

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 LineageProfiler database.

More information on these file types can be found here:

http://www.altanalyze.org/help_main.htm