

Criteria- Gene expression network

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Task	Tool
Alignment	? STAR
Read count	feature-count
Differential expression	DESeq2

Workflows:

1. Generating read count:

- **Step 1.** Creating/using GTF annotation file(s)
REQUIRIES: GTF file(s)
? ▪ Using latest reference genome
- **Step 2.** Mapping reads
REQUIRIES: fastq files
? ▪ Using STAR
- **Step 3.** Counting reads
REQUIRIES: bam files
? ▪ Using feature-count
- **Step 4.** Normalization
REQUIRIES: count tables
▪ DESeq

=> The read count files.

2. Generate cystoscope network