

# Using Galaxy for Bioinformatics

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# Galaxy Overview

## Welcome to Galaxy

Galaxy is web-based platform for reproducible computational analysis. Research in Galaxy is supported by 3 pillars: data, tools, and workflows. For an introduction to each, visit the below pages, or begin your analysis by setting a tool from the toolbar to the left.



How to get datasets into Galaxy,  
and modify them once they're  
imported.

[Data in Galaxy](#)



Analysis in Galaxy using  
computational tools.

[Tools in Galaxy](#)



Running full analyses in Galaxy  
with workflows.

[Workflows in Galaxy](#)

# Workflows in Galaxy

## Workflows in Galaxy

Workflows are Galaxy's chief mechanism for reproducibility. They allow a user to exactly recreate entire analyses they have performed previously, or simply assemble a pipeline from the ground up. Further, these workflows can be edited to tailor individual tool's parameters in the workflow to new data.



Generate Reproducible  
Workflows from Your Analysis

Extract Workflows from  
Analyses



Edit Workflows for New Data or  
Analyses

Modify Workflows with the  
Workflow Editor



Obtaining previously-run  
analyses from yourself or others,  
and recreating existing analyses.

Importing and Running  
Workflows

# Galaxy Tutorials

- Galaxy Training: <https://training.galaxyproject.org/>
- Select tutorials:
  - Galaxy 101 for everyone, <https://training.galaxyproject.org/training-material/topics/introduction/tutorials/galaxy-intro-101-everyone/tutorial.html>
  - Identification of variants in cancer, <https://usegalaxy.fr/training-material/topics/variant-analysis/tutorials/somatic-variants/tutorial.html>
  - Removal of human reads from SARS-Cov-2 sequencing data, <https://usegalaxy.fr/training-material/topics/sequence-analysis/tutorials/human-reads-removal/tutorial.html>

# Example analysis

- What chromosomes in humans have the most genes?