Galaxy Workflow ' bowtie2-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: Bowtie2

Is this single or paired library
Single-end

FASTQ file
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

Will you select a reference genome from your history or use a built-in index?
Use a genome from the history and build index

Select reference genome
Output dataset 'output' from step 2

Set read groups information?
Do not set

Select analysis mode
1: Default setting only

Do you want to use presets?
No, just use defaults

Save the bowtie2 mapping statistics to the history
False

Step 5: Flagstat

BAM File to report statistics of

Output dataset 'output' from step 4