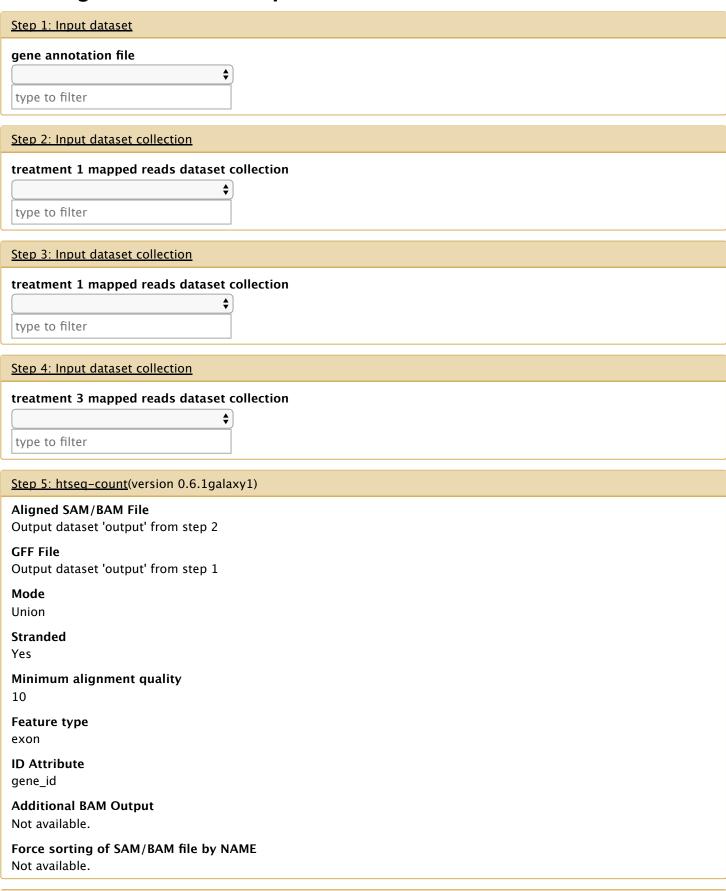
## Running workflow "deseq2-1-factor-3-levels"



Aligned SAM/BAM File

Step 6: htseq-count(version 0.6.1galaxy1)

**GFF File** Output dataset 'output' from step 1 Mode Union Stranded Yes Minimum alignment quality Feature type exon **ID Attribute** gene\_id **Additional BAM Output** Not available. Force sorting of SAM/BAM file by NAME Not available. Step 7: htseq-count(version 0.6.1galaxy1) Aligned SAM/BAM File Output dataset 'output' from step 4 **GFF File** Output dataset 'output' from step 1 Mode Union Stranded Yes Minimum alignment quality 10 Feature type exon **ID Attribute** gene\_id **Additional BAM Output** Not available. Force sorting of SAM/BAM file by NAME Not available. Step 8: DESeq2(version 2.11.39) **Factors** Factor 1

## **Factor levels**

**FactorName** 

Factor level 1

Output dataset 'output' from step 3

Specify a factor level, typical values could be 'tumor', 'normal', 'treated' or 'control'

Specify a factor name, e.g. effects\_drug\_x or cancer\_markers

```
FactorLevel_1
      Counts file(s)
      Output dataset 'counts' from step 5
      Factor level 2
      Specify a factor level, typical values could be 'tumor', 'normal', 'treated' or 'control'
      FactorLevel_2
      Counts file(s)
      Output dataset 'counts' from step 6
      Factor level 3
      Specify a factor level, typical values could be 'tumor', 'normal', 'treated' or 'control'
      FactorLevel_3
      Counts file(s)
      Output dataset 'counts' from step 7
 Choice of Input data
 Count data (e.g. from htseq-count or feature-count)
 Visualising the analysis results
 True
 Output normalized counts table
 Not available.
 Output all levels vs all levels of primary factor (use when you have >2 levels for primary factor)
 Not available.
 Fit type
 parametric
 Turn off outliers replacement (only affects with >6 replicates)
 Not available.
 Turn off outliers filtering (only affects with >2 replicates)
 Not available.
 Turn off independent filtering
 Not available.
Send results to a new history
```

```
tools used in this workflow:
```

```
"tool id": null,
"tool_id": null,
"tool_id": null,
"tool_id": null,
"tool id": "toolshed.g2.bx.psu.edu/repos/lparsons/htseq_count/htseq_count/0.6.1galaxy1",
"tool_id": "toolshed.g2.bx.psu.edu/repos/lparsons/htseq_count/htseq_count/0.6.1galaxy1",
"tool id": "toolshed.q2.bx.psu.edu/repos/lparsons/htseq_count/htseq_count/0.6.1qalaxy1",
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/deseq2/deseq2/2.11.39",
```