

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

Step	Annotation
------	------------

Step 1: Input dataset collection

Input Dataset Collection

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?

Individual unpaired reads

Reads

Output dataset 'output_file' from step 3

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