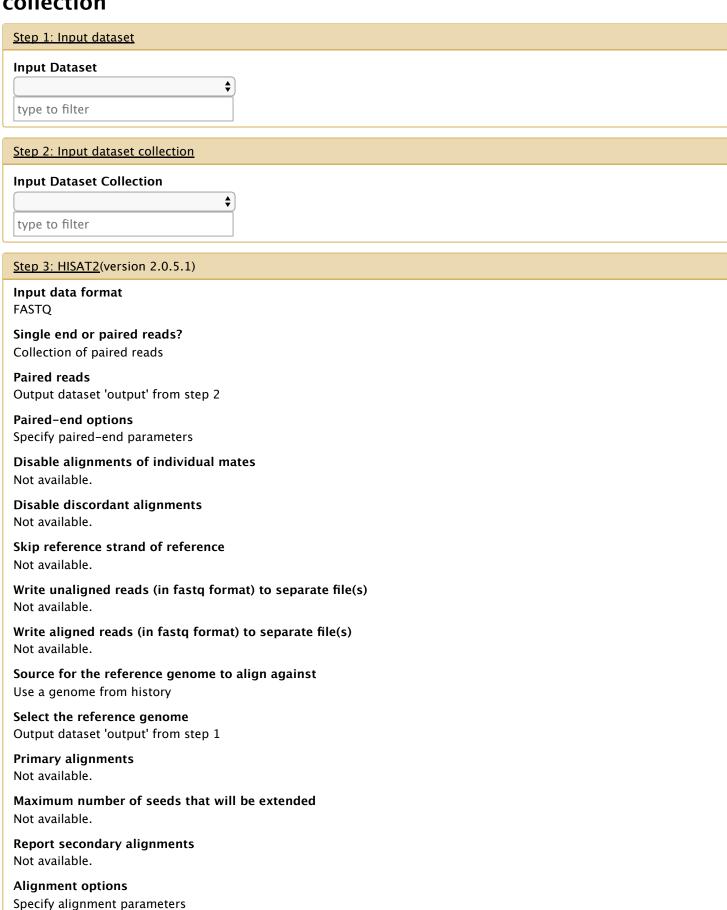
Running workflow "transcripts-assembly-paired-datasets-collection"



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 Minimum mismatch penalty 2 Disallow soft-clipping Not available. Ambiguous read penalty 1 Maximum soft-clipping penalty 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 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) Minimum intron length 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.

Step 4: StringTie(version 1.3.3)

Transcripts

Output dataset 'output_gtf' from step 4

Reference annotation to include in the merging

Selection is Optional \$

Minimum input transcript length to include in the merge

50

Minimum input transcript coverage to include in the merge

Not available.

Minimum input transcript FPKM to include in the merge

1.0

Minimum input transcript TPM to include in the merge

1.0

Minimum isoform fraction

0.01

Gap between transcripts to merge together

250

Keep merged transcripts with retained introns

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",
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/stringtie/stringtie/1.3.3",
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/stringtie/stringtie_merge/1.3.3",
```