

Running workflow "hisat2-alignment-paired-dataset-collections"

Step 1: Input dataset collection

reads in paired dataset collection

Step 2: Input dataset

reference genome

Step 3: HISAT2(version 2.0.5.1)

Input data format

FASTQ

Single end or paired reads?

Collection of paired reads

Paired reads

Output dataset 'output' from step 1

Paired-end options

Use default values

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

Not available.

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

Not available.

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

Not available.

Alignment options

Specify alignment parameters

Function type

Constant

Constant term (y)

Not available.

Coefficient (z)

Not available.

Ignore quality values

Not available.

Skip forward strand of reference

Not available.

Skip reverse strand of reference

Not available.

Input options

Specify input parameters

Skip the first N reads or pairs in the input

Not available.

Stop after aligning N reads

Not available.

Trim 5' end

Not available.

Trim 3' end

Not available.

Scoring options

Specify scoring parameters

Function type

Constant

Constant term (y)

Not available.

Coefficient (z)

Not available.

Set match bonus

2

Maximum mismatch penalty

6

Minimum mismatch penalty

2

Disallow soft-clipping

Not available.

Ambiguous read penalty

1

Maximum soft-clipping penalty

2

Minimum soft-clipping penalty

1

Read gap open penalty

5

Read gap extend penalty

3

Reference gap open penalty

5

Reference gap extend penalty

3

Spliced alignment parameters

Specify spliced alignment parameters

Penalty for canonical splice sites

Not available.

Penalty for non-canonical splice sites

3

Penalty for long introns with canonical splice sites

Constant

Constant term (y)

Not available.

Coefficient (z)

Not available.

Penalty for long introns with noncanonical splice sites

Natural logarithm [$f(x) = y + z * \log(x)$]

Constant term (y)

-8

Coefficient (z)

1

Minimum intron length

20

Maximum intron length

500000

Specify strand-specific information

FR Unstranded

Disable spliced alignment

True

Minimum fragment length for valid paired-end alignments

Not available.

Maximum fragment length for valid paired-end alignments

500

GTF file with known splice sites

Selection is Optional 

Transcriptome assembly reporting

Use default reporting.

Paired alignment parameters

Specify paired alignment parameters

Minimum fragment length

Not available.

Maximum fragment length

500

Disable finding alignments for individual mates

Not available.

Disable looking for discordant alignments

Not available.

Mates not dovetail

Not available.

Mates cannot contain others

Not available.

Mates cannot overlap

Not available.

☐ Send results to a new history

tools used in this workflow:

"tool_id": null,

"tool_id": null,

"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/hisat2/hisat2/2.0.5.1",