FastQC in Galaxy: Quality Control Made Easy

FastQC is fully integrated into the Galaxy platform, making it simple to assess the quality of your sequencing data without needing command-line skills. Here's how it works:

How to Use FastQC in Galaxy

Upload Your FASTQ Files: These contain your raw sequencing reads.

Run FastQC Tool:

Search for “FastQC” in the Galaxy tool panel.

Select your input file(s) and run the tool.

Review the Report:

Galaxy generates an HTML report with visual summaries.

Key metrics include base quality scores, GC content, adapter contamination, and overrepresented sequences.

What You’ll Learn from the Report

Per Base Sequence Quality: Are your reads high quality across their length?

Sequence Duplication Levels: Is there redundancy in your data?

Adapter Content: Do you need to trim adapters?

Overrepresented Sequences: Could indicate contamination or technical bias.

Next Steps

If issues are found, you can use tools like Cutadapt for trimming and MultiQC to summarize multiple FastQC reports.

Galaxy also supports workflows that automate these steps for batch processing.