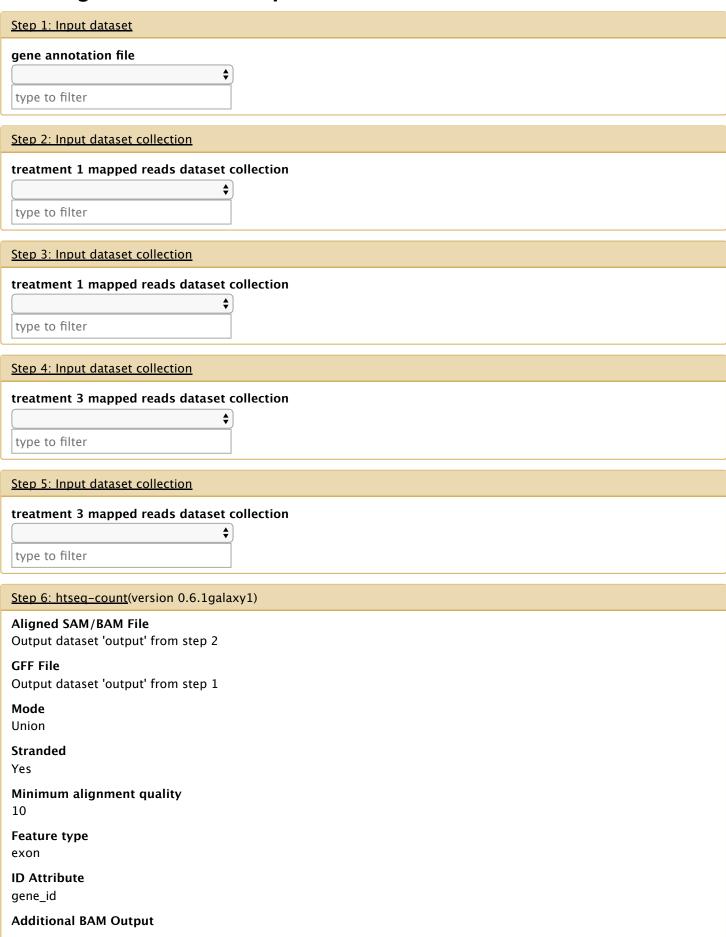
# Running workflow "deseq2-1-factor-4-levels"



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 3

#### **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: 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 9: htseq-count(version 0.6.1galaxy1)

# Aligned SAM/BAM File

Output dataset 'output' from step 5

# **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 10: DESeq2(version 2.11.39) **Factors** Factor 1 Specify a factor name, e.g. effects\_drug\_x or cancer\_markers **FactorName Factor levels** Factor level 1 Specify a factor level, typical values could be 'tumor', 'normal', 'treated' or 'control' FactorLevel 1 Counts file(s) Output dataset 'counts' from step 6 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 7 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 8 Factor level 4 Specify a factor level, typical values could be 'tumor', 'normal', 'treated' or 'control' FactorLevel 4

Counts file(s)



## 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": "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",
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```