



## GO-Enrichment Tool v2 App

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The GO-Enrichment App displays the results of a Gene-Ontology Enrichment analysis. For more information about Gene Ontology please have a look at <http://geneontology.org/>.

The likelihood for enrichment of a specific GO term is calculated using the “Fisher’s Exact Test”, under consideration of differentially expressed transcripts that belong to a specific GO term in relation to all GO terms and the transcripts members. The analysis is based on the R-package “TopGO”.

After selecting the comparison of interest, you can choose between the three main categories “Molecular Function” (**MF**), “Cellular Components” (**CC**) and “Biological Processes” (**BP**). The search window allows filtering for specific GO terms or transcripts of interest. Additionally, the tables can be filtered using the different options.

**The Graph Plot:** An interactive GO graph is generated from the filtered subset of the table. The plot can be accessed by clicking on the “Submit” button next to the “**Show graph plot for TOP xx enriched GO-Terms**” field. The number of top GO terms can be chosen.

Different colors of the GO terms indicate the likelihood for enrichment, with red, orange, yellow and white for strong likely to be enriched to less likely, respectively (see figure below). On the right side, an enlarged detail of the image is displayed. The size and zoom-factor can be manipulated with the mouse-wheel. An excerpt of the plot is depicted below.



the transcript in both samples on the two axes. Equally expressed transcripts are grouped in the diagonal line mounting from the lower left to the upper right corner of the plot.

The dots in red represent the transcripts belonging to the selected GO term. When browsing over the red dots, the information (description, p-value for DE, normalized frequencies) of the transcript is displayed (see figure below).