Gene Set ANOVA

The method used to detect changes in functional groups is ANOVA.There is one result per functional group based on the expression of all the genes contained in the group. Besides the factor specified in the ANOVA model, the following extra terms will be added to the model by Partek Flow 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** - Interaction of gene ID with the factor is added to detect changes within the expression of a gene set with respect to different levels of the factor, small p-value of this term means genes in the set behave differently on this factor -- the disruption of the categories expression pattern, we call it disruption effect.

Suppose there is an experiment to find genes differentially expressed in two tissues: t-test, or ANOVA can be used to analyze the data. The Gene Set ANOVA dialog allows you to specify the ANOVA model: tissue. However, under the hood, interaction term is added automatically in the model:

$y = \mu + T + G + T\,{}^{*}G +$

- y: expression of a functional group
- μ: average expression of the functional group
- T: tissue-to-tissue 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

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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