

ExpressionInput Directory

This directory contains all primary source data analyzed by AltAnalyze. This includes:

- Normalized expression files (exp. Prefix)
- Sample group file (groups. Prefix)
- Group comparison file (comps. Prefix)

Typically, there is one of each of these file types in the ExpressionInput directory. Additionally, the following files may also be present:

- RNA-Seq read counts (counts. Prefix)
- Affymetrix DABG p-values (stats. Prefix)
- Affymetrix residual probe values (residuals. Prefix)

Two exp. files will exist for alternative-exon or RNA-Seq analyses. The additional exp. file will have the suffix “steady-state.txt”, indicating gene-level rather than feature-level expression. For RNA-Seq analyses, two read-count files will also be present in this directory both with the prefix “counts.” and one with the suffix “steady-state.txt”. The stats. file provides a detection above background p-value for each probeset on the microarray for optional filtering in AltAnalyze (see below documentation). The residuals. file is used by AltAnalyze during calculation of FIRMA splicing scores when that option is selected.

Four additional directories may also be present in this folder:

- APT-output
- gProcessed
- rProcessed
- Non-Combat

The APT-output directory contains log files and QC from Affymetrix Power Tools, following microarray normalization (RMA). The gProcessed and rProcessed directories contain the combined green and red channel expression values for all microarray probes following extraction from Agilent Feature Extraction files, along with quantile normalized versions. The Non-Combat directory contains the original expression file used in the analysis prior to combat normalization (where applicable).

Additional details on these files and analyses can be found at:

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