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

Step 1: Input dataset collection

forward reads datasets collection

type to filter

Step 2: Input dataset collection

reverse reads datasets collection

type to filter

Step 3: FASTQ Groomer(version 1.0.4)

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: FASTQ Groomer(version 1.0.4)

File to groom
Output dataset 'output' from step 2

Input FASTQ quality scores type
Sanger & Illumina 1.8+

Advanced Options
Hide Advanced Options

Step 5: Trinity(version 2.4.0.0)

Paired or Single-end data?
Paired

Left/Forward strand reads
Output dataset 'output_file' from step 3

Right/Reverse strand reads
Output dataset 'output_file' from step 4

Strand specific data
Not available.

Jaccard Clip options
Not available.

Run in silico normalization of reads
True

Additional Options:

> **Minimum Contig Length**
> 200

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
1

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/devteam/fastq_groomer/fastq_groomer/1.0.4",
        "tool_id": "toolshed.g2.bx.psu.edu/repos/devteam/fastq_groomer/fastq_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

```
 7    <command detect_errors="aggressive"><![CDATA[
 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 &&
10        export PATH=/opt/galaxy/tool_dependencies/_conda/pkgs/jellyfish-2.2.6-0/bin:\$PATH &&
11        export PATH=/opt/galaxy/tool_dependencies/_conda/pkgs/parafly-r2013_01_21-0/bin:\$PATH &&
```