Galaxy Workflow ' hisat2-alignment-pe-dataset-collection'

Step **Annotation**

Step 1: Input dataset collection

input
select at runtime

Step 2: Input dataset

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: HISAT2

Input data format
FASTQ

Single end or paired reads?
Collection of paired reads

Paired reads
Output dataset 'output_file' from step 3

Paired-end options
Use default values

Write unaligned reads (in fastq format) to separate file(s)
False

Write aligned reads (in fastq format) to separate file(s)
False

Source for the reference genome to align against
Use a genome from history

Select the reference genome
Output dataset 'output' from step 2

Primary alignments

Not available.

Maximum number of seeds that will be extended
Not available.

Report secondary alignments
False

Alignment options
Use default values

Input options
Use default values

Scoring options
Use default values

Spliced alignment parameters
Use default values

Paired alignment parameters
Use default values

Step 5: Flagstat

BAM File to report statistics of
Output dataset 'output_alignments' from step 4