Running workflow "quality-control-paired-dataset-collections"

Step 1: Input dataset collection

reads in paired dataset collection

type to filter

Step 2: FASTQ Groomer(version 1.0.4)

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(version 0.65)

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

Contaminant list
Selection is Optional

Submodule and Limit specifing file
Selection is Optional

Step 4: Trimmomatic(version 0.32.3)

Paired end data?
True

Input Type
Dataset collection pair

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

Perform initial ILLUMINACLIP step?
Not available.

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(version 0.65)

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

Contaminant list

Selection is Optional

Submodule and Limit specifing file

Selection is Optional

Send results to a new history

tools used in this workflow:

"tool_id": null,
"tool_id": "toolshed.g2.bx.psu.edu/repos/devteam/fastq_groomer/fastq_groomer/1.0.4",
"tool_id": "toolshed.g2.bx.psu.edu/repos/devteam/fastqc/fastqc/0.65",
"tool_id": "toolshed.g2.bx.psu.edu/repos/pjbriggs/trimmomatic/trimmomatic/0.32.3",
"tool_id": "toolshed.g2.bx.psu.edu/repos/devteam/fastqc/fastqc/0.65",