



*usegalaxy.no tools and workflows*

*Given by who*

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



# Galaxy tools

Tools are available from the Tool menu

Organised under sub-menus

Possible to browse and search by name

You can make your own list of favourite tools

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'. A 'Using 16%' indicator is visible in the top right corner.

The 'Tools' menu is highlighted with a red border and contains the following items:

- 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

The main content area features a 'Welcome to usegalaxy.no' message from ELIXIR NORWAY, explaining that Galaxy is a web-based platform for data-intensive life science research. It includes a 'Quick Start Guide' link and a note about disc usage limitations (34.0 GB used, 200.0 GB total quota).

A tweet by ELIXIR Norway is displayed, mentioning a course from ELIXIR Norway and @DigitalLiv for PhD candidates and researchers. The tweet includes a link to a GitHub repository: [bit.ly/38VpdpS](https://github.com/korbinib/2021-02-01-DLN...).

The 'History' panel on the right shows a search for datasets and a list of two datasets: '2: Sample\_R2.fastq.gz' and '1: Sample\_R1.fastq.gz'.

A 'Galaxy version upgrade' notification is shown at the bottom, stating that UseGalaxy.no has been upgraded to version 20.09, with new features including direct data uploads and multimedia support.



# Galaxy tools = command line tools

Command line tools are wrapped into Galaxy so they become accessible with a GUI

Some Galaxy tools may have reduced the number of optional parameter settings for the tool

Example here is the assembly tool called SPAdes

The screenshot displays the Galaxy Norway interface for the SPAdes genome assembler. The 'Tools' sidebar on the left is highlighted with a red box, showing a search bar and a list of tools under categories like 'Assembly' and 'Graph/Display Data'. The 'SPAdes genome assembler for regular and single-cell projects' tool is selected. The main panel shows the tool's configuration options, including 'Single-cell?', 'Run only assembly? (without read error correction)', 'Careful correction?', 'Automatically choose k-mer values', 'Coverage Cutoff', and 'Libraries are IonTorrent reads?'. The 'History' panel on the right shows two datasets: '2: Sample\_R2.fastq.gz' and '1: Sample\_R1.fastq.gz'.

# Command line vs Galaxy

```
SPAdes genome assembler v3.11.1
Usage: /Users/service/tools/SPAdes-3.11.1-Darwin/bin/spades.py [options] -o <output_dir>

Basic options:
--o <output_dir>    directory to store all the resulting files (required)
--sc                this flag is required for MDA (single-cell) data
--meta              this flag is required for metagenomic sample data
--rna               this flag is required for RNA-Seq data
--plasmid           runs plasmidSPAdes pipeline for plasmid detection
--iontorrent        this flag is required for IonTorrent data
--test              runs SPAdes on toy dataset
-h/--help           prints this usage message
-v/--version        prints version

Input data:
--12 <filename>    file with interlaced forward and reverse paired-end reads
-1 <filename>       file with forward paired-end reads
-2 <filename>       file with reverse paired-end reads
-s <filename>       file with unpaired reads
--pe<#>-12 <filename> file with interlaced reads for paired-end library number <#> (<#> = 1,2,...,9)
--pe<#>-1 <filename>  file with forward reads for paired-end library number <#> (<#> = 1,2,...,9)
--pe<#>-2 <filename>  file with reverse reads for paired-end library number <#> (<#> = 1,2,...,9)
--pe<#>-s <filename>  file with unpaired reads for paired-end library number <#> (<#> = 1,2,...,9)
--pe<#>-<or> <filename> orientation of reads for paired-end library number <#> (<#> = 1,2,...,9; <or> = fr, rf, ff)
--s<#> <filename>    file with unpaired reads for single reads library number <#> (<#> = 1,2,...,9)
--mp<#>-12 <filename> file with interlaced reads for mate-pair library number <#> (<#> = 1,2,...,9)
--mp<#>-1 <filename>  file with forward reads for mate-pair library number <#> (<#> = 1,2,...,9)
--mp<#>-2 <filename>  file with reverse reads for mate-pair library number <#> (<#> = 1,2,...,9)
--mp<#>-s <filename>  file with unpaired reads for mate-pair library number <#> (<#> = 1,2,...,9)
--mp<#>-<or> <filename> orientation of reads for mate-pair library number <#> (<#> = 1,2,...,9; <or> = fr, rf, ff)
--hqmp<#>-12 <filename> file with interlaced reads for high-quality mate-pair library number <#> (<#> = 1,2,...,9)
--hqmp<#>-1 <filename>  file with forward reads for high-quality mate-pair library number <#> (<#> = 1,2,...,9)
--hqmp<#>-2 <filename>  file with reverse reads for high-quality mate-pair library number <#> (<#> = 1,2,...,9)
--hqmp<#>-s <filename>  file with unpaired reads for high-quality mate-pair library number <#> (<#> = 1,2,...,9)
--hqmp<#>-<or> <filename> orientation of reads for high-quality mate-pair library number <#> (<#> = 1,2,...,9; <or> = fr, rf, ff)
--nxmate<#>-1 <filename> file with forward reads for Lucigen NxMate library number <#> (<#> = 1,2,...,9)
--nxmate<#>-2 <filename> file with reverse reads for Lucigen NxMate library number <#> (<#> = 1,2,...,9)
--sanger <filename>    file with Sanger reads
--pacbio <filename>    file with PacBio reads
--nanopore <filename>  file with Nanopore reads
--tslr <filename>      file with TSLR-contigs
--trusted-contigs <filename> file with trusted contigs
--untrusted-contigs <filename> file with untrusted contigs

Pipeline options:
--only-error-correction runs only read error correction (without assembling)
--only-assembler        runs only assembling (without read error correction)
--careful                tries to reduce number of mismatches and short indels
--continue               continue run from the last available check-point
--restart-from <cp>      restart run with updated options and from the specified check-point ('ec', 'as', 'k<int>', 'mc')
--disable-gzip-output    forces error correction not to compress the corrected reads
--disable-rr             disables repeat resolution stage of assembling

Advanced options:
--dataset <filename>    file with dataset description in YAML format
-t/--threads <int>      number of threads
                        [default: 16]
-m/--memory <int>       RAM limit for SPAdes in Gb (terminates if exceeded)
                        [default: 250]
--tmp-dir <dirname>     directory for temporary files
                        [default: <output_dir>/tmp]
-k <int,int,...>        comma-separated list of k-mer sizes (must be odd and
```

Galaxy Norway

Analyze Data Workflow Visualize Shared Data Help User

Using 16%

SPAdes genome assembler for regular and single-cell projects (Galaxy Version 3.12.0+galaxy1) Favorite Options

Single-cell? Yes No

This option is required for MDA (single-cell) data. (--sc)

Run only assembly? (without read error correction) Yes No

(--only-assembler)

Careful correction? Yes No

Tries to reduce number of mismatches and short indels. Also runs MismatchCorrector – a post processing tool, which uses BWA tool (comes with SPAdes). (--careful)

Automatically choose k-mer values Yes No

k-mer choices can be chosen by SPAdes instead of being entered manually

K-mers to use, separated by commas 21,33,55

Comma-separated list of k-mer sizes to be used (all values must be odd, less than 128, listed in ascending order, and smaller than the read length). The default value is 21,33,55.

Coverage Cutoff Off

Libraries are IonTorrent reads? Yes No

History

search datasets

DEMO

2 shown

198.85 MB

2: Sample\_R2.fastq.gz

1: Sample\_R1.fastq.gz



# Running tools in Galaxy

Example running the tool  
SPAdes

Choose parameter  
settings

Select input files

Most tools comes with a  
detailed description of  
usage

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 left sidebar contains tool categories: 'Tools', 'Assembly', 'Graph/Display Data', and 'Create assemblies with Unicycler'. The 'SPAdes genome assembler for regular and single-cell projects' tool is highlighted in red. The main content area shows the tool configuration page for SPAdes, with a 'Single-cell?' toggle set to 'No'. The 'Files' section is highlighted in red, showing two input files: '1: Sample\_R1.fastq.gz' and '2: Sample\_R2.fastq.gz'. The 'Execute' button is also highlighted in red. The right sidebar shows the 'History' section with a search bar and a list of datasets, including '2: Sample\_R2.fastq.gz' and '1: Sample\_R1.fastq.gz', which are also highlighted in red. The bottom right corner features the 'elixir NORWAY' logo.

# Running tools in Galaxy

The result files are first displayed in grey boxes. This means the job is pending.

The screenshot displays the Galaxy Norway web interface. At the top, the navigation bar includes 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The main content area is a green notification box with a checkmark icon, stating: 'Executed SPAdes and successfully added 1 job to the queue. The tool uses 2 inputs: 1: Sample\_R1.fastq.gz, 2: Sample\_R2.fastq.gz. It produces 5 outputs: 3: SPAdes on data 2 and data 1: contig stats, 4: SPAdes on data 2 and data 1: scaffold stats, 5: SPAdes on data 2 and data 1: contigs (fasta), 6: SPAdes on data 2 and data 1: scaffolds (fasta), 7: SPAdes on data 2 and data 1: log. You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.'

On the left, the 'Tools' panel shows a search bar and categories: 'Assembly' (Shovill, rnaSPAdes, SPAdes), 'Create assemblies with Unicycler' (metaSPAdes), and 'Graph/Display Data' (Bandage Info, Bandage Image).

On the right, the 'History' panel shows a search bar and a list of datasets. A red box highlights the following entries: '7: SPAdes on data 2 and data 1: log', '6: SPAdes on data 2 and data 1: scaffolds (fasta)', '5: SPAdes on data 2 and data 1: contigs (fasta)', '4: SPAdes on data 2 and data 1: scaffold stats', '3: SPAdes on data 2 and data 1: contig stats', '2: Sample\_R2.fastq.gz', and '1: Sample\_R1.fastq.gz'. Each entry has an eye icon, a pencil icon, and a close icon.

# Running tools in Galaxy

When the job is running, the files turn yellow

The screenshot displays the Galaxy Norway web interface. At the top, the navigation bar includes 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. A 'Using 16%' indicator is visible in the top right corner.

The left sidebar contains a 'Tools' section with a search bar and several tool categories: 'Assembly' (including Showill, rnaSPAdes, and SPAdes), 'Create assemblies with Unicycler' (including metaSPAdes), and 'Graph/Display Data' (including Bandage Info and Bandage Image).

The main content area features a green notification box with a checkmark icon, stating: 'Executed SPAdes and successfully added 1 job to the queue.' Below this, it lists the tool's inputs and outputs:

- The tool uses 2 inputs:
  - 1: Sample\_R1.fastq.gz
  - 2: Sample\_R2.fastq.gz
- It produces 5 outputs:
  - 3: SPAdes on data 2 and data 1: contig stats
  - 4: SPAdes on data 2 and data 1: scaffold stats
  - 5: SPAdes on data 2 and data 1: contigs (fasta)
  - 6: SPAdes on data 2 and data 1: scaffolds (fasta)
  - 7: SPAdes on data 2 and data 1: log

Below the notification, a text block explains: 'You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.'

The right sidebar shows the 'History' panel with a search bar and a 'DEMO' section. The history list contains several entries, with the top five highlighted in yellow and enclosed in a red box:

- 7: SPAdes on data 2 and data 1: log
- 6: SPAdes on data 2 and data 1: scaffolds (fasta)
- 5: SPAdes on data 2 and data 1: contigs (fasta)
- 4: SPAdes on data 2 and data 1: scaffold stats
- 3: SPAdes on data 2 and data 1: contig stats
- 2: Sample\_R2.fastq.gz
- 1: Sample\_R1.fastq.gz

# Running tools in Galaxy

When the job finish successfully, the files turn green

The screenshot displays the Galaxy Norway web interface. At the top, the navigation bar includes 'NLS', 'Galaxy Norway', and menu items for 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. A 'Using 16%' indicator is visible in the top right corner.

The left sidebar contains a 'Tools' section with a search bar and several tool categories: 'Assembly' (including Showill, rnaSPAdes, and SPAdes), 'Create assemblies with Unicycler' (including metaSPAdes), and 'Graph/Display Data' (including Bandage Info and Bandage Image).

The main content area features a green notification box with a checkmark icon, stating: 'Executed SPAdes and successfully added 1 job to the queue.' Below this, it lists the tool's inputs and outputs:

- The tool uses 2 inputs:
  - 1: Sample\_R1.fastq.gz
  - 2: Sample\_R2.fastq.gz
- It produces 5 outputs:
  - 3: SPAdes on data 2 and data 1: contig stats
  - 4: SPAdes on data 2 and data 1: scaffold stats
  - 5: SPAdes on data 2 and data 1: contigs (fasta)
  - 6: SPAdes on data 2 and data 1: scaffolds (fasta)
  - 7: SPAdes on data 2 and data 1: log

Below the notification, a note explains: 'You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.'

The right sidebar shows the 'History' panel with a search bar and a list of datasets. The top entry is highlighted with a red box and contains the following items:

- 7: SPAdes on data 2 and data 1: log
- 6: SPAdes on data 2 and data 1: scaffolds (fasta)
- 5: SPAdes on data 2 and data 1: contigs (fasta)
- 4: SPAdes on data 2 and data 1: scaffold stats
- 3: SPAdes on data 2 and data 1: contig stats
- 2: Sample\_R2.fastq.gz
- 1: Sample\_R1.fastq.gz



# Tool output

It is possible to preview the output (result), view it in the main window or download the dataset

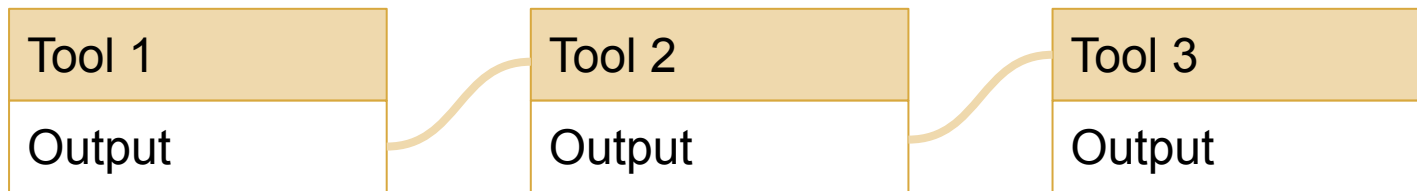
You can also copy the dataset over to another history

The screenshot displays the Galaxy Norway web interface. The top navigation bar includes 'NeLS', 'Galaxy Norway', and various action buttons like 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. A warning banner at the top states: 'This dataset is large and only the first megabyte is shown below. Show all | Save'. The left sidebar contains tool categories: 'Tools' (with a search bar), 'Assembly' (listing 'Showill', 'rnaSPAdes', and 'SPAdes'), 'Create assemblies with Unicycler' (listing 'metaSPAdes'), and 'Graph/Display Data' (listing 'Bandage Info' and 'Bandage Image'). The main content area shows the output of a tool, starting with a file path and followed by a large block of FASTA sequence data. The right sidebar shows the 'History' panel with a search bar and a list of datasets. The second dataset in the history, '6: SPAdes on data 2 and data 1: scaffolds (fasta)', is highlighted with a red box. This entry shows '7,853 sequences' and 'format: fasta, database: ?'. Below this, the command line is displayed: `/usr/local/bin/spades.py -o /data/part0/tmp/jobs/036/36193 /working --disable-gzip-output --careful -t 10 -m 150 -k 21,33,55 --pe1-fr --pe1-1 fastq.gz:/data/part0/008/dataset_8735.dat --pe1-2 fastq.gz:/data/part0/008/dataset_8736.dat`. At the bottom of the history entry, there is a 'Download' button and a preview of the first few lines of the FASTA output, which matches the main content area.



# Galaxy workflows

A workflow in Galaxy is basically a string of tools, where the output from one tool becomes the input for the next



# Galaxy workflows

The “nodules” indicate which output file from one acts as input for the next tool

Each workflow has a name and version

Additional text that describe the workflow and tags can be added

The screenshot displays the Galaxy Norway web interface. At the top, the navigation bar includes 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The main workspace shows a workflow titled 'Exercise II' with four tools connected in a sequence: 'Forward reads (R1)', 'Reverse reads (R1)', 'Trimmomatic', 'Kraken', and 'Convert Kraken'. The 'Trimmomatic' tool has several output options, with 'fastq\_out\_r1\_unpaired (input)' and 'fastq\_out\_r2\_unpaired (input)' selected. The 'Kraken' tool is configured with 'Kraken on input dataset(s): Classification (tabular)'. The 'Convert Kraken' tool is set to 'Choose dataset to convert' and 'out\_file (taxonomy)'. On the left, a 'Tools' sidebar lists various categories like 'Data Managers', 'Get Data', and 'Send Data'. On the right, a metadata panel for the workflow includes fields for 'Name' (Exercise II), 'Version' (Version 1, 6 steps (active)), and 'Annotation' (Taxonomic classification of metagenomes using Kraken). A 'Tags' section shows a 'Metagenomic' tag. A zoom control at the bottom indicates 80% magnification.

# Galaxy workflows

New tools can be added by clicking on the tool in the Tool menu

The tool will appear in the workflow editor

Tool parameter settings can be pre-set or made up to the user to set when running the workflow

The screenshot displays the Galaxy Norway interface for a workflow named "Exercise II". The "Tools" panel on the left lists various tools, with "Krona pie chart from taxonomic profile" highlighted in a red box. The workflow editor shows a sequence of steps: "Forward reads (R1)", "Reverse reads (R1)", "Trimmomatic", "Kraken", and "Convert Kraken". A "Krona pie chart" tool is added to the workflow, highlighted in a red box. The configuration panel for this tool is also highlighted in a red box, showing the following settings:

- Label:** (empty field)
- Add a step label:** (checkbox, unchecked)
- Annotation:** (empty text area)
- Add an annotation or notes to this step:** (checkbox, unchecked)
- What is the type of your input data:** Taxonomy (dropdown menu)
- Choose between Galaxy Taxonomy and generic table format (e.g. from MetaPhlan or mothur):** (checkbox, unchecked)
- Input file:** Data input 'input' (taxonomy)
- Select a taxonomy dataset:** (dropdown menu)
- show ranks from root to:** Class (dropdown menu)

# Galaxy workflows

The output from another tool can be connected as an input for the new tool

Remember to save the modified workflow

The screenshot displays the Galaxy Norway interface for a workflow named "Exercise II". The workflow consists of several steps: "Forward reads (R1)", "Reverse reads (R1)", "Trimmomatic", "Kraken", and "Convert Kraken". The "Convert Kraken" step is connected to a "Krona pie chart" step. A red box highlights the connection between the "Convert Kraken" step and the "Krona pie chart" step. The right sidebar shows the configuration for the "Krona pie chart" tool, including input file and taxonomy options.

**Tools**  
krona

**Inputs**

**Data Managers**

**Metagenomic Analysis**

- Format MetaPhlan2 output for Krona
- Krona pie chart from taxonomic profile
- LCAClassifier Perform taxonomic classification using the Lowest Common Ancestor algorithm
- Convert Kraken data to Galaxy taxonomy representation

**Mothur**

- Taxonomy-to-Krona convert a mothur taxonomy file to Krona input format

**Graph/Display Data**

- Visualize with Krona Visualise any hierarchical data

**Workflows**

**Krona pie chart**  
from taxonomic profile  
(Galaxy Version 2.7.1)

**Label**

Add a step label.

**Annotation**

Add an annotation or notes to this step. Annotations are available when a workflow is viewed.

**What is the type of your input data**

Taxonomy

Choose between Galaxy Taxonomy and generic table format (e.g. from MetaPhlan or mothur)

**Input file**

Data input 'input' (taxonomy)

Select a taxonomy dataset

show ranks from root to

Class

# Galaxy – Running workflows

Select input files

Tools in the workflow will run successively

You can view and download the result files

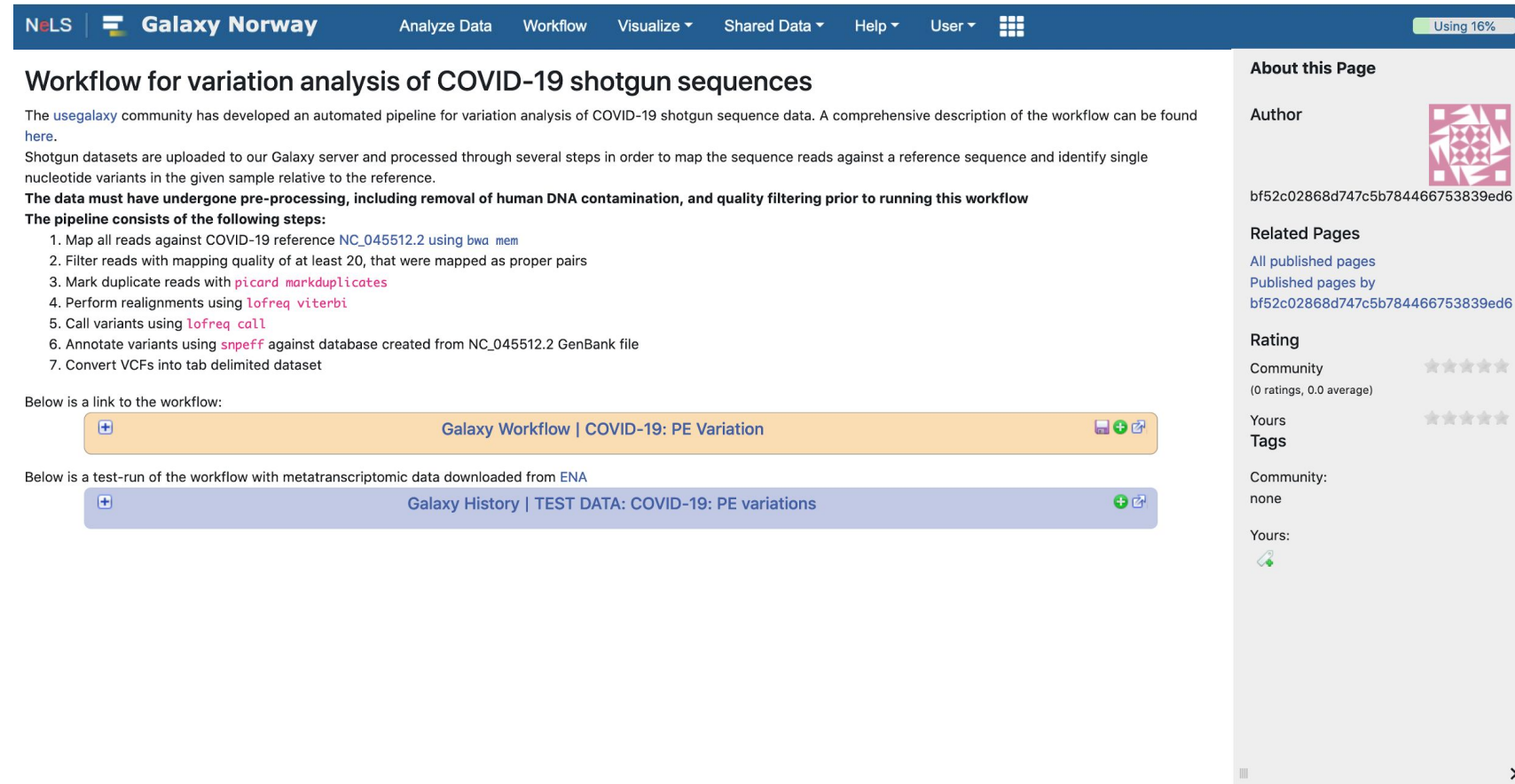
The screenshot displays the Galaxy Norway interface for configuring a workflow named "Taxonomic\_profiling\_Metaphlan2". The interface is divided into several sections:

- Tools:** A sidebar on the left lists various tools under categories like "Assembly", "Create assemblies with Unicycler", and "Graph/Display Data".
- Workflow Configuration:** The main area shows the workflow steps:
  - Step 1: Forward reads (R1)** and **Step 2: Reverse reads (R2)**: Both steps have a dropdown menu set to "1: read\_R1.fastq.gz".
  - Step 3: FastQC (Galaxy Version 0.72+galaxy1)**: This step is selected. Below it, there are sections for "Short read data from your current history" (outputting from step 1), "Contaminant list" (Nothing selected), and "Adapter list" (Nothing selected).
- History:** A sidebar on the right shows a list of datasets from a previous workflow named "test\_run\_16S". The list includes steps like "9: LCClassifier on data", "7: Taxonomic tree", "8: LCClassifier on data", "7: Taxonomic composition", "7: Megablast on data 6", "6: Predicted 16S rRNA reads from data 5", "5: FASTQ to FASTA on data 4", "4: Filter FASTQ on data 3", "3: Concatenate datasets on data 2 and data 1", "2: read\_R2.fastq.gz", and "1: read\_R1.fastq.gz".

# Workflow documentation in Usegalaxy.no

Each NeLS supported workflow is documented with instructions how to use it

Also test data sets available for each workflow



The screenshot displays the Galaxy Norway interface. At the top, the navigation bar includes 'NeLS', 'Galaxy Norway', and menu items for 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. A 'Using 16%' indicator is visible in the top right corner.

### Workflow for variation analysis of COVID-19 shotgun sequences

The usegalaxy community has developed an automated pipeline for variation analysis of COVID-19 shotgun sequence data. A comprehensive description of the workflow can be found [here](#).

Shotgun datasets are uploaded to our Galaxy server and processed through several steps in order to map the sequence reads against a reference sequence and identify single nucleotide variants in the given sample relative to the reference.

**The data must have undergone pre-processing, including removal of human DNA contamination, and quality filtering prior to running this workflow**

**The pipeline consists of the following steps:**

1. Map all reads against COVID-19 reference [NC\\_045512.2](#) using `bwa mem`
2. Filter reads with mapping quality of at least 20, that were mapped as proper pairs
3. Mark duplicate reads with `picard markduplicates`
4. Perform realignments using `lofreq viterbi`
5. Call variants using `lofreq call`
6. Annotate variants using `snpeff` against database created from NC\_045512.2 GenBank file
7. Convert VCFs into tab delimited dataset

Below is a link to the workflow:


[Galaxy Workflow | COVID-19: PE Variation](#)

Below is a test-run of the workflow with metatranscriptomic data downloaded from ENA

[Galaxy History | TEST DATA: COVID-19: PE variations](#)

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**Tags**

Community: none  
Yours: 

# Shared workflows in usegalaxy.no

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

You can import shared data to you user

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

The screenshot displays the Galaxy Norway web interface. The top navigation bar includes 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'User'. The 'Shared Data' menu is open, showing options for 'Data Libraries', 'Histories', 'Workflows', 'Visualizations', and 'Pages'. The 'Workflows' option is highlighted. Below the navigation bar, the 'Published Workflows' section is visible, featuring a search bar and a table of workflows. The table has columns for 'Name', 'Annotation', 'Owner', 'Community Tags', and 'Last Updated'. The workflow 'Pre-process COVID-19 PE single sample' is selected, and its context menu is open, showing 'Run', 'Import', and 'Save as File' options.

Name	Annotation	Owner	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



# Your imported and self made workflows

You can also create new workflows here

For beginners a good tip is to import an existing workflow, and modify it to meet your needs. The workflow will only be changed in your version

The screenshot displays the Galaxy Norway interface. The top navigation bar includes 'Analyze Data', 'Workflow' (highlighted), 'Visualize', 'Shared Data', 'Help', and 'User'. A search bar for workflows is present, along with '+ Create' and 'Import' buttons. The main content area shows a table of workflows:

Name	Tags	Updated	Sharing	Bookmarked
imported: miRNA differential expression (miRBase, hg38)		3 days ago		<input type="checkbox"/>
Taxonomic_profiling_Metaphlan2	metagenomics	2 months ago		<input type="checkbox"/>

A context menu is open over the second workflow, listing actions: Edit, Copy, Download, Rename, Share, View, and Delete. The right sidebar shows a 'History' section with two datasets: '2: Sample\_R2.fastq.gz' and '1: Sample\_R1.fastq.gz'.

# Sharing your workflows in usegalaxy.no

Self made or modified workflows can be shared with other usegalaxy.no users or made accessible via a link

You can also download a workflow and import it in another Galaxy

The screenshot displays the Galaxy Norway interface. The 'Workflow' tab is highlighted in the top navigation bar. A table lists workflows, with the 'Taxonomic\_profiling\_Metaphlan2' workflow selected. A context menu is open over this workflow, with the 'Share' option highlighted. A modal window titled 'Workflow 'Taxonomic\_profiling\_Metaphlan2'' is open, showing sharing options. The 'Share with a user' button is highlighted in red.

**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

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

**Share**

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

**Make Workflow Accessible via Link**  
Generates a web link that you can share with other people so that they can view and import the workflow.

**Make Workflow Accessible and Publish**  
Makes the workflow accessible via link (see above) and publishes the workflow to Galaxy's **Published Workflows** section, where it is publicly listed and searchable.

You have not shared this workflow with any users yet.

**Share with a user**

**Export**

**Download** workflow as a file so that it can be saved or imported into another Galaxy server.