

Gene Expression Analysis with Batch Effects

This tutorial will illustrate:

- [Importing the data set](#)
- [Adding an annotation link](#)
- [Exploring the data set with PCA](#)
- [Detect differentially expressed genes with ANOVA](#)
- [Removing batch effects](#)
- [Creating a gene list using the Venn Diagram](#)
- [Hierarchical clustering using a gene list](#)
- [GO enrichment using a gene list](#)

*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

The data for this tutorial is taken from an experiment that examined the effects of four treatment conditions at two time points on estrogen receptor-positive breast cancer cell lines *in vitro*. Each treatment/time combination has two replicates and there are two control samples for a total of eighteen samples. Gene expression analysis was performed using the Affymetrix GeneChip[®] Human U95A array. Values are transformed to log base 2 scale by $f(x) = \log_2(x+1)$.

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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