

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

Step 1: Input dataset

gene annotation file

Step 2: Input dataset collection

treatment 1 mapped reads dataset collection

Step 3: Input dataset collection

treatment 1 mapped reads dataset collection

Step 4: htseq-count(version 0.6.1galaxy1)

Aligned SAM/BAM File

Output dataset 'output' from step 2

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 5: 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 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",  
"tool_id": "toolshed.g2.bx.psu.edu/repos/iuc/deseq2/deseq2/2.11.39",
```