Galaxy Workflow ' quality-control-pe-dataset-collection'

Step **Annotation**

Step 1: Input dataset collection

input
select at runtime

Step 2: FASTQ Groomer

File to groom
Output dataset 'output' from step 1

Input FASTQ quality scores type
Sanger & Illumina 1.8+

Advanced Options
Hide Advanced Options

Step 3: FastQC

Short read data from your current history
Output dataset 'output_file' from step 2

Contaminant list
select at runtime

Submodule and Limit specifing file
select at runtime

Step 4: Trimmomatic

Single-end or paired-end reads?
Paired-end (as collection)

Select FASTQ dataset collection with R1/R2 pair
Output dataset 'output_file' from step 2

Perform initial ILLUMINACLIP step?
False

Trimmomatic Operations

> **Trimmomatic Operation 1**
>
> **Select Trimmomatic operation to perform**
> Sliding window trimming (SLIDINGWINDOW)
>
> **Number of bases to average across**
> 4
>
> **Average quality required**
> 20

Step 5: FastQC

Short read data from your current history
Output dataset 'fastq_out_paired' from step 4

Contaminant list
select at runtime

Submodule and Limit specifing file
select at runtime