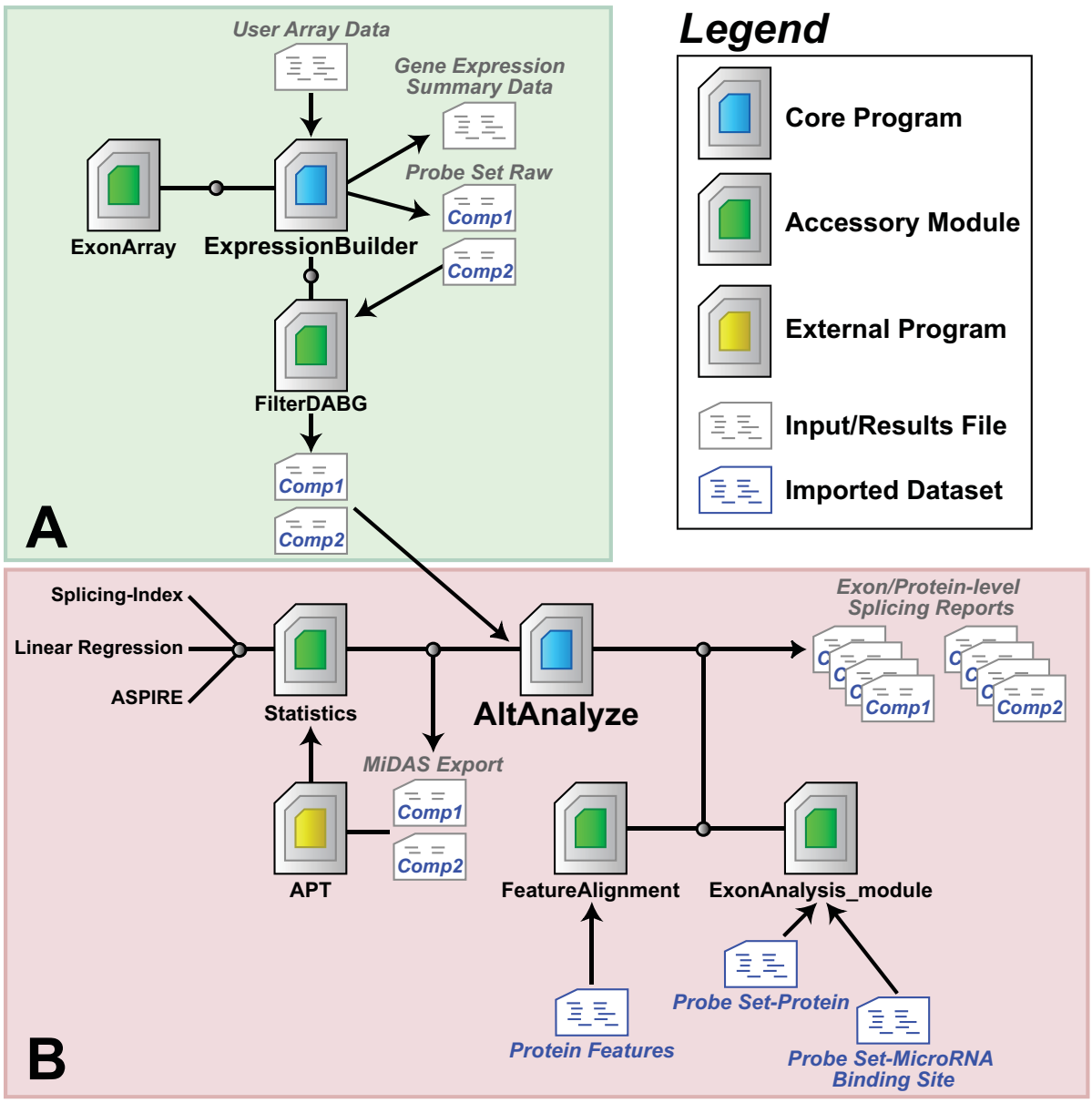

Figure 5.1. AltAnalyze Analysis Pipeline. The AltAnalyze workflow is depicted. The transparent green box highlights functions performed by the ExpressionBuilder module of AltAnalyze whereas the transparent red box highlights the AltAnalyze module. (A) User microarray data (probe set expression values and DABG p-values) are imported into AltAnalyze via the ExpressionBuilder module, which separates data for different biological array groups into user designated pair-wise comparisons (e.g.,

cancer vs. normal). For each pair-wise comparison, probe set expression values and DABG p-values are exported to separate files, and then analyzed by the module FilterDABG to exclude probe sets with poor detection parameters. The resulting files are inputs for alternative exon analysis. In parallel, a gene expression summary file is produced with Ensembl gene level expression (based on constitutive probe set expression) for each gene and array along with summary statistics (average, fold, and t-test p-value for all pair-wise comparisons) and annotations. (B) Using the ExpressionBuilder pair-wise comparison files, AltAnalyze re-calculates constitutive expression values, evaluates changes in probe set expression relative to constitutive (statistics module), and links probe sets with “significant” changes to aligning alternative protein sequence and predicted changes in protein and miR-BS architecture (ExonAnalyze and FeatureAlignment modules). The result is a series of probe set and gene summary files along with over-representation statistics for the regulation of protein and miR-BS features. Optionally, probe set and constitutive expression values can be exported to the bundled application Affymetrix Power Tools to calculate additional alternative exon statistics to be included in the AltAnalyze analysis.