Galaxy Workflow ' deseq2-analysis'

Step **Annotation**

Step 1: Input dataset collection

Input Dataset Collection
select at runtime

Step 2: Input dataset

input
select at runtime

Step 3: Input dataset

input
select at runtime

Step 4: htseq-count

Aligned SAM/BAM File
Output dataset 'output' from step 1

GFF File
Output dataset 'output' from step 2

Mode
Union

Stranded
Yes

Minimum alignment quality
10

Feature type
exon

ID Attribute
gene_name

Additional BAM Output
Do not output additional BAM file

Force sorting of SAM/BAM file by NAME
False

Step 5: DESeq2: DESeq

Count files from htseq-count

Output dataset 'counts' from step 4

sample table file
Output dataset 'output' from step 3

Design formula
~ time

Display analysis code in report?
False

Step 6: DESeq2: Visualization

Workspace from tool DESeq2: DESeq
Output dataset 'deseq_workspace' from step 5

Sample table file
Output dataset 'output' from step 3

Interest groups for PCA plots

> **Interest groups for PCA plot 1**
>
> **Interest group for PCA plot**
> 3

Interest groups for MDS plots

> **Interest groups for MDS plot 1**
>
> **Interest group for MDS plot**
> 3

Display analysis code in report?
False

Step 7: DESeq2: Results

Workspace from tool DESeq2: DESeq
Output dataset 'deseq_workspace' from step 5

Sample table file
Output dataset 'output' from step 3

Group for result contrast
3

Treatment level
earlyFlower

Condition level
lateFlower

Gene clustering groups

> **Gene clustering groups 1**
>
> **A phenotype column from the sample table**
> 3

Display analysis code in report?
False