



# Introduction to Galaxy

# Practical work



# Connecting to the Galaxy instance + TlaaS

<https://usegalaxy.fr/join-training/bilille-galaxy-2025>

The screenshot shows the 'Galaxy France' instance of the Galaxy platform. The left sidebar contains a navigation menu with sections like 'Tools', 'Get Data', 'Send Data', 'Collection Operations', 'GENERAL TEXT TOOLS', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'GENOMIC FILE MANIPULATION', 'Convert Formats', 'FASTA/FASTQ', 'FASTQ Quality Control', 'SAM/BAM', 'BED', 'VCF/BCF', 'Nanopore', 'COMMON GENOMICS TOOLS', 'Operate on Genomic Intervals', 'Fetch Alignments/Sequences', 'GENOMICS ANALYSIS', 'Annotation', 'Assembly', 'Mapping', 'Variant Calling', and 'RNA-Seq'. The main content area features a 'Welcome to usegalaxy.fr' banner with a message about accepting the 'Term Of Use'. Below this, there's a section titled 'Domain specific subdomains:' with links to 'Workflow4Metabolomics', 'Covid19', 'Metabarcoding', 'ProteoRE', and 'Ask the GalaxyCat'. The bottom of the page is 'Hosted by:' logos for 'IFB', 'elixir FRANCE', and 'TlaaS'. The right sidebar shows a 'History' panel with an 'Unnamed history' entry.

# Practical work

- Basic features

<https://training.galaxyproject.org/training-material/topics/introduction/tutorials/galaxy-intro-101-everyone/tutorial.html>

# Practical work

- To go further (if you have time)

- data manipulation

<https://training.galaxyproject.org/training-material/topics/introduction/tutorials/data-manipulation-olympics/tutorial.html>

- create, edit and import Galaxy workflows

<https://training.galaxyproject.org/training-material/topics/galaxy-interface/tutorials/workflow-editor/tutorial.html>

- workflow parameters

<https://training.galaxyproject.org/training-material/topics/galaxy-interface/tutorials/workflow-parameters/tutorial.html>

- visualisation with JBrowse

<https://training.galaxyproject.org/training-material/topics/visualisation/tutorials/jbrowse/tutorial.html>