

# Performing GO ANOVA

Preparing a data set for analysis requires importing the data, normalizing the data as appropriate for standard gene expression analysis, and inserting columns containing the experimental variables. Checkout [our tutorial page](#) for more details about preparing data. It is not necessary to perform a differential analysis of gene expression before GO ANOVA.

For the sake of example, the following walkthrough will consider an experiment that has been imported which includes two different tissues, brain tissue and heart tissue, extracted from a small set of patients.

The GO ANOVA function is available in the *Gene Expression*, *microRNA Expression*, *RNA-Seq*, and *miRNA-Seq* workflows.

- Select the **Gene Expression** workflow (or any of the other ones) from the Workflows drop-down on the upper right of the spread sheet
- Go to the **Biological Interpretation** section of the workflow
- Select **Gene Set Analysis** (Figure 1) and then **Gene Set ANOVA**
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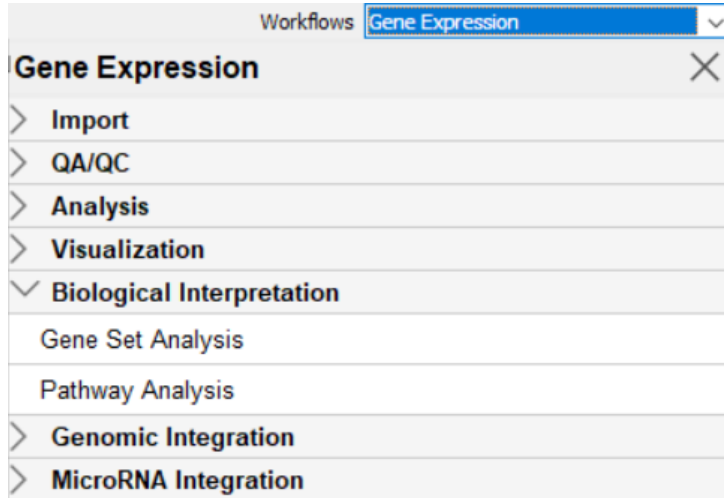


Figure 1. GO ANOVA dialog can be invoked via Gene Set Analysis option of the workflow

For this example analysis, the model was kept easy to interpret by including *Subject* and *Tissue* as the only ANOVA factors. Additionally, *Tissue* was added to the Disruption Factor(s). Including *Subject* controlled for person to person variation, and including *Tissue* allowed the analysis of differential expression and of functional category disruption between tissue types. For the sake of simplicity and minimizing run time, the term *Subject* was not added to the *Disruption Factor(s)* box. Including it would have helped correct for subject specific gene expression patterns, though the results were largely unaffected in this case.

Performing GO ANOVA analysis on very large GO categories can take quite a bit of time. More importantly, very large categories may have too large a scope to be useful. To speed the operation and analyze only smaller GO categories, specify 20 genes as the maximum size for an analyzed GO category.

For the sample dataset, the GO ANOVA dialog setup should appear as in Figure 2 below.

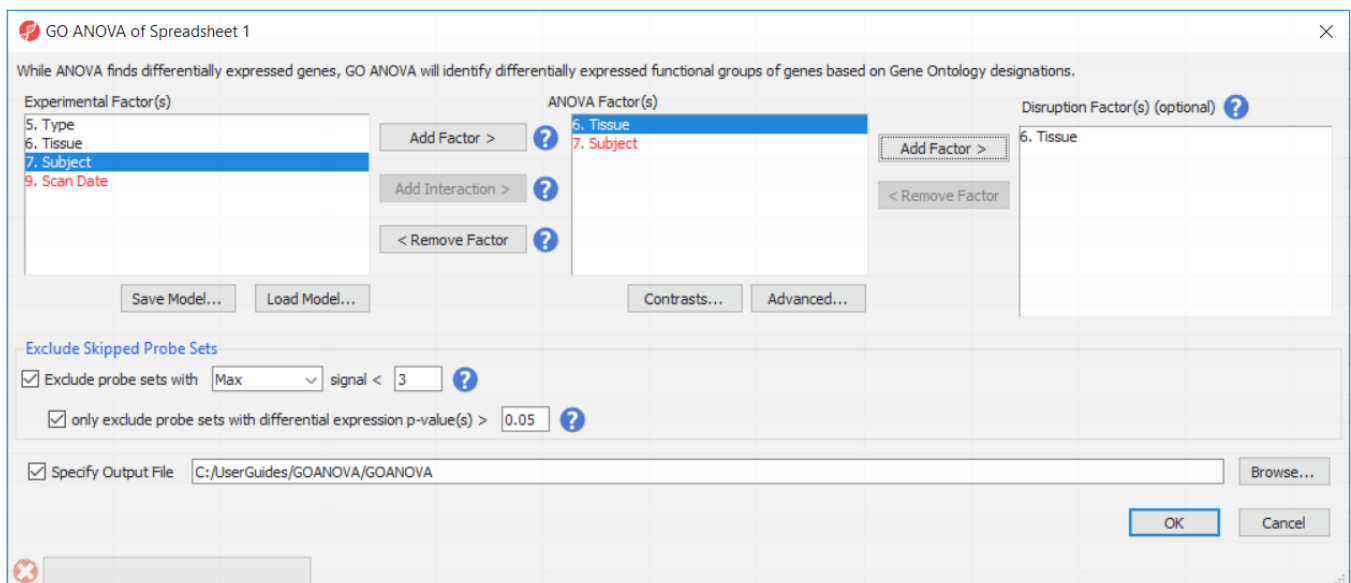


Figure 2. GO ANOVA configured for the user guide data set. Two factors added to the model

### Additional Assistance

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

