**Clustering Directory**

This directory contains fold-change expression files for differentially expressed genes (DEGs) to be used as input for clustering and heatmap/PCA visualization. These tab-delimited text files can consist of the following:

* DEG log2 folds relative to the row mean (SampleLogFolds Prefix)
* DEG log2 folds relative to the baseline mean (RelativeSampleLogFolds Prefix)
* Outlier DEG log2 folds relative to the row mean (OutlierLogFolds Prefix)
* LineageProfiler Z-scores (LineageCorrelations Prefix)

DEGs are defined based on the default or user-defined fold, p-value and p-value type thresholds. Significantly differentially expressed genes in these sets are defined as > 2 fold (up or down) regulated and comparison statistic p < 0.05 (any comparison), unless the options are changed in the GO-Elite options interface. Both the SampleLogFolds and RelativeSampleLogFolds have contain the same genes listed in an arbitrary order. Visualization of these results can be found in the folder DataPlots in the root results directory.

For SampleLogFolds, folds changes are calculated relative to the mean expression (all values in AltAnalyze or log2 values) for all samples in that row (not group).

The RelativeSampleLogFolds file returns these values as comparison folds for each sample relative to the mean expression of the baseline as indicated in the sample names.

The OutlierLogFolds file reports any gene with > 2-fold (up or down) regulated in any sample relative to the mean expression of all samples for that gene and not in the SampleLogFolds set.

The LineageCorrelations file contains enrichment Z scores for all analyzed samples relative to all cells and tissues in the LineageProflier database.

More information on these file types can be found here: <http://www.altanalyze.org/help_main.htm>