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

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
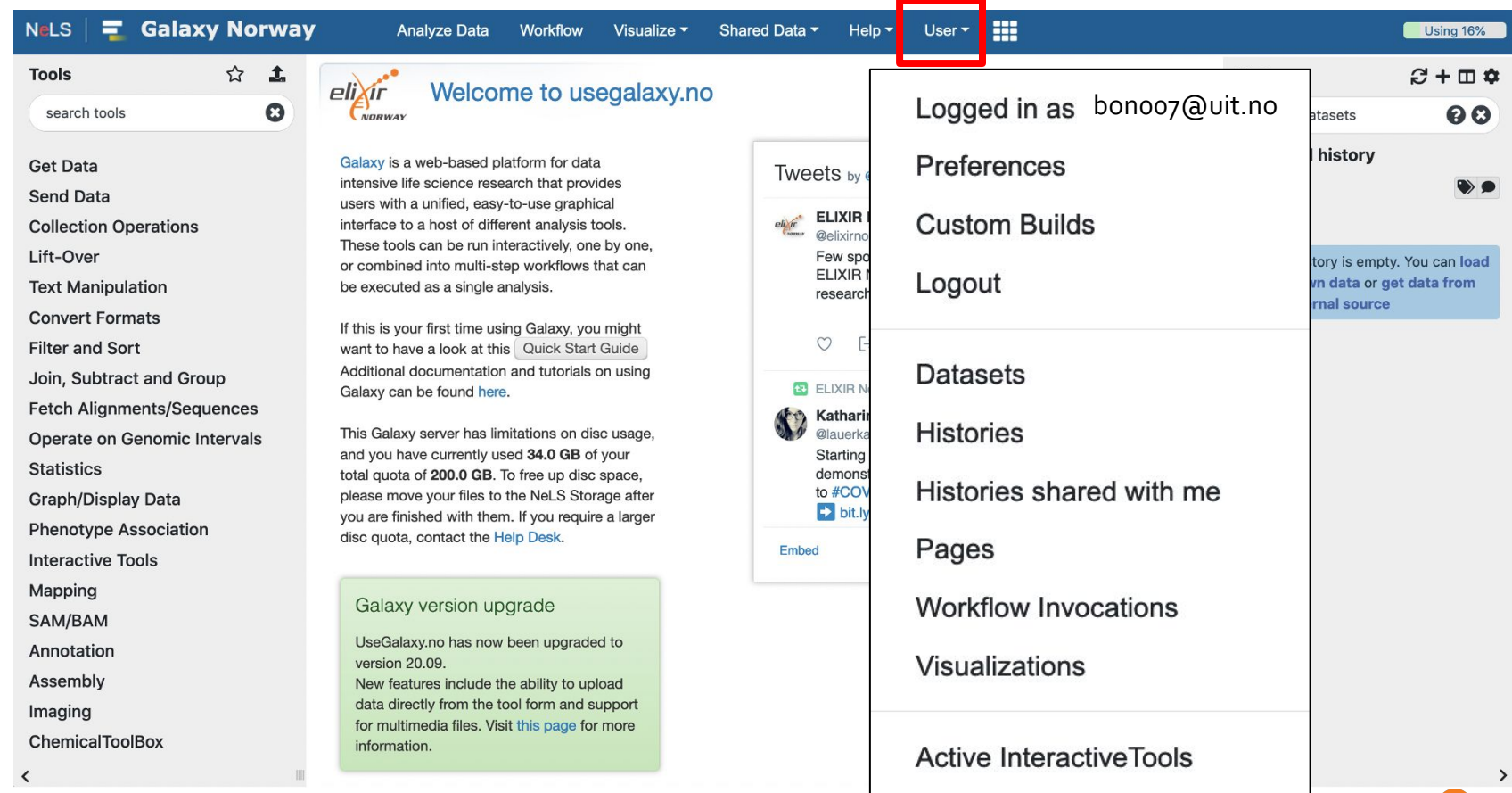

Tool menu

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

Support and tutorials

Contact ELIXIR Norway helpdesk for support

Access to Galaxy wiki, and tutorials

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

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

Workflows

Your workflows. These are the imported or the workflows you have made
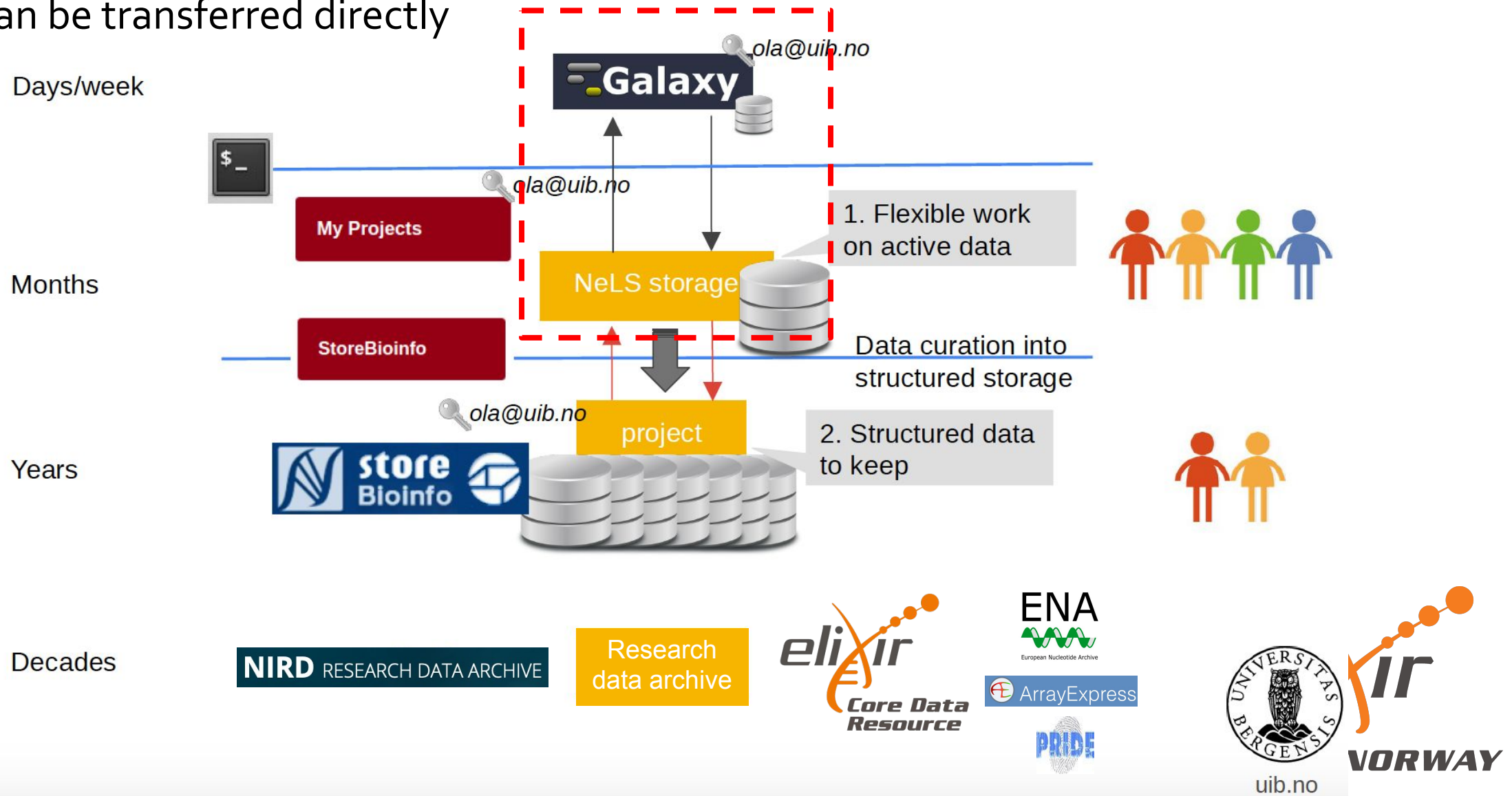
You can create new workflows here

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

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

Importing data from NeLS

Import data from Personal or Project folders in NeLS

Redirect to the NeLS portal (require login)

Files are selectable

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)

Use galaxy histories to organise data

The current history is "your current work space"

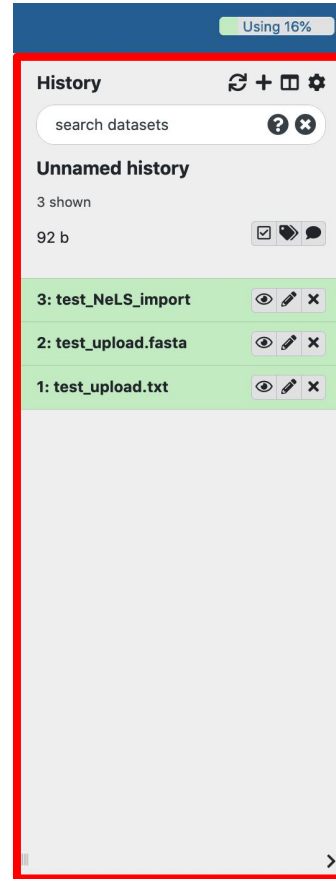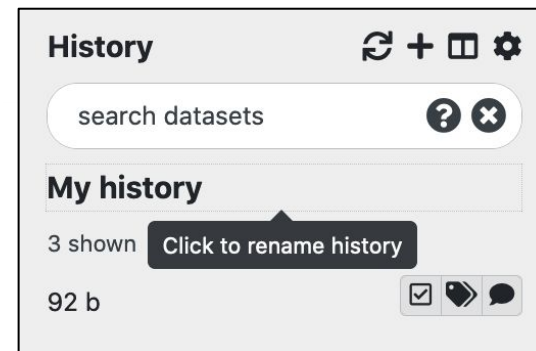The history panel displays datasets in the order in which they were created

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)
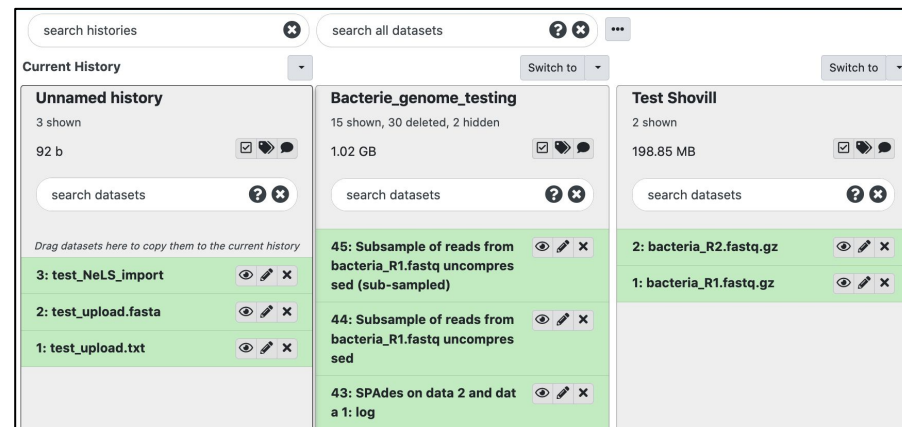
Datasets is equivalent to file(s)

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

Operations and information on datasets
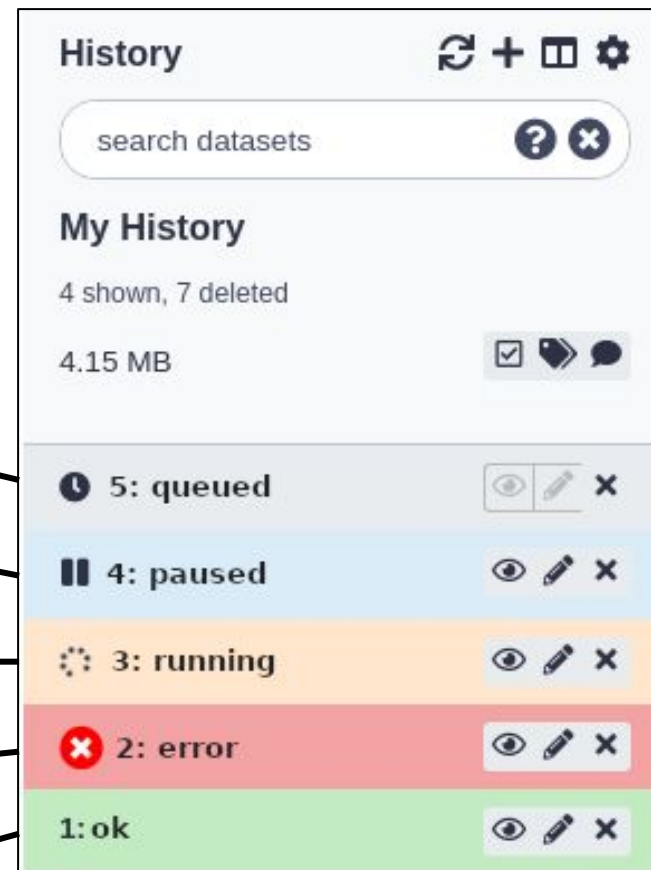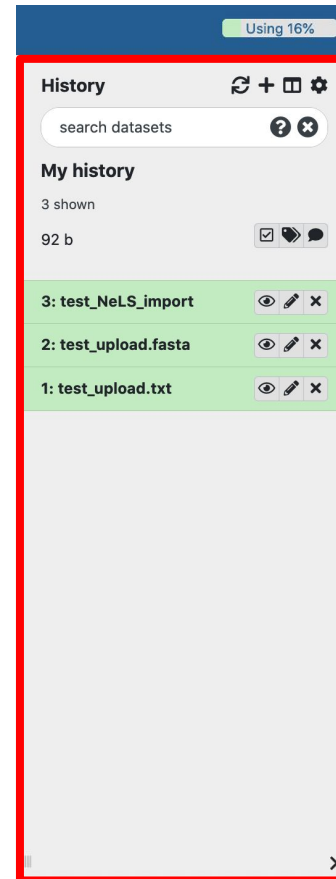
Multiple operations can be performed on each dataset

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

View data   Edit attributes   Delete data

3: test_NeLS_import 👁 ✏ ✖

2: test_upload.fasta 👁 ✏ ✖

1: test_upload.txt 👁 ✏ ✖

1 line

format: **txt**, database: **?**

uploaded txt file

Data description

Download data

Detailed information

Test file

Edit dataset attributes

≡ Attributes   ⚙ Convert   🗄 Datatypes   👤 Permissions

Change datatype   ↻ Detect datatype   ⇄ Change datatype

New Type

txt	▾

fasta	🔍

csfasta

fasta

fasta.gz

Upload File
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

elixir
NORWAY

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

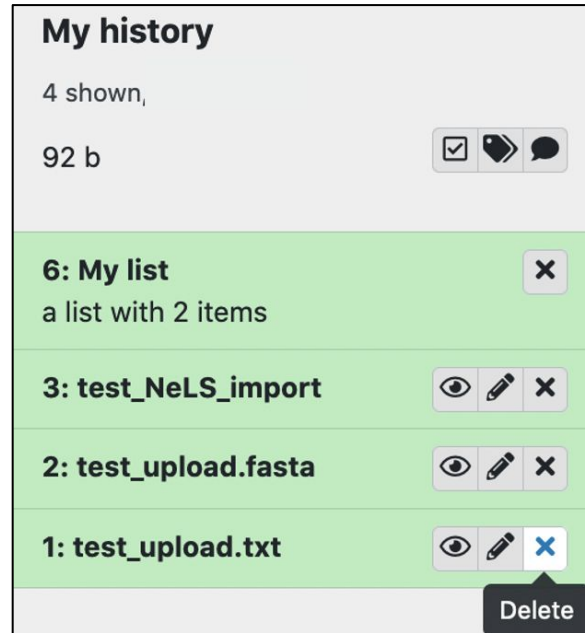After naming the collection/list, it will appear in your history

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

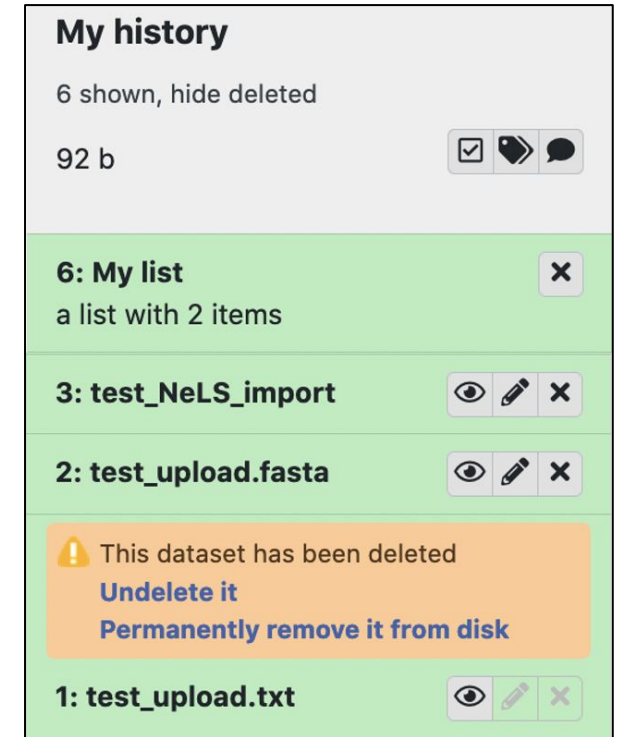Permanently deleting (purging) datasets (and histories) will free up disk space and cannot be recovered

Galaxy sharing data

An efficient method for sharing analysis with collaborators

Good practice to get support from the Helpdesk
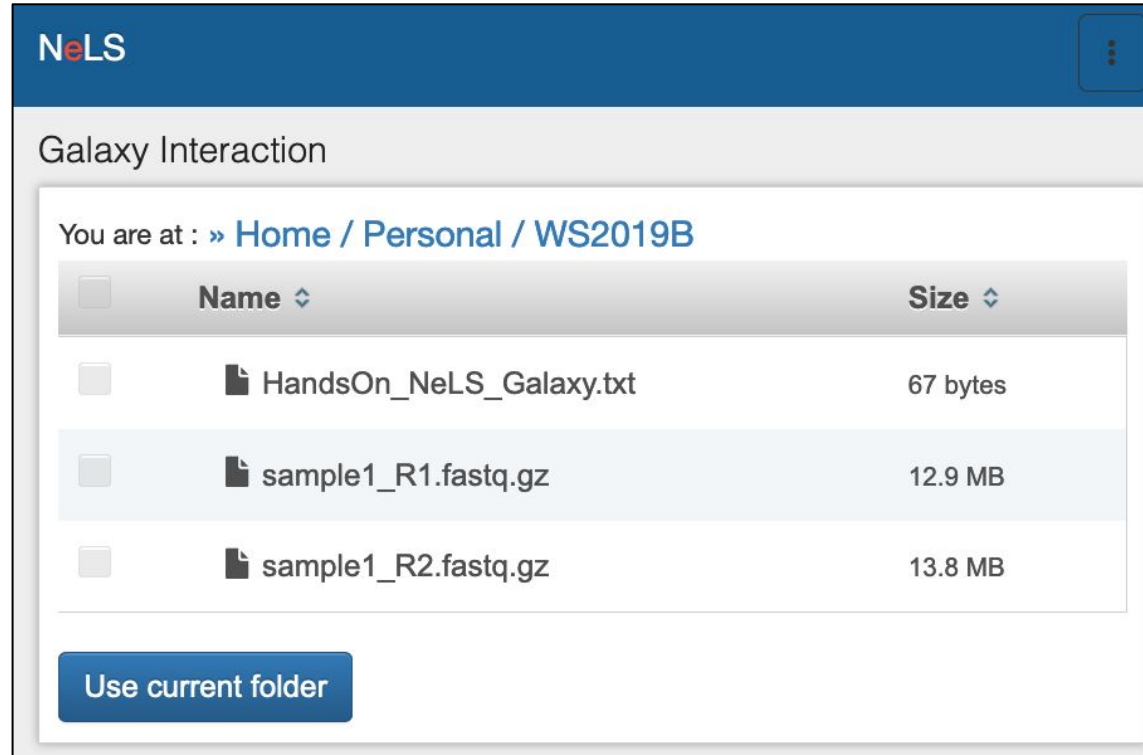
Exporting data

IMPORTANT: usegalaxy.no is not meant for storage

Please move your data when your data analysis is done

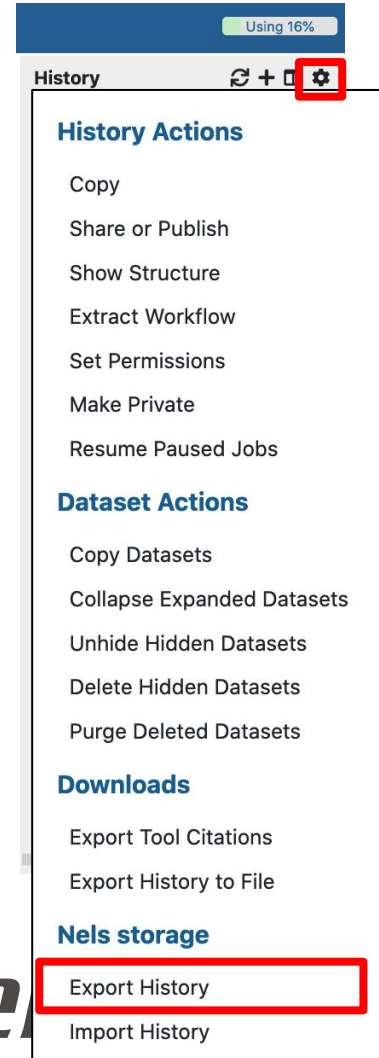You can export a complete history including datasets to a file on your local system or to NeLS