

Gene Ontology Enrichment

Gene ontology (GO), enrichment analysis has been incorporated into the gene expression, microRNA expression, exon, copy number, tiling, ChIP-Seq, RNA-Seq, miRNA-Seq and methylation workflows. The Gene Ontology Consortium [website](#) provides an excellent overview for new and experienced users of GO analysis. In brief, the common nomenclature of genes and gene products has been used to group genes into a functional hierarchy. This enables analyses to be compared across all types of genomic data, even data from different species. A broader understanding of experimental results is possible by grouping genes of interest into biological processes, cellular components and molecular functions of the genes. With the GO enrichment tool in Partek® Genomics Suite® you can take a list of genes (e.g. significantly differentially expressed genes) and see how they group in the functional hierarchy. This is analogous to going from looking at individual trees (genes) to see how the whole forest (gene ontology) is organized.

This tutorial illustrates how to:

- [Open a zipped project](#)
- [Perform GO enrichment analysis](#)

*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

This tutorial will provide a step-by-step guide to performing GO enrichment analysis. The data set used is based on 51 subjects run on the Illumina Human Ref-8 BeadChip platform. Twenty-six of the subjects were categorized as "Young" with an age range of 18 to 28. The other 25 subjects were categorized as "Old" with an age range of 65 to 84. Skeletal muscle, a type of striated muscle tissue, was obtained via biopsy from each subject. The total RNA was extracted from the skeletal cells, prepared and run on the BeadChips producing the data that is used for this tutorial.

The paper this data is based on can be found at [PLOS](#).

[Data and associated files for this tutorial](#) can be downloaded by going to *Help > On-line Tutorials* on the main menu toolbar within the Partek Genomics Suite software. Download the zipped file and store it on your local disk drive. There is no need to manually unzip the directory.

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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