

ExpressionOutput Directory

This directory contains all gene expression summarized data produced by AltAnalyze. If analyzing non-gene expression data, quantitative values associated with the input IDs will be provided here instead. Multiple file types are included in this directory, principally:

- Combined statistics, expression, annotation results (DATASET Prefix)
- Normalized expression statistics (GENMAPP Prefix)
- Summary significant results (SUMMARY Prefix)

The most critically useful file is the DATASET file, which includes all computed statistics (i.e., p-values, folds), annotations (i.e., gene, pathway, miRNA binding). The GENMAPP file contains just summary statistics and is more appropriate for analysis in the programs GenMAPP-CS and PathVisio. The SUMMARY file contains an overview of the number of genes and protein-coding potential associated with the user-defined analysis thresholds. These files are all presented in the root of the ExpressionOutput directory. However, a number additional files and folders may also be provided in this directory.

Additional file types found in the ExpressionOutput Directory are:

- Average biological group gene expression (AVERAGE Prefix)
- LineageProfiler cell/tissue correlation results (LineageCorrelation Prefix)

These files are both used in the calculation of LineageProfiler predictions. More on LineageProfiler can be found here:

<http://code.google.com/p/altanalyze/wiki/LineageProfiler>

Additional subdirectories can include:

- Clustering
- MarkerFinder

The Clustering folder includes differentially regulated genes and outlier predicted genes used for automated cluster visualization in AltAnalyze or outside

(<http://code.google.com/p/altanalyze/wiki/Heatmaps>). The MarkerFinder folder

(<http://code.google.com/p/altanalyze/wiki/MarkerFinder>).