



Galaxy

PROJECT

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What is Galaxy?

- A web-based research environment (just like a *web site*)
- Users
 - log in
 - select a tool/program to run
 - upload their input data
 - click on execute button

and Galaxy

- ★ executes the computations on the cluster
- ★ fetches the output data

... no previous knowledge in command-line and terminals is required

Galaxy is an open source code and has many instances in the world
(1 mln jobs / 11k users a month / 9k tools)

Galaxy USA:
<https://galaxyproject.org>

Galaxy Europe:
<https://usegalaxy.eu>

Galaxy Australia:
<https://usegalaxy.org.au/>



Communities sharing one coherent framework

- rna.usegalaxy.eu
- clipseq.usegalaxy.eu
- metagenomics.usegalaxy.eu
- hicexplorer.usegalaxy.eu
- cheminformatics.usegalaxy.eu
- proteomics.usegalaxy.eu
- imaging.usegalaxy.eu
- metabolomics.usegalaxy.eu
- ecology.usegalaxy.eu
- nanopore.usegalaxy.eu
- singlecellomics.usegalaxy.eu
- humancellatlas.usegalaxy.eu
- virology.usegalaxy.eu
- climate.usegalaxy.eu
- streetscience.usegalaxy.eu
- ml.usegalaxy.eu



Let's start : <https://galaxy.educloud.no>

**GALAXY-FOX-portal**



Login with your username and password

LOGIN

Apply for access

APPLY

About

Fox is a powerful HPC-cluster available to all users of the Educloud Research Infrastructure.

Educloud Research is a project-oriented self-service Platform as a Service that gives easy and fast access to a work environment for research projects, storage that is available from anywhere and low threshold HPC resources

More about Galaxy Framework 

Getting started

1. Apply for access to Educloud:
 - If you have a Norwegian electronic ID, click the Apply icon, go to the section Applications and then to Project membership (select project **ec73**). Your application will be handled shortly.
 - If you don't have a Norwegian electronic ID, please write to hpc-drift@usit.uio.no.
2. Galaxy on Fox requires a One-Time Password (OTP) generated for every login. See [explanation here](#) how to enable your smartphone to generate an OTP.

Once your access to project ec73 has been approved (step 1) and your smartphone authenticator has been set up (step 2), you can log into Galaxy FOX.

If you have an educloud account : **LOGIN** with your Educloud credentials



Log in

Educloud username

Example "ec-navnesen"

Password

[Reset password](#)

One time passcode (OTP)

Collected from your authentication app

[Reset OTP](#)

Log in

Contact information:

E-mail: ec-drift@uio.no

Phone: +47 22 84 00 04

Help:

[Support and user guide](#)

[Terms and conditions](#)

If you do not have an educloud account : **Apply** for project **ec73**

User privileges

Grant and revoke privileges for users, such as the right to export and publish files from a project, and to manage consent.



Group membership

Manage the members of the

Applications

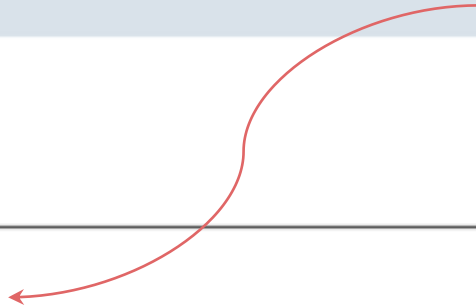
Project membership

Apply for membership in a project using a Norwegian electronic ID.



New project

Submit a new Educloud project



Galaxy is intuitive and easy: everything is on one screen

The screenshot displays the Galaxy web interface, which is designed to be intuitive and easy to use, with everything accessible on one screen. The interface is divided into three main sections:

- Activity Bar (Left):** Contains a sidebar with various tool categories and a search bar. The categories include: Upload, Tools, Workflows, Visualization, Histories, and Pages. The Tools section is expanded, showing sub-categories like GENERAL TEXT TOOLS, GENOMIC FILE FORMATS, FASTA/FASTQ, FASTQ Quality Control, SAM/BAM, BED, VCF/BCF, Nanopore, Convert Formats, Lift-Over, COMMON GENOMICS TOOLS, and GENOMICS ANALYSIS. The GENOMICS ANALYSIS section is further expanded, showing tools like Operate on Genomic Intervals, Fetch Sequences/Alignments, Assembly, Annotation, Mapping, Variant Calling, ChIP-seq, and RNA-seq.
- Center Panel:** The main workspace for data analysis. It features a large banner for GBCC2025 abstract submission and registration, which is now open. The banner includes a logo of a lighthouse and a DNA double helix, and text stating: "Join us for the first ever combined Galaxy BioConductor Community Conference (GBCC2025)". Abstract deadlines are listed: Talk: April 1, 2025 and Poster: May 1, 2025. Below the banner, there is a link to "See GBCC2025.org for more information and to submit your abstract". At the bottom of the Center Panel, there is a "Learn More" button and a link to "Want to learn the best practices for genome assembly using Galaxy? Visit the Galaxy VGP page at <https://galaxyproject.org/projects/vgp/>".
- History (Right):** A panel showing the user's history of datasets and workflows. It includes a search bar for datasets and a section for "Unnamed history". A message indicates that the history is empty and provides a link to "You can load datasets from the Galaxy Data Portal or get data from other sources like SRA".

At the bottom of the interface, there are logos for PennState, Johns Hopkins University, TACC, ACCESS, and Jetstream2. Text at the bottom states: "The Galaxy Team is a part of the Center for..." and "This instance of Galaxy is utilizing infrastructure generously provided by the Texas Advanced..."

Galaxy on FOX (UiO) outlook

The screenshot displays the Galaxy-FOX-portal interface. The top navigation bar includes links for Workflow, Visualize, Data, Admin, Help, and User, along with a 'Using 16.9 MB' indicator. The left sidebar contains a 'Tools' section with a search bar and a list of tools categorized by FASTA/FASTQ, Datamash, and other functions. The main content area shows the 'Barcode Splitter' tool configuration page. The tool parameters section includes a 'Barcodes to use' field set to '16: Line/Word/Character count on data 15', a 'Please provide a value for this option. Library to split' message, and a 'No compatible datasets available' warning. The 'Barcodes found at' section has a 'Start of sequence (5' end)' field. The 'Number of allowed mismatches' and 'Number of allowed barcodes nucleotide deletions' fields are both set to '0'. The 'Job Resource Parameters' section includes a 'Specify job resource parameters' field. The 'Project' section has a 'Select the project you want to run the job' dropdown. The 'Additional Options' section includes an 'Email notification' toggle set to 'No' and a 'Run Tool' button. The 'What it does' section states: 'This tool splits a Solexa library (FASTQ file) or a regular FASTA file into several files, using barcodes as the split criteria.' The right sidebar shows a 'History' section with a search bar and a list of datasets, including 'OBiWoW-2025' and '16: Line/Word/Character count on data 15'.

Galaxy-FOX-portal

Workflow Visualize Data Admin Help User Using 16.9 MB

Tools

search tools

Datamash

FASTA/FASTQ

Barcode Splitter

Clip adapter sequences

Collapse sequences

Combine FASTA and QUAL into FASTQ

Compute sequence length

Concatenate FASTA alignment by species

Cutadapt Remove adapter sequences from FASTQ/FASTA

fastsplit Split a FASTA file

FASTA Merge Files and Filter Unique Sequences Concatenate FASTA database files together

Fastx regular expression finder Search in fastx for regexp match

Fastx Statistics display summary statistics for a FASTA file

FASTA Width formatter

fastp fast all-in-one preprocessing for FASTQ files

FASTQ de-interlacer on paired end reads

FASTQ Groomer convert between various FASTQ quality formats

FASTQ Interlacer on paired end reads

FASTQ joiner on paired end reads

FASTQ Masker by quality score

FASTQ Quality Trimmer by sliding window

FASTQ splitter on joined paired end reads

FASTQ Trimmer by column

fastqjoin - Joins two paired-end reads on the overlapping ends

Filter by quality

Filter FASTA on the headers and/or

Barcode Splitter (Galaxy Version 1.6.1-galaxy2)

Tool Parameters

Barcodes to use

16: Line/Word/Character count on data 15

accepted formats

Please provide a value for this option.
Library to split **required**

No compatible datasets available

Barcodes found at

Start of sequence (5' end)

Number of allowed mismatches

0

(--mismatches)

Number of allowed barcodes nucleotide deletions

0

(--portals)

Job Resource Parameters

Specify job resource parameters

Project

Select the project you want to run the job

Project to assign resource allocation to.

Additional Options

Email notification

No

Send an email notification when the job completes.

Run Tool

Help

What it does

This tool splits a Solexa library (FASTQ file) or a regular FASTA file into several files, using barcodes as the split criteria.

History

search datasets

OBiWoW-2025

1.18 MB

16: Line/Word/Character count on data 15

15: Convert on data 8

16: Line/Word/Character count on data 9

9: Convert on data 8

8: two-column-table.txt

Galaxy use case

Bioinformatics analysis with Galaxy

Bioinformatics challenges

**Bioinformaticians
need to**



Manage storage
requirements &
compute power



Automate & scale-up
complex analysis



Maintain scientific
reproducibility

Bioinformaticians have multiple options

- Galaxy
- SLURM & HPC
- Workflow managers

Galaxy for bioinformatics

Target audience

Biologists & Clinicians

- Intuitive Web GUI
- Zero coding required
- Point & click
- Focus strictly on data

Reproducibility

Automatic

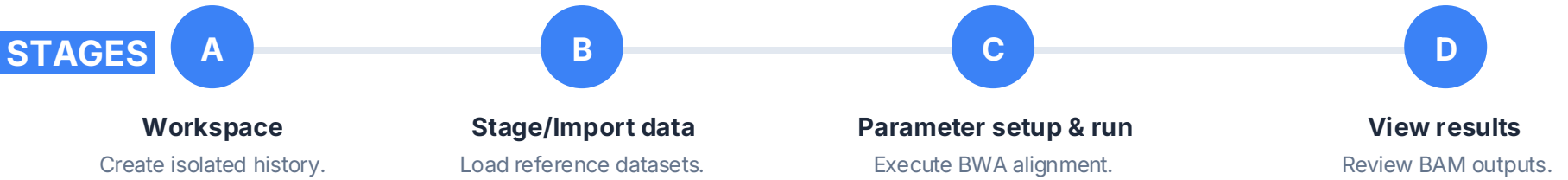
- Parameter recorded
- Extract/build workflows

Infrastructure

Admin-Managed

- Zero user setup
- Log in and analyze on provided clusters

Simple analysis using Galaxy



Simple analysis using Galaxy

STAGES

A

Workspace

Create isolated history.

B

Stage/Import data

Load reference datasets.

C

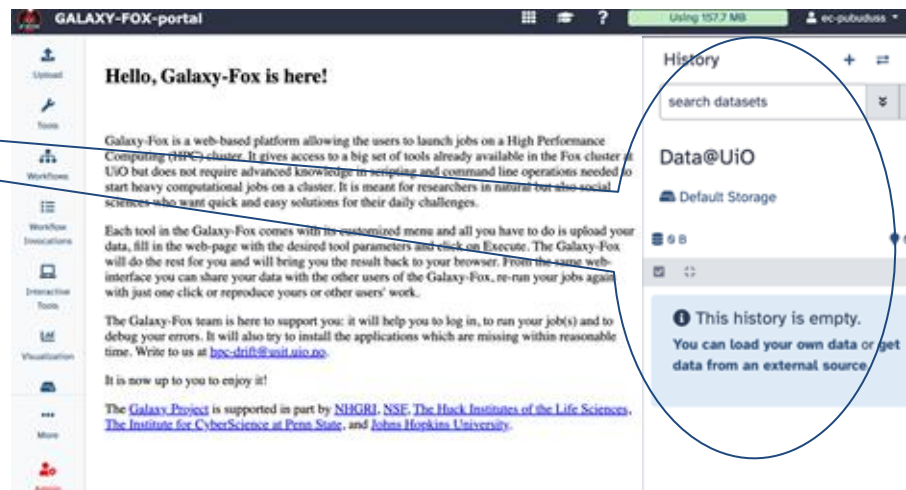
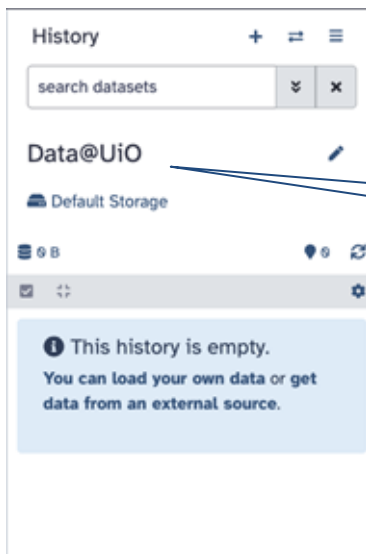
Parameter setup & run

Execute BWA alignment.

D

View results

Review BAM outputs.



Simple analysis using Galaxy

STAGES

A

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Create isolated history.

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Load reference datasets.

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Parameter setup & run

Execute BWA alignment.

D

View results

Review BAM outputs.

History

search datasets

Data@UiO

Default Storage

7.69 MB

2: NIST7035_TAAGGCGA_L001_R2_50k_R_trimmed.fastq.gz

1: NIST7035_TAAGGCGA_L001_R1_50k_R_trimmed.fastq.gz

GALAXY-FOX-portal

Using 187.7 MB

ec-pubsub

Hello, Galaxy-Fox is here!

Galaxy-Fox is a web-based platform allowing the users to launch jobs on a High Performance Computing (HPC) cluster. It gives access to a big set of tools already available in the Fox cluster at UiO but does not require advanced knowledge in scripting and command line operations needed to start heavy computational jobs on a cluster. It is meant for researchers in natural but also social sciences who want quick and easy solutions for their daily challenges.

Each tool in the Galaxy-Fox comes with its customized menu and all you have to do is upload your data, fill in the web-page with the desired tool parameters and click on Execute. The Galaxy-Fox will do the rest for you and will bring you the result back to your browser. From the same web-interface you can share your data with the other users of the Galaxy-Fox, re-run your jobs again with just one click or reproduce yours or other users' work.

The Galaxy-Fox team is here to support you: it will help you to log in, to run your job(s) and to debug your errors. It will also try to install the applications which are missing within reasonable time. Write to us at hsc@scifi@uit.no.

It is now up to you to enjoy it!

The Galaxy Project is supported in part by [NHGRI](#), [NSE](#), [The Hack Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Johns Hopkins University](#).

History

search datasets

Data@UiO

Default Storage

7.69 MB

2: NIST7035_TAAGGCGA_L001_R2_50k_R_trimmed.fastq.gz

1: NIST7035_TAAGGCGA_L001_R1_50k_R_trimmed.fastq.gz

Simple analysis using Galaxy

STAGES

A

Workspace

Create isolated history.

B

Stage/Import data

Load reference datasets.

C

Parameter setup & run

Execute BWA alignment.

D

View results

Review BAM outputs.

The screenshot shows the Galaxy-FOX-portal interface. The 'Map with BWA' tool is selected, and the 'Tool Parameters' section is visible. The 'Will you select a reference genome from your history or use a built-in index?' dropdown is set to 'Use a built-in genome index'. The 'Using reference genome' dropdown is set to 'Human (Homo sapiens) (38): hg38'. The 'Select input type' dropdown is set to 'Paired fastq'. The 'Select first set of reads' dropdown is set to '1: NIST7935_TAAGGCGA_L961R1_56k_R1_trimmed.fastq.gz'. The 'Select second set of reads' dropdown is set to '2: NIST7935_TAAGGCGA_L961R2_56k_R1_trimmed.fastq.gz'. The 'accepted formats' section is visible at the bottom.

The screenshot shows the Galaxy-FOX-portal interface. The 'Map with BWA' tool is selected, and the 'Tool Parameters' section is visible. The 'Will you select a reference genome from your history or use a built-in index?' dropdown is set to 'Use a built-in genome index'. The 'Using reference genome' dropdown is set to 'Human (Homo sapiens) (38): hg38'. The 'Select input type' dropdown is set to 'Paired fastq'. The 'Select first set of reads' dropdown is set to '1: NIST7935_TAAGGCGA_L961R1_56k_R1_trimmed.fastq.gz'. The 'Select second set of reads' dropdown is set to '2: NIST7935_TAAGGCGA_L961R2_56k_R1_trimmed.fastq.gz'. The 'accepted formats' section is visible at the bottom.

Simple analysis using Galaxy

STAGES

A

Workspace

Create isolated history.

B

Stage/Import data

Load reference datasets.

C

Parameter setup & run

Execute BWA alignment.

D

View results

Review BAM outputs.

GALAXY-FOX-portal

Using 157.7 MB

ec-pubtools

8: Map with BWA on dataset 5 and 6 (mapped reads in BAM format)

9.1 MB

format bam, database hg38, size 9.1 MB

Preview Raw Visualize Details Edit

You can display your dataset with the following links:

1. display at UCSC (main)
2. display with IGV (local)
3. display in IGB (View)

or select a visualization from below.

search visualizations

IGV Interactive Genomics Viewer

Explore genomic data

Trackster

Fast, interactive visualization for large, NGS/HTS datasets using only a web browser.

History

search datasets

Data@UIO

Galaxy-FOX server storage

24.9 MB

5: Map with BWA on dataset 5 and 6 (mapped reads in BAM format)

9.1 MB

format bam, database hg38

[bwaaln] 17bp reads: max_diff = 2

[bwaaln] 38bp reads: max_diff = 3

[bwaaln] 64bp reads: max_diff = 4

Binary bam alignments file

6: NIST7035_TAAGGCGA_L001_R1_50k_R_trimmed.fastq.gz

5: NIST7035_TAAGGCGA_L001_R2_50k_R_trimmed.fastq.gz

8: Map with BWA on data 6 (mapped reads in BAM format)

5.7 MB

format bam, database hg19

[bwaaln] 17bp reads: max_diff = 2

[bwaaln] 38bp reads: max_diff = 3

[bwaaln] 64bp reads: max_diff = 4

Binary bam alignments file

6: NIST7035_TAAGGCGA_L001_R1_50k_R_trimmed.fastq.gz

5: NIST7035_TAAGGCGA_L001_R2_50k_R_trimmed.fastq.gz

When & Who

Empowering research?

**Do not have direct access to HPC?
or
Biologists & Clinicians?**



Galaxy

Workflows - a sequence of tasks

The screenshot displays the GALAXY-FOX-portal interface. At the top, a dark header bar contains the portal name, navigation icons, a memory usage indicator (Using 879.5 MB), and a user profile (ec-torfin). A left sidebar lists navigation options: Upload, Tools, Workflows, Workflow Invocations, Interactive Tools, Visualization, Histories, History Multiview, More, and Admin. The main content area features a 'Hello, Galaxy-Fox is here!' message, followed by a paragraph about the platform's purpose, a paragraph about tool customization, a support statement, and a list of supporting institutions. A right sidebar shows a 'History' panel with a search bar, a list of datasets (including 'Default Storage'), and a message stating 'This history is empty. You can load your own data or get data from an external source.'

GALAXY-FOX-portal

Using 879.5 MB ec-torfin

Hello, Galaxy-Fox is here!

Galaxy-Fox is a web-based platform allowing the users to launch jobs on a High Performance Computing (HPC) cluster. It gives access to a big set of tools already available in the Fox cluster at UiO but does not require advanced knowledge in scripting and command line operations needed to start heavy computational jobs on a cluster. It is meant for researchers in natural but also social sciences who want quick and easy solutions for their daily challenges.

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It is now up to you to enjoy it!

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History

search datasets

Unnamed history

Default Storage

9 B

This history is empty. You can load your own data or get data from an external source.

<https://workflowhub.eu/>

GALAXY-FOX-portal Using 679.5 MB ec-torfin

Attributes

Name
Paired end variant calling in haploid sys

Version
1 Sep 23rd 2026, 16 steps

Short Description
Workflow for variant analysis against a reference genome in GenBank format

This short description will be visible when this workflow is viewed and should be limited to a sentence or two.

License
MIT License

Creator
Anton Nekrutenko
Add a new creator - either a person or an organization.

Digital Object Identifier (DOI)
Add a new DOI

Tags
generic WuPath Haploid

Add Tags

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

Readme
[Show Readme](#)

A detailed description of what the workflow does. It is best to include descriptions of what kinds of data are required. Researchers looking for the workflow will see this text. Markdown is enabled.

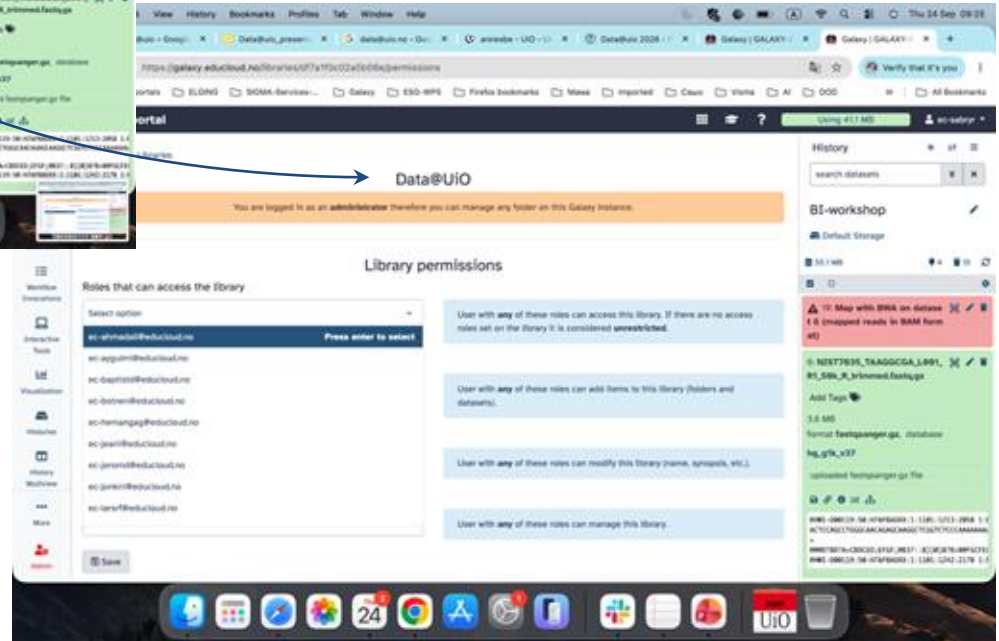
Help

A detailed description of how to use the workflow and debug problems with it.

Paired end variant calling in haploid system (imported from URL)

```
graph LR; A[Map with BWA] --> B[SAM/BAM/CRAM data set]; B --> C[Filter by readnames]; C --> D[SAMtools view]; D --> E[SAMtools stats]; E --> F[MarkDuplicates]; F --> G[MultiQC]; G --> H[Realign reads]; H --> I[Call variants]; I --> J[Text reformating];
```

The workflow diagram illustrates the process of paired end variant calling in a haploid system. It begins with 'Map with BWA', which leads to 'SAM/BAM/CRAM data set'. This step then flows into 'Filter by readnames', which leads to 'SAMtools view'. From 'SAMtools view', the workflow branches into 'SAMtools stats' and 'MarkDuplicates'. 'SAMtools stats' leads to 'MultiQC', which then leads to 'Realign reads'. 'MarkDuplicates' leads to 'Call variants'. 'Realign reads' also leads to 'Call variants'. Finally, 'Call variants' leads to 'Text reformating'. The workflow is titled 'Paired end variant calling in haploid system (imported from URL)'.



Visit Galaxy Training pages

Just click here
in the top menu:



 Galaxy Training!

Contributors Learning Pathways Help Settings Search Tutorials

Welcome to Galaxy Training!

Collection of tutorials developed and maintained by the worldwide Galaxy community

Galaxy for Scientists

We have separated the tutorials into several categories based on field and technology. We are exploring other ways to organise the tutorials going forward!

Start Here

Topic	Tutorials
Introduction to Galaxy Analyses	14
Using Galaxy and Managing your Data	27

Not sure where to start?

Try the NGS Basics Learning Path!

[Start Learning](#)

Scientific Fields

Topic	Tutorials
Climate	14

Quickstart

Learning Pathways



Galaxy for SysAdmins



Galaxy for Developers



Galaxy for Teachers



Upcoming Events

Check out upcoming events around the Galaxy!

December 3, 2025
Introduction to Galaxy, the Open-Source Platform for FAIR Data Analysis (in German)

<https://training.galaxyproject.org/training-material/>

Time for questions

Contact and user support

hpc-drift@usit.uio.no