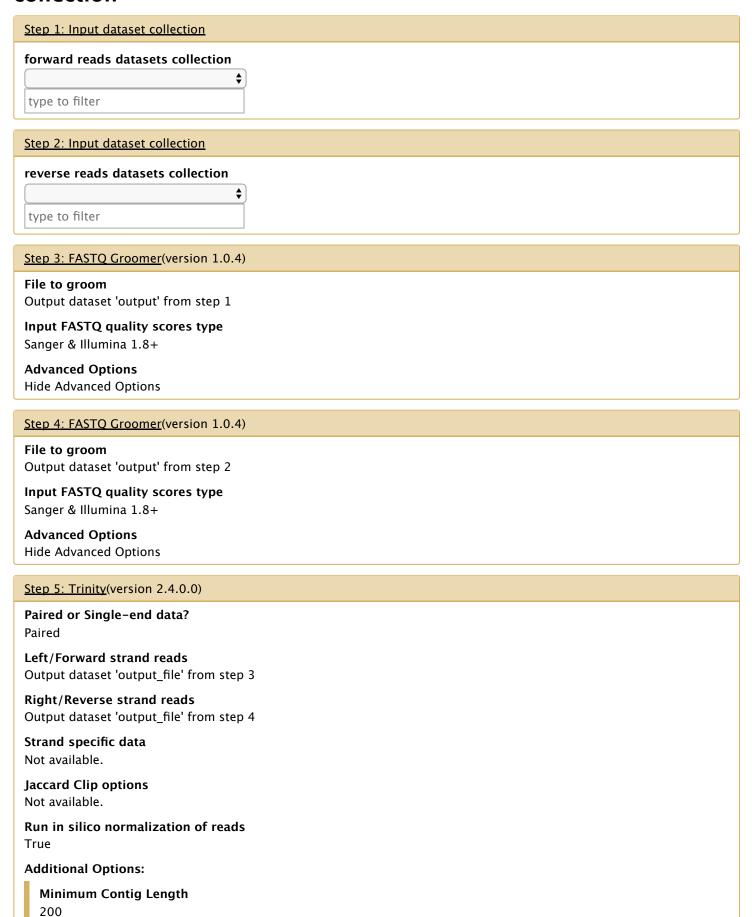
## Running workflow "trinity-transcriptom-assembly-datasets-collection"



```
Use the genome guided mode?
No
Error-corrected or circular consensus (CCS) pac bio reads
 Selection is Optional $
Minimum count for K-mers to be assembled
```

Send results to a new history

10

11

```
tools used in this workflow:
       "tool_id": null,
       "tool_id": null,
       "tool_id": "toolshed.g2.bx.psu.edu/repos/devteam/fastq_groomer/fastq_groomer/1.0.4",
       "tool id": "toolshed.g2.bx.psu.edu/repos/devteam/fastg_groomer/fastg_groomer/1.0.4",
       "tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/trinity/trinity/2.4.0.0",
tools added to the command line section in the trinity.xml file
     <command detect_errors="aggressive"><![CDATA[</pre>
 8
       export PATH=/opt/galaxy/tool_dependencies/_conda/pkgs/trinity-2.4.0-5/bin:\$PATH &&
 9
       export PATH=/opt/galaxy/tool_dependencies/_conda/pkgs/bowtie2-2.2.6-py27_0/bin:\$PATH &&
```

export PATH=/opt/galaxy/tool\_dependencies/\_conda/pkgs/jellyfish-2.2.6-0/bin:\\$PATH &&

export PATH=/opt/galaxy/tool\_dependencies/\_conda/pkgs/parafly-r2013\_01\_21-0/bin:\\$PATH &&