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

Step 1: Input dataset

gene annotation file

type to filter

Step 2: Input dataset collection

treatment 1 mapped reads dataset collection

type to filter

Step 3: Input dataset collection

treatment 1 mapped reads dataset collection

type to filter

Step 4: Input dataset collection

treatment 3 mapped reads dataset collection

type to filter

Step 5: Input dataset collection

treatment 3 mapped reads dataset collection

type to filter

Step 6: 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 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:

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