RNA-Seq Analysis

RNA-Seq is a high-throughput sequencing technology used to generate information about a sample's RNA content. Partek Genomics Suite offers convenient visualization and analysis of the high volumes of data generated by RNA-Seq experiments.

This tutorial illustrates:

- Importing aligned reads
- Adding sample attributes
- RNA-Seq mRNA quantification
- Detecting differential expression in RNA-Seq data
- Creating a gene list with advanced options
- Visualizing mapped reads with Chromosome View
- Visualizing differential isoform expression
- Gene Ontology (GO) Enrichment
- Analyzing the unexplained regions spreadsheet

*Note: the workflow described below is enabled in Partek Genomics Suite version 7.0 software. Please fill out the form on Our support page to request this version or use the **Help > Check for Updates** command to check whether you have the latest released version. The screenshots shown within this tutorial may vary across platforms and across different versions of Partek Genomics Suite.*

Description of the Data Set

In this tutorial, you will analyze an RNA-Seq experiment using the Partek Genomics Suite software RNA-Seq workflow. The data used in this tutorial was generated from mRNA extracted from four diverse human tissues (skeletal muscle, brain, heart, and liver) from different donors and sequenced on the Illumina® Genome Analyzer™. The single-end mRNA-Seq reads were mapped to the human genome (hg19), allowing up to two mismatches, using Partek Flow alignment and the default alignment options. The output files of Partek Flow are BAM files which can be imported directly into Partek Genomics Suite 7.0 software. BAM or SAM files from other alignment programs like ELAND (CASAVA), Bowtie, BWA, or TopHat are also supported. This same workflow will also work for aligned reads from any sequencing platform in the (aligned) BAM or SAM file formats.

Data and associated files for this tutorial can be downloaded by going to Help > On-line Tutorials from the Partek Genomics Suite main menu or using this link - RNA-Seq Data Analysis tutorial files. Once the zipped data directory has been downloaded to your local drive:

- Unzip the downloaded files to C:\Partek Training Data\RNA-seq or to a directory of your choosing. Be sure to create a directory or folder to hold the contents of the zip file

Additional Assistance

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