



Workflows in Galaxy

Demo: Importing, creating and modifying workflows in Galaxy

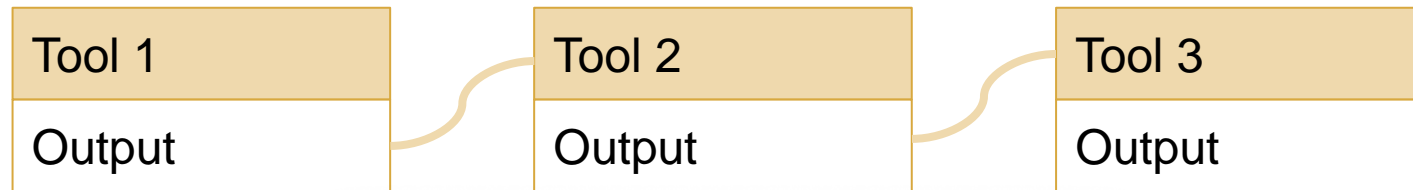


Erik Hjerde

Workflows in Galaxy

Galaxy is a workflow manager with a graphical user interface

Workflows in Galaxy are strings of tools connected in the correct order so that the output from one tool becomes the input for the next tool



```
exercise2 — ehj000@gold: ~/projekter/strain_analysis/metaspades/PIN52-B_S5_L001_R1...
fp3-ntf-m0053:exercise2 service$ /location/of/tool1 -input [FILE] -parameterA [INT] -parameterB [INT] -output [FILE] | /location/of/tool2 -input [FILE] -parameterA [INT] -parameterB [INT] -output [FILE] | /location/of/tool3 -input [FILE] -parameterA [INT] -parameterB [INT] -output [FILE] > result.txt
```

A terminal window showing a Galaxy workflow command. The command is a pipeline of three tools, each with its own input and parameters, connected by pipes. The output of the final tool is redirected to a file named result.txt.

Workflows in Galaxy



Live demo – feel free to join

Finding existing workflows in Galaxy

Modifying workflows in Galaxy

Sharing workflows in Galaxy

Constructing new workflows in Galaxy

Running workflows in Galaxy

The screenshot displays the NeLS Galaxy web interface at galaxy-uit.bioinfo.no. The top navigation bar includes links for Analyze Data, Workflow, Shared Data, Visualization, Admin, Help, and User. A left sidebar lists various tools under the heading 'GENERAL GALAXY TOOLS', including Get Data, Send Data, Collection Operations, Text Manipulation, Filter and Sort, Join, Subtract and Group, Convert Formats, Extract Features, Metagenomics, Statistics, NGS: QC and Manipulation, NGS: Picard, NGS: Mapping and Sequence analysis, and NGS: GATK Tools. The main content area features a 'Welcome to the NeLS Galaxy installation in Tromsø' message, a brief description of Galaxy as a web-based platform for data-intensive life science research, and a 'Quick Start Guide' link. A 'History' panel on the right shows a search for datasets, with results for 'ELIXIR workshop Exercise I' (2 shown, 2.38 KB), including '2: file2.txt' and '1: file1.txt'. A 'Tweets' section by @elixirnorway is also visible, featuring a tweet from Inge Jonassen (@ingejonassen) about an all hands meeting in Oslo.



The remaining slides are repetition of the most important things from the demo for later use when you go home and have forgotten everything you learned😊



Workflows in Galaxy

Create, import or upload a workflow

NeLS galaxy-uit.bioinfo.no

Analyze Data Workflow Shared Data Visualization Admin Help User

Tools

search tools

GENERAL GALAXY TOOLS

- Get Data
- Send Data
- Collection Operations
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Metagenomics
- Statistics
- NGS: QC and Manipulation
- NGS: Picard
- NGS: Mapping and Sequence analysis
- NGS: GATK Tools
- Assembly and Validation
- Transcriptomics
- NGS: SAM-tools
- Genome Diversity

Workflows

- All workflows

Your workflows

Workflow page

search for workflow...

Name	Tags	Owner	# of Steps	Published	Show in tools panel
My first workflow		You	0	No	<input type="checkbox"/>

Details

Edit Workflow Attributes

Name:
My first workflow

Tags:

Apply tags to make it easy to search for and find items with the same tag.

Annotation / Notes:
Describe or add notes to workflow
Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

Context menu

- Edit
- Run
- Share
- Download
- Copy
- Rename
- View
- Delete

Workflows in Galaxy

NeLS galaxy-uit.bioinfo.no

Analyze Data Workflow Shared Data Visualization Admin Help User

Using 48%

Tools Workflow Canvas | My first workflow Details

search tools

GENERAL GALAXY TOOLS

- [Get Data](#)
- [Send Data](#)
- [Collection Operations](#)
- [Text Manipulation](#)
- [Filter and Sort](#)
- [Join, Subtract and Group](#)
- [Convert Formats](#)
- [Extract Features](#)
- [Metagenomics](#)
- [Statistics](#)
- [NGS: QC and Manipulation](#)
- [NGS: Picard](#)
- [NGS: Mapping and Sequence analysis](#)
- [NGS: GATK Tools](#)
- [Assembly and Validation](#)
- [Transcriptomics](#)
- [NGS: SAM-tools](#)
- [Genome Diversity](#)

Workflows

- All workflows

Tools

Canvas navigation

Edit Workflow Attributes

Name:
My first workflow

Tags:

Apply tags to make it easy to search for and find items with the same tag.

Annotation / Notes:
Describe or add notes to workflow
Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

Workflows in Galaxy

NeLS galaxy-uit.bioinfo.no

Analyze Data Workflow Shared Data Visualization Admin Help User

Tools Workflow Canvas | My first workflow

search tools

Inputs

- Input dataset
- Input dataset collection

GENERAL GALAXY TOOLS

- Get Data
- Send Data
- Collection Operations
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Metagenomics
- Statistics
- NGS: QC and Manipulation
- NGS: Picard
- NGS: Mapping and Sequence analysis
- NGS: GATK Tools
- Assembly and Validation
- Transcriptomics
- NGS: SAM-tools
- Genome Diversity
- Data Manager Tools
- Workflows

Select tool

Selected tool

Tool attributes

Input dataset

output

Input dataset

Label

Add a step label.

Annotation

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

Workflows in Galaxy

NeLS galaxy-uit.bioinfo.no

Analyze Data Workflow Shared Data Visualization Admin Help User

Tools Workflow Canvas | My first workflow

search tools

Inputs

GENERAL GALAXY TOOLS

[Get Data](#)

[Send Data](#)

[Collection Operations](#)

[Text Manipulation](#)

[Filter and Sort](#)

[Join, Subtract and Group](#)

[Convert Formats](#)

[Extract Features](#)

[Metagenomics](#)

[Statistics](#)

NGS: QC and Manipulation

- **fastp** – fast all-in-one preprocessing for FASTQ files
- **pe-sync**: Paired-end synchronization check The Paired-end synchronization check program determines if the reads in paired-end fastq files are in the proper order (synchronized).
- **resync**: Paired-end resynchronization Resynchronize a pair of paired-end fastq files
- **FASTQ Groomer** convert between various FASTQ quality formats
- **FLASH** adjust length of short reads
- **seqtk_sample** random subsample of fasta or fastq sequences

Workflow Canvas | My first workflow

Connect tools

Input dataset x

output

fastp x

Input 1

outputpaired_coll

out1

out2

report_html (html)

report_json (json)

fastp – fast all-in-one preprocessing for FASTQ files (Galaxy Version 0.19.5+galaxy1)

Label

Add a step label.

Annotation

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

Single-end or paired reads

Single-end

Input 1

Data input 'in1' (fastq or fastq.gz)
Input FASTQ file #1 (-i)

Adapter Trimming Options

☒ **Disable adapter trimming**

Yes No

Adapter trimming is enabled by default. If this option is specified, adapter trimming is disabled. (-A)

☒ **Adapter sequence for input 1**

The adapter for read1. For SE data, if

Workflows in Galaxy

NeLS galaxy-uit.bioinfo.no

Analyze DataWorkflowShared DataVisualizationAdminHelpUser

Using 48%

Tools

search tools

GENERAL GALAXY TOOLS

[Get Data](#)

[Send Data](#)

[Collection Operations](#)

[Text Manipulation](#)

[Filter and Sort](#)

[Join, Subtract and Group](#)

[Convert Formats](#)

[Extract Features](#)

[Metagenomics](#)

[Statistics](#)

[NGS: QC and Manipulation](#)

[NGS: Picard](#)

[NGS: Mapping and Sequence analysis](#)

[NGS: GATK Tools](#)

[Assembly and Validation](#)

[Transcriptomics](#)

[NGS: SAM-tools](#)

[Genome Diversity](#)

Workflows

All workflows

My first workflow

Your workflows

search for workflow...

+

↑

Name	Tags	Owner	# of Steps	Published	Show in tools panel
<div>My first workflow</div>		You	2	No	<input checked="" type="checkbox"/>

Sharing a workflow in Galaxy

[Go back to Workflows List](#)

Workflow ' My first workflow'

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.

This workflow must be accessible. Please use the option above to "Make Workflow Accessible and Publish" before receiving a URL for importing to another Galaxy.

Create image of workflow in SVG format

Export to the www.myexperiment.org site.

myExperiment username:

username 

myExperiment password:

password 

Export to myExperiment

Import shared history

Histories shared by other users can be copied into your history

NeLS galaxy-uit.bioinfo.no Analyze Data Workflow **Shared Data** Visualization Admin Help User Using 46%

Published Histories

search name, annotation, owner, and tags
[Advanced Search](#)

Data Libraries
Histories
Workflows
Visualizations
Pages

Name	Annotation	Owner	Community Rating	Community Tags	Last Updated↓
WP4 workshop Oct 2019		ehj000	☆☆☆☆☆		~5 seconds ago

Published Histories | [ehj000](#) | WP4 workshop Oct 2019 **Import history**

WP4 workshop Oct 2019
799.49 MB

search datasets


Dataset	Annotation
2: read_R2.fastq.gz	
1: read_R1.fastq.gz	

Accessing the documentation

The documentation in Pages can be accessed by users under the “Pages” tab


NeLS galaxy-uit.bioinfo.no Analyze Data Workflow **Shared Data** Visualization Admin Help User Using 46%

Published Pages



[Advanced Search](#)

Visualization
Data Libraries
Histories
Workflows
Visualizations
Pages

Title	Annotation	Owner	Community Rating	Community Tags	Last Updated↓
Taxonomic profiling PE reads	Metagenomic analysis	ehj000			~12 seconds ago

Accessing the documentation

The description of the workflow including an embedded overview is available

NeLS galaxy-uit.bioinfo.no

Analyze DataWorkflowShared DataVisualizationAdminHelpUser

Using 46%


Published Pages | ehj000 | Taxonomic profiling PE reads

About this Page




Workflow for Taxonomic Classification of Metagenomic shotgun sequences

We have developed an automated pipeline for taxonomic classification of metagenomic shotgun sequences integrated with Galaxy. Shotgun datasets are uploaded to our Galaxy server and processed through several steps in order to create a summary and overview of the taxonomy of a given sample. The pipeline consists of the following steps:


1. Upload FASTQ file(s) to Galaxy: Use "Get Data" on the menu, and upload your files
2. Reduce the input files by random subsampling reads
3. Quality filtering: Filter FASTQ is used to discard short sequences and sequences with low quality scores.
4. Concatenate forward and reverse reads
5. Assigning taxonomy to sequences using MetPhlAn2
6. Convert to Krona input
7. Visualize the taxonomic composition: Krona is used to generate interactive pie-charts for visualizing the structure of the taxonomic hierarchy in the sample.



Galaxy Workflow | WP4_demo
Taxonomic profiling of PE reads





Author
ehj000



Related Pages
[All published pages](#)
[Published pages by ehj000](#)

Rating
Community
(0 ratings, 0.0 average)
Yours

Tags
Community: none
Yours:

