

Genomic data Science Capstone- Week 6- Gene expression Count

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Gene expression levels in the 8 samples were counted using the FeatureCounts tool in galaxy. The BAM files obtained in week4 alignment step were used to run Featurecounts. The strand option was selected as 'Unstranded'. The gtf file used was featureCounts built-in for hg19. In 'Options for Paired-end reads', 'Count fragments instead of reads' was set to 'enabled'. Remaining parameters were set to 'Default'.

The counts tables obtained for each of the 8 sample were joined together using 'Column join on collections' tools in galaxy. The output was a tabular file with one gene per row and one sample per column.

The table was submitted as the result of week 6 analysis.