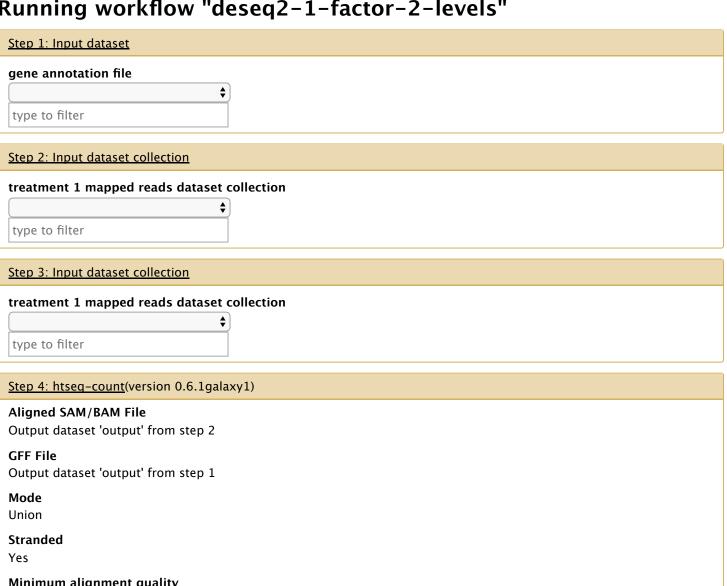
Running workflow "deseq2-1-factor-2-levels"



Minimum alignment quality 10 Feature type exon **ID Attribute** gene id **Additional BAM Output** Not available. Force sorting of SAM/BAM file by NAME

Step 5: htseq-count(version 0.6.1galaxy1)

Aligned SAM/BAM File

Output dataset 'output' from step 3

GFF File

Not available.

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 6: 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 4

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 5

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": "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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