Galaxy Workflow ' trinity-transcriptome-assembly-pe-dataset-collection'

Step **Annotation**

Step 1: Input dataset collection

input
select at runtime

Step 2: Input dataset collection

input
select at runtime

Step 3: 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 4: FASTQ Groomer

File to groom
Output dataset 'output' from step 2

Input FASTQ quality scores type
Sanger & Illumina 1.8+

Advanced Options
Hide Advanced Options

Step 5: Trinity

Paired or Single-end data?
Paired

Left/Forward strand reads
Output dataset 'output_file' from step 3

Right/Reverse strand reads
Output dataset 'output_file' from step 4

Strand specific data
False

Jaccard Clip options
False

Run in silico normalization of reads
True

Additional Options:

> **Minimum Contig Length**
> 200

Use the genome guided mode?
No

Error-corrected or circular consensus (CCS) pac bio reads
select at runtime

Minimum count for K-mers to be assembled
1