Hands-on: Galaxy Platform

Galaxy: Web-based NGS Analysis

- User-friendly interface - no command line required

- Pre-installed tools and workflows

- Reproducible analysis with workflow sharing

- Public server: usegalaxy.org

Galaxy Workflow Example

Step 1: Upload Data
Upload FASTQ files from your computer or URL

Step 2: Quality Control
Run FastQC → Review reports → Trim if needed

Step 3: Alignment
Map with BWA-MEM → Select reference genome

Step 4: Variant Calling

FreeBayes or GATK → Generate VCF

Step 5: Annotation

SnpEff → Download annotated results

Access Galaxy training materials at training.galaxyproject.org