successfully



The screenshot shows the 'History' panel in Galaxy. It features a search bar for datasets, a 'My History' section with 4 items shown and 7 deleted, and a total size of 4.15 MB. Below this is a list of jobs with their states and associated datasets:

Job ID	State	Dataset(s)
5	queued	test_upload.txt
4	paused	test_upload.fasta
3	running	test_NeLS_import
2	error	test_upload.fasta
1	ok	test_upload.txt



This screenshot is a zoomed-in view of the 'History' panel, showing the search bar and the 'My history' section. It lists three items:

Job ID	State	Dataset(s)
3	running	test_NeLS_import
2	paused	test_upload.fasta
1	ok	test_upload.txt

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

E.g. version of the tool and database used in an analysis

The screenshot illustrates the Galaxy web interface for dataset management. At the top, three labels with arrows point to icons: 'View data' (eye icon), 'Edit attributes' (pencil icon), and 'Delete data' (X icon). The main panel shows a list of datasets:

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

The selected dataset, '1: test_upload.txt', is expanded to show its details:

- 1 line
- format: **txt**, database: ?
- uploaded txt file
- Download data icons: download, info, chart, help
- Test file

Annotations on the left side of the interface:

- 'Data description' points to the format and database information.
- 'Download data' points to the download icon.
- 'Detailed information' points to the 'Test file' label.

An inset window titled 'Edit dataset attributes' is shown on the right, with tabs for 'Attributes', 'Convert', 'Datatypes', and 'Permissions'. The 'Datatypes' tab is active, showing options to 'Change datatype', 'Detect datatype', and 'Change datatype'. A 'New Type' dropdown menu is open, listing 'txt', 'fasta', 'csfasta', 'fasta', and 'fasta.gz', with 'fasta' selected.

At the bottom, a detailed view of the 'Upload File' dataset is shown:

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

Dataset Collections for operation on multiple files

You can create dataset collections or list of multiple datasets that will be sent through the same analysis

Different types of collections and list are created by selecting dataset from your history

After naming the collection/list, it will appear in your history

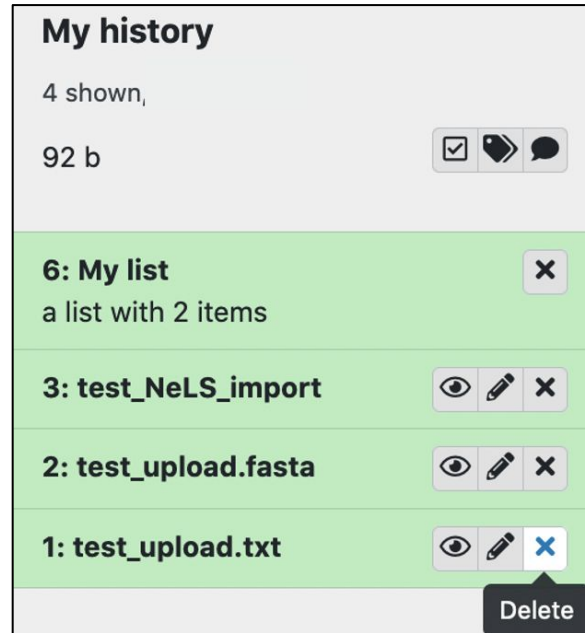
The image shows a sequence of three screenshots from the Elixir interface. The first screenshot shows the 'History' panel with a search bar and a list of datasets: '3: test_NeLS_import', '2: test_upload.fasta', and '1: test_upload.txt'. A context menu is open over the selected datasets, with 'Build Dataset List' highlighted. The second screenshot shows the 'My history' panel with a list of collections: '6: My list' (a list with 2 items), '3: test_NeLS_import', '2: test_upload.fasta', and '1: test_upload.txt'. The third screenshot is a dialog box titled 'Create a collection from a list of datasets'. It contains a list of datasets to be included in the collection: 'test_upload.fasta' and 'test_upload.txt', each with a 'Discard' button. There is a checkbox for 'Hide original elements?' and a text input field for 'Name:' containing 'My list'. 'Cancel' and 'Create list' buttons are at the bottom.

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

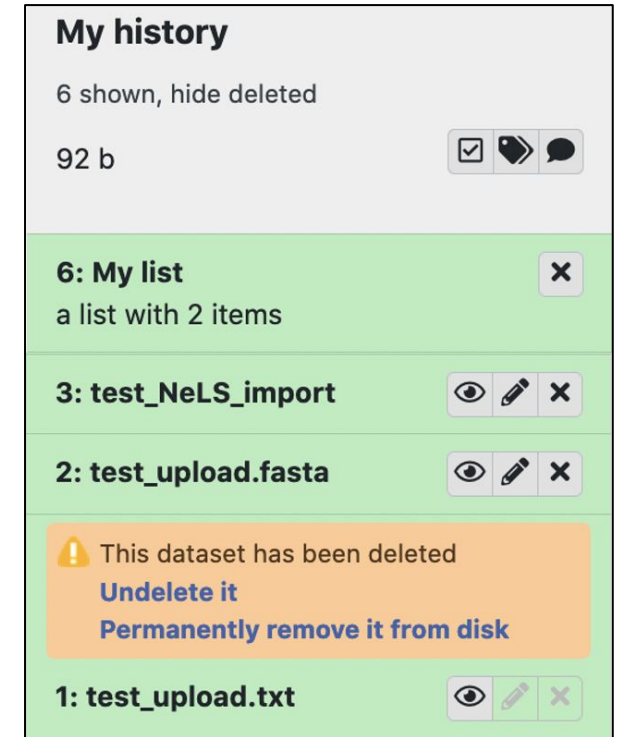
6: My list a list with 2 items

3: test_NeLS_import

2: test_upload.fasta

1: test_upload.txt

Delete



My history
6 shown, hide deleted
92 b

6: My list a list with 2 items

3: test_NeLS_import

2: test_upload.fasta

This dataset has been deleted
[Undelete it](#)
[Permanently remove it from disk](#)

1: test_upload.txt

Galaxy sharing data

An efficient method for sharing analysis with collaborators

Good practice to get support from the Helpdesk

Tools

- Get Data
- Send Data
- Collection Operations
- Lift-Over
- Text Manipulation
- Convert Formats
- Filter and Sort
- Join, Subtract and Group
- Fetch Alignments/Sequences
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Phenotype Association
- Interactive Tools
- Mapping
- SAM/BAM
- Annotation
- Assembly
- Imaging
- ChemicalToolBox

Share or Publish History `My history`

Make History Accessible via Link and Publish It

This history is currently restricted so that only you and the users listed below can access it. You can:

- Make History Accessible via Link**
 - Also make all objects within the History accessible.
 - Generates a web link that you can share with other people so that they can view and import the history.
- Make History Accessible and Publish**
 - Also make all objects within the History accessible.
 - Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Share History with Individual Users

You have not shared this history with any users.

- Share with a user**

History

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

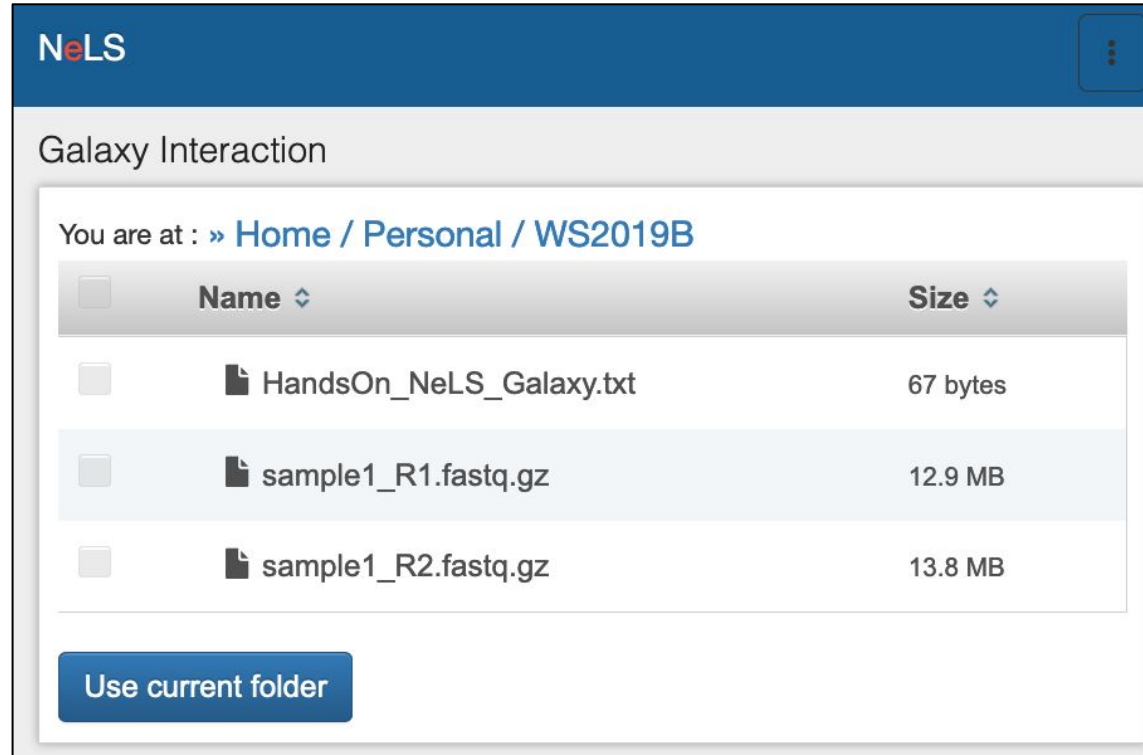
- Export History
- Import History

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



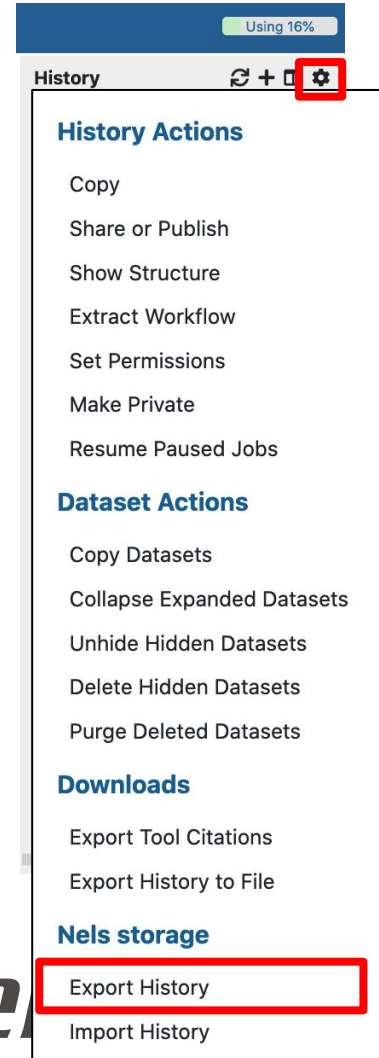
NeLS

Galaxy Interaction

You are at : » [Home](#) / [Personal](#) / [WS2019B](#)

<input type="checkbox"/>	Name ↕	Size ↕
<input type="checkbox"/>	HandsOn_NeLS_Galaxy.txt	67 bytes
<input type="checkbox"/>	sample1_R1.fastq.gz	12.9 MB
<input type="checkbox"/>	sample1_R2.fastq.gz	13.8 MB

[Use current folder](#)



Using 16%

History [↻](#) [+](#) [⊞](#)

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