

Implementation Details

The method used to detect changes in functional groups is ANOVA. For detailed information about ANOVA, see Chapter 11 of the Partek User Manual. There is one result per functional group based on the expression of all the genes contained in the group. Besides all the factors specified in the ANOVA model, the following extra terms will be added to the model by Partek Genomics Suite automatically:

- **Gene ID** - Since not all genes in a functional group express at the same level, gene ID is added to the model to account for gene-to-gene differences
- **Factor * Gene ID** (optional) - Interaction of gene ID with the factor can be added to detect changes within the expression of a GO category with respect to different levels of the factor, referred to in this document as the disruption of the categories expression pattern or simply disruption

Suppose there is an experiment to find genes differentially expressed in two tissues: Two different tissues are taken from each patient and a paired sample t-test, or 2-way ANOVA can be used to analyze the data. The GO ANOVA dialog allows you to specify the ANOVA model, which includes the two factors: tissue and participant ID. The analysis is performed at the gene level, but the result is displayed at the level of the functional group by averaging of the member genes' results. The equation of the model that can be specified is:

$$y = \mu + T + P +$$

- y: expression of a functional group
- μ : average expression of the functional group
- T: tissue-to-tissue effect
- P: participant-to-participant effect (a random effect)
- : error term

When the tissue is interacted with the gene ID then the ANOVA model becomes more complicated as demonstrated in the model below. The functional group result is not explicitly derived by averaging the member genes as the new model includes terms for both gene and group level results:

$$y = \mu + T + P + G + T * G +$$

- y: expression of a functional group
- μ : average expression of the functional group
- T: tissue-to-tissue effect
- P: patient-to-patient effect (this can be specified as a random effect)
- G: gene-to-gene effect (differential expression of genes within the function group independent of tissue type)
- T*G: Tissue-Gene interaction (differential patterning of gene expression in different tissue types)
- : error term

In the case that there is more than one data column mapping to the same gene symbol, Partek Genomics Suite will assume that the markers target different isoforms and will not treat the two markers as replicated of the same gene. Instead, each column is treated as a gene unto itself.

If there are only two samples in the spreadsheet then, Partek Genomics Suite cannot calculate a type by gene ID interaction. In this case, the result spreadsheet will contain a column labeled *Disruption score*. First, for each gene in the functional group *Partek Genomics Suite* will calculate the difference between the two samples. A z-test is used to compare the difference between each gene and the rest of the genes in the functional group. The disruption score is the minimum p-value from the z-tests comparing each gene to the rest in the functional group. A low disruption score therefore indicates that at least one gene behaves differently from the rest. This implies a change in the pattern of gene expression within the functional group and potential disruption of the normal operation of the group. The category as a whole may or may not exhibit differential expression in addition to the disruption.

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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