Bulk RNA-Seq

This tutorial gives an overview of RNA-Seq analysis with Partek® Flow®. It will guide you through creating an RNA-Seq analysis pipeline. The goals of the analysis are to create a list of differentially expressed genes, visualize these gene expression signatures by hierarchical clustering, and interpret the gene lists using gene ontology (GO) enrichment.

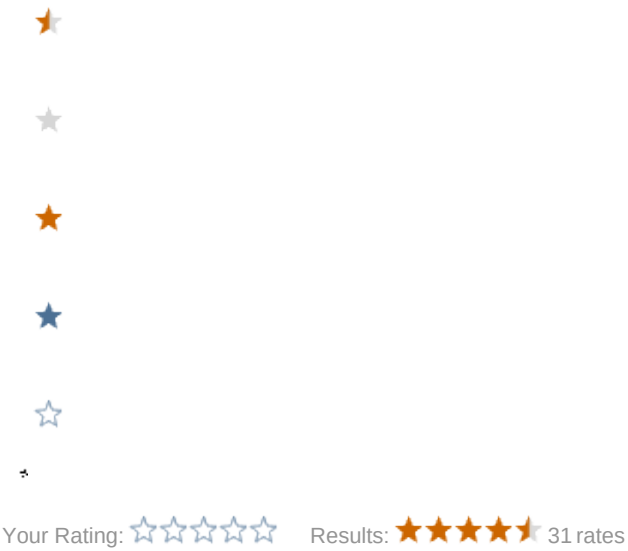
This tutorial will illustrate:

Description of the Data Set

This tutorial uses a subset of the data set published in Xu et al. 2013 (PMID: 23902433). In the experiment, mRNA was isolated from HT29 colon cancer cells treated with the drug 5-aza-deoxy-cytidine (5-aza) at three different doses: 0M (control), 5M, or 10M. The mRNA was sequenced using Illumina HiSeq (paired end reads). The goal of the experiment was to identify differentially expressed genes between the different treatment groups.

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.



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