GO-Elite Directory Description

AltAnalyze is distributed with its own biological and statistical enrichment analysis software called GO-Elite (http://genmapp.org/go_elite). When this analysis is performed (optional), users can identify biological pathways that are over-represented in a particular set of regulated genes in addition to increased cell populations, disease associated factors, transcriptional regulators and targets of microRNAs to name a few. GO-Elite is run on automatically produced lists of regulated genes (differential gene expression and alternative exon expression). The GO-Elite directory contains a set folders used as input for GO-Elite and output, including graphical outputs (heatmaps and networks). The subdirectories in this folder include:
1. input
2. denominator
3. MarkerFinder
4. GO-Elite_results

The input directory contains tab-delimited text files with regulated IDs, whereas the denominator directory contains all examined IDs. The input file also contains comparison p-values and fold changes to optionally visualize upon WikiPathways or networks. All files in the input directory are automatically analyzed for all available gene-set types (e.g., WikiPathways, KEGG, Gene Ontology, Disease Ontology, Transcription Factor binding sites, Cellular biomarkers).

The MarkerFinder directory contains predicted marker genes for each condition analyzed. These are not analyzed automatically but can be with the associated file in the denominator directory when run from the Additional Analyses menu in AltAnalyze.

The GO-Elite_results directory contains all results produced from a GO-Elite analysis. Although optionally produced by GO-Elite, the WikiPathways image folder is saved to the root directory rather than here. In the GO-Elite_results directory, four results files can be found along with three addition subdirectories. The principle results file is named pruned-results_z-score_elite.txt. This file lists all enriched GO-Elite biological categories with non-redundant terms pruned out for all biological ontologies using the GO-Elite pruning function. Associated gene names and IDs are also listed in this file. In the folder heatmaps, over-represented terms are visualized as colored heatmaps to identify similar biological trends. In the folder networks, the relationship between biologically over-represented terms and genes or other IDs visualized as a network to identify unique and common molecules associated with these terms. In the WikiPathways directory, pathways and associated gene or metabolite IDs are colored based on their indicated regulation (up or down, red or blue).

Other subdirectories in the GO-Elite_results directory contain results for individual input files and all scores and gene associations for all analyzed IDs.

More information on these file types can be found at:
http://www.altanalyze.org/help_main.htm and
http://www.genmapp.org/go_elite/help_main.htm