#### 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

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Collection Operations Lift-Over Text Manipulation	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.	ELIXIR Norway     @elixirnorway     Few spots left on the @swcarpentry course from     ELIXIR Norway and @DigitaltLiv for PhD candida     researchers korbinib.github.io/2021-02-01-DLN	ates & your own data or get data fr
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Join, Subtract and Group Fetch Alignments/Sequences	Additional documentation and tutorials on using Galaxy can be found here.	ELIXIR Norway Retweeted	¥
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Annotation Assembly	UseGalaxy.no has now been upgraded to version 20.09. New features include the ability to upload		
maging ChemicalToolBox	data directly from the tool form and support for multimedia files. Visit this page for more information.		



# 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

#### **Galaxy Norway** -Using 16% User -NeLS Analyze Data Workflow Visualize -Shared Data -Help -Tools ☆ **1** History 2+00 elixir Welcome to usegalaxy.no search tools 8 88 search datasets **Unnamed history** Galaxy is a web-based platform for data Get Data Tweets by @eliximorway intensive life science research that provides (empty) Send Data users with a unified, easy-to-use graphical **ELIXIR Norway** eli ir **Collection Operations** interface to a host of different analysis tools. @elixirnorway These tools can be run interactively, one by one, Lift-Over Few spots left on the @swcarpentry course from 1 This history is empty. You can load or combined into multi-step workflows that can ELIXIR Norway and @DigitaltLiv for PhD candidates & your own data or get data from **Text Manipulation** be executed as a single analysis. researchers korbinib.github.io/2021-02-01-DLN... an external source Convert Formats If this is your first time using Galaxy, you might $\bigcirc$ [> Jan 19, 2021 Filter and Sort want to have a look at this Quick Start Guide Additional documentation and tutorials on using Join, Subtract and Group ELIXIR Norway Retweeted Galaxy can be found here. Fetch Alignments/Sequences Katharina Lauer This Galaxy server has limitations on disc usage, @lauerkatharina **Operate on Genomic Intervals** and you have currently used 34.0 GB of your Starting on 20 Jan, a series of 6 webinars will Statistics total quota of 200.0 GB. To free up disc space, demonstrate that *#openscience* is key for responding to #COVID19 and public health crises please move your files to the NeLS Storage after Graph/Display Data bit.lv/38VpdpS you are finished with them. If you require a larger Phenotype Association disc quota, contact the Help Desk. Embed View on Twitter Interactive Tools Mapping Galaxy version upgrade SAM/BAM UseGalaxy.no has now been upgraded to Annotation version 20.09 Assembly New features include the ability to upload data directly from the tool form and support Imaging for multimedia files. Visit this page for more ChemicalToolBox information. Tool menu Main window History

Main menu

#### 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

NeLS   🗧 Galaxy Norway	V Analyze Data Workflow Visualize <del>v</del>	Shared Data ▼ Help ▼	User -	Using 16%
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Imaging	for multimedia files. Visit this page for more			
	information.		Active InteractiveTools	
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#### Support and tutorials

Contact ELIXIR Norway helpdesk for support

Access to Galaxy wiki, and tutorials

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Imaging ChemicalToolBox	data directly from the tool form and support for multimedia files. Visit this page for more information.				



#### 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

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Mapping SAM/BAM Annotation Assembly maging ChemicalToolBox	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.				



# 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

Nels   🚍 Galaxy Norway	Analyze Data Workflow Vis	sualize - Shared I	oata <del>▼</del> Help <del>▼</del>	User 🕶	<b>=</b>		Using 16%
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Text Manipulation Convert Formats	NGS Pipeline for Paired End Reads (R1 and R2)	kjetil- klepper	****		Oct 17, 2020	your own data or an external source	get data from e
Filter and Sort Join, Subtract and Group	miRNA differential expression (miRBase, hg38)	kjetil- klepper	*****	nels	Oct 15, 2020		
Fetch Alignments/Sequences Operate on Genomic Intervals	miRNA differential expression (MirGeneDB, hg38)	kjetil- klepper	****	nels	Oct 14, 2020		
Statistics Graph/Display Data	COVID-19: PE Variation 🔻	kjetil- klepper	kkkk	nels	Oct 13, 2020		
Phenotype Association Interactive Tools	Pre-process COVID-19 PE collections	kjetil- klepper	****	nels	Oct 13, 2020		
Mapping SAM/BAM	Pre-process COVID-19 PE single sample	kjetil-	*****	nels	Oct 13, 2020		
Annotation Assembly		Run					
		Import					
		Save as	File			11	

# Workflows

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

You can create new workflows here

Nels   🔁	Galaxy N	orway	Analyze Data	Workflow	Visualize <del>-</del>	Shared Data	Help -	User -				Using 16%
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# Usegalaxy.no is connected to NeLS



# 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

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# 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

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perate on Genomic Intervals tatistics raph/Display Data	This Galaxy server has limitations on disc usage, and you have currently used <b>34.0 GB</b> of your total quota of <b>200.0 GB</b> . To free up disc space, please move your files to the NeLS Storage after you are finished with them. If you require a larger	<ul> <li>Katharina Lauer</li> <li>@lauerkatharina</li> <li>Starting on 20 Jan, a series of 6 webina demonstrate that #openscience is key i to #COVID19 and public health crises</li> <li>bit.ly/38VpdpS</li> </ul>	ars will for responding		
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elixir

# Importing data from NeLS

Import data from Personal or Project folders in NeLS

Redirect to the NeLS portal (require login)

Files are selectable

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# 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)

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elixir

# 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

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**HIXI** 

# 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)



45: Subsample of reads from

44: Subsample of reads from 🛛 🕢 🗙 bacteria\_R1.fastq uncompres

43: SPAdes on data 2 and dat ( ) \* ×

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Drag datasets here to copy them to

3: test\_NeLS\_import

2: test upload.fasta

1: test upload.txt

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• / ×



2: bacteria R2.fastg.gz

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1: test_upload.txt	<ul> <li>● # ×</li> </ul>

#### 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 <ul> <li>Import</li> <li>Import</li> </ul>	
	2: test_upload.fasta	Edit dataset attributes
	1: test_upload.txt 💿 🖋 🗙	Change datatype
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Data	format: <b>txt</b> , database: <b>?</b>	fasta
description		csfasta
	uploaded txt file	fasta
		fasta.gz
data		
	Test file	
Detailed		
information		
	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	

# 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

My history		My histor
4 shown,		6 shown, hid
92 b		92 b
6: My list a list with 2 items	×	6: My list a list with 2
3: test_NeLS_import	• • ×	3: test_NeL
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1: test_upload.txt	• # ×	👍 This data
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My history				
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<b>6: My list</b> a list with 2 items	×			
3: test_NeLS_import	# ×			
2: test_upload.fasta	<i>i</i> ×			
A This dataset has been deleted Undelete it Permanently remove it from disk				
1: test_upload.txt	Ø X			



# Galaxy sharing data

An efficient method for sharing analysis with collaborators

Good practice to get support from the Helpdesk

NeLS   🚍 Galaxy Norway	Analyze Data Workflow Visualize - Shared Data - Help - User -	Using 16%
Tools 🟠 🛓	Chara ar Dublich Lliston, 'My biston,'	History 记 🕇 🕻 🌣
search tools	Share of Publish History My history	History Actions
Get Data		Сору
Send Data	Make History Accessible via Link and Publish It	Share or Publish
Collection Operations	This history is currently restricted so that only you and the users listed below can access it. You can:	
Lift-Over		Show Structure
Text Manipulation	Make History Accessible via Link	Extract Workflow
Convert Formats	Also make all objects within the History accessible	Set Permissions
Filter and Sort		Make Private
Join, Subtract and Group	Generates a web link that you can share with other people so that they can view and import the history.	
Fetch Alignments/Sequences		Resume Paused Jobs
Operate on Genomic Intervals	Make History Accessible and Publish	Dataset Actions
Statistics	Also make all objects within the History accessible.	O D. t t.
		Copy Datasets
Interactive Tools	Makes the history accessible via link (see above) and publishes the history to Galaxy's Published Histories	Collapse Expanded Datasets
Mapping	section, where it is publicly listed and searchable.	Unhide Hidden Datasets
SAM/BAM		Delete Hidden Datasets
Annotation	Share History with Individual Users	Purgo Delated Datasets
Assembly	You have not charad this history with any usars	Fuige Deleted Datasets
Imaging		Downloads
ChemicalToolBox	Share with a user	Export Tool Citations
<		Export History to File





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	1	Using 16%
Galaxy Interaction		History Actions
You are at : » Home / Personal / WS2019B		Copy Share or Publish
Name ≎	Size \$	Extract Workflow
HandsOn_NeLS_Galaxy.txt	67 bytes	Set Permissions Make Private
sample1_R1.fastq.gz	12.9 MB	Resume Paused Jobs Dataset Actions
sample1_R2.fastq.gz	13.8 MB	Copy Datasets Collapse Expanded Datase
Use current folder		Unhide Hidden Datasets Delete Hidden Datasets Purge Deleted Datasets
		Downloads
		Export Tool Citations
		Export History to File

Nels storage Export History Import History