

AlternativeOutput Directory Description

Comparison Specific Files

When performing alternative exon analyses on microarray or RNA-Seq datasets, all significant alternative exons, junctions and splicing events along with function protein and mRNA-level predictions will be saved to this directory. These files include predicted alternative exons, splicing-events, alternative promoters, corresponding annotations, genomic coordinates, protein-level predictions and effected protein domains, motifs and microRNA binding sites. The principal file types for each specific biological comparison in this directory are:

1. Top-scoring alternative exon results ([exon-inclusion-results.txt](#) Suffix)
2. Gene-level summaries of #1 ([exon-inclusion-GENE-results.txt](#) Suffix)
3. Enrichment of effected protein domains ([ft-domain-zscores.txt](#) Suffix)
4. Enrichment of effected miRNA binding sites ([microRNA-zscores.txt](#) Suffix)

Preceding each of these file suffixes is the statistical method applied to each file. These can include splicing-index (normalized exon or junction expression), FIRMA (exon or junction-level), ASPIRE and Linear Regression (reciprocal junction analysis). For junction sensitive platforms, both reciprocal junction and alternative exon analyses are performed in tandem. A detailed description of the fields in these files can be found at:

- <http://code.google.com/p/altanalyze/wiki/ProteinDirectionIndicator>
- http://www.altanalyze.org/help.htm#results_overview

The most critical useful file among these is the [exon-inclusion-results](#) file. This reports all of the most significant alternative exons, junctions, splicing events and related functional annotations and statistics for a given comparison.

Agglomerated Result Files

In addition to comparison specific result files, several comparison files are produced that include comparison of results between the different biological comparisons and/or different statistical analyses for a single comparison (e.g., ASPIRE and splicing-index results).

5. Reciprocal and alternative exon comparisons from #1 ([comparison-evidence.txt](#) Suffix)
6. Summary statistics from #1 ([summary-results.txt](#) Suffix)
7. Combination of all comparisons results from #1 ([all-genes-comparisons-events.txt](#) Suffix)
8. Combination of all comparisons results from #1 ([all-genes-GENE-comparisons-events.txt](#) Suffix)

More information on these file types can be found at:

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