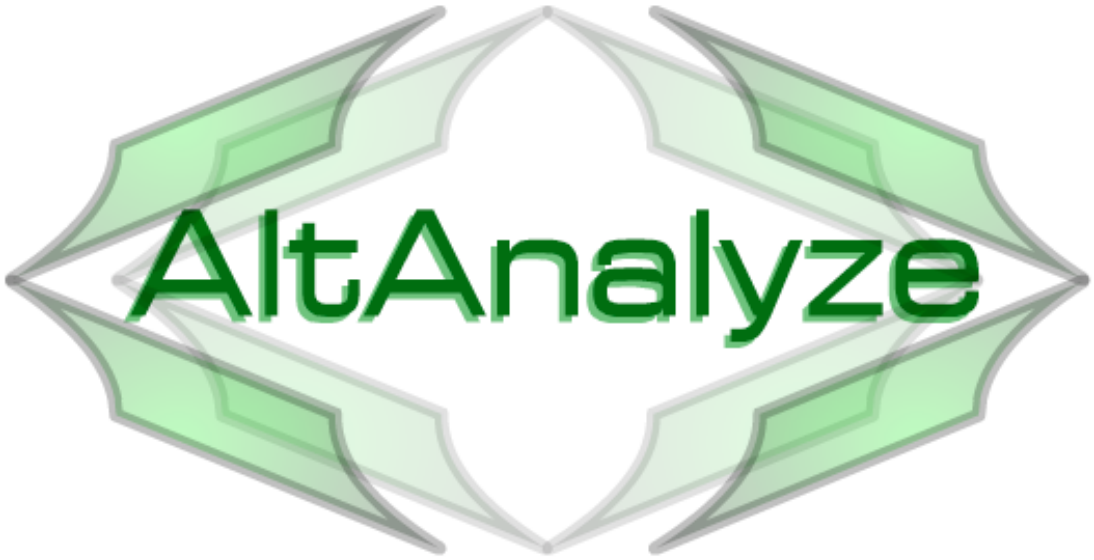

AltAnalyze Information and Instructions

Version 2.0

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Section 1 - Introduction

1.1 Program Description

AltAnalyze (http://altanalyze.org) is a freely available, easy-to-use, cross-platform application for the end-to-end analysis of **microarray**, **RNA-Seq**, proteomic, metabolomic and other quantitative datasets. These analyses include QC, gene-expression summarization, **alternative exon/junction identification**, expression clustering, **single-cell analysis**, PCA, network analysis, cell type and sample classification, alternative exon visualization, batch effects removal, ID-mapping, Venn diagram analysis, pathway/TF target enrichment and pathway visualization. For splicing-sensitive platforms (RNA-Seq and Affymetrix Exon, Gene and Junction arrays), AltAnalyze specializes in evaluating changes in protein sequence, domain composition, and microRNA targeting that result from differential isoform expression. To do this, AltAnalyze associates user sequence-level changes in exon or junction expression that lead to the alternative expression of associated mRNAs. This software requires no advanced knowledge of bioinformatics programs or scripting. Once the analysis is complete, a user-friendly **Results Viewer** can be run as an independent program or directly from AltAnalyze. As input from RNA-Seq experiments, AltAnalyze accepts **raw RNA sequence** files, **aligned BAM** files, genomic **aligned exons and junctions** from several external packages, or previously **normalized expression values**. For Affymetrix analyses, all that is required are your microarray files or a list of regulated probe sets along with some simple descriptions of the conditions that you're analyzing. Step-by-step tutorials are available from our support site at http://www.altanalyze.org.

AltAnalyze is composed of a set of modules designed to (A) summarize, organize and filter exon and junction-level data; (B) annotate and calculate statistics for differential gene expression, (C) calculate scores for alternative splicing (AS), alternative promoter selection (APS) or alternative 3' end-processing; (D) annotate regulated alternative exon events (e.g., mutually-exclusive splicing); and (E) assess downstream predicted functional consequences at

the level of protein domains, microRNA binding sites (miR-BS) and biological pathways. The resulting data will be a series of text files (results and over-representation analyses) that you can directly open in a computer spreadsheet program for analysis and filtering (Figure 1.1). Graphical QC plots, hierarchical clustering heatmaps, PCA, network diagrams, exon expression graphs and pathway diagrams are also produced. In addition, export files are created for the Cytoscape (1) program DomainGraph to graphically view domain and miR-BS exon alignments and AltAnalyze statistics.

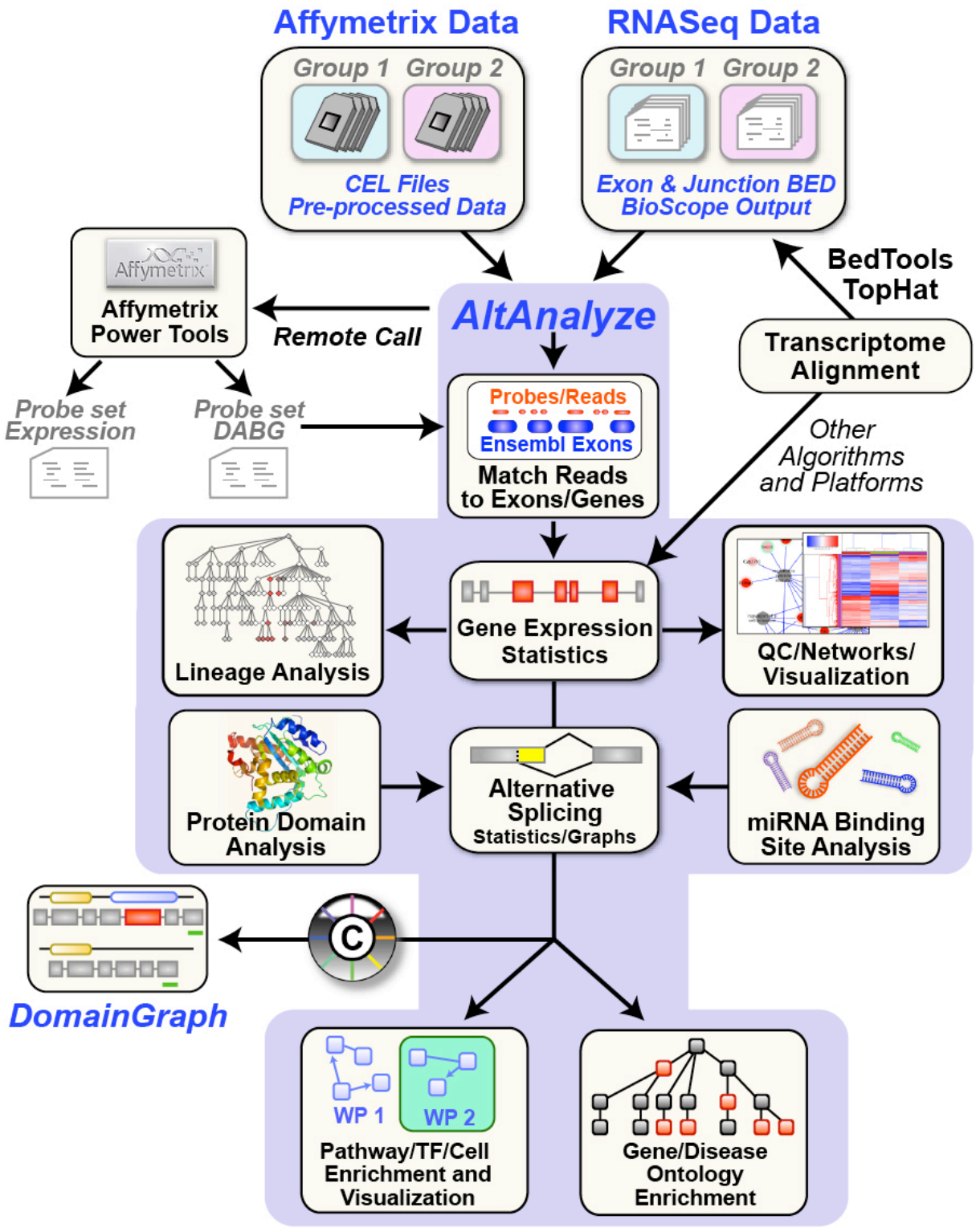


Figure 1.1. AltAnalyze Overview. Simplified graphic illustration of the analysis steps and output files produced by AltAnalyze. All of these results can be easily browsed from using the **AltAnalyze Results Viewer**.

Alternative exon analysis is currently compatible with the RNA-Seq unaligned and aligned exon and junction data, Affymetrix Exon 1.0 ST, Affymetrix Gene 1.0 ST, Affymetrix HJAY, HTA2.0, MJAY, hGLUE, HTA2.0 arrays and the custom exon-junction Affymetrix AltMouse A array, however, data from **other platforms** can be imported if supplied in BED format for over 50 species (Section 1.6). Analysis of these and conventional Affymetrix microarrays is supported for array normalization (**RMA**), batch effects removal (**combat**), calculation of array group statistics, dataset annotation and pathway over-representation analysis. For non-Affymetrix arrays, all these steps are supported with exception to array normalization.

1.2 Updates

Program updates, new features and bug fixes for all AltAnalyze versions can be found at: http://code.google.com/p/altanalyze/wiki/News

1.3 Implementation

AltAnalyze is provided as a stand-alone application that can be run on Windows or Mac OS X operating systems, **without installation of any additional software**. This software is composed of a set of distinct modules written entirely in the programming language Python and distributed as stand-alone programs and source-code. Python is a cross-platform compatible language; therefore, AltAnalyze can be run on any operating system that has Python and Tkinter for Python installed. On many operating systems, including Linux and any Mac OS X operating systems the necessary python components are included by default, however, on some operating systems, such as Ubuntu, Tkinter may need to be installed when using the graphical user interface. AltAnalyze can be run from either an intuitive graphic user interface or from the command-line. Additional source-code dependencies can be optionally installed to support additional visualization options. To run AltAnalyze from source-code, rather than through the compiled executables, see section 1.5 and 2.2 for more information. *Note*: some features may not be compatible with all executable operating system versions.

1.4 Requirements

The basic installation of AltAnalyze requires a minimum of 1GB of hard-drive space for all required databases and components. Species databases are downloaded separately by the user from within the program, for various database versions. *Species gene databases, Affymetrix library and annotation files can all be automatically downloaded by AltAnalyze.* A minimum of 4GB of RAM and Intel Pentium III processor speed are further required. At least an additional 1GB of free hard-drive space is recommended for building the required output files. Additional RAM (up to 16GB) and hard-drive space (up to 4GB free) is recommended for large exon or junction studies.

1.5 Installation

Prior to downloading AltAnalyze, determine the version that is appropriate to use for your operating system (e.g., Win64 for Windows, OSX for Mac). The operating system specific applications will include all necessary dependencies. If this application fails to run, we recommending downloading the source-code version and installing any necessary dependencies (see below). **For RNA-Seq analyses, it is essential to know the genome version your sequences were aligned against and which Ensembl databases support these versions in AltAnalyze. See the Ensembl website (http://ensembl.org) for details.**

Compiled Stand-Alone Version

Download the installer package (Mac OS X) or zip archive to your machine. To install on Mac OS X, double-click on the dmg to mount the AltAnalyze disk image to your Desktop. After opening the disk image, drag the folder “AltAnalyze” to any desired directory. For zip archives, extract the archive file to any accessible location using the appropriate zip extraction tool (e.g., WinZip, default tool). Once extracted, open the AltAnalyze program directory and double-click on the file named “AltAnalyze” to start the GUI.

Source-Code Version

When using AltAnalyze in headless mode (command-line only – **Section 2.3**), only Python is required (Python 2.6 or 2.7 is recommended). When using the GUI, both Python and Tkinter are required at a minimum. Tkinter is typically installed with Python but is not included with some Linux implementations (e.g., Ubuntu), unless manually installed. Scipy (http://www.scipy.org) is optional (improves performance when performing a Fisher Exact Test). Numpy (http://www.numpy.org) and MatPlotLib (http://www.matplotlib.org) are required for all quality control and clustering analyses and visualization. To support WikiPathways visualization, install the python web service client package lxml (http://pypi.python.org/pypi/lxml). If the Python imaging library Pillow is installed (https://pypi.python.org/pypi/Pillow) direct visualization of pathways in the GUI is supported as opposed to with the default operating system PNG image viewer. Additional dependency information and instruction details can be found here: http://code.google.com/p/altanalyze/wiki/StandAloneDependencies.

Extract the zip archive to any accessible folder. From a command-prompt change directories to the AltAnalyze program folder and enter “python AltAnalyze.py” to initiate the GUI. For headless-mode, supply AltAnalyze with the appropriate command-line arguments (see the end of Section 2 - Running AltAnalyze Locally Using the Command-Line Option).

1.6 Pre-Processing, External Files and Applications

RNA Sequence Alignment and Aligned Data

Several options now exist for importing RNA-Seq data into AltAnalyze, including the direct alignment of raw RNA-Seq as well as alignment result files. We recommend reading our online instructions (http://code.google.com/p/altanalyze/wiki/ObtainingRNASeqInputs) to see which method best suits your data. In general, we recommend **TopHat2/BowTie2** as a sensitive method for obtaining known and novel junctions, in addition to exon-spanning reads.

The latest versions of AltAnalyze support direct alignment of RNA-Seq fastq or fastq.gz format files, using the extremely fast and lightweight tool kallisto (http://pachterlab.github.io/kallisto/). As kallisto’s license has some restrictions, please read

before using this option. Gene and isoform level results are generated from kallisto, but not exon and junction.

When analyzing data from already aligned RNA-Seq reads, AltAnalyze can import data in the **BAM alignment** file (.bam) produced by the TopHat or STAR software, UCSC BED format (http://genome.ucsc.edu/FAQ/FAQformat.html#format1), as output from the Applied Biosystems software **BioScope**, or junction expression files supplied by the Cancer Genome Atlas (**TCGA**). The junction BED file can be produced by various RNA-Seq exon-exon junction alignment applications, including TopHat (junction.bed), HMMSplicer (canonical.bed) and SpliceMap (junction_color.bed). These files provide genomic coordinates and corresponding aligned read counts for unique junctions. For AltAnalyze, all junction BED files must be given unique names and saved to a single folder for an experiment (minimum of two files belonging to two different experimental groups). When processing BAM files, both junction and exon format BED files will be produced from each BAM. Upon import, AltAnalyze will match the splice-site coordinates of each junction to Ensembl and UCSC mRNA annotated exon-junctions, individual exon splice sites, exons and introns. AltAnalyze will also identify trans-splicing events, where an aligned junction contains splice sites found with two distinct genes. If neither splice site of detected junction aligns to an Ensembl gene (between the 1st and last exons), the junction will be excluded from the analysis. Junctions and corresponding read counts will be saved to the folder "ExpressionInput" (user-defined output directory), with re-assigned standard AltAnalyze IDs (e.g., ENSMUSG00000033871:E13.1-E14.1). Reciprocal junctions will be analyzed for any known or novel junction predicted to alternatively regulate an associated exon (see section 3.2 – Reciprocal Junction Analysis). For SOLiD sequencing, a viable alternative to these methods is the software BioScope, which produces both exon and junction expression estimates. The counttag (exon-level) and alternative-splicing (junction-level) files can be loaded once the extension Is changed from .txt to .tab. For junction count files from the **TCGA**, after downloading to your hard-drive, the extension "**.junction_quantification.txt**" must be added to all files for AltAnalyze to recognize the proper input format.

Affymetrix Array Analyses

AltAnalyze can process raw Affymetrix image files (CEL files) using the RMA algorithm. This algorithm is provided through Affymetrix Power Tools (APT) binaries that are distributed with AltAnalyze in agreement with the GNU distribution license (see agreement in the AltDatabase/afffymetix/APT directory). Alternatively, users can pre-process their data outside of AltAnalyze to obtain expression values using any desired method. Example methods for obtaining such data include ExpressionConsole (Affymetrix) and R (Bioconductor), either of which can be used if the user desires another normalization algorithm rather than RMA (e.g., GC-RMA, PLIER, dCHIP). Likewise, users with non-Affymetrix data can use an appropriate normalization method (e.g. http://chipster.csc.fi). *FIRMA alternative exon analysis is only supported when users have previously analyzed CEL files for the dataset of interest, since FIRMA scores are calculated from RMA probe-level residuals, rather than probe set expression values.*

If alternative exon, gene or junction Affymetrix CEL files are processed directly by AltAnalyze (using APT and RMA), two files will be produced; an expression file (containing probe set and expression values for each array in your study) and a detection above background (DABG) p-value file (containing corresponding DABG p-values for each probe set). As mentioned, if FIRMA is selected as the alternative exon analysis algorithm, APT will first perform a separate RMA run to produce probe residuals for gene-level metaprobesets (Ensembl associated AltAnalyze core, extended or full probe sets). The results produced by AltAnalyze will be identical to those produced by APT or ExpressionConsole(http://www.affymetrix.com/products/software/specific/expression_console_software.affx). For some exon arrays, users can choose to exclude certain array probes based on genomic cross-hybridization (section 2.3).

For array summarization, all required components are either pre-installed or can be downloaded by AltAnalyze automatically (Affymetrix library and annotation files) for most array types. If the user is prompted for a species library file that cannot be downloaded, the user will

be asked to download the appropriate file from the Affymetrix website. Offline analyses require the user to follow the instructions in Section 2.3.

Agilent Feature Extraction Files

AltAnalyze directly process Agilent Feature Extraction files produced from Agilent scanned slide images using Agilent's proprietary Feature Extraction Software. Feature Extraction text files can be loaded in AltAnalyze using the **Process Feature Extraction Files** option and selecting the appropriate color ratio or specific color channel from which to extract expression values from. Quantile normalization is applied by to Agilent data processed through this workflow.

Other Splicing-Sensitive Platforms

With the latest version of AltAnalyze (version 2.0.3 and later), any user exon and junction expression data can be imported into AltAnalyze. This is accomplished by treating the input expression data the same as the RNA-seq input files (i.e., stored as junction or exon coordinates and counts in the UCSC BED format). Analyses, annotations and results are the same as with RNA-seq data.

Example junction BED input: http://code.google.com/p/altanalyze/wiki/JunctionBED

Example exon BED input: http://code.google.com/p/altanalyze/wiki/ExonBED

Other Quantitative Expression Data

Previously normalized or non-normalized expression values for any experimental data can also be imported into AltAnalyze for analysis. Most analytical functions will be available provided the data is formatted in a compatible manner (e.g., log2, non-zero values). Non-normalized data can be directly normalized in AltAnalyze using the quantile normalization option. When loading gene, protein, RNA or metabolite associated data, biological annotations, pathway enrichment analysis, network visualization and pathway visualization options are also supported. Simply

select the Data Type **Other IDs** from the **Main Menu** (Section 2.2) and the appropriate identifier system from the platform selection pulldown.

1.7 Help with AltAnalyze

Additional documentation, tutorials, help, and user discussions are available at the http://code.google.com/p/altanalyze/wiki/Tutorials. Downloads, tutorials and help for DomainGraph can be found at http://domaingraph.bioinf.mpi-inf.mpg.de.

Section 2 – Running AltAnalyze

2.1 Where to Save Input Expression Files?

When performing analyses in AltAnalyze, the user needs to store all of their Affymetrix CEL files, Agilent Feature Extraction files or sequence alignment count files (BED or TAB) in a single directory. This directory can be placed anywhere on your computer and will be later selected in AltAnalyze. Example files can be downloaded from:

Affymetrix Exon Array Data

ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/series/GSE13297/GSE13297_RAW.tar.

BED and TAB Files

http://code.google.com/p/altanalyze/wiki/RNASeq_sample_data

Extract any downloaded TAR and/or GZIP compressed files prior to analysis.

For Affymetrix array analyses, if the user has already run normalization on their CEL files outside of AltAnalyze or have downloaded already analyzed expression data from another source, you can save the expression and DABG p-value file (optional) anywhere on your computer. These files should be tab delimited text files that only consist of probe sets, expression values and headers for each column. Example files can be downloaded http://AltAnalyze.org/normalized_hESC_differentiation.zip.

If beginning with a tabular expression file, simply save this file to an accessible file location and create an appropriate output directory, prior to starting AltAnalyze. If using the command-line for analysis, you will need to create you groups and comps files prior to calling AltAnalyze as described here:

http://code.google.com/p/altanalyze/wiki/GroupsAndComps

http://code.google.com/p/altanalyze/wiki/ManualGroupsCompsCreation

2.2 Running AltAnalyze from the Graphic User Interface

Windows and Mac Directions:

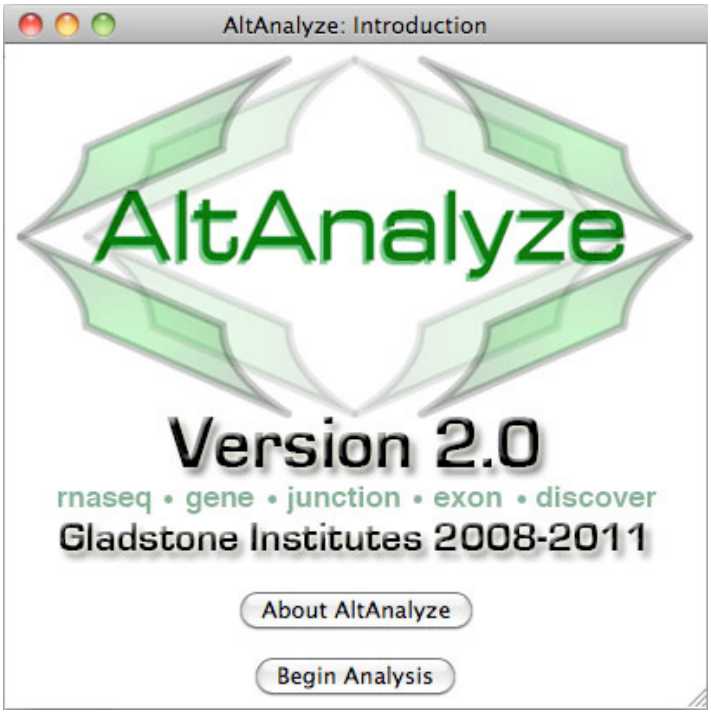
Once you have saved your BAM, FASTQ, BED, TAB, CEL, TXT or normalized expression value files to a single directory on your computer, open the AltAnalyze application folder and double-click on the executable file named “AltAnalyze.exe” (Windows) or “AltAnalyze” (Mac). This will open a set of user interface windows where you will be presented with a series of program options (see following sections). These compiled versions of AltAnalyze can also be run via a command-line to run remotely or as headless processes (see **Section 2.3**). Once the analysis is complete, you can open the other application **AltAnalyzeViewer** to easily browse your results, rather than navigate the result files stored on your computer (see the ViewerManual for details or https://code.google.com/p/altanalyze/wiki/InteractiveResultsViewer).

Unix/Linux and Source Code Directions:

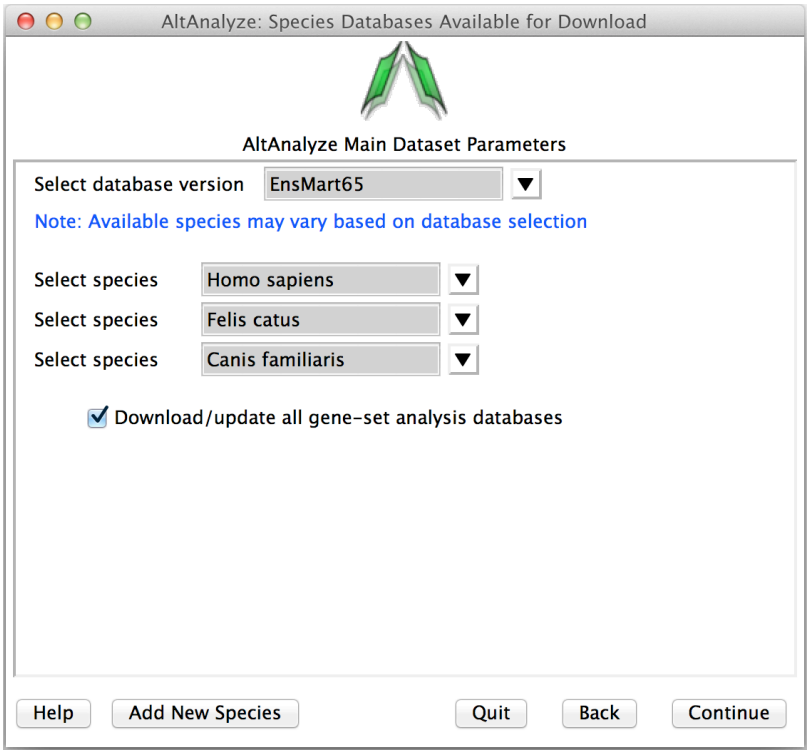
On Linux, download the Linux executable and python source code archive version of AltAnalyze. To run the compiled version, double-click the executable file named “AltAnalyze” or open this file from command-line (./AltAnalyze). These compiled versions of AltAnalyze can also be run via a command-line to run remotely or as headless processes (see **Section 2.3**). If this file is not compatible with your configuration, you should download the Python source-code version instead. Start AltAnalyze by opening a terminal window and changing directories to the AltAnalyze main program (e.g. “cd AltAnalyze_v.2.X.X” from the program parent directory). Once in this directory, typing “python AltAnalyze.py” in the terminal window will begin to run AltAnalyze (you should see the AltAnalyze main menu within a matter of seconds). Prior to running, you will likely wish to install dependencies required for visualization and advanced analyses. To do so, see the instructions listed at: http://code.google.com/p/altanalyze/wiki/StandAloneDependencies.

AltAnalyze Graphical Interface Options:

There are many options in AltAnalyze, which allow the user to customize their output, the types of analyses they run and the stringency of those analyses. The following sections show the sequential steps involved in running and navigating AltAnalyze. Section 2.4 describes each option in detail. Interactive tutorials for different analyses are provided from the AltAnalyze website. ***Please note: if you will be using AltAnalyze on a machine that does NOT have internet access, follow instructions 1-5 below on an online machine and then copy the AltAnalyze program directory to an offline machine.***



1) Introduction Window – Upon opening AltAnalyze, the user is presented with the AltAnalyze splash screen and additional information. To directly open the AltAnalyze download page, follow the hyperlink under “About AltAnalyze”, otherwise select “Begin Analysis”.



2) Species Database Installation – The first time AltAnalyze is used, the user will be prompted to download one or more species database (requires internet connection). Independent of the data source (e.g., RNASeq or array type) you are analyzing, select a species and continue. The user can select from different versions of Ensembl. If your species is not present, select the button **Add New Species**. **Selecting the option Download/update all gene-set analysis databases** will additionally download GO-Elite annotation databases needed for performing a wide-array of biological enrichment analyses (pathways, ontologies, TF-targets, miR-targets, cellular biomarkers) and network visualization analyses.

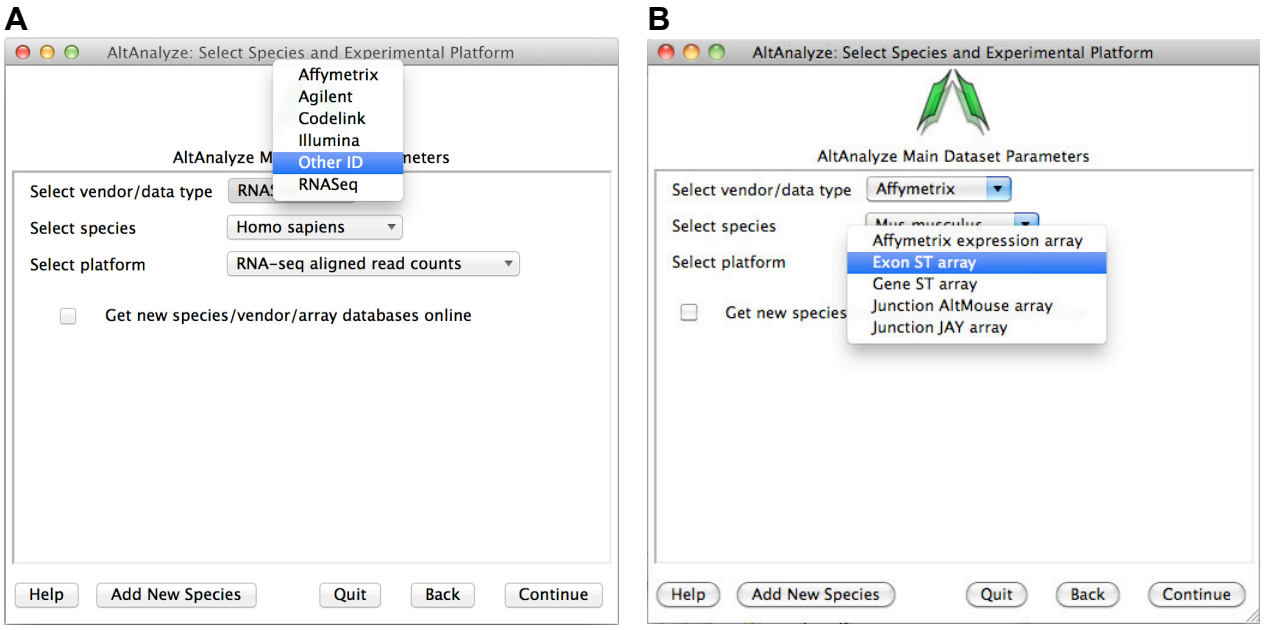


Figure 2.1. Select a Species and Vendor or Data Type for Analysis. A) Options for selecting currently supported species, array vendors or data types (RNASeq). Select the check box to download the latest AltAnalyze gene and exon databases.

3) Select species and platform – Next, the user must select a species, array vendor or data type and platform for analysis (Figure 2.1). Array vendors include Affymetrix, Illumina, Agilent and Codelink. The data type, **Other ID** can be selected if loading non-normalized or normalized values from a different data source (select ID type under Select Platform). This applies also to RNA-Seq normalized gene values from a different workflow, such Cufflinks, eXpress or RSEM. In these cases, match the input ID type (e.g., Symbol, Ensembl) under Select Platform. If multiple database versions have been downloaded, the user will also be able to select a version pull-down menu. After selecting these

options click **Continue**.

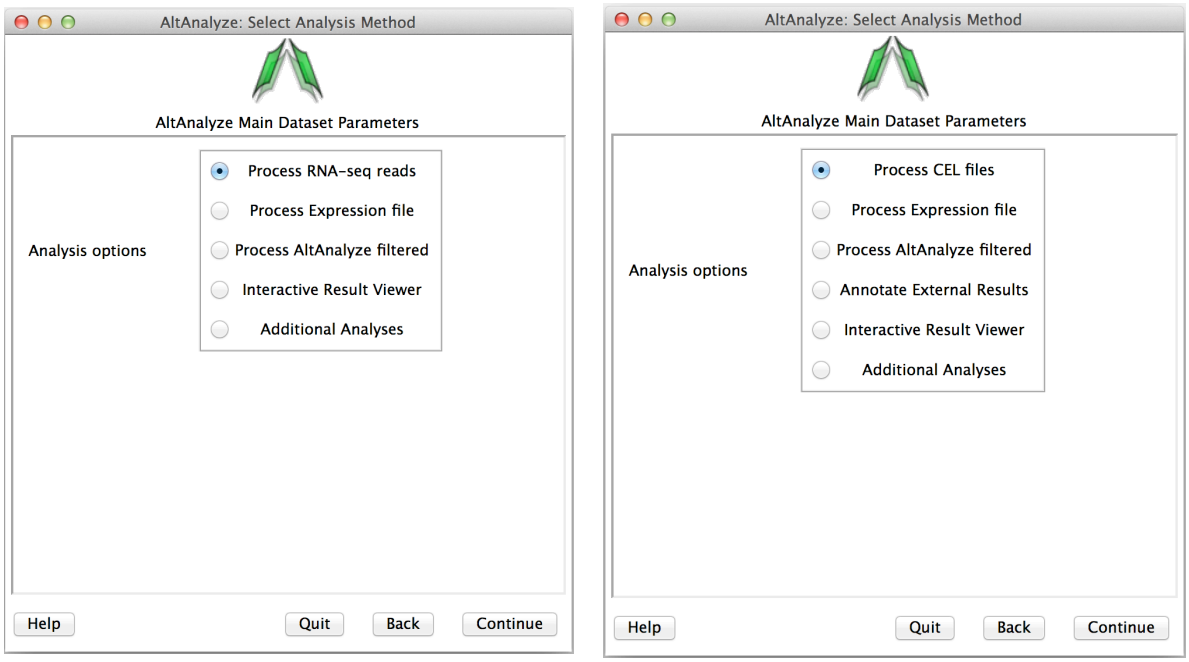
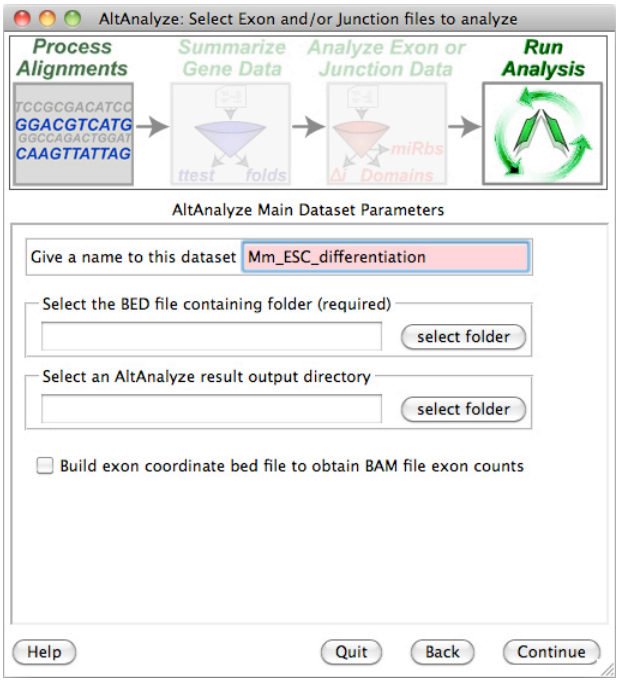


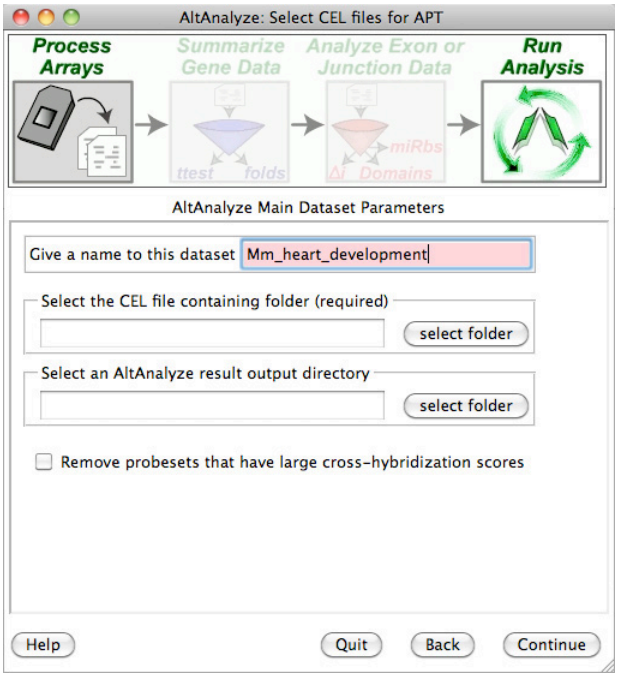
Figure 2.2. Select the Analysis Type. Options available for the select species and array or data type. AltAnalyze filtered is only available for alternative exon analyses.

4) Select analysis option– In this window, the user must select the type data being analyzed. There are four main types of data; A) FASTQ, BAM, BED, CEL or Feature Extraction files, B) Expression files (normalized or read counts), C) AltAnalyze filtered files and D) results from 3rd party applications (Annotate External Results), E) open the Interactive Results Viewer or F) perform **Additional Analyses**. Processing of CEL files will produce the two file types (expression and DABG), while processing of BED files will produce a file of exon and/or junction counts. Processing of Expression files, allows the user to select tab-delimited text files where the data has already been processed (e.g. RMA or read counts), which will also produce AltAnalyze filtered files. AltAnalyze filtered files are written for any splicing array analysis (not for gene expression only arrays).

These later files allow the user to directly perform splicing analyses, without performing the previous steps. The AltAnalyze filtered files are stored to the folder “AltExpression” under the appropriate array and species directories in the user output folder. Since CEL file normalization and array filtering and summarization can take a considerable amount of time (depending on the number of arrays), if re-performing an alternative exon analysis with different parameters, it is recommended that the user select the **Process Expression file** or **Process AltAnalyze filtered**, depending on which options the user wants to change. Users can also import lists of regulated probe sets with statistics obtained from a 3rd party application (e.g., JETTA) other than AltAnalyze using the **Annotate External Results** option. In addition, expression clustering, pathway visualization, pathway enrichment and lineage classification can be independently run on a user expression file using the option **Additional Analyses**.

A





B

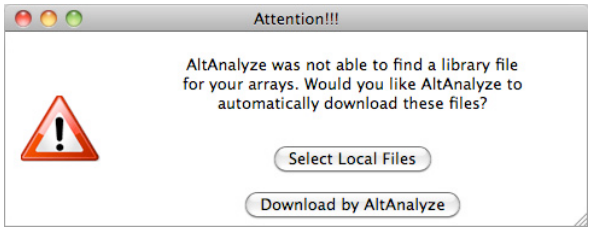


Figure 2.3. Select Folder and File Locations. (A) Pre-built BED or TAB files are currently required to run AltAnalyze on RNA-Seq data. To properly run RMA using the APT software (included with AltAnalyze), the user must select a valid folder containing CEL files. (B) The first time you analyze a certain type of array you will be prompted to download a library file(s) for that array. For some arrays, you will be prompted for AltAnalyze to download these plus annotation files for you. Otherwise, you will be prompted by the program for such files.

5) Processing CEL, Feature Extraction or Exon/Junction Files- If you selected the first option from "Main Dataset Parameters", you will be presented with a new window for selecting the location of your CEL/FE/BED/TAB files and desired output directory. Clicking the "select folder" icon will allow you to browse your hard-drive to select the folder with these data files. You can double-check the correct directory is selected by looking at the adjacent text display. For Agilent Feature Extraction files, you will be presented with the option of selecting which channels or channel ratios to extract data from. For Affymetrix CEL files, this window will be followed by an indicator window that will automatically download the library and annotation files for that array. If the array type is unrecognized and you do not already have Affymetrix library files for your array (e.g. PGF or CDF), you will need to download these files from the Affymetrix website. To do so, select the link at the bottom left side of this window named "Download Library Files". Select the array type being analyzed from the web page and select the appropriate library files to download and extract to your computer (requires an Affymetrix username and password) (Figure 2.3 B). For RNA-Seq data, the user selects the folder containing their exon and junction input files in either BED (e.g., TopHat) or TAB (BioScope) files. If the

user is analyzing junction alignment results but does not have exon-level results, the user can build an annotation file for the program BEDTools, to derive these results from an available BAM file (e.g., produced by TopHat). To do this, select the option "Build exon coordinate bed to file obtain BAM file exon counts". Instead of running the full AltAnalyze pipeline, AltAnalyze will immediately produce the exon annotation file for BEDTools to the BAMtoBED folder in the user output directory. Additional details can be found at: http://code.google.com/p/altanalyze/wiki/BAMtoBED.

A **B**

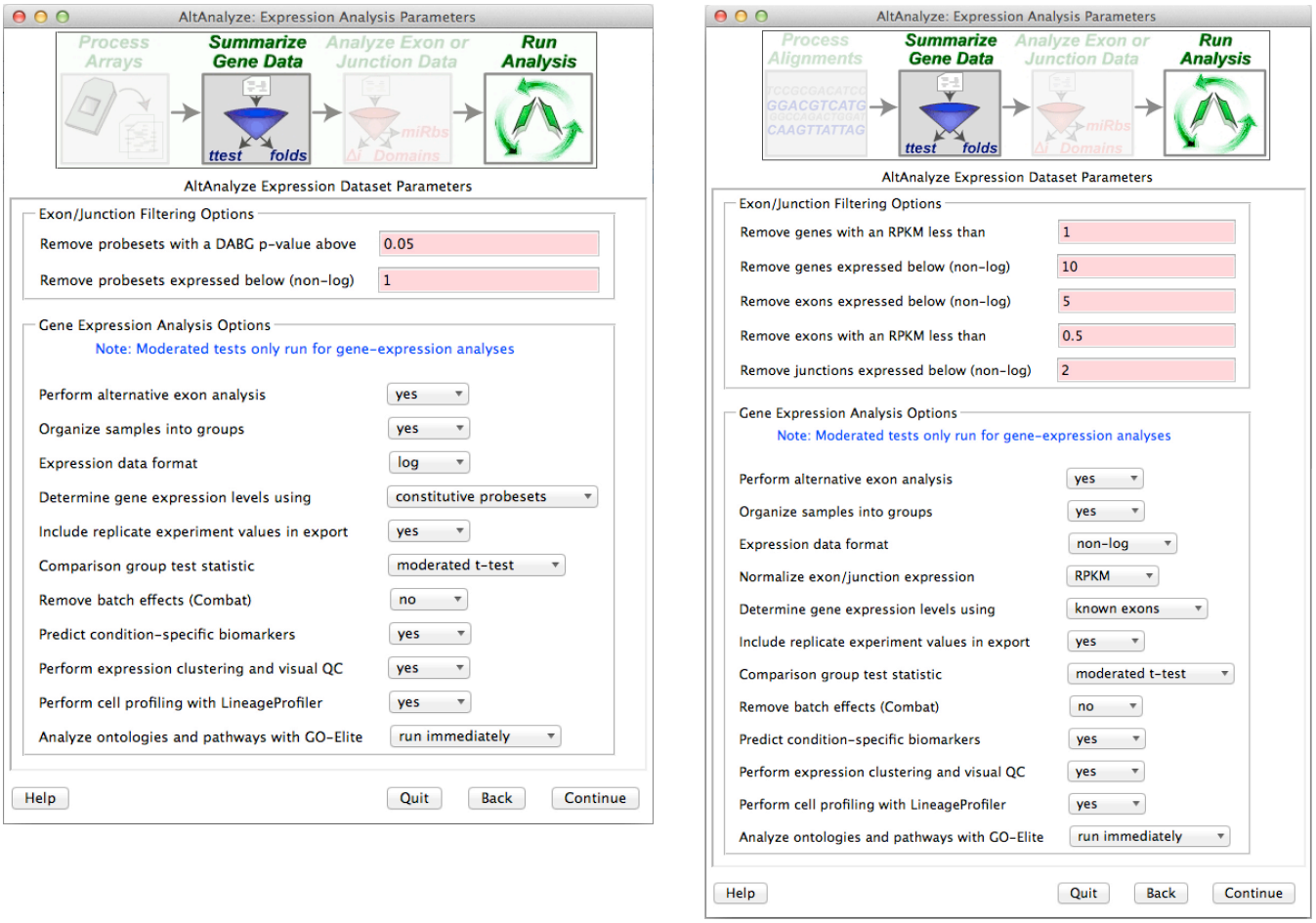


Figure 2.4. Select Summarization and Filtering Options. Users are presented with options for filtering RNA-Seq reads or probe sets for alternative exon analyses (DAGB and mean group expression) and options for how to derive gene expression

values.

6) Summarizing Gene Data and Filtering For Expression – After obtaining summary read counts or normalized CEL expression values, a number of options are available for summarizing gene level expression data, filtering out RNA-Seq reads and probe sets prior to alternative exon analysis and performing additional automated analyses (Figure 2.4). Selection of a comparison group test statistic, allows the user to calculate a p-value for gene expression and splicing analyses based on different tests (e.g., paired versus unpaired t-test). Batch-effect correction can be optionally performed with the combat library (https://github.com/brentp/combat.py). For applicable platforms, the option to perform quantile normalization is also provided here. For Affymetrix splicing arrays, AltAnalyze calculates a "gene-expression" value based on the mean expression of all "core" (Affymetrix core probe sets and those aligning to known transcript exons) or "constitutive" (probe sets aligning to those exon regions most common among all transcripts) probe sets that have a mean DABG p-value less than and a mean expression value greater the user indicated thresholds for each gene. The same methods are used for RNA-Seq exon or junction counts, using the same Ensembl and UCSC combined constitutive evidence. Rather than observed counts, RPKM normalized counts are selected by default, with counts as an alternative options (Section 3.2). These values are used to report predicted gene expression changes (independent of alternative splicing) for all user-defined comparisons (see following section). In addition, fold changes and ttest p-values are calculated for each of these group comparisons. These statistics along with several types of gene annotations exported to a file in the folder "ExpressionOutput" in the user-defined results directory. Along with this tab-delimited text file, a similar file with those values most appropriate for import into the pathway analysis program GenMAPP will also be produced (Figure 5.1). For splicing analyses, RNA-Seq reads or probe sets with user defined splicing cutoffs (expression and DABG p-values) will be retained for further analysis (see section 5.2 – ExpressionBuilder algorithm). Other

analyses, such as QC, PCA, hierarchical clustering (significant genes and outliers), prediction of which cell lineages are detected and pathway analysis are also automatically run using these options. If the user selects no for any these, they can be run again later using the **Additional Analyses** option from the **Select Analysis Method** menu.

Figure 2.5. Select Summarization and Filtering Options. Splicing analysis options for (A) RNA-Seq or junction arrays and (B) exon arrays (e.g., Exon 1.0 and gene 1.0).

7) Select Alternative Exon Analysis Parameters – If using a junction (RNA-Seq or junction array) or exon-sensitive array (e.g., Human Affymetrix Exon 1.0 or Gene 1.0 ST), the user will be presented with specific options for that platform (Figure 2.5). These options

include alternative exon analysis methods, statistical thresholds, and options for additional analyses (e.g., MiDAS), however, the default options are typically recommended. Users can also choose whether to analyze biological groups as pairwise group comparisons, comparison of all groups to each other or both. These include combining values for exon-inclusion junctions and restricting an analysis to a conservative set of Affymetrix probe sets (e.g., **core**) and changing the threshold of splicing statistics. Note: that AltAnalyze's **core** includes any probe set associated with a known exon. When complete, the user can select "Continue" in AltAnalyze to incorporate these statistics into the analysis.

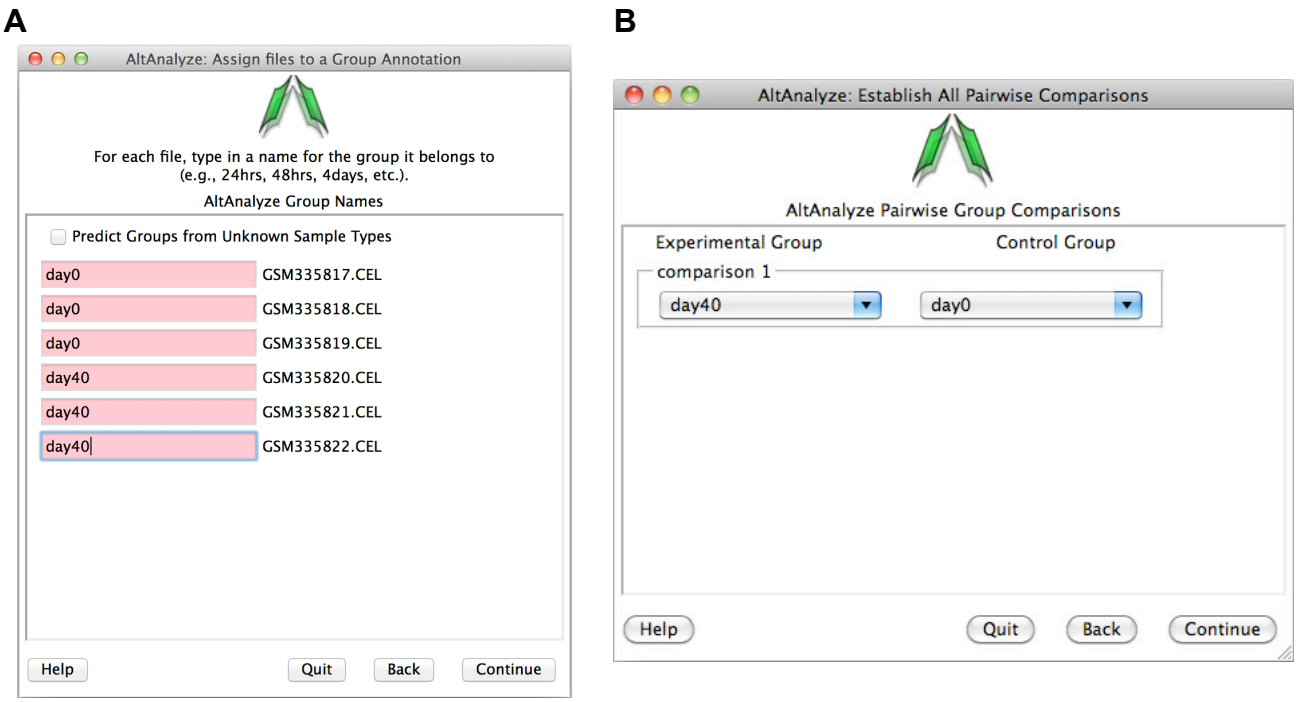
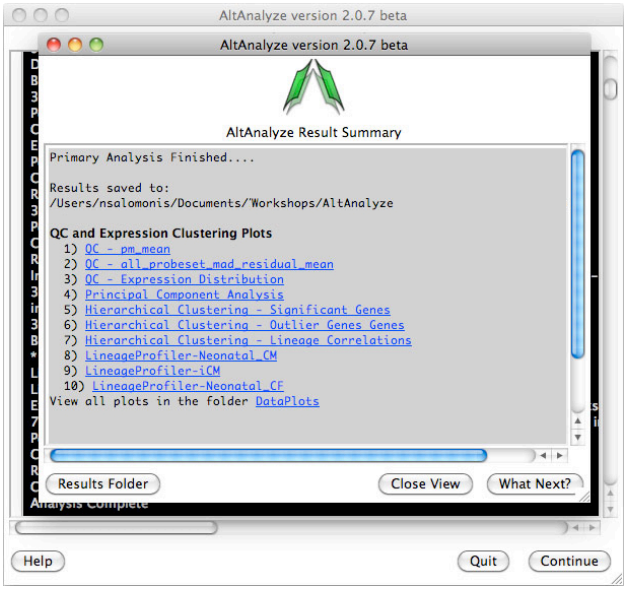


Figure 2.6. Establish Groups and Comparisons. (A) Enter a name for each group for all samples. Optionally, select "Predict Groups from Unknown Sample Types" to predict groups. (B) Enter all group comparisons for any possible pairwise group comparisons (in this case there is only one). These relationships can be created in advance in a spreadsheet program for command-line analysis in AltAnalyze or for large sample datasets. For more details see the following webpage: http://code.google.com/p/altanalyze/wiki/ManualGroupsCompsCreation.

8) Assigning Groups to Samples – When analyzing a dataset for the first time, the user will need to establish which samples correspond to which groups. Type in the name of the group adjacent to each sample name from in your dataset (Figure 2.6 A). When selecting batch-effect correction (**combat**), an additional menu similar to the group annotation will appear afterwards asking the user to enter the batch effect for each one. For **single-cell datasets** or other datasets where you wish to predict de novo groups, select the **Predict Groups from Unknown Sample Types** option to discover clustered sample groups for further analysis in AltAnalyze (See #11 below and **Section 3.2** for details.)

9) Establishing Comparisons between Groups – Once sample-to-group relationships are added, the user can list which comparisons they wish to be performed (Figure 2.6 B). For splicing and non-splicing arrays, folds and p-values will be calculated for each comparison for the gene expression summary file. For RNA-Seq read or splicing arrays, each comparison will be run in AltAnalyze to identify alternative exons. Thus, the more pairwise comparisons the longer the analysis. If the user designates to compare "all groups" and not designate a pairwise comparison, this window will not be displayed.

A



B

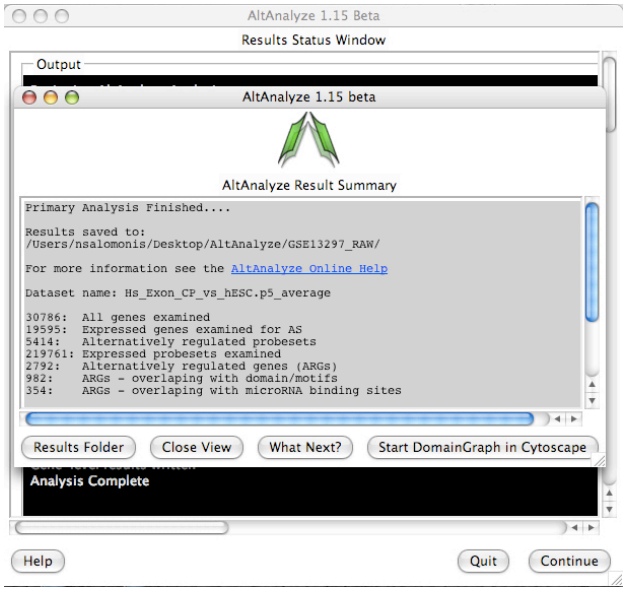


Figure 2.8. AltAnalyze Status. The AltAnalyze status window will appear once all user options are defined. Analysis run-time will depend on the number of samples, comparisons and array type. (A) Gene expression analysis results are shown for Affymetrix array data (alternative exon analysis omitted). Links to data plots (PNG files) are shown for the default selected QC, clustering and lineage analyses. (B) Summary of alternative exon results is shown for an exon or junction-sensitive platform. By Selecting the option **Start DomainGraph in Cytoscape**, users can immediately proceed to results visualization in DomainGraph at the level of transcripts, proteins, domains, exons and microRNA binding sites.

10) AltAnalyze Status Window - While the AltAnalyze program is running, several intermediate results files will be created, including probe set or RNA-Seq read, gene and dataset level summaries (Section 2.4). The results window (Figure 2.8) will indicate the progress of each analysis as it is running. When finished, AltAnalyze will prompt the user that the analysis is finished and a new “Continue” button will appear. A summary of results appears containing a basic summary of results from the analysis. This window contains buttons that will open the folder containing the results and suggestions for downstream interpretation and analysis. Selecting the button “Start DomainGraph in Cytoscape” will allow the user to directly open a bundled version of Cytoscape and DomainGraph (Section 8). In addition to viewing the program report, this information is written to a time-stamped log text file in the user-defined output directory.

A **B**

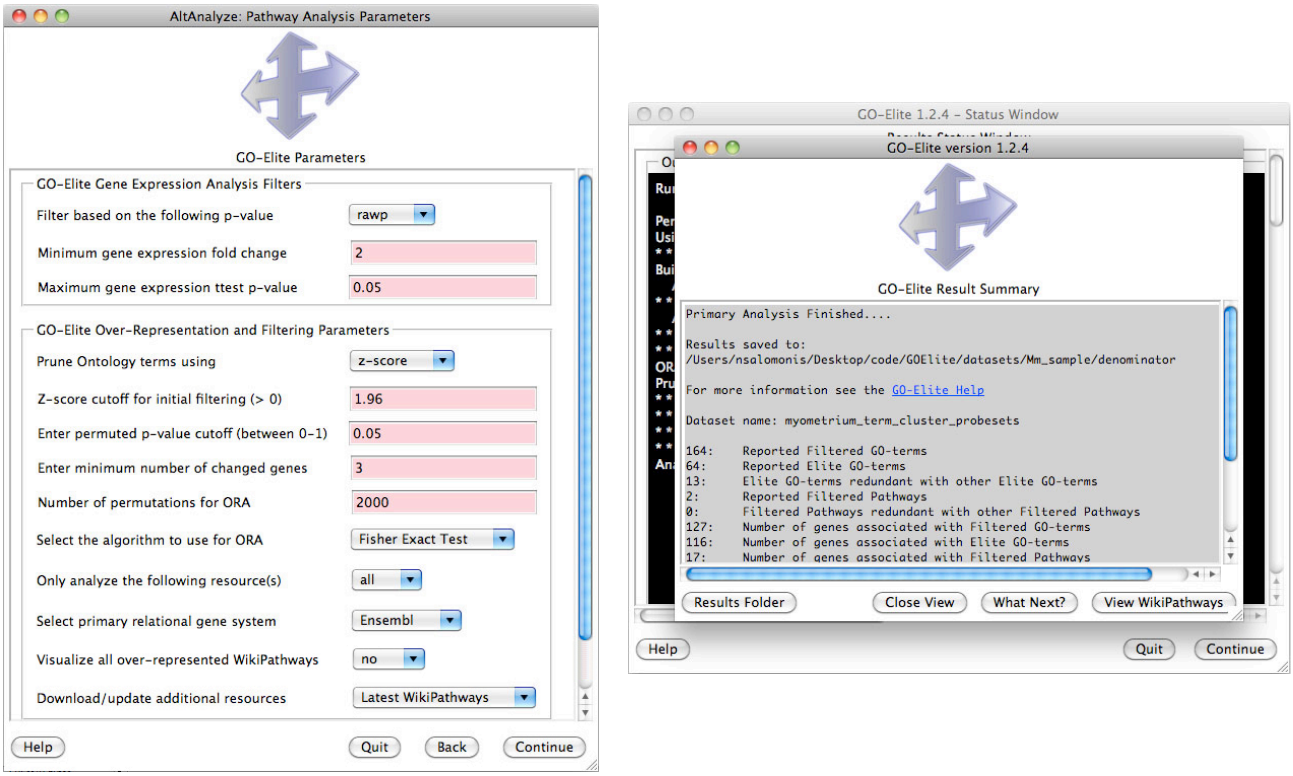


Figure 2.9. Perform Pathway Over-representation Analysis. (A) Options to analyze both differentially expressed and alternative expressed genes from AltAnalyze summary statistics. Options include how stringent the gene expression statistics are, whether or not to visualize pathways and methods for redundancy filtering between Gene Ontology (GO) terms from the program GO-Elite. Additional ontologies (Disease, Phenotype), pathways (KEGG, PathwayCommons) and gene-sets (e.g., BioMarkers, transcription factor targets) can be updated and analyzed. (B) Results are reported for GO and WikiPathways are reported when the user runs GO-Elite after the primary analysis.

11) Analyze ontologies and pathways with GO-Elite – If the user selects this option during the analysis or following, they will be presented with a number of options for filtering their expression data to identify significant regulated genes, perform pathway, ontology or gene-set over-representation analyses and filter/prune the subsequent results. Selecting to visualize WikiPathways may significant time to the analysis. Regulated alternative exons will also be analyzed using GO-Elite. A similar summary results window as above

will also appear with the GO-Elite WikiPathways and Gene Ontology results (Figure 2.9). For additional information, see: http://genmapp.org/go_elite

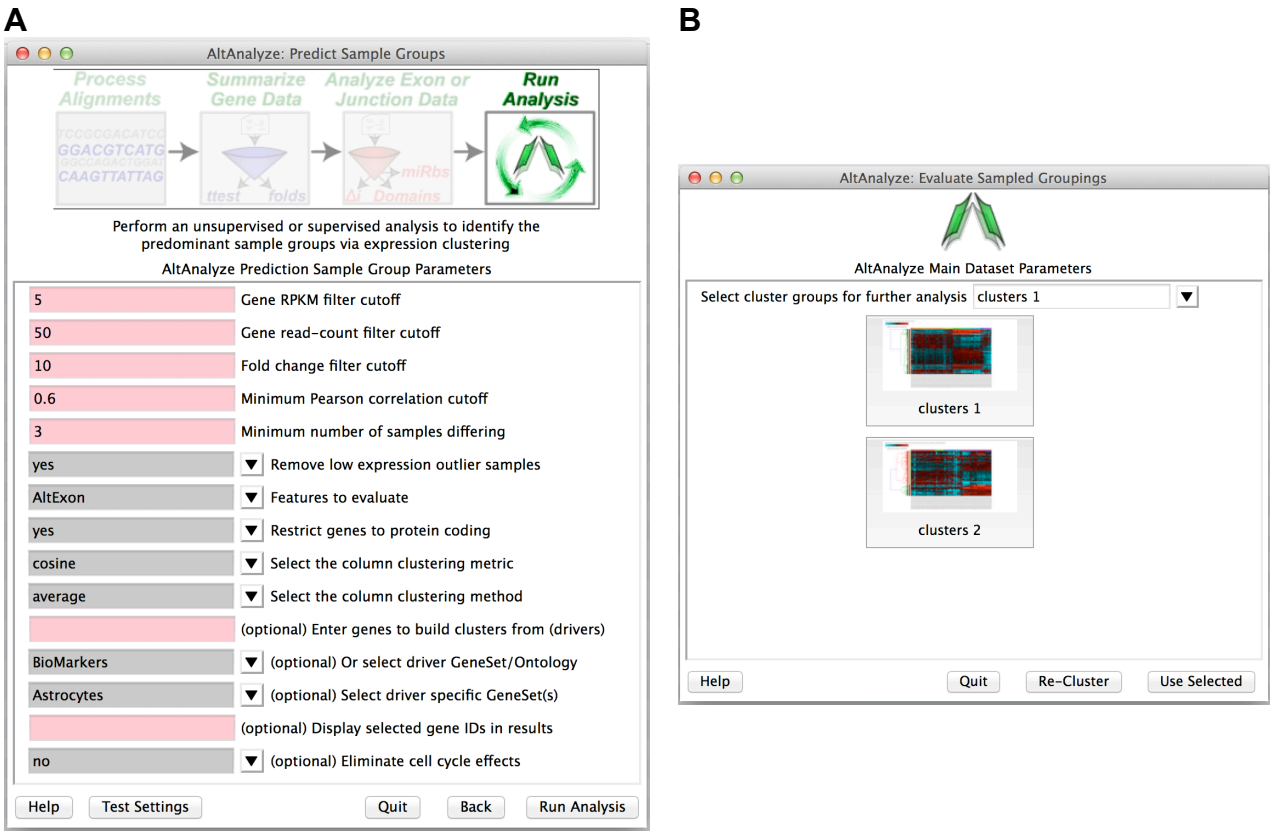


Figure 2.10. Iterative Pattern Discovery. (A) Available options for de novo identification of differentially regulated gene sets and sample clusters from the predict sample groups menu. These include the selection of specific pathways from which to correlate to all other genes to build coherent gene clusters, removal of cell-cycle effects and initial filtering and correlation parameters. (B) Resulting hierarchically clustered results from which to select from for further downstream comparison analyses in AltAnalyze. Selection of each icon will preview the entire cluster (specific genes can be identified from the resulting files saved in the ExpressionInput directory). Cluster options can be selected from the top pulldown menu for further comparison analyses.

12) Predict Groups from Unknown Sample Types – When a priori sample groups are unknown, such as with Single-Cell RNA-Seq analyses, it is recommended that the user discover sample groups clustered based on highly distinct gene or alternative isoform expression patterns. This can be accomplished by selecting the predict option from the Group selection menu. This menu implements a robust algorithm for iteratively filtering, correlating and clustering the data to find coherent gene expression patterns that can inform which sample groups are present. The resulting menu (**Figure 2.10**), will present the user with options for filtering their dataset (RNA-Seq or other input datasets), based on the maximal non-log expression for each row (Gene RPKM filer cutoff), number of associated reads for each gene (if applicable, otherwise set equal to the above), minimum required fold change difference between the minimum and maximum expressed samples for each gene and associated number of samples for this comparison, correlation threshold between genes for identification of coherent gene set clusters, which features to evaluate (gene, alternative exons, or both) and which gene sets to optionally build off. Although designed for RNA-Seq, any datasets can be analyzed with these menu options. The results will be presented in the form of clustered heatmaps, from which you can select from different options. Each heatmap will have somewhat distinct sample clusters from which you can select to perform the conventional AltAnalyze comparison analysis workflows, using the parameters established in the prior menu options. As results can vary based on the clustering algorithm used, we recommend that you have R installed on your computer (not required), to use the HOPACH clustering algorithm which provides improved results. For Windows operating systems, you will need to register R in your system path (https://code.google.com/p/altanalyze/wiki/SetRPath). Additional online tutorials and example videos are available to assist in this analysis: https://code.google.com/p/altanalyze/wiki/Tutorials

Additional Analysis Options

Many of the analysis tools present in AltAnalyze can be run independent of the above described workflows on user input text files. The input text files are either a table of log2 expression values, fold-changes or identifiers for over-representation analysis in GO-Elite. The options are available from the menu **Additional Analyses** from the menu **Select Analysis Methods** (Figure 2.2) as well as from the command-line. In addition to the below overviews, more information on these methods and available options can be found in **Section 2.5 and 2.6.**

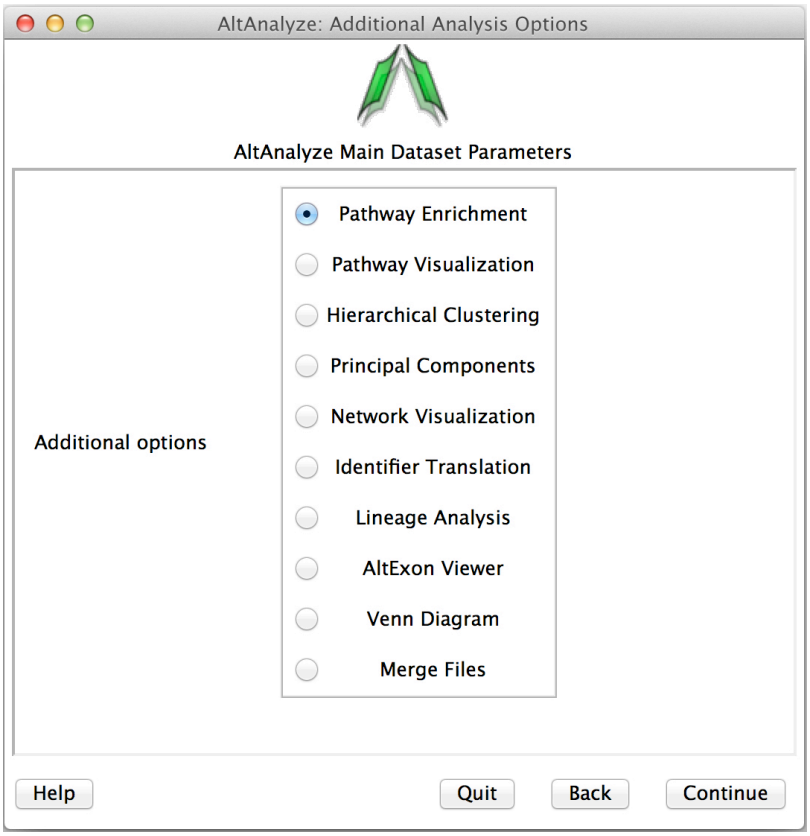


Figure 2.10. Additional Analysis Options. Analyses that can be run on any properly formatted user data. This includes pathway over-representation, visualization, hierarchical clustering, principal component, lineage analysis, network visualization, alternative exon graphs, Venn diagrams, identifier translation and file merging options.

1) Pathway Enrichment – Performs GO-Elite analysis as described in the previous section on any existing directory of input and denominator identifiers. This method runs GO-Elite independent of other AltAnalyze functions. In addition to saving lists of enriched biological categories, this tool produced hierarchically clustered heatmaps of enriched terms between input ID lists along with network graphs displaying interactions between genes and enriched pathways, ontology terms or gene sets. When the pathway visualization option is also selected, all enriched WikiPathways will also be exported as colored PDF and PNG images. If selecting already produced GO-Elite inputs produced by AltAnalyze, see the folder **GO-Elite/input** in the AltAnalyze results folder.

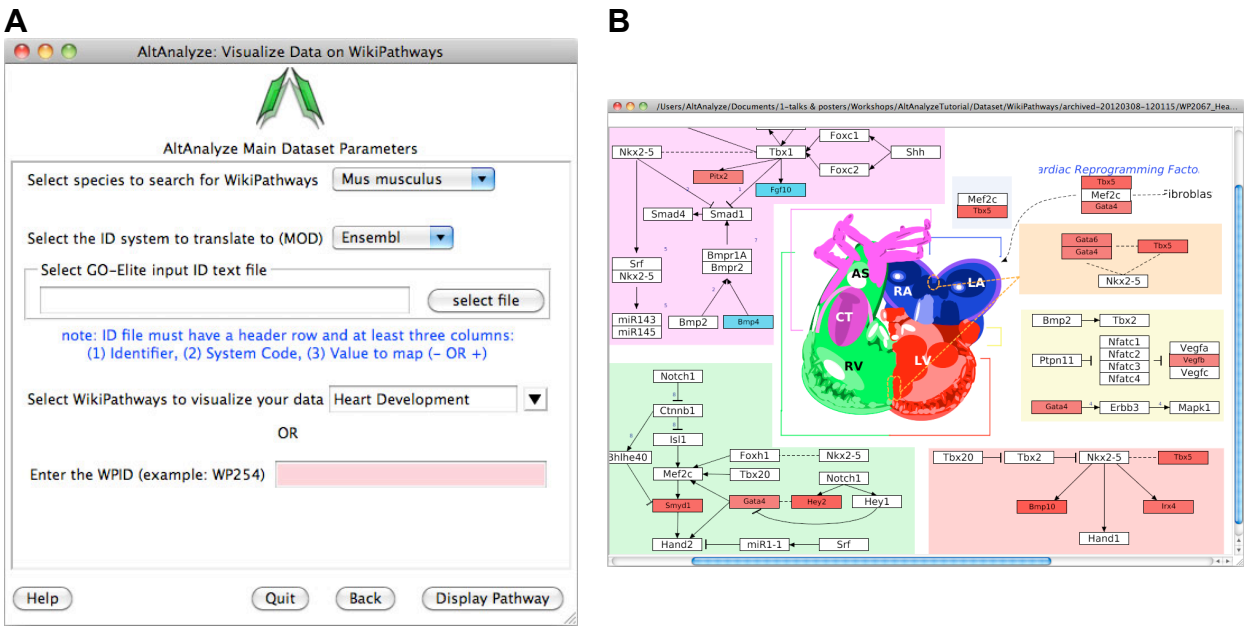
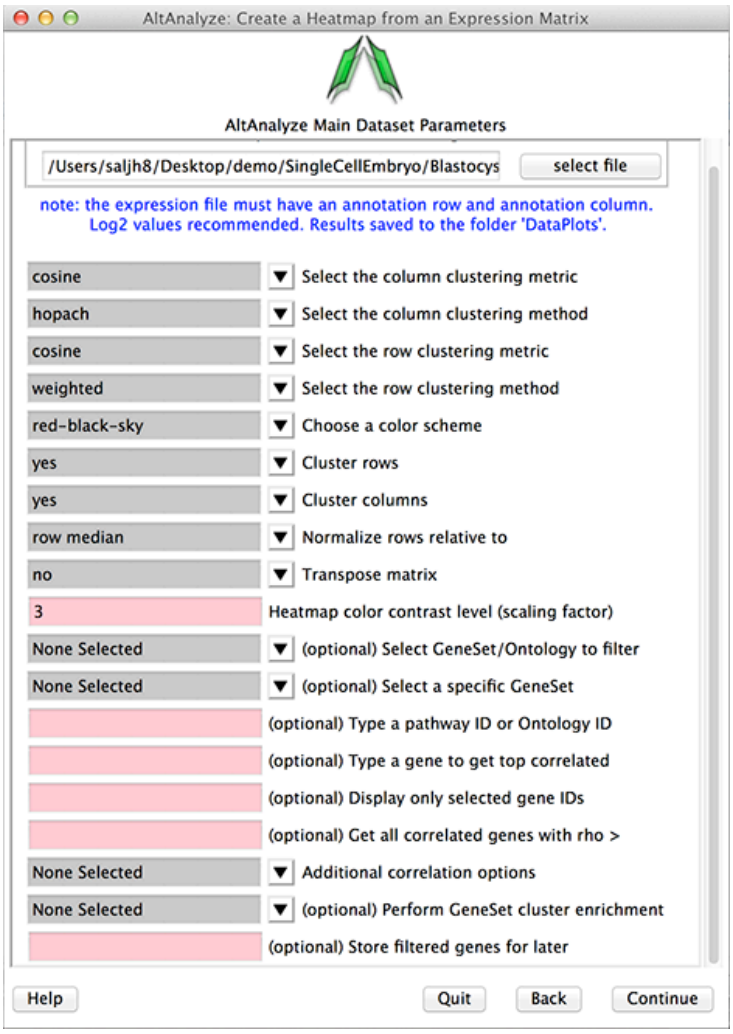


Figure 2.11. Visualize WikiPathways in AltAnalyze. Users can select pathways to visualize their GO-Elite input files upon for any WikiPathway. (A) The selection window opened from the **Additional Analyses** menu and (B) an example visualized pathway is shown. Default red = positive values, blue = negative values.

2) Pathway Visualization – Using the same GO-Elite input files, the user can select any current WikiPathway and visualize log2 fold changes on the selected pathway through

the AltAnalyze user interface. The input file must have three columns (ID, SystemCode, FoldChange). Images will be saved as PNG and PDF files to the same directory as the input file. When running from source-code, ensure that the python package lxml is installed (Section 1.5).

A



B

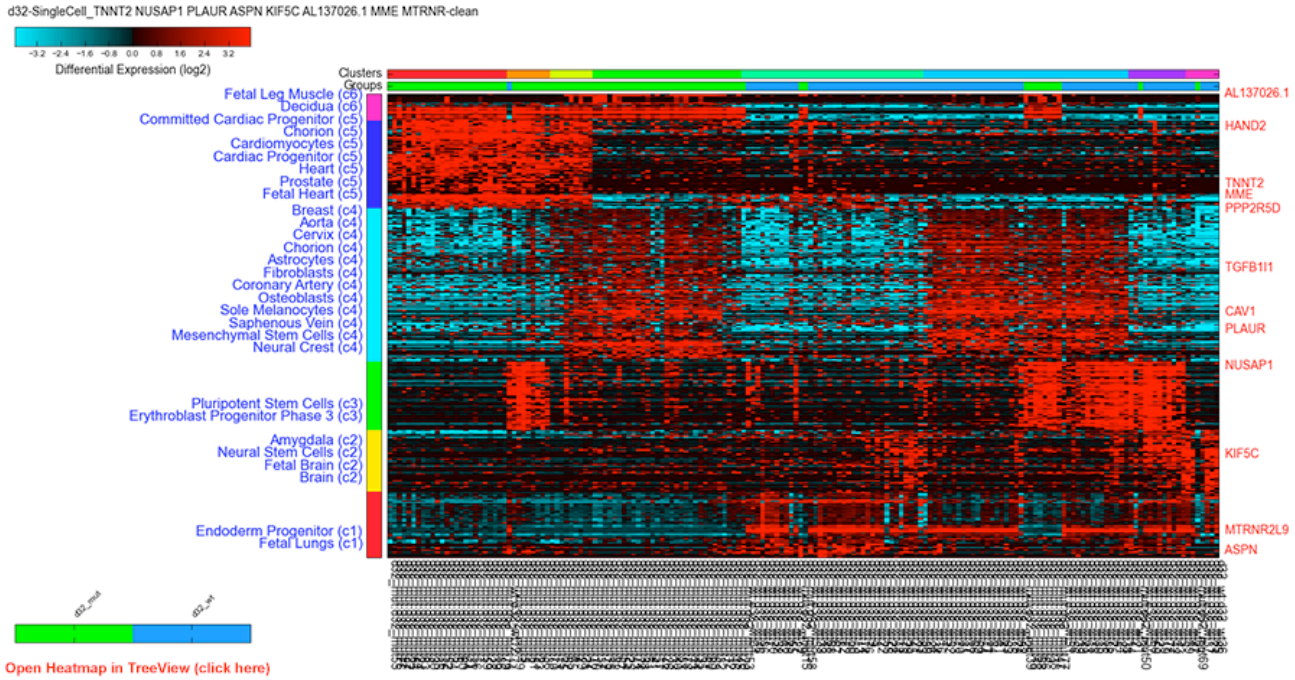


Figure 2.12. Hierarchical Cluster and Heatmap Visualization. This function can be used to identify global patterns of expression from any user input text file. (A) The basic and advanced parameters for clustering and visualization or shown as well as (B) an example heatmap derived by clustering columns and rows from an input text file of log2 folds, associated enriched pathways on the left and genes used selected by the software to build clusters from on the right (optional). In this example, single-cell RNA-Seq data (unpublished) was subjected to iterative driver gene discovery, beginning with PCA stored derived gene-sets, positive, top correlated genes (rho>0.4) with driver identification and BioMarker enrichment analysis. Additional advanced options are described in **Section 2.6**. Default red = positive values, blue = negative values.

3) Hierarchical Clustering – This interface will output a clustered heat map of rows and columns for any user supplied input text file. This file must have column names (e.g., samples) and row names (e.g., probesets), with the remaining data as values. The user can choose the clustering algorithm or metrics to use, whether to cluster rows or columns and what colors to use. This algorithm is automatically run when using the default

AltAnalyze workflows on two gene-sets: 1) all significantly differentially expressed genes and 2) outlier regulated genes. These files are available in the folder ExpressionOutput/Clustering. 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 interface. Outlier genes are those 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 significantly differentially expressed list. Many additional advanced options, including filtering by **pathways**, **ontology terms** and other **gene sets** and single-cell discovery analysis options are described in **Section 2.6**. Resulting clusters are interactive, allowing for viewed genes to be explored in online databases, pathways to be evaluated for associated genes and connections and deeper visualization in TreeView by selection of the TreeView viewer option in the lower left hand corner of the heatmap. Additionally, visualization of pre-assigned sample groups can be viewed by adding the group prefix prior to the sample name as a colon separated annotation (e.g., group_name:sample_name) or analyzing the expression files in the directory **ExpressionInput**.

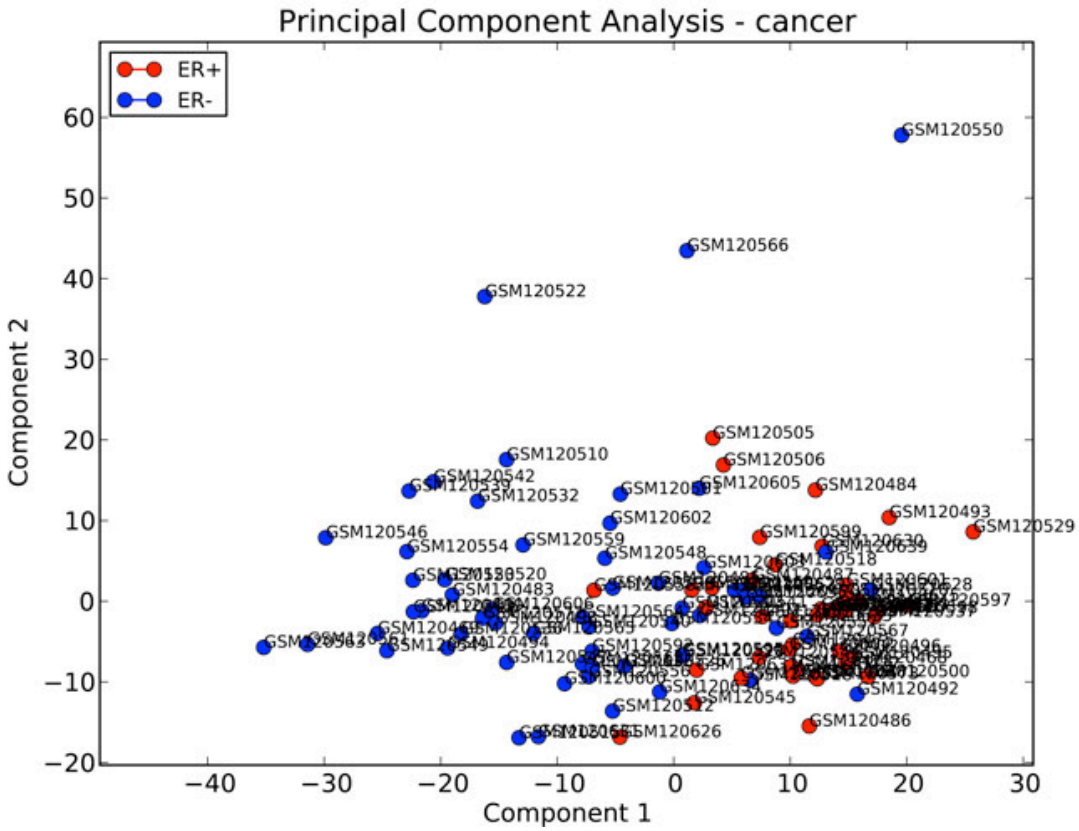
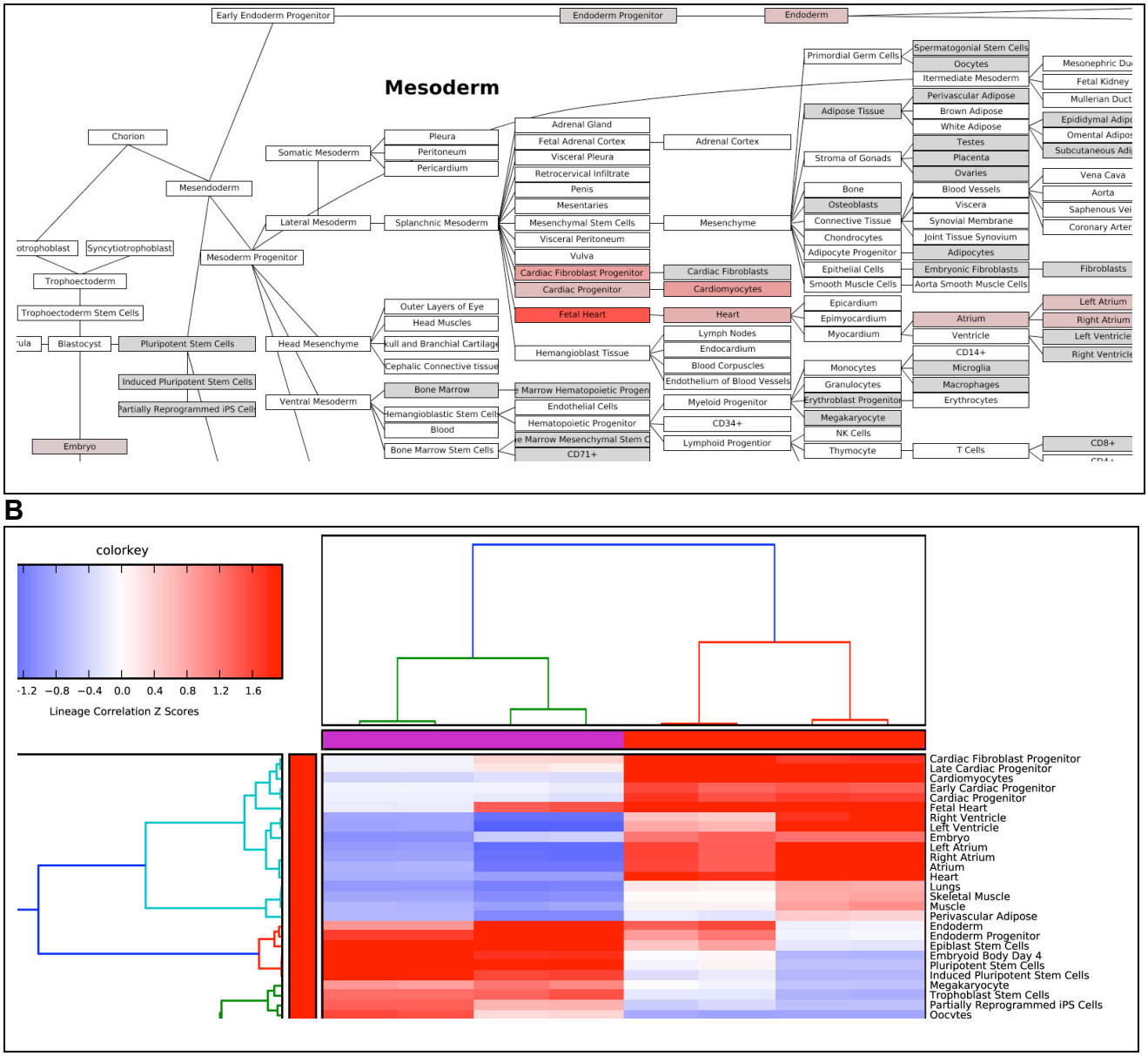


Figure 2.13. Principal Component Analysis. This function can be used to identify sample or gene similarities any user input text file. An example output image derived from the 1st and 2nd components are shown for the GEO dataset GSE5325, grouped by estrogen receptor status. Groups are defined in the input file by the presence of the group name proceeding the sample name and separated by a colon (e.g., cancer:sample1.txt).

4) Principal Component Analysis – This analysis takes the same input as hierarchical clustering (see above) and outputs a plot of samples clustered based on the first two principal components. Resulting genes associated with each principal component can be stored by entering a name for the analysis options menu, for further analysis in the above hierarchical clustering tool. This analysis is useful for determining how similar samples and biological groups are two each other in the 2D or interactive 3D space (see **Section 2.6** for more details).

A



B

Figure 2.14. Lineage Profiler Analysis. Lineage Profiler output for RNA-Seq cardiac differentiation time-points gene expression data. Visualization of correlation-based Z scores for (A) a single differentiation time-point along a comprehensive lineage network and (B) comparison of lineage associations for all samples examined after hierarchical clustering.

5) Lineage Analysis – This option allows the user to identify correlations to over 70 tissues and cell types for a group of biological sample. The input file must be tab-delimited and have expression values (log2 for microarray datasets) for each array (e.g., probeset)

identifier. Visualization of these results is provided for Z scores calculated from the lineage correlation coefficients upon a comprehensive Lineage WikiPathways network and as a hierarchically clustered heat map. Additional options for alternative modes of sample classification and custom reference sets are described in **Section 2.6**.

6) Network analysis – This option (aka NetPerspective) allows users to build and view biological interaction networks built using input sets of genes, protein, metabolite identifiers along with data indicating the regulation of these genes. See **Section 2.6** for more details.
7) Venn Diagram visualization – To identify the overlap between identifiers found in two or more files, users can select this menu options to obtain overlapping Venn Diagrams of the IDs overlapping in distinct files. Two methods are available for visualization of these diagrams: (A) Standard overlapping Venn's and (B) ID membership weighted (See **Section 2.6** for more details).
8) Alternative Exon Visualization – This method allows users to view either raw exon expression (e.g., RPKMs, probeset intensity) or gene-normalized normalized expression values (splicing-index) for all exon-regions for a given set of genes. Users must first select the AltResults folder from a given experiment. When more than two groups of samples are present in a given study, it is recommended that the user also perform the alternative exon anlaysis for all group comparisons (rather than pairwise) to simultaneously view all biological groups. When viewed in this context, distinct sample groups are displayed as different colored lines with error bars indicated by the standard error. Individually entered genes or files containing many genes can be displayed or saved to the users hard disk (exported to the folder **ExonPlots**). For more details, see **Section 2.6**.
9) Identifier Translation – This method can be used to translate from one gene, protein or metabolite ID system to another. Simply load a file of interest and select the input ID system and output ID system. A new file will be saved to the same directory in which the input file is in with the extension name of the output ID system.

10) Merge Files – This function allows users to identify sets of IDs that overlap or that are distinct from each other from a set of distinct files. As many as four files can be selected, using the options **Union** or **Intersection**.

2.3 Running AltAnalyze from Command-Line

In addition to using the default AltAnalyze graphical user interface (GUI), AltAnalyze can be run by command line options by calling the python source code in a terminal window or through other remote services. This option can be used to run AltAnalyze on a remote server, to batch script AltAnalyze services or avoid having to select specific options in the GUI. To do this, the user or program passes specific flags to AltAnalyze to direct it where files to analyze are, what options to use and where to save results.

Methods for Command-Line Processing

- When installing source code, run from within the AltAnalyze program directory by calling AltAnalyze.py followed by command-line arguments
- When running with OS-specific binaries of AltAnalyze directly call the binary files themselves:
    - Windows OS `AltAnalyze.exe`
    - Mac OS X `AltAnalyze.app/Contents/MacOS/AltAnalyze`
    - Ubuntu OS `./AltAnalyze`

Examples and Flag description

Detailed examples, flag descriptions, default values and associated information can be found at: http://code.google.com/p/altanalyze/wiki/CommandLineMode

2.4 AltAnalyze Analysis Options

There are a number of analysis options provided through the AltAnalyze interface. This section provides an overview of these options for the different compatible analyses (gene expression

arrays, exon arrays, junction arrays and RNA-Seq data). For new users, we recommend first running the program with the pre-set defaults and then modifying the options as necessary.

Selecting the Platform and Species

When beginning AltAnalyze, the user can select from a variety of species and platform types. Only array manufacturers and array types supported for each downloaded species will be displayed along with support for RNA-Seq analysis. When multiple gene database versions are installed, a drop-down box at the top of this screen will appear that allows the user to select different gene database versions. These gene databases include all resources necessary for gene annotation, alternative exon analysis (where applicable) and Gene Ontology and pathway analysis. Expression normalization, summarization, annotation and statistical analysis options are available for all input data types (e.g., microarray, RNASeq, proteomics, metabolomics data). At the bottom of this interface is a check-box that the user can select to download updated species gene databases, which will bring-up the database downloader window.

Selecting the RNA-Seq Analysis Method

Similar to microarray analysis options (see below), users can choose to analyze; 1) BED/TAB files, 2) an already built RNA-Seq expression file or 3) an AltAnalyze filtered RNA-Seq expression file. Since options 2 and 3 produce files from option 1, users will want to begin by loading a directory of RNA-Seq counts (junction and/or exon) from their analysis junction alignment analysis. Various programs can be used to produce the junction .bed format files that are used as AltAnalyze input. These include HMMSplicer (http://derisilab14.ucsf.edu/software/hmmsplicer/) and TopHat (http://tophat.cbcb.umd.edu/). Exon .bed files are produced using BAM files and an AltAnalyze produced input exon coordinate BED file with BEDTools (http://code.google.com/p/altanalyze/wiki/BAMtoBED). Future implementations of AltAnalyze will likely allow users to download these applications from within AltAnalyze and automatically call these applications through a python subprocess. The junction

and exon BED files consist of junction splice-site coordinates along with the number of reads from a sequencing run that correspond to that junction.

BED and TAB File Summarization

After loading junction BED files, AltAnalyze will like link each junction to an Ensembl gene and known splice-sites based on the provided genomic coordinates. When novel splice-sites are encountered, AltAnalyze will create a novel junction annotation for the splice-site (5' or 3'). In some cases, the splice-sites may be present in two different genes, indicating trans-splicing. The number of known-splice sites, novel splice sites and trans-splicing junctions will be reported upon import and in the log file. The resulting file, saved to the folder ExpressionInput/exp.NameYouEnter.txt, will contain unique identifiers indicating the Ensembl gene and associated exon-junction (e.g., E13.1-E14.1), indicating the exon block (e.g., "E13") and exon region (e.g., ".1") that the splice site positions aligns to. When the splice-site is novel it will be annotated as aligning to the corresponding exon, intron or UTR region with the additional notation "_position", where position is the genomic splice-site coordinate, following the exon region (e.g., E13.1_1000347, I13.1_1000532, U15.1_1001023). If exon .bed files are present in this same directory have the same prefix name (e.g., sample1__exon.bed and sample1__junction.bed), the exon coordinates will be matched to AltAnalyze annotated exon and intron regions (Ensembl/UCSC) and novel exon regions inferred from the junction BED locations. Both junction expression and exon expression will be written to the same file with the prefix "exp.". This file can subsequently be loaded as option 2 ("Process Expression File"). The same process is applied to .tab files from BioScope, accept that exon and junction count files are produced simultaneously and output to different format files.

Selecting the Microarray Analysis Method

After the user has selected the species of interest, they must choose what type of data they will next be analyzing. Data can consist of; 1) Affymetrix CEL files, 2) an already processed expression text files, 3) properly formatted and filtered AltAnalyze expression input text file or 4)

restricted list of probe sets to be directly analyzed. If beginning with Affymetrix CEL files all three of these file types are produced in series (see following section) and automatically processed without any user intervention. If all CEL files from your study already been previously in AltAnalyze or in another program, the user can load this file be selecting the option “expression file” and choosing this text file from your computer. This file needs to contain data from arrays corresponding to at least two biological groups. Users may wish to re-analyze these files to change their expression filtering parameters to be more or less stringent. For the two or more biological groups (see how to define in Figure 2.6), AltAnalyze will segregate the raw data based on the user-defined pairwise group comparisons and filter the containing probe sets based on whether they match the user-defined thresholds for inclusion and are associated with Ensembl genes (see the below section: Expression Analysis Parameters). These files will be saved to the folder “AltExpression” in the user-defined output directory. These files can be later selected by choosing the option “AltAnalyze filtered”, if the user wishes to re-run or use different AltAnalyze alternative exon analysis options (see below section: Alternative Exon Analysis Parameters).

CEL File Summarization

CEL files are one of the file types produced after scanning an Affymetrix microarray. The CEL file is produced automatically from the DAT file (an image file, similar to a JPEG), by the Affymetrix software by overlaying a grid over the microarray florescent image and assigning a numeric value to each cell or probe. From this file, expression values for each probe set can be calculated and normalized for all arrays in the study using various algorithms.

When choosing to analyze CEL files in AltAnalyze, the user will be prompted to identify the folder containing the CEL files and the folder in which to save these other results to. The user will also need to assign a name to the dataset. These CEL files will be summarized using the RMA algorithm using the program Affymetrix Power Tools (APT). The APT C++ module “apt-probeset-summarize” is directly called by AltAnalyze when running AltAnalyze on a Mac, PC or Linux operating system. Unlike some other applications, APT is packaged with AltAnalyze and thus does not require separate installation. However, because it is a separate application

there may be unknown compatibility issues that exist, depending on your specific system configuration and account privileges. For human and mouse exon arrays, AltAnalyze also allows for the masking of probes with cross-hybridization potential, prior to running RMA. This is performed through an experimental APT function (--kill-list), masking probes that are indicated in files produced for the MADS application (http://biogibbs.stanford.edu/~yxing/MADS/Annotation.html) that cross-hybridize to an off-target transcript within 3bp mismatches and a person correlation coefficient > 0.55, as per the MADS recommendations. The probes with cross-hybridiation potential are indicated in the AltAnalyze directory "AltDatabase/Hs/exon/Hs_probes_to_remove.txt".

APT requires the presence of a library file(s) specific for that array. AltAnalyze will automatically determine the array type and can install these files if the user wishes (currently most human, rat and mouse arrays supported). If AltAnalyze does not recognize the specific array type or the user chooses to download these files themselves, they will need to select the appropriate files when prompted in AltAnalyze. For exon, gene and junction arrays, a PGF, CLF and antigenomic BGP file are required. These files will be automatically downloaded and installed if the user selects "Download" when prompted. For the AltMouse and 3'arrays, the appropriate CDF file will be downloaded. In addition to these library files, a NetAffx CSV annotation file will be downloaded that allows for addition of gene annotations (non-exon arrays) and Gene Ontology pathway annotations (all arrays). Once installed, AltAnalyze will recognize these files and automatically use them for all future analyses. Once the user selects the appropriate directories and files, the user will be prompted to select the remaining options in AltAnalyze, before APT is run. Once run, a tab-delimited text expression file will be produced for all probe sets on the array and a detection-above background (DABG) p-value file (not applicable to AltMouse or 3'arrays).

Loading a Processed Expression File

If performing an RNA-Seq analysis, this is the file produced immediately after loading and aligning the junctions to exons, introns and UTR regions. For Affymetrix arrays, if CEL files are

processed outside of AltAnalyze, the user must save the resulting expression text file in tab-delimited format. It is all right if the first rows in the file have run information as long as they are preceded by a pound sign (#).

Expression Analysis Parameters

The options presented in this interface (Figure 2.4) allow the user to determine what fields are present in the gene expression output file, what scale the data is in (e.g. logarithmic), which RNA-Seq reads or probe sets (aka features) to use when calculating gene expression and how to filter features for subsequent analyses.

1) Perform an alternative exon analysis - Selecting the option “just expression” will halt the analysis after the gene expression result file has been written, such that no splicing analysis is performed. This option is only available for splicing-sensitive platforms.
2) Expression data format - Indicates the format in which the normalized expression values or counts have been written. When CEL files have been processed by AltAnalyze, ExpressionConsole, APT, RMAExpress or through R, the file format will be logarithmic base 2 (log). The default format of RNA-seq counts is non-log. If the user designates “non-log”, then expression values will be log base 2 (log_2) transformed prior to analysis.
3) Determine gene expression levels using - For splicing RNA-Seq and sensitive microarrays, the user has the choice to alter the way in which gene expression values are calculated and how to filter their feature-level expression files prior to alternative exon analysis. When “core” features are selected for this option, all core features (Affymetrix core annotated and any exon aligning feature) linked to a unique gene will be used to calculate a measure of gene expression by taking the mean expression of all associated feature values. When the “constitutive” is selected, only those features that have been annotated as constitutive or common to the most isoforms will be used for gene expression calculation. In either case, only features with at least one array possessing a DABG p-value less than the user threshold (Affymetrix only) will be retained (if a DABG

p-value file is present). In order to exclude this threshold, set the minimum DABG p-value equal to 1.

4) Include replicate experimental values in the export - Instructs AltAnalyze whether to include the expression values associated with each BED or CEL file in the output file. If not selected only the mean expression value of all BED or CEL files for each biological group will be written.
5) Remove probesets with a DABG p-value above – When a DABG file has been produced (default when summarizing CEL files with AltAnalyze for exon-arrays), this option is applied. The default DABG p-value cutoff is $p<0.05$. This will filter out any non-constitutive probe set that has a mean DABG $p>0.05$ for both compared biological groups. For probe sets used in determining gene expression levels, both biological groups must have a DABG p < user-value. In order to exclude this option, you can remove the DABG file (contains the prefix “stats.”), or set this value equal to 1.
6) Remove probesets/reads expressed below (non-log) – Filters can be applied to both Affymetrix array data and RNA-Seq datasets to exclude non-expressed probesets, genes, exons or junctions. In all cases, the expression of a feature is examined (non-log value) to see if that feature meets the indicated threshold. If not, it is excluded or considered non-expressed. This can be critical for comparisons where neither condition demonstrates gene or exon expression and hence can be considered an artifact. To exclude this option, set the default value to 1 for probeset or read count thresholds and 0 for RPKM filters.
7) Comparison group test statistic – Allows the user to calculate a p-value for gene expression and splicing analyses based on different tests (e.g., paired versus unpaired t-test, rank sum, Mann Whitney, Kolmogorov Smirnov). These test apply to two sample group comparisons, whereas any multi-group comparison analyses rely only on an f-test statistic. For unpaired t-test, the f-test statistic is also used. These tests are provided through a module of the open-source statistical package Salstat (http://salstat.sourceforge.net/).

8) Perform expression clustering and visual QC – This option will automatically generate various quality control plots and hierarchical clustering heatmaps based on the user input dataset analyzed. Basic quality control metrics include the: 1) distribution of normalized log2 expression values, 2) raw signal intensities (Affymetrix - prior to APT), 3) deviation of residuals from the mean (Affymetrix – post RMA), 4) Feature-level (exon, junction, intron) expression box-plots (RNA-Seq) and 5) the total expression of each feature (RNA-Seq) for all analyzed samples. Principal component analysis and hierarchical clustering are also applied to all significantly regulated genes (default or user-defined criterion). Hierarchical clustering is also applied to genes with outlier expression values to identify poor-replicating samples. When this option is selected, the results will be available as PDF and PNG in the folder DataPlots and from the GUI once the analysis is finished (Figure 2.8A). When run from source-code, requires installation of MatPlotlib and Numpy.
9) Perform cell profiling with LineageProfiler – Lineage Profiler is a novel tool designed to analyze and visualize the cellular composition of supplied RNA profiles. Only RNA profiling data with gene expression values (e.g., Affymetrix and RNA-Seq), as opposed to folds only, are currently supported. Lineage Profiler produced pearson correlation coefficients and associated Z scores for each sample analyzed. These Z scores are visualized as a hierarchically clustered heatmap for all samples and as a comprehensive lineage network for the biological groups (Figure 2.14). When running from source-code this tool requires the python libraries lxml, MatPlotLib and Numpy for results visualization and is optimized to run with Scipy.
10) Perform ontologies and pathways with GO-Elite – Choosing “decide later” will allow the user to view the GO-Elite pathway and Gene Ontology over-representation analysis options after the main gene expression and/or alternative exon analysis is run. This will prompt a separate status window and results summary window displaying over-representation statistics for pathway analysis. If the option “run immediately” is selected, GO-Elite will run right away without a separate window. Please note, GO-Elite analysis can take up to an hour per criterion when using the default parameters, when analyzing

all possible gene-sets, pathways and ontologies. For this reason, multithreading has been implemented in GO-Elite version 1.2.6 and greater. For more details on this analysis see: http://www.genmapp.org/go_elite/help_main.htm

Alternative Exon Analysis Parameters

The options presented in this menu (Figure 2.5) instruct AltAnalyze what statistical methods to use when determining alternative exon expression, which features to select for analysis, what domain-level and miR-BS analyses to perform and what additional values to export for analyses in other tools. Details on each analysis algorithm are covered in detail in section 3.2.

1) Select the alternative exon algorithm – For exon and gene arrays, the splicing index and FIRMA methods are available and for RNA-Seq and junction arrays the ASPIRE and linear regression methods are available. RNA-Seq and junction analyses can also include single junction analyses (e.g., Splicing-index, MiDAS), following the reciprocal junction analysis. These methods are used to calculate an alternative exon score, relative to gene expression levels. The default value for splicing-index and FIRMA analyses is 2, indicating that an adjusted expression difference greater than two fold (up- or down-regulated) is required for the probe set to be reported. Based on the algorithm, different values and scales will apply. For junction analyses, the ASPIRE algorithm default cutoff is 0.2, whereas the linear-regression algorithm is 2. For linear-regression (linearregres), a minimum value of 2 will select any linear-regression fold greater than 2 (result folds are reported in log 2 scale, however), up- or down-regulated, whereas ASPIRE's scores ranging from -1 to 1. See algorithm descriptions for more details (section 3.2).
2) Minimum alternative exon score – This value will vary based on the alternative exon analysis method chosen (see above options).
3) Max MiDAS/normalized intensity p-value – This is the p-value cutoff applied to MiDAS and splicing-index or FIRMA ttest p-values for single exon/junction analyses. Currently, the user cannot set different p-value thresholds for these two statistics. More on MiDAS can be found below and in section 3.2.

4) Select probesets to include – This option is used to increase or decrease the stringency of the analysis. In particular, this option allows the user to restrict what type of features are to be used to calculate an alternative exon score. In the case of junction analyses, this option includes the ability to merge the expression values of junctions/exons that measure the same differential inclusion of an exon (combined-junctions). For exon and gene arrays, there are three options, “core”, “extended” and “full”. Although these are the same probe set class names used by Affymetrix to group probe sets, AltAnalyze uses a modification of these annotations. Specifically, probe sets with the core annotation include all Affymetrix core probe sets that specifically overlap with a single Ensembl gene (2) (based on genomic position) along with any probe set that overlaps with an Ensembl or UCSC exon (3). Likewise, extended and full probe sets are those remaining probe sets that also align to a single Ensembl gene, with the Affymetrix extended or full annotation. For RNA-Seq and junction arrays, options include “all”, “exons-only”, “junctions-only”, “combined-junctions”.
5) Maximum absolute gene-expression change – This value indicates maximum gene expression fold change (non-log, up- or down-regulated) that is allowed for a gene to be reported as alternatively regulated. The default is 3-fold, up or down-regulated. This filter is used with assumption that alternative splicing is a less critical factor when a gene is highly differentially expressed.
6) Perform permutation analysis - (***Junction Analyses Only***) This analysis reports a p-value that represents the likelihood of the observed alternative exon score occurring by change, after randomizing the expression values of all samples.
7) Maximum reciprocal-junction permutatep – (***Junction Analyses Only***) This p-value cutoff applies to the permutation based alternative exon score p-values when performing ASPIRE or linearregres (see section 3.2).
8) Export all normalized intensities – This option can be used to compare alternative exon scores prior to filtering for biological multiple comparisons, outside of AltAnalyze. For example, if comparing multiple tissues, the user may wish to export all normalized

intensities (feature non-log expression divided by gene-expression) for all tissue comparisons. The results will be stored to the AltResults/RawSpliceData folder in the user-defined output-directory. For junction analyses, the ratio of the normalized intensities (NI) is reported for the two reciprocal-junctions (j1 and j2).

9) Calculate MiDAS p-values – This statistic is analogous to the ttest p-value calculated during the splicing-index analysis (see section 3.2 for more details). If not selected, then only the splicing-index or FIRMA (depending on the user selection) fold and p-value will be used to filter alternative exon results.
10) Calculate normalized intensity p-values – Indicates whether to calculate the splicing-index or FIRMA ttest p-values and filter using the above threshold.
11) Filter results for predicted AS – This option instructs AltAnalyze to only include regulated exons in the output that have been assigned a valid splicing annotation (e.g., alternative-cassette exon) provided by AltAnalyze. These annotations exclude exons with no annotations or those with only an alternative N-terminal exon or alternative promoter annotation.
12) Align feature to protein domains using – This option is used to restrict the annotation source for domain/motif over-representation analysis. If “direct-alignment” is chosen, only those features that overlap with the genomic coordinates of a protein domains/motif will be included in the over-representation analysis, otherwise, the inferred method is used (see section 3.2 for more details).
13) Number of algorithms required for miRNA binding site reporting – This option is used to filter out miR-BS predictions that only occur in one of the four miR-BS databases examined. For more miR database information see section 6.5.
14) Type of group comparison to perform –This option indicates whether to only perform pairwise alternative exon analyses (between two groups) or to analyze all groups, without specifying specific comparisons.

2.5 Overview of Analysis Results

AltAnalyze will produce three sets of results:

1) Gene expression (GE)
2) Alternative exon
3) Diagnostic and exploratory visualization

These files are all saved to the user-defined output directory and can be explored through the use of a spreadsheet data viewer, such as Microsoft Excel or OpenOffice, and a PDF viewer. Issues reading these spreadsheets may occur on non-US Windows configurations that (e.g., improper processing of numbers of with decimals). Additional information on the statistical methods used and source of annotations can be found in Section 3.

Gene Expression Summary Data

There are five primary GE summary result files produced by AltAnalyze. These files contain raw data, summary statistics and/or comprehensive annotations..

1) DATASET file – Gene annotations, comparison and ANOVA statistics, raw expression values and counts (saved to **ExpressionOutput**).
2) GenMAPP file – Comparison statistics (saved to **ExpressionOutput**).
3) Summary statistics file – Overview statistics for protein and non-coding genes, up- and down-regulated counts and microRNA binding site statistics (saved to **ExpressionOutput**).
4) Clustering input file – Contains all differentially expressed genes based on user comparisons (saved to **ExpressionOutput/Clustering**).
5) GO-Elite input files – Lists of differentially expressed genes as input for pathway over-representation (saved to the folder **GO-Elite**).

The first is a file is a complete dataset summary file with the prefix "**DATASET**-" followed by the user-defined dataset name containing all array expression values (gene-level for RNA-Seq and

tiling-arrays), calculated group statistics (mean expression, folds, raw and adjusted t-test and f-test p-values) and gene annotations (e.g., gene symbol, description, Gene Ontology, pathway and some custom groups, genomic location, protein coding potential, miRNA binding sites). For microRNA arrays, other annotations from the Affymetrix annotation CSV will replace these (user supplied). For RNA-Seq and tiling arrays, the gene expression values are derived from either RNA-Seq reads or probe sets most informative for transcription (known exons or constitutive) (see "Select expression analysis parameters", in Section 2.3). **For RNA-Seq, if only junctions are present, then constitutive junctions or known junctions will be used, however, if exon reads are present, these will be used over junction reads.** Constitutive features are determined by finding discrete exon regions that are common to the most mRNA transcripts (Ensembl and UCSC) for all transcripts used in the AltAnalyze database build (section 6). For junction arrays (hGlue, HJAY, HTA2.0 and MJAY), both constitutive exon aligning probe sets and constitutive junction aligning junction probe sets (most common junctions in mRNAs) are used, whereas for RNA-Seq, constitutive exons are used. When one or more gene expression reporting probe sets have DABG p-values with at least one biological group with a mean value below the user defined threshold, these probe sets will be used to calculate gene expression, otherwise, all gene expression reporting probe sets will be used.

The second file, with the prefix "**GenMAPP-**", contains a subset of columns from the dataset summary file for import into GenMAPP (4) or PathVisio (5) (http://www.pathvisio.org/PathVisio2). This file has the prefix "GenMAPP" and excludes all gene annotations and individual sample expression values. This text file can be imported into these programs to create criterion and color the associated results on pathways (see tutorials here: http://code.google.com/p/altanalyze/wiki/PathwayAnalysis).

The third file, with the prefix "**SUMMARY-**", contains overview statistics for that dataset. These results are divided in to Ensembl protein coding and non-coding genes. Counts for up- and down-regulated genes are provided separately. Genes called "expressed" are most relevant for RNA-Seq analyses, where raw counts incremented by 1 for fold calculation purposes (gene-level). A microRNA count is provided for a single miRNA (miR-1 by default). To change this,

users must manually edit the file `ExpressionBuilder.py` (exportGeneRegulationSummary function).

The fourth file, with the prefix "**SampleLogFolds-",** provides all log2 fold changes relative to the mean expression of all samples in the dataset for all "regulated" genes. Genes included in this file are those that have greater than 2 fold (up or down) change in gene expression and comparison statistic $p < 0.05$ for any user indicated comparison. To change these defaults, the user must currently select "run immediately" for the GO-Elite analysis option and change the associated defaults. This file will be used for (A) hierarchical clustering and (B) principal component analysis, when these options are selected.

The fifth file type, saved to the folder "GO-Elite/input" are differentially or alternative expressed genes and summary statistics for all comparisons. These files are primarily used as input for performing ontology, pathway or gene-set enrichment analysis using the GO-Elite option. This analysis can be run along with the default AltAnalyze workflows, immediately afterwards, or independently using the **Additional Analyses** menu (**Pathway Enrichment** option). These lists can also be used for **Pathway Visualization** also from the Additional Analyses menu. These files contain all differentially expressed genes (prefix **GE.**), alternative regulated (prefix **AS.**), as well as up and downregulated genes (suffix **–upregulated** or **–downregulated**). The IDs listed will be either the primary microarray identifier or an Ensembl gene ID, based on the platform analyzed. Also included are the log2-fold changes and p-values associated with the indicated comparisons. These files may also be of use in external analysis programs.

Alternative Exon Summary Data

These results are produced from all features (RNA-Seq reads or probe sets) that may suggest alternative splicing, alterative promoter regulation, or any other variation relative to the gene expression for that gene (derived from comparisons file). When the user chooses to either analyze all groups rather than just pairwise comparisons or both, the same output files will be produced but report MiDAS p-values comparing all conditions and the maximum possible

splicing index fold between all conditions (Section 3.2). Each set of results corresponds to a single pairwise comparison (e.g., cancer vs. normal) and will be named with the group names you assigned. Four sets of results files are produced in the end:

6) RNA-Seq or probe set-level – Feature-level statistics, exon annotations, AS/APS annotations, and functional predictions (protein, domain and miRNA binding site).
7) Gene-level – Gene-level summary of data in feature-level file.
8) Domain-level – Over-representation analysis of gene-level domain changes due alternative exon regulation.
9) miRNA binding sites - Over-representation analysis of gene-level, predicted miRNA binding sites present in alternatively regulation exons.
10) DomainGraph input file – Direct or inferred Affymetrix Exon 1.0 ST probe set IDs and summary statistics (see file #4) for analysis in DomainGraph. For non-exon arrays (e.g., RNA-Seq, Affymetrix junction or gene arrays), corresponding regulated exons are translated to the overlapping exon ID (see Section 8).
11) All processed splicing scores – Feature-level statistics (see file #4) above for all analyzed features (not just significant). This is in the same format as the DomainGraph export file (see file #7).
12) All feature-normalized intensities– (optional) Feature-level normalized intensities (see file #4) used to calculate splicing-index statistics or FIRMA fold changes for each sample. To obtain this file "Export all normalized intensities" option.
13) Summary statistics file – Global statistics, reporting the number of genes alternatively regulated, number differentially expressed and summary protein association information (e.g., mean regulated protein length).

Each file is a tab delimited text file that can be opened, sorted and filtered in a spreadsheet program. These files are saved to the user-defined output directory under "**AltResults/AlternativeOutput**", all with the same prefix (pairwise group comparisons). AltAnalyze will analyze all pairwise comparisons in succession and combine the feature-level

and gene-level results into two additional separate files (named based on the splicing algorithm chosen).

Feature- and Gene-Level Alternative Exon Result Files

The feature-level file contains alternative exon data for either one probe set (exon-array), exon/junction IDs or reciprocal junctions (RNA-Seq and junction arrays). More information on these fields can be found at http://code.google.com/p/altanalyze/wiki/ProteinDirectionIndicator. In general, these file include:

- Gene and feature annotations (e.g., description, symbol, exon/junction or probe set ID, feature exon ID, transcript clusters, links to Ensembl/UCSC exons, ordered exon-region IDs).
- Mean feature expression values for the regulated feature(s).
- Gene expression changes and baseline expression.
- Statistical results (e.g., splicing-index score, deviation value, normalized intensity p-value, adjusted normalized intensity p-value, MiDAS p-values, raw feature p-value).
- Alternative exon annotations (e.g., splicing-events, alternative promoters, alternative annotation confidence score).
- Protein- and microRNA-level associations (e.g., associated IDs, sequence, pattern of regulation, regulated domains/microRNA binding sites).
- Genomic coordinates of the regulated exon or pairs of reciprocal junctions regulated.

The gene-level file contains a summary of the data at the gene level, with each row representing a unique gene. This file also includes:

- Gene Ontology and pathway information for each gene obtained from Ensembl.

Protein Domain/Motif and miRNA Binding Site Over Representation Files

Over-representation analyses, (files 3 and 4) have the same structure:

- Column A is the name of the miR-BS or protein domain (e.g., sequence motif).

- Column B is the number of unique genes associated with alternatively regulated features for that sequence motif (aka Changed).
- Column C is the number of genes analyzed for over-representation that correspond to that sequence motif (aka Measured).
- Column D is the percentage Changed (Changed/Measured).
- Column E is the over-representation z-score (see Section 3 - Algorithms) for all unique genes aligning to the sequence motif that are alternatively regulated. A value of 1.96 is approximate to a p-value of 0.05 assuming a normal distribution.
- Column F is the Fisher Exact test p-value to assess the likelihood of this observation occurring by chance.
- Column G is the Benjamini-Hochberg adjusted p-value of F, to take into account multiple hypothesis correction.
- Column H contains all gene symbols for all unique genes changed.

Comparison Evidence File

A common question for biologists analyzing alternative exon profiles is which events are most likely true versus false positive predictions. RNA-Seq and junction microarrays allow for independent detection of alternative splicing events using only exon-junctions or only detected exons. The comparison evidence file examines results from the reciprocal junction analysis (ASPIRE or Linear Regression) and the single feature (exon or junction) analysis (splicing-index), to determine which events are predicted by both analyses or only be one. Those splicing-events predicted by both represented independently verified events that are most likely to represent valid known or novel alternative splicing events in the dataset. This file includes:

- Gene, exon and junction annotations (e.g., description, symbol, junction or probe set ID, feature exon ID, links to Ensembl/UCSC exons, ordered exon-region IDs).
- Statistical results (e.g., splicing-index score, deviation value, normalized intensity p-value, adjusted normalized intensity p-value, MiDAS p-values, raw feature p-value).

- Alternative exon annotations (e.g., splicing-events, alternative promoters, alternative annotation confidence score).
- Protein- and microRNA-level associations (e.g., associated IDs, sequence, pattern of regulation, regulated domains/microRNA binding sites).
- Algorithm from which the event was predicted (e.g., ASPIRE, splicing-index).

Diagnostic and Exploratory Visualization Results

In addition to the results files listed in the previous sections, various image plots are produced by AltAnalyze to assess quality control (QC), cluster gene or sample profiles (clustering) and identify associated cell types represented in each sample (Lineage Profiler). All plots are saved to the folder **DataPlots** in the user-defined output directory. Unlike the other AltAnalyze methods, these analyses require the installation of non-default Python packages if running directly from the Python source-code (see Section 1.5). However, these dependencies are already included in the OS specific binary distributions.

Basic Quality Control

Multiple basic quality control plots are produced by AltAnalyze to evaluate sample quality and overall technical similarity to other samples in the dataset. Different QC metrics are applied based on whether the input data is from: (A) AltAnalyze normalized Affymetrix files, (B) RNA-Seq data or (C) pre-processed expression files.

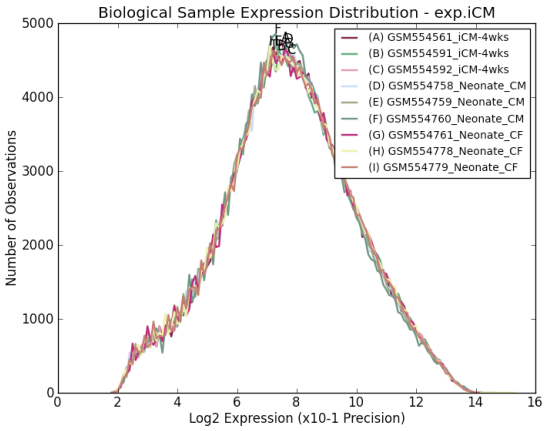
If data from (A) applies, three output QC files will be generated: 1) distribution of normalized log2 probeset intensity values, 2) mean raw signal intensities of each array and 3) mean absolute deviation (MAD) of the RMA residuals for each array (Figure 2.15 A-C). The source data for all of these three QC metrics are derived from Affymetrix Power Tools (Section 1.6) RMA analysis built into AltAnalyze. For more details see: http://bib.oxfordjournals.org/content/early/2011/04/15/bib.bbq086.full.

If data from (B) applies, three groups of QC files will be generated: 1) distribution of log2 read-counts (exon and junction), 2) feature-level box-plots for the distribution of exon, junction

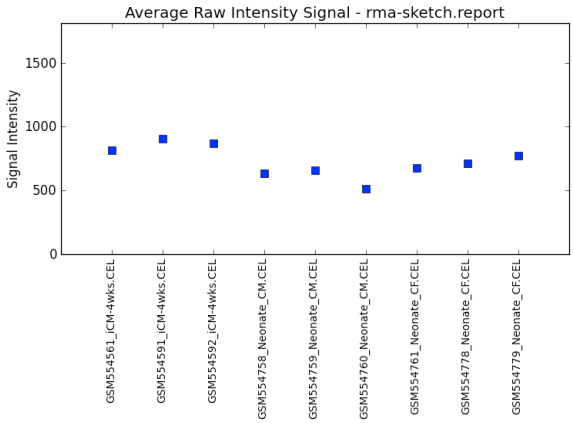
and intron read-counts and 3) total number of reads for each sample, broken down by exon, junction and intron aligning (Figure 2.15 D-F). This source data for these plots is obtained from the file with the prefix counts in the folder **ExpressionInput**, which includes where each feature aligns to and the total number of associated read counts.

Data from (C) consist only of the distribution of log2 values in the input file.

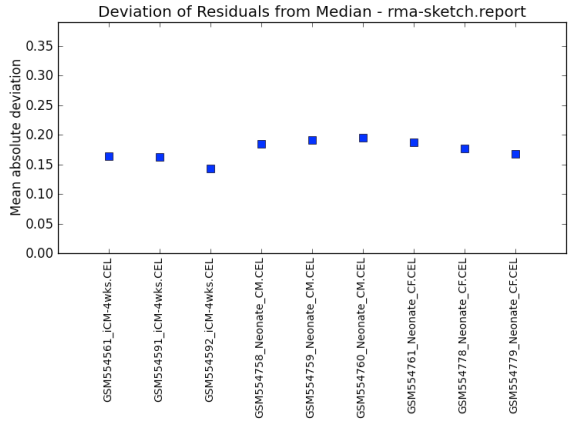
A



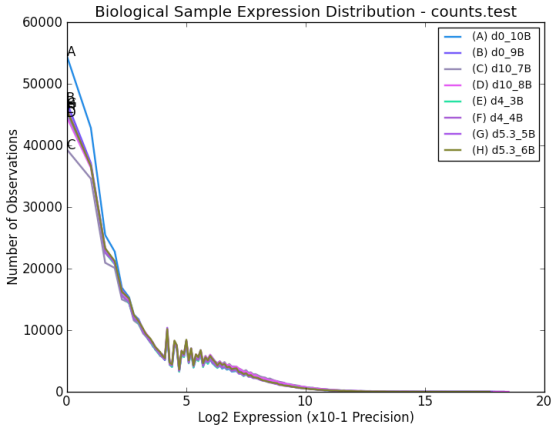
B



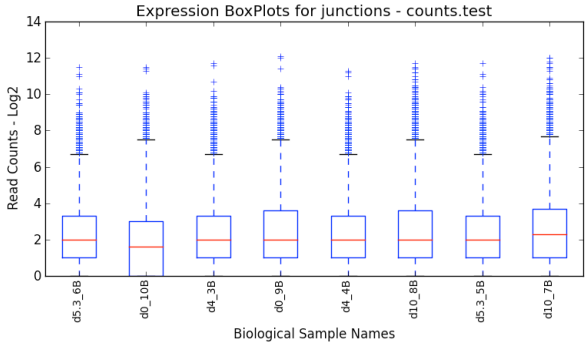
C



D



E



F

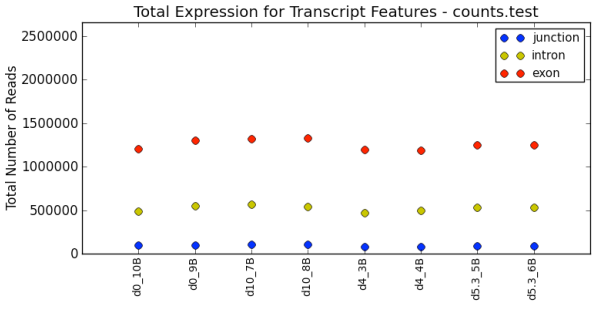


Figure 2.15. Basic QC Plots. Example AltAnalyze QC plots produced for normalized Affymetrix array (A-C) and RNA-Seq data (D-F). Only summarized junction count data is shown in E.

Expression Clustering

Two main expression clustering methods are currently output by AltAnalyze, hierarchical clustering and principal component analysis (PCA). Hierarchical clustering is used to identify overall patterns of gene expression shared by groups of genes and samples whereas PCA is used to visualize similarities between samples within and between groups in 2D dimension space. Hence, both methods can be used to evaluate the quality of the data as well as explore sample or gene relationships.

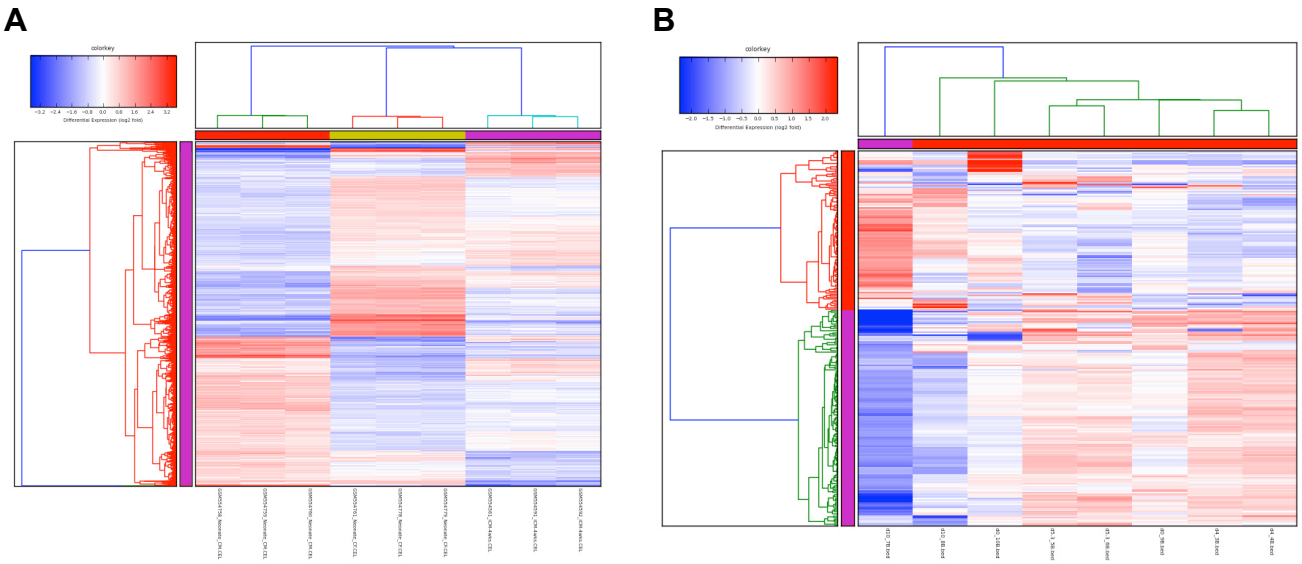


Figure 2.16. Hierarchical clustering heatmaps. Example AltAnalyze hierarchical clustering heatmaps for (A) significantly regulated genes in multiple comparisons and (B) outlier regulated genes. Genes are displayed as rows and samples as columns. Red indicates upregulation and blue indicates down. The vertical and horizontal bars adjacent to the heatmaps are colored based on a flat cluster threshold of 0.7 (distance criterion). In some cases, colors in the heatmap may not relate to colors in

the dendrograms or flat cluster bars.

Hierarchical clustering is applied by default to both significantly differentially expressed genes and outlier regulated genes from the entire dataset. Genes considered significantly regulated are those that have greater than 2 fold (up or down) change in gene expression and comparison statistic $p < 0.05$ for any user indicated comparison (see GO-Elite options for details on changing the defaults – Figure 2.9). Outlier genes are those with a greater than 2 fold difference relative to the mean of all samples, for any gene not in the significantly regulated set. For significantly regulated genes, sample folds are calculated as compared to the mean of all samples for each gene or based on the group comparisons designated by the user (called "Relative"). Although default clustering metrics, methods and coloring options are applied to the resulting heatmaps, these options can be changed after running AltAnalyze (see **Additional Analyses** - Section 2.2). Vector based versions of these plots are available in the PDF outputs in the folder **DataPlots**. A text file representing the clustered matrix, identifiers and flat-clusters will be exported to the **DataPlots** directory along with a TreeView compatible .cdt file. Note: Only row names are included when the number of rows visualized is less than 100. Clustering is accomplished using Scipy's cluster.hierarchy method. For additional details and workflows, see associated online Tutorials: https://code.google.com/p/altanalyze/wiki/Tutorials.

PCA is applied only to the significantly differentially regulated gene set, by default. In this plot, the values of 1st component are plotted against the values of the second component for each sample (Figure 2.13). This analysis will visualize each sample as a colored circle, with the color corresponding to the different assigned biological groups. The sample names will be displayed to the right of the sample circle.

Lineage Profiler Analysis

Lineage Profiler is a new method introduced in AltAnalyze version 2.07. This algorithm correlates user supplied sample expression profiles with previously collected expression profiles from a large compendium of publically available cell types and tissues (aka lineages). The

underlying lineage data is biased towards adult, fetal and progenitor cell types arising throughout differentiation, as opposed to disease states or cell lines. It is capable of characterizing both microarray and RNA-Seq datasets for a diverse database of cell lineages.

The compendium itself is built on top of either exon or 3'array publically available datasets (human and mouse) combined from a large number of studies. From the entire compendium dataset, only the top 60 cell-specific markers are used for the lineage correlation analysis (see AltDatabase/EnsMart65/ensembl/Hs/Hs_exon_tissue-specific_protein_coding.txt). The top markers are selected during the LineageProfiler database build process, based on their overall expression correlation to a specific-cell type relative to all other cell types examined. Additional details on the LineageProfiler algorithm can be found at http://code.google.com/p/altanalyze/wiki/LineageProfiler.

Three main output files are currently provided by LineageProfiler: (1) sample-to-cell type correlation statistic flat-files, (2) hierarchically clustered heatmap of correlation statistics and (3) visualization of the correlation statics along a comprehensive lineage network. The primary statistic used form these analyses is a Z score calculated from the distribution of Pearson correlation coefficients for each user supplied RNA-profile to all analyzed lineages.

The correlation statistics flat-files are produced by LineageProfiler: (A) Pearson-correlation coefficients (ExpressionOutput/LineageCorrelations-**<dataset_name>**.txt), (B) derived Z scores (ExpressionOutput/LineageCorrelations-**<dataset_name>**-zscores.txt) and (C) average Z scores for each biological group (ExpressionOutput/Clustering/LineageCorrelations-**<dataset_name>**-zscores-groups.txt). These files are all tab-delimited text files that can be easily explored in a spreadsheet viewer, such as Excel.

The hierarchically clustered heatmap output (2) is based on file (B). An example of this output is shown in Figure 2.14B. This output is particularly useful for identifying changes in lineage associations during developmental transitions.

To further understand which cell fate decisions or lineage pathways are regulated in particular biological conditions, visualization along a comprehensive lineage network is provided (3) derived from file (C). An example of this output is shown in Figure 2.14A. The lineage

network is a community curated network posted at WikiPathways (http://wikipathways.org/index.php/Pathway:WP2062). This network is visualized using the WikiPathways API (`Wikipathways_webservice.py > viewLineageProfilerResults()`). When running AltAnalyze from source-code, this function requires installation of the lxml library.

2.6 Accessory Functions

In addition to the streamlined AltAnalyze pipeline analyses, a number of individual useful functions can be run independently of these workflows. These include:

1. Pathway Enrichment
2. Pathway Visualization
3. Hierarchical Clustering
4. Principal Component Analysis
5. Lineage Analysis and Sample Classification
6. Network Analysis and Visualization
7. Biological Identifier Translation
8. Alternative Exon Visualization
9. Venn Diagram Analysis
10. File Merging Functionality

These functions provide a wide array of solutions for genomics analysis that are easily accessible to bioinformaticians and experimental biologists alike. These functions can be accessed through the Additional Analyses menu after selecting a species and platform type in the main menu. Alternatively, the functions can be run from the command-line for batch customized analytical and batch pipelines (see Section 2.4).

Pathway Analysis and Visualization

Pathway enrichment and visualization methods are identical to those provided in the independent analysis package GO-Elite. Enrichment analysis is available using a multiple algorithms, user defined thresholds and can be run on over a dozen distinct biological gene and metabolite categories. This tool provides an optimized list of enriched biological categories (e.g., Ontology term pruning) for description of input ID lists. In addition to tabular result files, hierarchically clustered heatmaps are displayed showing enrichment of terms between distinct conditions analyzed as well as networks of enriched terms with corresponding regulated genes. For more details see http://genmapp.org/go_elite/help_main.htm.

Hierarchical Clustering and Visualization

AltAnalyze can perform hierarchical clustering using default options (see Section 2.5 – Expression Clustering) or using customized options. These include the ability to change visualization modes (e.g., colors, contrast), clustering algorithm (e.g., cosine, euclidean, hopach), row normalization, matrix transposition and biological group coloring. In addition, several advanced options are available including the ability to cluster and visualize genes associated with certain GO-Elite pathways, ontologies or gene-sets and obtaining clusters of genes most correlated with a single candidate. These advanced options allow any users to easily and quickly obtain highly specialized expression views using a large selection set of biological categories, visualization options and advanced clustering algorithms from a single interface (Figure 2.17A). More details on these options and parameters are described at http://code.google.com/p/altanalyze/wiki/Heatmaps.

Principal Component Analysis (PCA)

In addition to the default pipeline output of two-dimension PCA plots (first two components – see Section 2.5), PCA can be run on its own using multiple customized options. These include optionally displaying sample labels and viewing a PCA plot interactively in three-dimensions as shown in Figure 2.17B. The percentage of variance explained for each component is annotated in the component label. The top correlated and anti-correlated genes associated with the top

four principal components are stored in the folder DataPlots/PCA.txt and can optionally be stored as an available gene set for other downstream analyses by entering a name for the analysis in the GUI.

Lineage Analysis and Sample Classification

This menu provides a number of flexible options for classifying samples relative to either (A) pre-compiled tissue/cell type references built from various transcriptome measurement platforms or (B) relative to a user supplied set of reference measurements. For tissue and cell-type classification, the LineageProfiler algorithm is employed, in which each loaded sample is matched to a set of tissue-specific markers determined from AltAnalyze's MarkerFinder algorithm and then correlated to all available compendium cell type or tissue expression values. Although the overall correlation (Pearson correlation coefficient) between distinct platforms may be low (e.g., RNA-Seq versus exon array profiles), these sample specific correlations most typically are accurate, especially where many distinct sample types are being compared (manuscript in preparation). Results are output as a lineage correlation heatmap and as a WikiPathway network for lineage differentiation (**DataPlots** folder). The results in these files are z-scores derived from the distribution of observed correlations for all samples analyzed in a given experiment.

In addition to lineage classification, this algorithm can be applied to custom references and even distinct gene-models, discovered using the LineageProfilerIterate.py script provided with AltAnalyze. Using this method, samples can be classified using user-supplied references for all analyzed genes or subsets of gene-models provided in a gene-model file. Additional information on these methods, example workflows and example files are provided online at:
http://code.google.com/p/altanalyze/wiki/LineageProfiler
http://code.google.com/p/altanalyze/wiki/SampleClassification

A **B**

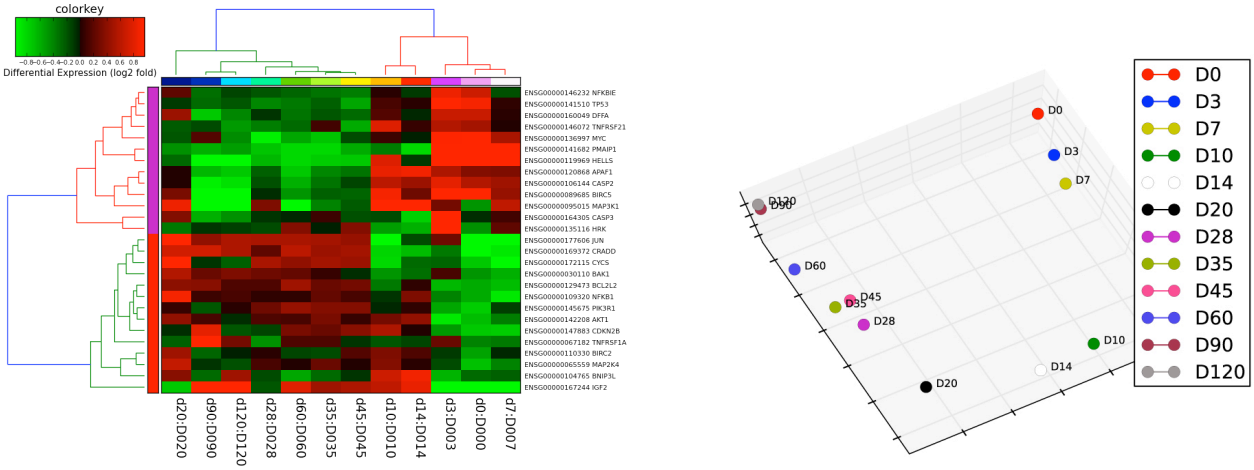


Figure 2.17. Advanced Clustering Options. Additional Analysis menu options available for hierarchical clustering of genes belonging to particular biological class (A) and PCA of samples in three dimensions (B), is shown. (A) Genes corresponding to the WikiPathway Apoptosis is displayed using the red-black-green color pallet and samples colored by biological category in the top color bar. (B) 3D PCA of Cardiac differentiation with display of sample labels turned on.

Network Analysis and Visualization (NetPerspective)

NetPerspective is a new tool introduced in AltAnalyze 2.0.8 that allows users to quickly and easily identify hypothetical biological networks between interacting genes, proteins, RNAs and metabolites with a single query. NetPerspective uses a collection of highly curated interactions from WikiPathways, KEGG and HMDB, experimentally derived transcription factor targets, annotated drug-protein interactions, microRNA target predictions (Section 3.7) and speculative protein interactions from BioGRID. Networks can be generated from lists of input IDs, existing interactions or GO-Elite pathways/gene-sets/ontologies, visualized with regulated gene, proteins and metabolites. Connections between sets of IDs can be identified using direct interactions, indirect or from the shortest path of possible connections. These networks are automatically displayed when run from the GUI and are also saved as PDF and PNG files to the folder **network** in the input file directory (Figure 2.19). When run from the command-line, automated generation of networks and images can be performed for an unlimited number of input lists run

sequentially or in parallel. More details on these options and parameters are described at http://code.google.com/p/altanalyze/wiki/NetPerspective.

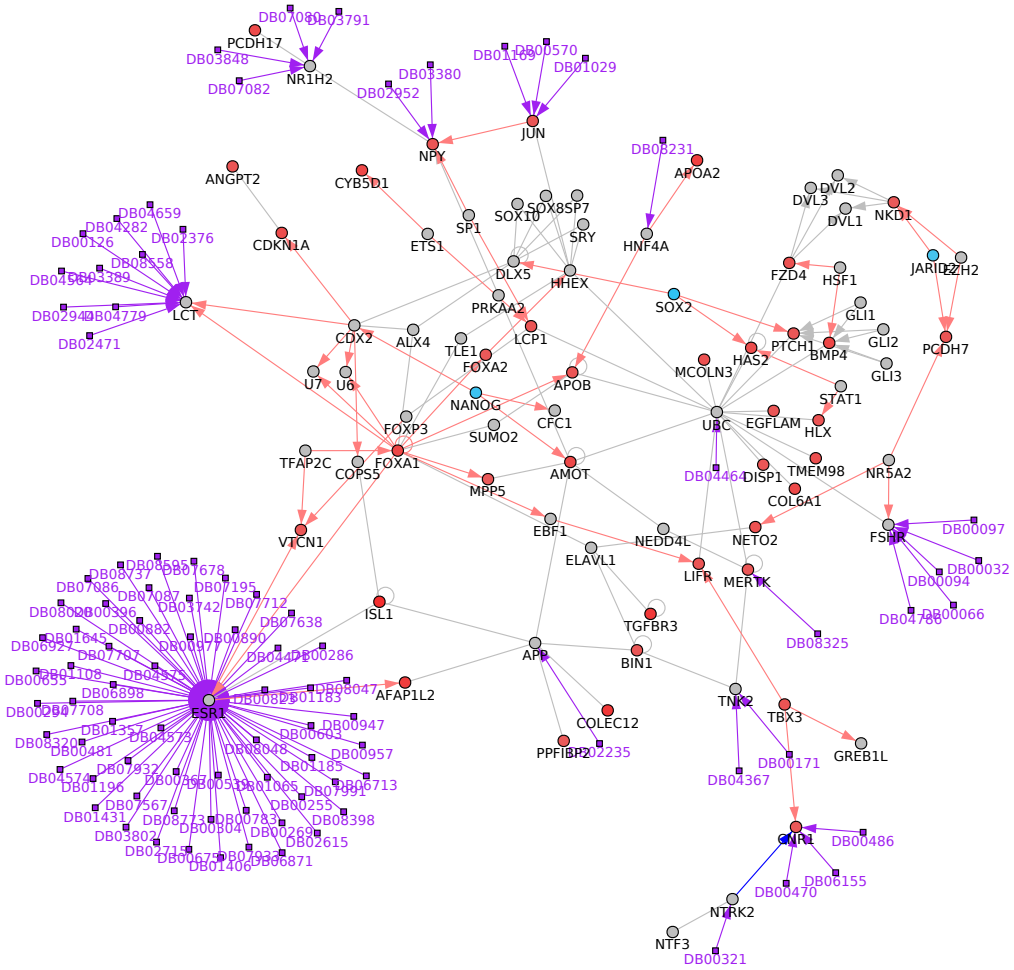


Figure 2.19. Automated Network Analysis and Visualization. Example output from NetPerspective. Nodes are colored as up or down-regulated (red or blue), with red edges indicating transcriptional regulation, blue indicating annotated inhibitory interactions, arrows indicating annotated directed interactions, purple arrows indicating drug interactions and green edges indicating microRNA-mediated interactions (not shown).

Alternative Exon Visualization (AltExonViewer)

An important means for initial validation of alternative exon expression (e.g., alternative splicing, alternative promoter regulation) is visualization of feature expression in the context of all measured gene features. In addition to visualization of alternative exons in the Cytoscape plugin DomainGraph (**Section 8**), AltAnalyze contains a built in alternative exon viewer called AltExonViewer. This function allows users to display gene data in the form of a 1) **line graph** depicting exons along the X-axis and exon-expression or splicing index fold change along the Y-axis, 2) a **heatmap** of all exons across all samples and 3) a **Sashimi-Plot** genomic view. For the line **graph option**, expression values from each group are summarized as a single line color, with standard-error values included. One gene or multiple genes can be displayed at a time using a manual text entry field (e.g., SOX2 NANOG POU5F1 TCF7L1) or through a file selection option. Probed UTR regions and Introns can also be optionally displayed. To visualize exon-expression, select the **raw expression** option. This option requires that input expression files have already been generated and analyzed with AltAnalyze (conforming to the standard file locations – e.g., ExpressionInput/exp. file). To visualize alternative exon-expression directly, select the **splicing-index** option. This option works for already produced alternative exon results, which are saved to the folder AltResults/RawSpliceData (**Figure 2.20**). When analyzing a dataset with more than two groups, re-run the AltAnalyze workflow beginning with the Process AltAnalyze Filtered option and selecting the **all groups** selection for **Comparisons to Perform** option.

For the **heatmap** view, a standard AltAnalyze heatmap is produced with all exon region expression values (median normalized), ordered from beginning to end along the y-axis. The **Sashimi-Plot** option, directly interfaces with the Sashimi-Plot source python code (http://miso.readthedocs.org/en/latest/sashimi.html), to produce high resolution splicing plots. Additional details on these options and parameters are described at http://code.google.com/p/altanalyze/wiki/AltExonViewer.

A **B**

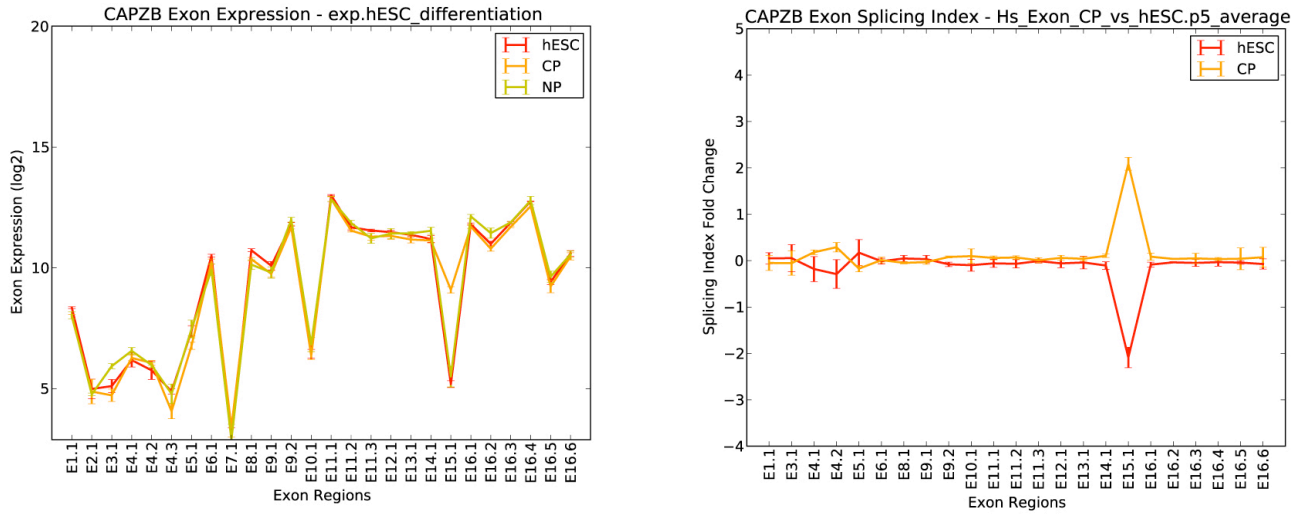


Figure 2.20. Alternative Exon Visualization. Visualization of exon expression is shown for a single gene (CAPZB). (A) In the first plot, three conditions (hESC, CP, NP) are shown indicating the relative expression of probesets corresponding to the below indicated exon regions (**Section 3.5**). (B) Analysis of a single pairwise-comparison (CP versus hESC) for splicing-index associated expression values. In both plots, E15.1 would be predicted to be "splice-out" upon differentiation to cardiac or neural lineages.

Venn Identifier Comparison Analyses

To evaluate commonalities and difference between different gene sets or other IDs obtained from AltAnalyze or outside programs, two tools are available within AltAnalyze for merging files and/or visualizing ID overlaps. To visualize the overlap between identifiers in two or more files (max of 4), select the Venn Diagram option in AltAnalyze (**Additional Analyses** menu). *For this analysis, species and platform selection are not important.* Select the different files of interest, containing comparable IDs in the first column of those files. Select an output directory for which you want the two types of Venn Diagrams to be saved to. Two methods are available for visualization of these diagrams: (A) Standard overlapping Venn's and (B) ID membership weighted. The standard overlapping Venn will have equally sized circles or ovals representing IDs from each individual files (**Figure 2.21**). Selection of the associated numbers will prompt a new window to appear with the associated identifiers for that subset (automatically copied to your computers clipboard). This open-source code for this library can be found at:

https://github.com/icetime/pyinfor/blob/master/venn.py. The ID membership weighted Venn was also obtained from another open-source project, matplotlib-venn (http://pypi.python.org/pypi/matplotlib-venn). This output will weight the circles in the Venn based on the relative overlap of IDs in each file (max of 3 files). Both of these outputs are automatically produced and saved to the indicated output directory with a time-stamp in the filename.

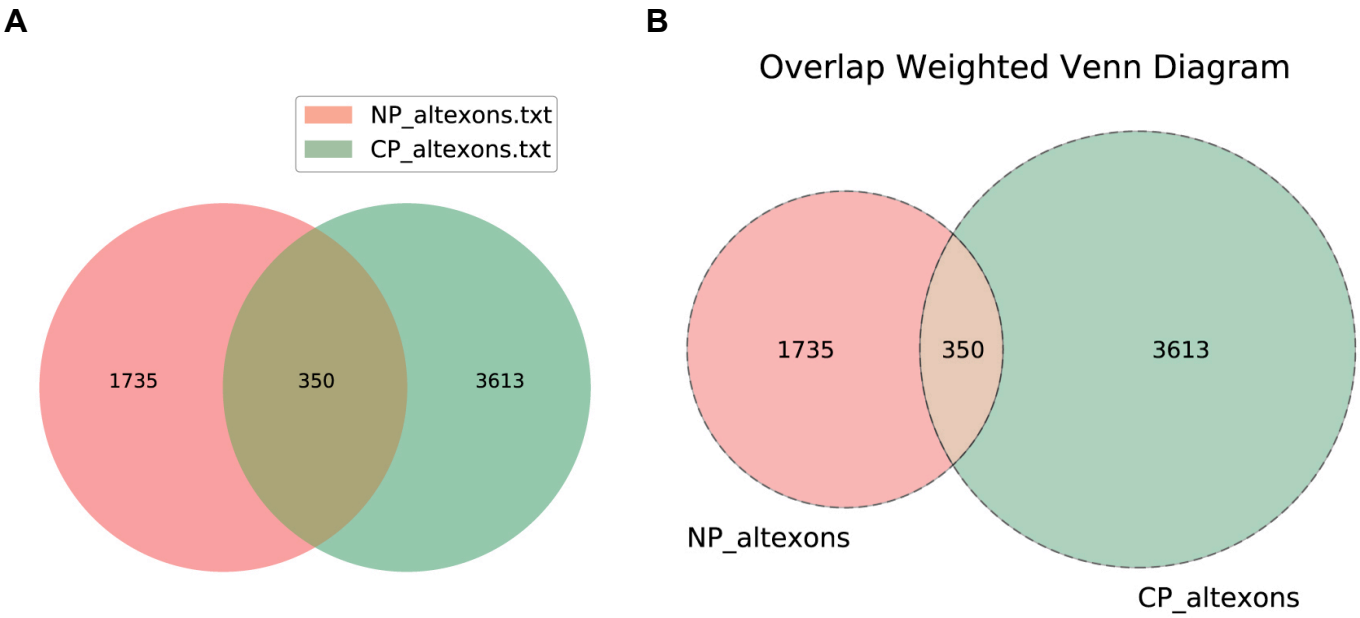


Figure 2.21. Venn Diagram Analysis in AltAnalyze. Venn Diagrams exported for two comparisons (alternative exons in neural and cardiac differentiation) for the (A) standard and (B) overlapping output image files.

File Merging Tool

Like the Venn diagram tool, this tool identifies differential overlaps between input identifier files and outputs a tab-delimited text file containing the original file contents for intersecting (**Intersection** option) or all combined IDs (**Union**). *For this analysis, species and platform selection are not important.* Up-to-four files can be selected for overlap. An output directory must also be selected for which to save the combined output (**MergedFiles.txt**) to. All columns contained in the original files will also be in the output with the column names followed by the

source file (column-name.source-file.txt). Additional options are available for only returning unique IDs for each file or all possible combinations of matching IDs in the output (important when more than identical ID is present in the first column of a file).

Identifier Translation

A common use case for biologists dealing with genomics datasets is conversion of one identifier type to another. To accomplish this, users can access the Identifier Translation menu, load a file containing the IDs to be translated (must be the first column of values and obtain a new file in which the first column of values matches the desired ID type. These translations are accomplished through use of relationships obtained from Ensembl and HMDB (GO-Elite database > AltDatabase/EnsMart72/goelite/Hs/uid-gene). All original IDs and other column data will be present in the output file, along with the Ensembl or HMDB IDs used for translation. Where multiple Ensembl or HMDB IDs are related to the input ID, only one will be chosen (last listed).

Section 3 – Algorithms

Multiple algorithms are available in AltAnalyze to identify individual features (for exon-sensitive platforms (EP)) or reciprocal probe sets (exon-exon junction platforms (JP)) that are differentially regulated relative to gene expression changes. These include the splicing index method (EP & JP), FIRMA (EP & JP), MiDAS (EP & JP), ASPIRE (JP) and Linear Regression (JP). For junction sensitive platforms (RNA-Seq and junction arrays), single feature analyses (e.g., splicing-index) are performed immediately after reciprocal junction analyses (e.g., ASPIRE) on the same list of expressed features. This allows the user to examine alternative exons predicted by pairs of reciprocal junctions in addition to those predicted by a single regulated exons/junctions (JP). In addition to these statistical methods, several novel methods are used to predict which alternative proteins correspond to a regulated exon, which protein domain/features differ between these and which RNA regulatory sequences differ between the associated transcripts (e.g., miR-BS).

3.1 Default Methods

The default options are stored in external text files in the folder “Config” as “defaults-expr.txt”, “defaults-alt_exon.txt”, and “defaults-funct.txt”.

defaults-expr.txt	Default expression analysis options (Figure 2.4)
defaults-alt_exon.txt	Default alternative exon analysis options (Figure 2.5)
defaults-funct.txt	Default functional analysis options (Figure 2.5)

These options correspond to those found in the configuration file “options.txt”. The user is welcome to modify the defaults and theoretically even the options in the “options.txt” file, however, care is required to ensure that these options are supported the by the program. Since AltAnalyze is an open-source program, it is feasible for the user to add new species and array support or to do so with AltAnalyze support. The default algorithms for the currently supported arrays are as follows:

Exon/Gene	splicing-index (score > 2 and t-test p<0.05), no MiDAS
Junction/RNA-Seq	ASPIRE (score > 0.2 and permute p<0.05)
3' array	NA

3.2 Algorithm Descriptions

Expression Normalization

For Affymetrix array analyses, AltAnalyze calls the software Affymetrix PowerTools, distributed with the GPU license. For conventional 3' expression arrays, the RMA methods is applied to all Affymetrix CEL files (all supported formats) in the input user directory. Expression values are computed based on corresponding probeset annotations in the downloaded CDF file (automatically recognized and downloaded by AltAnalyze or supplied by the user). For exon, gene and junction arrays, RMA is also applied but for exon/junction-level probesets and not transcript cluster probesets (gene-level). In addition, detection above background (DABG) p-values are calculated for these arrays to evaluate likelihood of exon expression for calculating gene expression estimates and assessing probeset-level alternative exon expression (Section 3.3-3.4).

For RNA-Seq studies, data is imported as junction and exon counts per region (junction or defined exon region). These counts can be analyzed directly in AltAnalyze, since alternative exon and junction expression are evaluate on a sample-by-sample basis, which allows for normalization of these values within a biological group and between group comparisons. However, gene expression will still be non-normalized when counts are used directly, hence, gene expression estimates may be incorrect, impacting all AltAnalyze gene expression fold changes. To account for this, the user can choose to normalize using the RPKM method (http://www.clcbio.com/manual/genomics/Definition_RPKM.html). Users can choose between these normalization methods or no normalization methods (direct analysis of counts). Upon import of RNA-Seq counts, counts are incremented by 1, in order to calculate summary statistics without encountering zero-division errors. While the reported counts for gene expression and

alternative splicing analyses will reflect the non-adjusted counts (e.g., zero, where applicable) for raw and quantile normalized counts, RPKM values will always reflect the adjusted values. In cases where RPKM adjusted counts are selected, an original zero read count in two compared groups will be interpreted as a fold change of 1, rather than reflecting the actual adjusted RPKM comparison value (values will differ between samples since the total number of reads per sample will vary).

Agilent Feature Extraction files can also be loaded and normalized using a workflow similar to that for Affymetrix microarrays. Agilent Feature Extraction files are produced from Agilent scanned slide images using Agilent's proprietary Feature Extraction Software. Feature Extraction text files can be loaded in AltAnalyze using the **Process Feature Extraction Files** option and selecting the appropriate color ratio or specific color channel from which to extract expression values from. Quantile normalization is applied by to Agilent data processed through this workflow.

For all additional expression dataset types, both quantile normalization and batch-effects removal are available. Batch effect removal is provided using the combat python package, which provides nearly identical results to that of the R version of combat (https://github.com/brentp/combat.py). Additional information about combat in AltAnalyze can be found here: http://code.google.com/p/altanalyze/wiki/combat.

Gene Expression Analysis

For the simple gene expression output files saved to the ExpressionOutput directory, several basic expression statistics are calculated. These statistics are performed for any user specified pairwise comparisons (e.g., cancer versus normal) and between all groups in the user dataset (e.g., time-points of differentiation). Expression values are reported as log2 values for all microarray analyses and as non-log values for RNA-Seq analyses. These statistics are comprised of the following: (1) rawp, (2) adjp, (3) log-fold, (4) fold change, (5) ANOVA rawp, (6) ANOVA adjp and (7) max log-fold. The rawp is a one-way analysis of variance (ANOVA) p-value calculated for each pairwise comparison (two groups only). The adjp is the Benjamini-Hochberg

(BH) 1995 adjusted value of the rawp. The log-fold is the log2 fold calculated by geometric subtraction of the experimental from the control groups for each pairwise comparison. The fold change is the non-log2 transformed fold value. The ANOVA rawp is the same as the comparison rawp, but for all groups analyzed (note, this is reduced to the rawp when only two groups are analyzed). The ANOVA adj is the BH adjusted of the ANOVA rawp. The max log-fold is the log2 fold value between the lowest group mean and the highest group expression mean for all conditions in the dataset. These statistics are intended for further data filtering and prioritization in order to assess putative transcription differences between genes. For non-RPKM RNA-Seq analyses, these values will be the average of exon or junction read counts (exons when both present) for known or constitutive annotated features. When RPKM normalization is selected, gene expression will be based on the RPKM of all “expressed” exons or junctions in any of the sample groups (user defined filtering thresholds), taking into account the total read counts for “expressed” exons, their sequence length and the total number of reads per sample. Filtering thresholds for exons and junctions are separate variables, since the likelihood of obtaining a junction read count are typically lower than an exon read count, due smaller sequence regions and algorithms available to identify both. To calculate a fold-change, the final gene-level counts are incremented by 1, prior to calculating the RPKM. These same gene RPKM values are used for alternative exon analyses. An additional column is present for RNA-Seq analyses with the total reads per gene shown, in order to filter for low versus high absolute expression (also available from the file “counts.YourDataset-steady-state.txt”).

Statistical Testing Procedures

Multiple conventional statistical tests are provided for the various comparison analyses available (e.g., differential gene expression, alternative exon expression). For group comparisons involving greater than two groups, a standard f-test statistic is used. For pairwise group comparisons, users can choose from unpaired and paired t-test’s (assuming equal variance), rank sum, Mann Whitney and Kolmogorov Smirnov. These tests are made available from the open-source statistical package SalStat (http://salstat.sourceforge.net/). In addition to these un-

moderated tests, AltAnalyze provides a moderated t-test option (unpaired, assuming equal variance), based on the limma empirical Bayes model. This model calculates an adjusted variance based on the variance of all genes or exons analyzed for each comparison. Unlike a standard limma analysis, only the variances for the two groups being compared are used to compute the adjusted variance (s2 prior and df prior) for each comparison as opposed to variance from all groups analyzed (when greater than 2). For these calculations (gamma functions), AltAnalyze uses the python mpmath library (http://code.google.com/p/mpmath). For q-value calculations, AltAnalyze imports the python adapted qvalue library (https://github.com/nfusi/qvalue/blob/master/LICENSE.txt).

Predict Group Selection Algorithm (aka Single-Cell Group Discovery)

A novel algorithm was developed to identify similar sample or cell groups where no or limited prior information exists on the identity of individual samples. This algorithm employs an iterative filtering, correlation, clustering and driver selection workflow that results in a coherent set of differentially expressed genes and predicted sample groups. By itself, these gene sets can be utilized for further investigation (e.g., lineage differentiation pathways). Both the predict groups menu option and the hierarchical clustering **Additional Analyses** menu can perform the major elements of this analysis. (**Step 1**) The algorithm begins by importing all supplied expression values from an input dataset, empirically determining whether the data should be log2 adjusted, filtering the data based on the supplied RPKM and maximal gene count expression thresholds, examining only protein coding genes in the AltAnalyze Ensembl gene database and searching for genes with at least N number of samples differing between for a given gene based on the indicated fold cutoff (e.g., the 3rd lowest expressing gene versus the 3rd highest expression gene, with at least a 5 fold difference, for n=3 and a minimum 5 fold difference). (**Step 2**) This results in a filtered gene set from which to perform all pairwise correlations and select only those genes that are correlated to at least 10 distinct genes. Because an individual sample can drive the correlations, only gene sets that remain intra-correlated following removal of the most highly expressed gene are retained (except in cases where only one sample difference are selected

from the **Minimum number of samples differing** option). This pioneering round gene set is clustered using the supplied clustering algorithms (cluster 1) and used for further downstream filtering. (**Step 3**) In the next round, iterative filtering steps are applied using different correlation thresholds to select no more than 20 genes for each clustered "pattern", which are then re-clustered (cluster 2). (**Step 4**) The resulting cluster is re-supplied to the prior algorithm, with additional option to select to select the top correlated gene(s) for each cluster (drivers) to other genes in that gene cluster. Multiple transcription factor genes are selected from each cluster, if present; otherwise a single driver gene is selected. If the user indicated that cell-cycle genes should be excluded, any clusters from this set with more than one cell-cycle gene will be excluded. These driver genes are then correlated to those produced from **Step 1** (filtered from the original set based on expression, annotation and fold change) using the user supplied correlation cutoff to identify positively correlated genes (maximum of 50 per driver gene) (cluster 3). (**Step 5**) This last step is re-iterated using the results of cluster 3 to further refine the results (cluster 4). All clustered options are presented to the user for sample groups selection, for downstream AltAnalyze workflow differential expression and splicing analyses (if applicable). When performing this workflow for alternative exons (AltExon option), only the **Minimum number of samples differing** is considered and is applied to the AltAnalyze **Reciprocal isoform Percent Spliced In** (Ri-PSI) in analysis (see algorithm details below).

Reciprocal Junction Analysis

Alternative exon analyses differ for exon-based analyses as compared to junction sensitive analyses. For an exon-level analysis, alternative exon regulation is determined by comparing the normalized expression of one exon in two or more conditions (pairwise versus all groups analysis). Normalized expression is the expression of an individual exon (aka a probe set) divided by the gene-expression value (collective expression of gene features that best indicate constitutive versus alternative expression). In contrast, junction sensitive analyses (e.g., RNA-Seq and junction arrays) assess the expression of junctions often in addition to exons. For alternative splicing and often alternative promoter selection, two junctions (or an inclusion exon

and exclusion junction) are differentially expressed in opposite directions, leading to the inclusion or exclusion of exons, exon-regions or introns. Thus, these methods are more sensitive in detecting alternative exon expression and the precise splicing-event that is occurring, as opposed to identifying on the exon features that are regulated (Figure 3.1). Although this method is more accurate at detecting true alternative splicing events, single exon or junction analyses are still useful at detecting other forms of alternative exon-region expression (e.g., alternative promoter selection and alternative 3' end-processing). While junction arrays contain exon features for assessing alternative 3' end-processing, RNA-Seq junction-only data does not, thus, details on alternative polyadenylation will likely be missing.

1.

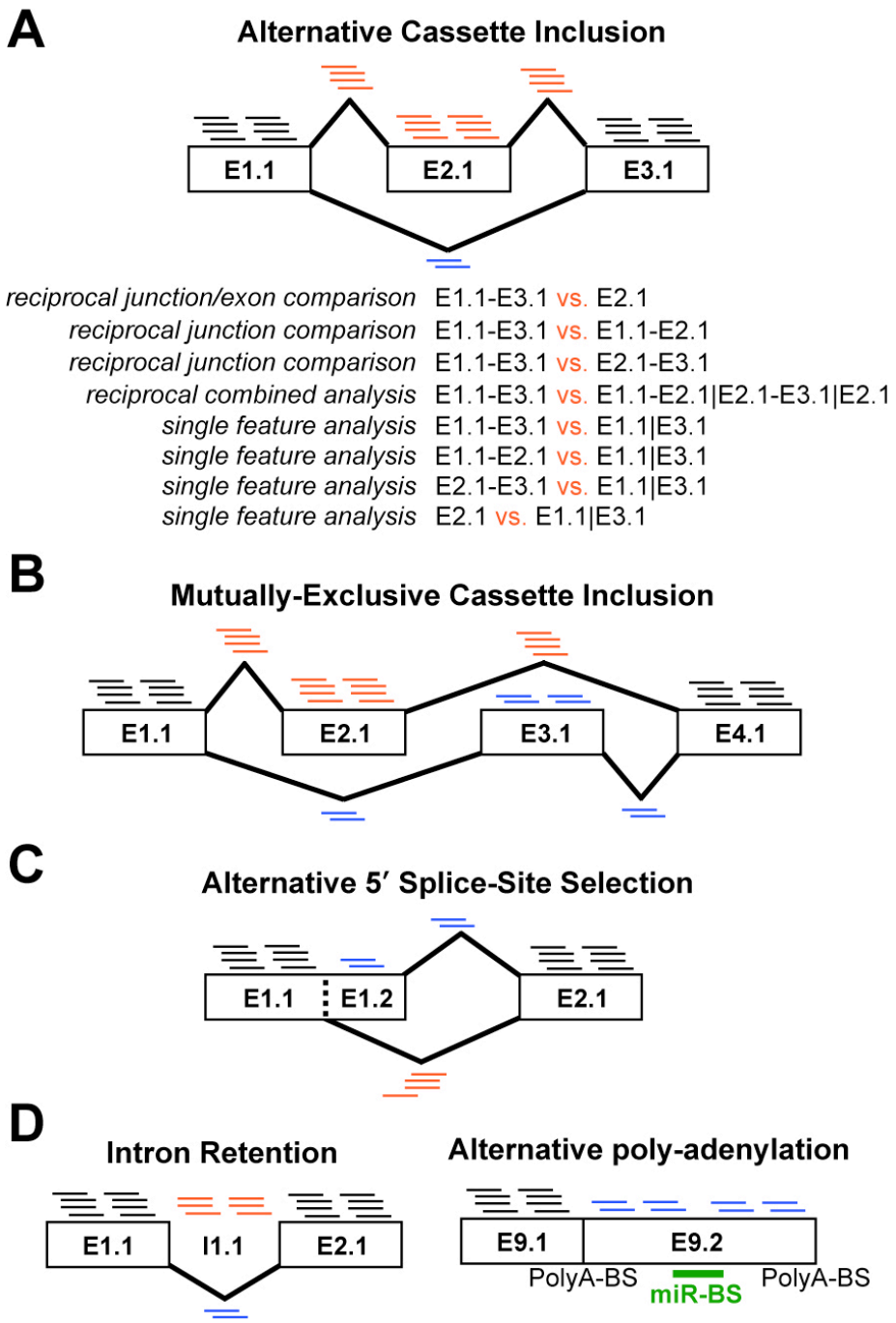


Figure 3.1. Splicing and Alternative Exon Events Detected by Different Algorithms. Examples are shown for features (RNA-Seq reads or Affymetrix probe sets) that can be used to detect distinct alternative events. A) Alternative cassette-exon inclusion is shown with increased inclusion of exon E2.1 (AltAnalyze exon block-region notation). Exon E2.1 and junctions E1.1-E2.1 and E2.1-E3.1 (inclusion junction) are expressed higher in this example (more

associated reads) relative to junction E1.1-E3.1 (exclusion junction). While this indicates that alternative splicing is occurring in one condition, AltAnalyze looks at changes in the expression or ratio of expressed isoforms between at least two experimental conditions. Listed are the possible exon and junction analyses available to infer an alternative cassette splicing is occurring between two conditions. These include 1) comparison of the exclusion junction to the inclusion exon, 2) comparison of the exclusion junction and one of the inclusion junctions, 3) comparison of the exclusion junction and the mean expression of all inclusion features and 4) comparison of any exclusion or inclusion features relative to exons that are not alternatively spliced. Options 1-3 are performed only by junction arrays and exon/junction RNA-Seq using reciprocal junction analysis (e.g., ASPIRE), while option 4 is used for junction-arrays, exon arrays and RNA-Seq (e.g., splicing-index). Figures B-D represent other examples of alternative exon inclusions. None of the examples in Figure D can be detected by junction-only RNA-Seq analyses.

To identify alternative exons from junction analyses, AltAnalyze first identifies reciprocal junctions or pairs of exon-junctions, one measuring the inclusion of an exon and the other measuring exclusion of the exon. This algorithm allows for the identification of novel exon junctions detected by RNA-Seq that overlap in the genome with known junctions and splice to at least one known splice site. If exon expression is also measured, an exclusion junction can be directly compared to the expression of an included exon. For the reciprocal junction algorithms used by AltAnalyze (ASPIRE, Linear Regression, Ri-PSI), the expression of the exclusion junction is directly compared to the expression of the inclusion junction or exon for each sample. In this way, these algorithms don't require normalization of expression, which is useful for RNA-Seq analyses were read counts are directly used. ASPIRE does use the gene expression estimate as an additional factor, however, since these values are calculated on a per sample basis, normalization is not an issue. Pairs of reciprocal junctions or reciprocal junction/exon

pairs are extracted from the AltAnalyze gene database for known junctions (Ensembl and UCSC) by comparing the exon block and region structure of transcripts (Section 6.2) in addition to at runtime for novel junctions detected from an RNA-Seq experiment. For junction arrays, novel reciprocal junctions are included in the gene database from Affymetrix predicted junctions, using the same exon block and region comparison strategy. For the AltMouse array, reciprocal probe set pairs are determined using the `ExonAnnotate_module.py` module using the "identifyPutativeSpliceEvents" function, by comparing AltMerge exon block and region annotations from Affymetrix. These methods allow for the identification of cassette exon inclusion, alternative 5' and 3' splice-site selection, mutually-exclusive cassette inclusion, alternative promoter selection, intron-retention and trans-splicing (RNA-Seq only).

Splicing Index Method

This algorithm is described in detail in the following publications:
(6, 7). In brief, the expression value of RNA-Seq feature or probe set for a condition is converted to log space (if necessary). For each feature examined, its expression (log_2) is subtracted from the mean gene expression of value to create a gene expression corrected log ratio (subtract instead of divide when these values are in log space). This value is the normalized intensity. This normalized intensity is calculated for each experimental sample, using only data from that sample. To derive the splicing-index value, the group-normalized intensity of the control is subtracted from the experimental. This value is the change in exon-inclusion (delta I, δI, or splicing index fold change).

$$NI(probeset_i) = \left(\frac{probeset\ intensity}{ex\ pression\ level\ of\ \ gene} \right)$$

$$SI(probeset_i) = \log_2 \left(\frac{NI(probeset_i)_{sample1})}{NI(probeset_i)_{sample2})} \right)$$

An f-test p-value is calculated (two tailed, assuming unequal variance) by comparing the normalized intensity for all samples between the two experimental groups. A Benjamin-Hochberg adjusted p-value from this f-test p is also calculated. A negative SI score of -1 thus indicates a two-fold change in the expression of the RNA-Seq feature or probe set, relative to the mean gene expression, with expression being higher in the experimental versus the control. When more than two-groups are being compared in AltAnalyze (“all groups” or “both options" for “Type of group comparisons to perform”), the splicing-index value is calculated between the two biological groups with the lowest and highest normalized intensities. The two groups being compared are indicated in the alternative exon results file.

A deviation value is also included from the splicing-index statistic (Yamashita et. al, 2012 Journal of Human Genetics) across the entire gene to evaluate overall gene-level variation in exon-expression relative to the exon-region of interest. The authors of the study that introduce the deviation value or DV, recommend a DV>3.0 be considered as one variable contributing to a greater likelihood of alternative exon differential expression. For additional information, see the following webpage: http://code.google.com/p/altanalyze/wiki/DeviationValue

FIRMA Analysis

FIRMA or Finding Isoforms using Robust Multichip Analysis (8) is an alternative to the splicing-index approach, to calculate alternative splicing statistics. Rather than using the probe set expression values to determine differences in the relative expression of an exon for two or more conditions, FIRMA uses the residual values produced by the RMA algorithm for each probe, corresponding to a gene. The median of the residuals for each probe set, for each array sample is compared to the median absolute deviation for all residuals and samples for the gene.

Although the core FIRMA methods are the same as the original implementation in R, AltAnalyze FIRMA differs in several important ways:

1) The standard AltAnalyze core, extended, or full probe set definitions define the probe composition of each gene, rather than the Affymetrix transcript cluster definitions. Thus, each probe must correspond to a single Ensembl gene to be analyzed.
2) While FIRMA scores for each sample and probe set are calculated, only summary statistics are reported in the standard AltAnalyze output files. This statistic is the average FIRMA score for all samples in the experimental group minus the average of the FIRMA scores in the designated baseline group. If no comparisons are specified, the two groups with the largest difference in scores are reported.
3) FIRMA scores are organized into groups for calculation of summary statistics (FIRMA fold change and t-test p-values). However, scores for each probe set and sample can be optionally exported.

Users can define whether to use the AltAnalyze core, extended or full annotations in the program interface or using the `--probetype` flag in the command-line interface. An unique numerical ID corresponding to each Ensembl gene and all associated gene probe sets for FIRMA analysis are stored in a metaprobeset file in the array annotation directory (e.g., AltDatabase/EnsMart54/Hs/exon/Hs_exon_core.mps). This file is used to define gene level probe sets by the program APT.

Similar to splicing-index analysis of exon-tiling data, expression and DAGB filtering of probe set expression, FIRMA score p-value filtering and gene expression reporting/filtering based on either constitutive or all exon aligning probe sets. To export FIRMA scores for each probe set and sample, select the option “Export all normalized intensities” from the “Alternative Exon Analysis Parameters” window, or by using the flag `--exportnormexp` in the command-line interface.

MiDAS

The MiDAS statistic is described in detail in the white paper:

www.affymetrix.com/support/technical/whitepapers/exon_alt_transcript_analysis_whitepaper.pdf . This analysis method is available from the computer program APT, mentioned previously. APT uses a series of text files to examine the expression values of each probe set compared to the expression of user supplied gene expression reporting probe sets. This method can also be used with RNA-Seq junctions when performing single feature-level analyses. Since AltAnalyze uses only features found to align to a single Ensembl gene (with the exception of RNA-Seq for trans-splicing events), AltAnalyze creates it's own unique numerical gene identifiers (different than the Affymetrix transcript clusters). When written, a conversion file is also written that allows AltAnalyze to translate from this arbitrary numerical ID back to an Ensembl gene ID. These relationships are stored in the following files along with the feature expression values:

meta-Hs_Exon_cancer_vs_normal.txt	Relates feature to gene
gene-Hs_Exon_cancer_vs_normal.txt	Gene expression values (non-log)
exon-Hs_Exon_cancer_vs_normal.txt	Feature expression values (non-log)
commands-Hs_Exon_cancer_vs_normal.txt	Contains user commands for APT
Celfiles-Hs_Exon_cancer_vs_normal.txt	Relates sample to group
probeset-conversion-Hs_Exon_cancer_vs_normal.txt	Relates arbitrary gene IDs back to Ensembl

When the user selects the option "Calculate MiDAS p-values", AltAnalyze first exports expression data for selected RNA-Seq feature or probe sets (e.g., AltAnalyze "core" annotated – Figure 2.5) to these files for all pairwise comparisons. Once exported, AltAnalyze will communicate with the APT binary files packaged with AltAnalyze to run the analysis remotely. MiDAS will create a folder with the pairwise comparison dataset name and a file with MiDAS p-values that will be automatically read by AltAnalyze and used for statistical filtering (stored in the AltAnalyze program directory under "AltResults/MiDAS"). These statistics will be clearly labeled in the results file for each feature and used for filtering based on the user-defined p-value thresholds (Figure 2.5). When more than two-groups are being compared in AltAnalyze ("all groups" or "both options for "Type of group comparisons to perform"), the MiDAS p-value is reported for all groups designated by the user in combined array files or expression dataset file.

Note: Different versions of the APT MiDAS binary have been distributed. AltAnalyze is distributed with two versions that report slightly different p-values. The older version (1.4.0) tends to report larger p-values than the most recent distributed (1.10.1). Previous versions of AltAnalyze used version 1.4.0, while AltAnalyze version 1.1 uses MiDAS 1.10.1 that produces p-values that are typically equivalent to those as the AltAnalyze calculated splicing-index p-values (larger).

ASPIRE

For exon-exon sensitive junction platforms (RNA-Seq, HJAY, HTA2.0, MJAY, hGlue, AltMouse), the algorithm analysis of splicing by isoform reciprocity or ASPIRE was adapted from the original report (9) for inclusion into AltAnalyze. Similar to the splicing-index method, for each reciprocal junction, a ratio is calculated for expression of the junction (non-log) divided by the mean of all gene expression reporting junctions and exons (non-log), for the baseline and experimental groups. The ASPIRE δI is then calculated for the inclusion (ratio1) and exclusion (ratio2) junctions, as such:

R_{in} = baseline_ratio1/experimental_ratio1

R_{ex} = baseline_ratio2/experimental_ratio2

I_1=baseline_ratio1/(baseline_ratio1+baseline_ratio2)

I_2=experimental_ratio1/(experimental_ratio1+experimental_ratio2)

in_1= ((R_{ex}-1.0)*R_{in})/(Rex-Rin)

in_2= (R_{ex}-1.0)/(R_{ex}-R_{in})

$\delta I = -1*((in_2-in_1)+(I_2-I_1))/2.0$

If (R_{in}>1 and R_{ex}<1) or (R_{in}<1 and R_{ex}>1) and the absolute δI score is greater than the user supplied threshold (default is 0.2), then the δI is retained for the next step in the analysis. By default, AltAnalyze will calculate a one-way ANOVA p-value for the sample ASPIRE scores (relative to the compared condition group means) and a false-discovery rate p-value of this one-

way ANOVA (Benjamin-Hochberg). In place of these statics, the user can choose to perform a permutation analysis of the raw input data to determine the likelihood of each ASPIRE score occurring by chance alone. This permutation p-value is maximally informative when the number of experimental replicates is > 3. This permutation p-value is calculated by first storing all possible combinations of the two group comparisons. For example, if there are 4 samples (A-D) corresponding to the control group and 5 (E-H) samples in the experimental group, then all possible combinations of 4 and 5 samples would be stored (e.g, [B, C, G, H] and [A, D, E, F]). For each permutation set, ASPIRE scores were re-calculated and stored for all of these combinations. The permutation p-value is the number of times that the absolute value of a permutation ASPIRE score is greater than or equal to the absolute value of the original ASPIRE score (value = x) divided by the number of possible permutations that produced a valid ASPIRE score ((R_{in}>1 and R_{ex}<1) or (R_{in}<1 and R_{ex}>1)). If this p-value is less than user defined threshold, or x<2 (since some datasets have a small number of samples and thus little power for this analysis), the reciprocal junctions are reported.

Linear Regression

When working with the same type of reciprocal junction data as ASPIRE, a linear regression based approach can be used with similar results. This method is based on previously described approach (11). This algorithm uses the same input ASPIRE (junction comparisons, constitutive adjusted expression ratios). To derive the slope for each of the two biological conditions (control and experimental), the constitutive corrected expression of all samples for both reciprocal junctions is plotted against each other to calculate a slope for each of the two biological groups using the least squared method. In each case, the slope is forced through the origin of the graph (model = y ~ x – 1 as opposed to y ~ x). The final linear regression score is the $\log_2$ ratio of the slope of the baseline group divided by the experimental group. This ratio is analogous to a fold change, where 1 is equivalent to a 2-fold change. When establishing cut-offs, select 2 to designate a minimum 2-fold change. The same permutation analysis used for ASPIRE is also available for this algorithm.

Note: For previous published analyses ((11) and Salomonis et al. in preparation), linear regression was implemented using the algorithm `rlm`, which is apart of the R `mass` package from bioconductor. The Python R interpreter `rpy`, was used to run these analyses (which requires installation of R). In AltAnalyze version 2.0.X, this functionality is available using a pure python solution but may provide the exact same values.

Ri-PSI: Reciprocal isoform-Percent Spliced In

Ri-PSI is a new splicing algorithm introduced in AltAnalyze version 2.0.9, designed to be maximally sensitive to known and novel valid isoform differences while remaining very stringent. The PSI algorithm is available for both RNA-Seq junction-sensitive analyses and HTA2.0 arrays. This algorithm is run by default in addition to other splicing analyses or from the **Predict Groups** menu option. The primary results are saved to AltResults/Alternative Output/*species*_RNASeq_top_alt_junctions-PSI.txt. Because this algorithm is focused on reciprocal junctions counts, which do not have to be normalized within each individual sample, the results tend to be higher confidence. However, currently, the results are provided without comparison statistics. Nonetheless, such statistics can be easily calculated in software such as Excel (e.g., ttest function), ignoring samples without any reported PSI values that should be ignored due to insufficient detection. This method can only be applied to RNA-Seq datasets, in particular those that directly report counts for each exon-exon junction (e.g., TopHat, TCGA junction files). This algorithm examines the ratio of junction counts for the minor isoform (isoform with the fewest occurrences in the examined dataset) to the sum of the major and minor isoform junction counts. Both the numerator and denominator are incremented by 1 count, to ensure non-zero ratios. Thus, the maximal ratio can be 1 and then minimum must be greater than zero. Because the algorithm compares all possible pairwise reciprocal isoforms, it is possible for two minor isoforms to be compared. For this reason, the maximum expression of the minor isoform compared to the maximum expression of the most highly expressed junction for that gene is also reported in a secondary result field (**Max Inclusion PSI**). Results with a maximum difference between the **Minimum number of samples differing** indicated in the **Predict Groups** menu (optional)**,** will be additionally filtered for at least a 0.25 difference in PSI between

samples. Currently, splicing event type and functional predictions are not included in these results, but will be in later versions. Although comparison statistics are currently not generated from these results, a file written to the same output folder with the suffix **PSI-ANOVA.txt** with all splice events possessing an ANOVA p<0.05 are reported. These results are used for the automated **Sashimi-Plot** visualization, if associated BAM files are present in the same directory as the input RNA-Seq BED files.

External Alternative Exon Analysis File Import

In addition to providing several alternative exon analysis algorithms options in AltAnalyze (MiDAS, FIRMA, splicing-index), users can import Affymetrix alternative exon results from other programs for downstream functional annotation analyses. These analyses consist of alternative exon annotation (alternative splicing and alternative promoter selection), protein isoform, protein domain and microRNA binding site disruption analysis and pathway over-representation. Two options for external probe set analysis are now available:

1) Annotation of 3rd party alternative exon data in AltAnalyze
2) Restricted analysis of probe sets using a pre-defined list

Both options are conceptually similar; provide AltAnalyze with a list of probe sets and optionally statistics, and AltAnalyze will return alternative exon statistics (option 2) and/or functional annotations for the input probe sets (option 1 and 2).

Option 1 – Import and annotation of 3rd party probe set results

For this option, no raw data is required (e.g., CEL files or expression values) just a list of probe sets of interest. This option is simply available by selecting the main analysis option "Annotate External Results" and selecting a tab-delimited probe set list. The probe sets supplied in this list can be produced by any alternative exon analysis program the user prefers, as long as the output is exon-level Affymetrix probe sets. Users can provide direct output files from

JETTA or provide results in a more generic format, consisting of regulated probe sets and result statistics (optional).

The generic file format for alternative exon results import is:

1) (Column 1) Probe set ID ***(required)***
2) (Column 2) Alternative-exon fold ***(optional)***
3) (Column 3) Alternative-exon p-value ***(optional)***
4) (Column 4-100) Ignored data ***(optional)***

In addition to this generic format, results from the program JETTA can also be directly imported. Since this method produces two p-values for the MADS algorithm, the smallest of the two p-values is used. The results from this analysis are typical AltAnalyze result files, including input for DomainGraph and include any alternative exon statistics supplied with the probe set list.

Option 2 – Restricted probe set analysis (Advanced Feature)

This option can be performed with any of the main AltAnalyze analysis options (e.g., Process CEL Files, Expression Files or AltAnalyze Filtered). It is triggered by supplying a list of probe sets for each comparison of interest in the directory "filtering" in the AltAnalyze program directory (AltAnalyze_v1release/AltDatabase/filtering). The restricted filtering files are tab-delimited text files containing the corresponding exon probe set ID (Column 1) and optionally exon statistics and annotations (Columns 1-100). While the statistics and annotations provided in the restricted filtering file are not used for any computation, they are appended as extra columns in the alternative exon results file. Multiple files, corresponding to specific biological comparisons (e.g., Tumor_vs_wild-type) can exist in this folder and only those files who's name matches the comparison name will be matched and used for restricted analysis. For example, if biological sample groups A, B and C are being compared, to filter C_vs_A, the restricted probe set file must be named C_vs_A.txt. Note: If the user enters any filters (e.g., maximum DABG p value threshold, minimum alternative exon score), these will further restrict which "significant" probe sets are reported. To report all probe sets found in the AltAnalyze database, make sure to

set all thresholds to the minimum or maximum value (e.g., `--dabgp` 1 `--rawexp` 1 `--altp` 1 `--probetype` full `--altscore` 1 `--GEcutoff` 10000 – Section 2.3). Alternatively, users working with the command-line interface can use the option **`--returnAll`** to automatically enter this minimum values (see section 2.3).

Domain/miR-BS Over-Representation Analysis

A z-score is calculated to assess over-representation of specific protein sequence motifs (e.g., domains) and miR-BS's found to overlap with a probe set or RNA-Seq exon/junction (feature) that are alternatively regulated according to the AltAnalyze user analysis. This z-score is calculated by subtracting the expected number of genes in with a protein feature or miR-BS meeting the criterion (alternatively regulated with the user supplied thresholds) from the observed number of genes and dividing by the standard deviation of the observed number of genes. This z-score is a normal approximation to the hypergeometric distribution. This equation is expressed as:

$$z = \frac{(observed - expected)}{std.deviation(observed)} \qquad z = \frac{\left(r - n\frac{R}{N}\right)}{\sqrt{n\left(\frac{R}{N}\right)\left(1-\left(\frac{R}{N}\right)\left(1-\frac{n-1}{N-1}\right)\right.}}$$

n = All genes associated with a given motif

r = Alternatively regulated genes associated with a given motif

N = All genes examined

R = All alternatively regulated genes

Once z-scores have been calculated for all protein motifs and miR-BS linked to alternatively regulated features, a permutation analysis is performed to determine the likelihood of observing these z-scores by chance. This is done by randomly selecting the same number of regulated features from all features examined and recalculating z-scores for all terms 2000 times. The likelihood of a z-score occurring by chance is calculated as the number of times a permutation z-score is greater than or equal to the original z-score divided by 2000. A

Benjamini-Hochberg correction is used to transform this p-value to adjusted for multiple hypothesis testing.

Gene Ontology and Pathway Over-Representation Analysis

To perform advanced pathway, gene-set and Ontology (e.g., GO) over-representation AltAnalyze includes core python modules from the program GO-Elite (version 1.2) in AltAnalyze (http://www.genmapp.org/go_eite). GO-Elite currently provides a dozen distinct enrichment analyses for a large array of gene-sets, pathway databases and biological ontologies. The over-representation statistics used are identical to those for domain/miR-BS over-representation analysis (ORA) (e.g., z-score, Fisher's Exact p-value, BH p-value calculation). After ORA, all Ontology terms and gene-sets are filtered using user-defined statistical cut-offs (z-score, permutation p-value and number of genes changed), with Ontology terms further pruned to identify a minimally redundant set of reported Ontology terms, based on hierarchical relationships and ORA scores (see GO-Elite documentation). The gene database used for GO-Elite is specific to the version of Ensembl in the downloaded AltAnalyze gene database (Plus versions only with associations directly from Affymetrix included). All result files normally produced by GO-Elite will be produced through AltAnalyze.

AltAnalyze generates two types of gene lists for automated analysis in GO-Elite; differentially expressed genes and alternatively regulated genes. Criterion for differentially expressed genes are defined by the user in the GO-Elite parameters window (e.g., fold difference > 2 and t-test $p < 0.05$). The user can choose to use the rawp (one-way ANOVA, two groups) or adjp (BH adjusted value of the rawp) in the software. All genes associated with alternative exons are used for GO-Elite analysis. Genes with alternative exons that also have alternative splicing annotations can be further selected using the "Filter results for predicted AS" option. Results are exported to the "GO-Elite" directory in the user-defined output directory, while input gene lists can be found in the folders "GO-Elite/input" and "GO-Elite/denominator". The gene lists for differentially expressed genes have the prefix "GE." while the alternative exon files have the prefix "AS.". The appropriate denominator gene files for each is selected by GO-

Elite. Species and array specific databases for GO-Elite analysis are downloaded automatically from AltAnalyze when the species database is installed. Array types supported for each species include any Affymetrix supported at the time the Ensembl database was released along with any arrays supported by Ensembl.

3.3 Probe set and RNA-Seq Filtering

Prior to an Affymetrix alternative exon analysis, AltAnalyze can be used to remove probe sets that are not deemed as sufficiently expressed. For the two conditions that AltAnalyze compares (e.g., cancer versus normal), a probe set will be removed if neither condition has a mean detection above background (DABG) p value less than the user threshold (e.g., 0.05). Likewise, if neither condition has a mean probe set intensity greater than the user threshold (e.g., 70), then the probe set will be excluded from the analysis. When comparing two conditions (pairwise comparison) for probe sets used to determine gene transcription (e.g., constitutive aligning), both conditions will be required to meet these expression thresholds in order to ensure that the genes are expressed in both conditions and thus reliable for detecting alternative exons as opposed to changes in transcription. When comparing all biological groups in the user dataset, however, these additional filters are not used. For RNA-Seq analyses, the read counts associated with each exon or junction are used as a surrogate for the expression. These same filters applied to constitutive annotated exons or junctions and junctions used for reciprocal junction analysis.

3.4 Constitutive and gene expression calculation

Identifying exons and junctions for gene expression calculations

A reliable estimate of transcriptional activity for each gene is required to both report basic gene expression statistics and perform alternative exon analysis. Affymetrix exon and junction arrays probe most well annotated exon regions, many introns, untranslated regions and theoretically

transcribed regions. Gene expression values can be calculated in one of two ways from AltAnalyze; (A) using features aligned to constitutive exons, (B) using features aligned to all known exons. Using constitutive exons are recommended for use for all analyses.

Constitutive exons in AltAnalyze are classified as exons that align to a pre-determined set of exon regions that are most common to all mRNA transcripts used when the AltAnalyze database is created. RNA transcript exon structures and genomic positions are extracted from analogous versions of Ensembl and the UCSC genome browser database. While AltAnalyze database versions EnsMart49 and EnsMart52 used mRNA annotations from the Affymetrix probe set annotation file, EnsMart54 and later exclusively derives constitutive exon annotation from UCSC and Ensembl exon structures (Figure 3.1). If only one exon region is considered constitutive then the grouped exon regions with the second highest ranking (based on number of associated transcripts) are included as constitutive (when there at least 3 ranks). For next generation Affymetrix junction arrays (hGlue, HJAY, HTA2.0 and MJAY), constitutive exons are obtained as described above. Constitutive junctions from these arrays are currently determined by two methods; 1) determine if both of the exons in the junction are annotated as constitutive and 2) determine if the junction is annotated as a putative ‘alternative’ probe set according to the manufacturer annotation file (e.g., mjay.r2.annotation_map). If both lines of evidence indicate the probeset is constitutive, then the probeset is annotated accordingly. Probe set annotations are provided in “AltDatabase/EnsMart55/Hs/junction/Hs_Ensembl_probesets.txt” (modify for your species, Ensembl version and array type). For RNA-Seq analyses, junctions are considered constitutive if the 5’ and 3’ splice sites of the detected junction map to the corresponding splice sites of two exons that are; 1) annotated as constitutive and 2) not annotated as alternative from the transcript reciprocal junction comparison analysis. Constitutive RNA-Seq junctions are only evaluated when no exon reads are present.

In addition to constitutive exons, users have the option to use all features that have an Affymetrix core probe set annotation or align to an AltAnalyze defined exon region. Affymetrix defines probe sets according to three criterion, "core", "extended" and "full". The Affymetrix core annotations are recommended for calculation of constitutive levels by Affymetrix, however,

these are often a mix of known alternative exons and AltAnalyze annotated constitutive exons. In addition to these Affymetrix core exons, the AltAnalyze core set consists of any probe set that aligns to an exon region, but excludes probe sets aligning to any non-exon features, including introns and untranslated regions (Figure 3.1). In version 2.0 of AltAnalyze, users are no longer restricted to genes containing constitutive annotated exons/junctions for alternative exon analysis. Prior to version 2.0, AltAnalyze removed genes during the filtering process that had no exon or junctions with constitutive annotation prior to the alternative exon analysis. To address this issue, all exon or junction features that align to known mRNAs are used to assess gene expression when no constitutive features are deemed “expressed” according to the user’s filtering parameters.

Calculating gene expression values

Gene expression values are calculated twice during an exon array analysis; (1) To report gene expression fold changes and summary statistics, (2) To calculate gene expression normalized intensities for alternative exons. While both analyses use the same set of starting exons, junctions or probe sets (constitutive or mRNA aligning), they differ in how filtering of these features occurs. These differences are important when trying to eliminate false positive alternative exon predictions.

For gene expression summary reporting, expression values from all constitutive or core features (user defined) are filtered and then averaged. For this analysis, the constitutive or core features are first identified from the AltAnalyze database (Ensembl_probeset or Ensembl_exon file) and corresponding expression and detection probabilities extracted from the APT RMA result files from the input array files. For RNA-Seq analyses only total number of counts associated with each exon/junction are considered. For each biological group (typically containing replicates), the mean expression and mean detection above background probabilities are calculated for each feature. If the mean expression and the mean detection above background probabilities for at least one group does not meet the user defined thresholds (by default $p<0.05$ and expression>70), then this feature will not be used to calculate the gene

expression value for the corresponding gene. The average expression for all remaining features, for each sample will calculated to obtain a mean gene expression value for each feature for each replicate. Thus, any differences between features used to calculate gene expression will be averaged. For example, when all core features are used, the expression of any alternative exons will be averaged with the non-alternative exons. If no constitutive or core features for a gene meet these criterion (see below), then all will be used to calculate gene expression. Only one set of gene expression values is reported for each Ensembl gene.

This same strategy is used for calculating a gene expression value for the alternative exon analysis with the following differences: (1) a feature used to calculate gene expression must demonstrate evidence expression (expression and detection probability filtering) in both conditions (pairwise comparisons only) or it is removed and (2) if no feature remain after expression and detection probability filtering, then features for the gene will NOT be analyzed for the alternative exon analysis. If all groups are being compared for the alternative exon analysis, rather than direct comparison of two groups, then only one biological group must meet the expression and detection probability thresholds for the gene expression (same as for gene expression summary reporting, above). These additional requirements ensure that the gene is expressed at sufficient levels to assess alternative splicing in both compared biological groups. This is important in eliminating false positive changes in feature expression that can occur when the gene is expressed in only one condition.

3.5 Alternative Splicing Prediction

To predict whether or not a single feature (EP) or reciprocal junction-pair (JP) associates with an alternative splicing or alternative promoter sequence, AltAnalyze uses two strategies; 1) Identify alternative exons/introns based on *de novo* isoform comparison and 2) Incorporating splicing predictions from UCSC's "known_alt.txt" file.

De Novo Splicing Prediction and Exon Annotation

In order to identify exons with alternative splicing or promoters, AltAnalyze compares all available gene transcripts from UCSC and Ensembl to look for shared and different exons. To achieve this, all mRNA transcripts from UCSC's species-specific "mRNA.txt" file that have genomic coordinates aligning to a single Ensembl gene and all Ensembl transcripts from each Ensembl build are extracted. Only UCSC transcripts that have a distinct exon composition from Ensembl transcripts are used in this analysis, excluding those that have a distinct genomic start or stop position for the first and last exon respectively (typically differing 5' and 3' UTR agreement), but identical exon-structure.

When assessing alternative splicing, cases of intron retention are identified first. These regions consist of a single exon that spans an two adjacent exons at least one another transcript for that same gene. These retained introns are stored for later analysis, but eliminated as annotated exons. Remaining exons are clustered based on whether their genomic positions overlap (e.g., alternate 5' or 3' start sites). Each exon cluster is considered an exon block with one or more regions, where each block and region is assigned a numerical ID based on genomic rank (e.g., E1.1, E1.2, E2.1, E3.1). For each exon in a transcript, the exon is annotated as corresponding to an exon block and region number (Figure 3.1). All possible pairwise transcript comparisons for each gene are then performed to identify exon pairs that show evidence of alternative exon-cassettes, alternative 3' or 5' splice sites or alternative-N or -C terminal exons (Figure 3.1). All transcript exon pairs are considered except for those adjacent to a retained intron. This analysis is performed by comparing the exon block ID and region IDs of an exon and it's neighboring exons to the exon blocks and regions in the compared transcript. Ultimately, a custom heuristic assigns the appropriate annotation based on these transcript comparisons.

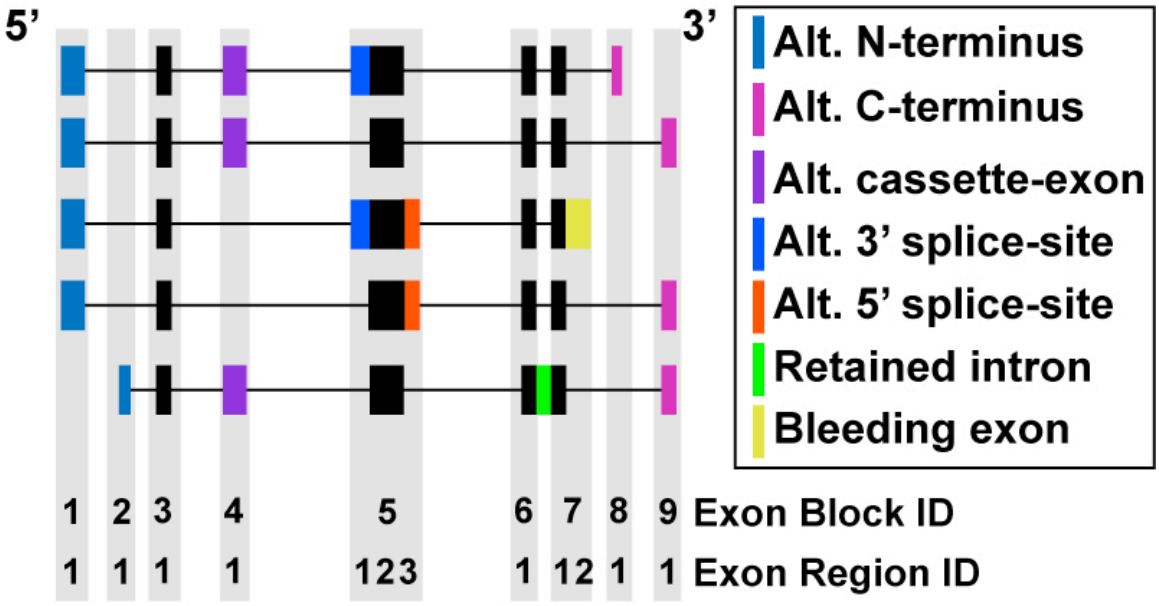


Figure 3.2. Comparison of mRNA Exon Composition. To determine alternative splicing and alternative promoter regulation, all analyzed transcripts (Ensembl and UCSC) were compared based on exon genomic positions and subsequently annotated by a custom heuristic. Exon block and regions definitions are shown. The different types of alternative exon events are illustrated by different colored exons among five theoretical transcripts for the same gene. The black filled boxes represent exon regions that are most common to all mRNA transcripts. These regions are annotated as constitutive by AltAnalyze. Features that overlap with the constitutive regions can be used to calculate gene expression. All non-intron regions that align to an exon block can also optionally be used to calculate gene expression.

Incorporating UCSC Splicing Predictions

In addition to all *de novo* splicing annotations, additional splicing annotations are imported from the UCSC genome database and linked to existing exon blocks and regions based on genomic coordinate overlap. This comparison is performed by the `alignToKnownAlt.py` module of

AltAnalyze (called from `EnsemlbImport.py`). *De novo* and UCSC splicing annotations are stored along with feature Ensembl gene alignment data in the file <species>_Ensembl_probesets.txt (Affymetrix) or ensembl/<species>/<species>_Ensembl_exon.txt file (RNA-Seq). These Affymetrix annotations are used by AltAnalyze and DomainGraph for annotation and visualization. In the AltAnalyze result file, UCSC KnownAlt the major splicing annotation types are altFivePrime, altThreePrime, cassetteExon, altPromoter, bleedingExon and retainedIntron. In comparison, the major AltAnalyze determined splicing annotation types alt-5', alt-3', cassette-exon, alt-N-term, intron-retention, exon-region-exclusion and alt-C-term. These splicing annotations are determined by comparing relative exon-junction positions for all analyzed transcripts for each gene (see proceeding section). The annotation "exon-region-exclusion" is the opposite of intron-retention (region most commonly described as exon rather than intron), alt-N-term is similar to altPromoter (distinct 5' distal-transcript exon with shared 3' exons) and alt-C-term is the opposite of alt-N-term. To better understand these annotations, look at specific probe set examples through the NetAffx website (www.affymetrix.com/analysis/index.affx) using the UCSC browser option.

Filtering for Alternative Splicing

As mentioned in previous sections, AltAnalyze includes the option restrict alternative exon results to only those probe sets or reciprocal junction-pairs predicted to indicate alternative splicing. AltAnalyze considers alternative splicing as any alternative exon annotation other than an alternative N-terminal exon or alternative promoter annotation derived from *de novo* or UCSC genome database annotations.

Incorporating Alternative Poly-Adenylation Predictions

Poly-adenylation (polyA) sites are identified using the polyA database (http://polya.umdnj.edu/) version 2. This database provides polyA site genomic coordinates for human, mouse, rat, chicken and zebrafish, generated in 2006 from various genomic database builds. Of these, only

human polyA sites are provided as an annotation track in the UCSC genome database. For human, the polyA sites for the appropriate human genome build are downloaded and parsed using the same methods for the knownAlt UCSC annotation track. If multiple polyA sites are observed in a given Ensembl gene, exon regions overlapping with these binding sites are reported as “alternative_polyA” along with the alternative splicing annotations. To report these same annotations for other species, annotations from the polyADB_2 flat-file were converted to UCSC BED format and batch converted to the latest genome build using http://www.genome.ucsc.edu/cgi-bin/hgLiftOver. In some cases, multiple lift-over translations were required. Intermediate files are available at http://www.altanalyze.org/archiveDBs/. Due to missing chromosome annotations for most predictions in zebrafish, these annotations were not included.

3.6 Protein/RNA Inference Analysis

Identifying Alternative Proteins Protein Domains

RNA-Seq and probe set sequences are used to identify which proteins align to or are missing from transcripts for that gene. To do this, all Ensembl and UCSC mRNA transcripts are extracted for a gene that corresponds to a given feature (probe set or RNA-Seq junction). For each transcript, all exon genomic coordinates are stored. For exon-level analyses, transcripts with exons that contain the probe set (or RNA-Seq exon region) genomic coordinates are considered transcript aligning, while all others are considered non-aligning. For junction analyses, if two reciprocal junctions (or junction and an exon) align to distinct isoforms, these relationships are stored rather than the aligning and non-aligning isoforms, however, if both isoforms do not align to distinct transcripts, then the one with a aligning and non-aligning set of transcripts is stored for further exon comparisons.

If a set of aligning and non-aligning isoforms (competitive) is identified for a single feature or reciprocal junction pair, all possible aligning and non-aligning pairwise combinations are identified to find those pairwise comparisons with the smallest difference in exon composition. This is accomplished by determining the number of different and common exons each transcript

pair contains (based on genomic start and stop of the exon). When comparing the different transcript pairs, the most optimal pair is selected by first considering the combined number of distinct exons in both transcripts and second the number of common transcripts. Thus, if one transcript pair has 4 exons in common and 2 exons not in common, while a second pair has 5 exons in common and 3 exon not in common, the prior will be selected as the optimal since it contains less overall differences in exon composition (even though it has less common exons than the other pair). A theoretical example is illustrated in Figure 3.2.

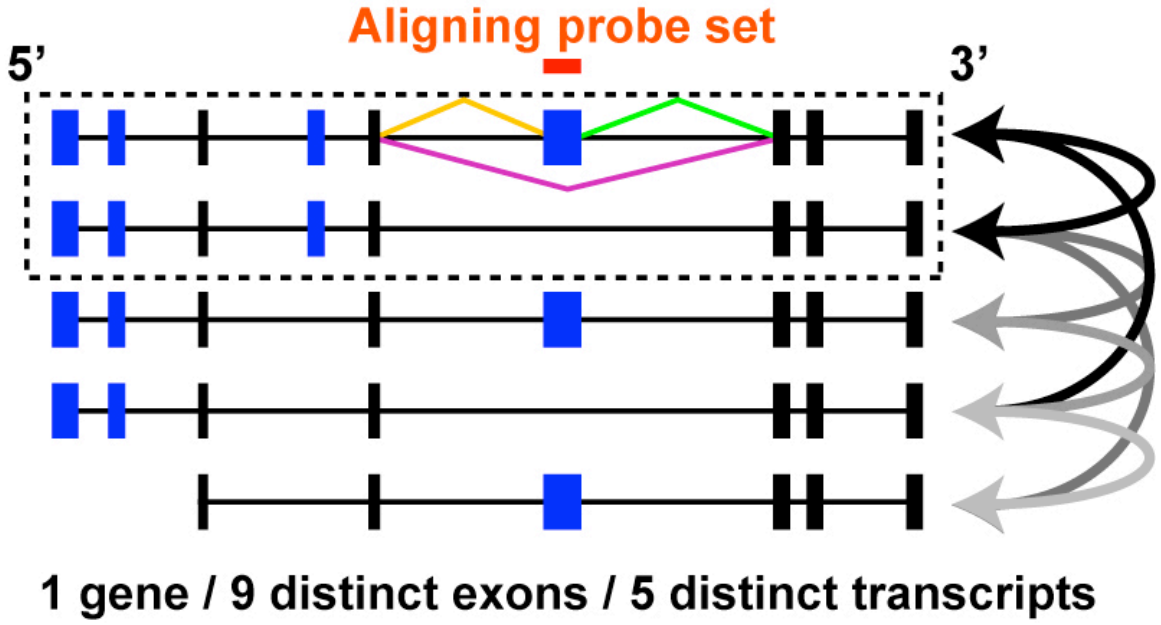


Figure 3.3. Comparison of probe set aligning and non-aligning mRNAs. A theoretical gene is shown with 9 distinct exons and 5 distinct mRNA transcripts with different exon combinations. Four exons are alternatively expressed in different transcripts (blue exons) while five are common or constitutive to all transcripts (black exons). All possible pairwise transcript combinations are shown (arrows) between mRNAs that contain and probe set aligning exon and those that do not. Ultimately, a single pair is selected that has the most common exons and the least uncommon exons (dashed box). The same strategy is used for junction analyses as exon, however, for junction sensitive platforms, aligning transcripts are identified by direct junction (orange, green, purple)

sequence alignment to the mRNAs prior to comparing exon composition as described above.

Once a single optimal isoform pair has been identified, protein sequence is obtained for each by identifying protein IDs that correspond to the mRNA (Ensembl or NCBI) and if not available, a predicted protein sequence is derived based on *in silico* translation. Although such a protein sequence may not be valid, given that translation of the protein may not occur, these sequences provide AltAnalyze the basis for identifying conservative changes predictions for a change in protein size, sequence and domain composition. Domain/protein features are obtained directly from UniProt's sequence annotation features or from Ensembl's InterPro sequence annotations (alignment e-value <1) (see section 5 data extraction protocols). Any InterPro sequences with a description field or any UniProt sequence annotation feature that is not of the type "CHAIN", "CONFLICT", "VARIANT", "VARSPLIC" and "VAR_SEQ" are examined by AltAnalyze. To compare domain or motif sequence composition differences, the protein sequence that corresponds to the amino-acid start and stop positions of a domain for each transcript is searched for in each of the compared protein isoforms. If the length of a motif sequence is less than 6 amino-acids, flanking sequence is included. If a domain is present in one but not another isoform, that domain is stored as differentially present. To identify differences in protein sequence (e.g., alternative-N-terminus, C-terminus, truncation coding sequence and protein length), the two protein sequences are directly compared for shared sequence in the first and last five residues and comparison of the entire sequences. If the N-terminal sequence is common to both isoforms but there is a reduction in more than 50% of the sequence length, the comparison is annotated as truncated. If an Ensembl transcript, non-coding and nonsense mediated decay annotations are included from the Ensembl translation annotations. All of these annotations are stored for each junction, exon or probe set for import into AltAnalyze, with each new database build.

Direct Domain/Motif Genomic Alignment

The above strategy allows AltAnalyze to identify predicted protein domains and motifs that are found in one isoform but not the other (aligning to a feature and not aligning). In addition to these “inferred” domain predictions, that include protein domains/motifs that do not necessarily overlap with the regulated feature, AltAnalyze includes a distinct set of annotations that only corresponds to domain/motif protein sequence that directly overlaps with a feature. Alignment of features to InterPro IDs is achieved by comparing feature genomic coordinates to InterPro genomic coordinates. To obtain InterPro genomic start and end positions are determined by first identifying the relative amino-acid positions of an InterPro region in an Ensembl protein, finding which exon and at what position the InterPro region begins and ends and finally stroing the genomic position of these relative exon coordinates.

These feature-InterPro overlaps can be of two types; 1) features whose sequence is present in the domain coding RNA sequence and 2) features whose sequence is not present in the domain coding RNA sequence. The second type of overlap typically occurs in the gene introns. While these associations are typically meaningful, false “indirect” associations are possible. To reduce the occurrences of these false positives, any feature that aligns to the UTR of an Ensembl gene or that occurs in the first or last exon of an mRNA transcript are excluded. These heuristics were chosen after looking at specific examples that the authors considered to be potential false positives. For junction analyses (RNA-Seq and junction array), the associated critical exon genomic position rather than probe set is used.

Identifying microRNA Binding Sites associated with Alternative Exons

MicroRNA binding site (miR-BS) sequence is obtained and compared from five different microRNA databases (see section 6.5), and compared to identify miR-BSs in common to or distinct to different databases. Probe set sequences are obtained from Affymetrix, while critical exon sequences (corresponding to two reciprocal junctions) are obtained from chromosome FASTA sequence files (see section 6.7). Each miR-BS sequence is searched for within probe set or critical exon sequence to identify a match. These relationships are stored with each new database build and are used by AltAnalyze and DomainGraph.

Exhaustive Protein Domain/Motif Analysis

Very similar to the competitive protein domain/motif analysis is the exhaustive protein comparison analysis. This feature is currently not available by default in AltAnalyze and requires replacement database files from AltAnalyze support. The purpose of these files is to obtain the most conservative possible domain-level prediction results from the competitive analysis. This done by storing all pairwise aligning and non-aligning isoform comparisons (Figure 3.2) and then obtaining protein sequence for each transcript, as described in earlier sections and storing all domain/motifs differentially found between all possible competitive isoforms. From these stored results, all possible competitive isoforms are themselves compared to find isoforms that ideally show only differences in central regions of the protein (no N-terminal or C-terminal differences), next for those that contain as few possible domain-level predictions and finally for those with the smallest overall differences in protein length. For detailed algorithm information see the `IdentifyAltIsoforms` module and the function "compareProteinFeaturesForPairwiseComps".

3.7 Gene Annotation Assignment

AltAnalyze extracts useful gene annotations for determining whether a gene (A) encodes for protein, (B) is likely "drug-able", (C) is a transcriptional regulator, (D) has putative microRNA targets, (E) participates in known pathways, (F) localizes to specific cellular compartment and (G) is a housekeeping gene. To obtain these annotations, AltAnalyze extracts various annotations for several public genomic databases (Ensembl, UniProt, miRBase, TargetScan, miRanda, Pictar, miRNAMap, WikiPathways, Gene Ontology, Affymetrix). Extracted from Ensembl are annotations for protein coding potential in addition to pseudogenes, rRNA, miRNAs, snoRNAs, lincRNA and other gene types. From UniProt, annotations for kinase, GPCR and coupling pathway, single transmembrane receptors transcriptional regulator and cellular

compartment. Annotations for Gene Ontology termas and WikiPathways are extracted on the fly from the downloaded Official GO-Elite annotation databases. Housekeeping gene predictions are extracted from this same database, by searching for Ensembl-Affymetrix associations for probesets containing the ‘AFFX’ notation. Any microRNA targeting prediction from miRBase, TargetScan, miRanda, Pictar, miRNAMap (Section 6.5) are reported along with the source of the annotation and overlapping predictions.

Section 4 – Using R with AltAnalyze

While AltAnalyze is a largely a stand-alone program, some statistical analyses can be included that depend on external applications. These require prior installation of these tools using operating system installers and properly interfacing them with AltAnalyze.

4.1 Interactivity with R

Although installation of R is not required for any of the AltAnalyze analyses, for users who wish to use more advanced statistics (e.g., advanced clustering), installation of R may be needed. AltAnalyze connects to R using the python library pypeR (PYthon-piPE-R), included with AltAnalyze. Using this library, AltAnalyze is able to connect to R, access libraries and run them remotely. Currently, clustering using the hopach algorithm is the only R library supported. To run, you will only need to have R installed and recognized from a terminal window. Most R installers should include this functionality by default, without any user-required interaction. AltAnalyze will install hopach in a local directory when first run. R interactivity is supplied using the R_interface.py module. Additional functionality has been built into this module (gcrma, multtest, combat, limma), but is not currently connected to any main analysis options within AltAnalyze. Advanced users wishing to exploit this code are welcome to contribute to AltAnalyze development. Please note, that some limma and combat functionality are already supported using existing python libraries in AltAnalyze.

Section 5 - Software Infrastructure

5.1 Overview

AltAnalyze consists of more than 30 modules and over 10,000 lines of code. The core modules for AltAnalyze consist of the programs ExpressionBuilder and AltAnalyze, which can be used in tandem or separately through the AltAnalyze GUI. The user will never likely need to deal directly with these modules names when running AltAnalyze, but these distinct core modules are used for different analysis functions (Figure 5.1).

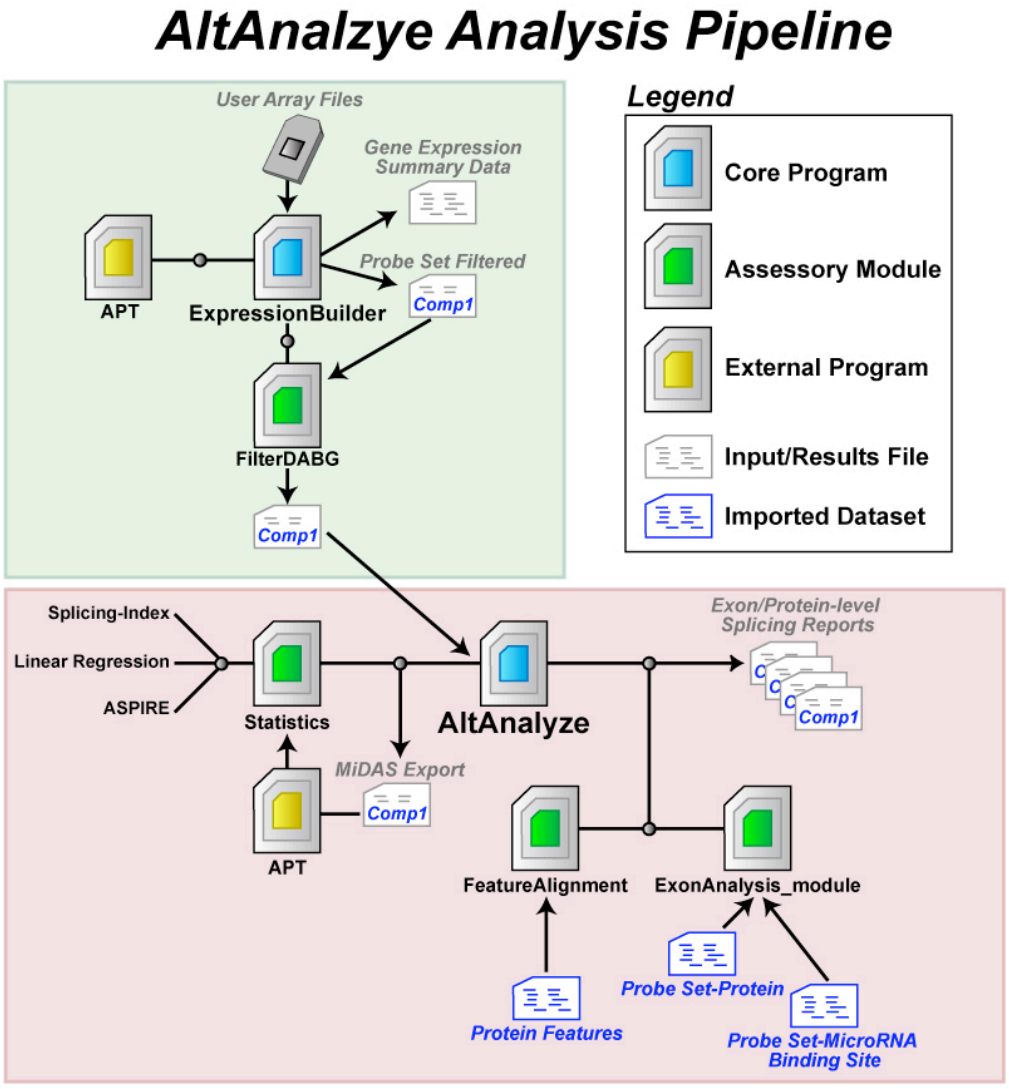


Figure 5.1. AltAnalyze Analysis Pipeline. The AltAnalyze workflow is depicted, using Affymetrix arrays as an example (for RNA-Seq data, substitute RNA-Seq

alignment files for CEL file and exon/junction for probe set). 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) or CEL files are imported into AltAnalyze via the `ExpressionBuilder` module, which separates data for different biological array groups into user designated pairwise comparisons (e.g., cancer vs. normal). For each pairwise 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 values (based on constitutive probe set expression) for each gene and array along with summary statistics (average expression, fold, and t-test p-value for all pairwise comparisons) and annotations. (B) Using the `ExpressionBuilder` pairwise 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.

The ExpressionBuilder component builds constitutive gene expression summary files as well as filters the exon, junction or probe set expression data prior to alternative-exon analysis.

The AltAnalyze module performs all of the alternative-exon analysis and MiDAS p-value calculations.

5.2 ExpressionBuilder Module

The ExpressionBuilder program is principally designed to perform the following tasks:

1) Import user expression data from tab-delimited files.
2) ***(Alternative Exon Analysis)*** For Affymetrix arrays, exclude probe sets where no samples have a DABG p<user-threshold (only applicable when DABG p-values exist) or an expression value > user-threshold. For RNA-Seq, this module filters out exons or junctions where no samples have a read count > user-threshold (e.g., 2 reads).
3) Organize your data according to biological groups and comparisons (specified by the user from custom text files).
4) ***(Alternative Exon Analysis)*** Calculate gene transcription levels for all Ensembl genes.
5) Export calculated gene expression values along with folds, t-test and f-test p-values and gene annotations for all genes and all user indicated comparisons.
6) ***(Alternative Exon Analysis)*** Export all gene-linked feature expression and DABG data for all pairwise comparisons for further filtering (next step).
7) ***(Alternative Exon Analysis)*** Filter the resulting feature data using mean expression values and probabilities specific for each pairwise comparison and user-defined thresholds (Figure 2.4).

The above tasks are performed in order by the ExpressionBuilder module. Detection probabilities are assessed at two steps (2 and 7). In step 2, import of DABG p-values are for the purpose of calculating a transcription intensity value only for those constitutive features (present in all or most transcripts) that show detection above background, since some probe sets will have weaker expression/hybridization profiles as others for Affymetrix analyses and some junction counts are too low to be considered biologically significant for RNA-Seq. If no features have a DABG p-value less than the default or user supplied threshold (for at least one sample in your dataset), all selected features will be used to calculate expression (constitutive aligning only if default is selected).

In step 7, the probe set DABG p-values are examined to include or exclude features for alternative splicing analysis. This step is important in minimizing false positive splicing calls. False positive splicing calls can occur when a feature is expressed below detectable limits and results in a transcription-corrected expression value that artificially appears to be alternatively regulated. For Affymetrix expression and DABG p-value files output from APT, probe set expression values are initially filtered to remove any probe sets where the expression and dabg p-values are below the user defined threshold for all biological groups examined and export all pairwise comparison group files (expression and dabg) for further filtering. For exons or probe sets used to determine gene expression levels (constitutive or known exons), the module FilterDABG is used to remove features that are expressed below user defined thresholds (expression and dabg) in the two comparison groups for all pairwise comparisons. If a feature is not used to determine gene expression levels, then for at least one of the two biological groups, the same criterion must be true (mean DABG p-value and expression). These filters ensure that: 1) the gene is "expressed" in both conditions and 2) the feature is "expressed" in at least one condition. The feature and expression values passing these user defined filters are exported to a new file that is ready to use for splicing analyses, stored to the user output directory under "AltExpression/ExonArray/*species*". This file can also be directly selected in future AltAnalyze runs as input for analysis ("AltAnalyze filtered file" – Figure 2.2).

Runtime of ExpressionBuilder is dependent on the number of conditions and array type being analyzed (10 minutes plus for Affymetrix Exon 1.0 ST arrays). When analyzing junction-only RNA-Seq data, runtime is relativity fast (1-5 minutes), since the sequence space (pre-aligned junctions) is less than exon and junction tiling arrays. However, analysis of combined exon and junction RNA-Seq data is typically longer and more memory intensive than Affymetrix junction arrays. If multiple comparisons are present in a single expression file, input files for AltAnalyze will all be generated at once and thus runtimes will take longer.

Note 1*: While this pipeline is mainly for use with alternative exon/junction platforms, it is also compatible with a standard 3' Affymetrix microarray dataset to calculate folds, t-test p-values, and assign*

annotations to this data. This is useful when you have many comparisons in your dataset and you don't wish to manually calculate these values.

***Note 2**: You do not need to run ExpressionBuilder if you have an alternative way of building AltAnalyze input files for Affymetrix arrays. To do so, your file headers for each arrays must have the name "group:sample_name", where your group names are different for each group and the denominator group is listed first and the numerator is listed second. Below the header line should only be probe set IDs and log2 expression values.*

5.3 AltAnalyze Module

The AltAnalyze module is the primary software used for all alternative exon analyses. This software imports the filtered expression data and performs all downstream statistical and functional analyses. This program will analyze any number of input comparison files that are in the "AltExpression" results directory for that array type. The main analysis steps in this program are:

1) Import exon or junction annotations, to determine which exon, junctions or probe sets to analyze, which are predicted constitutive and which correspond to known AS or APS events.
2) Import the user expression data for the pairwise comparison.
3) Store feature level data (e.g., junction or probe set) for all features corresponding to either a constitutive exon (or junction) or for splicing event, while storing the group membership for each value.
4) Calculate a constitutive expression value for each gene and each sample (used for the splicing score later on). OPTIONAL: If the user selected a cut-off for constitutive fold changes allowed to look at alternative exon regulation, then remove genes from the analysis that have a gene-expression difference between the two groups > cut-off (up or down).

5) ***(Alternative Exon Analysis Only)*** OPTIONAL: exports input for the Affymetrix Power Tools (APT) program to calculate a MiDAS p-value for each probe set or RNA-Seq feature.
6) Calculate a splicing score and t-test p-value from the junction or probe set and constitutive expression values. This calculation requires that splicing ratios are calculate for each sample (exon/constitutive expression) and then compared between groups. For exon arrays, the splicing index method (SI) is calculated for each probe set. For junction analyses, ASPIRE, Linear Regression are used with the pre-determined reciprocal junctions or alternatively are calculated for individual features using the SI method.
7) ***(Junction Analysis Only)*** OPTIONAL: performs a permutation analysis of the sample ASPIRE input values or Linear Regression values to calculate a likelihood p-value for all possible sample combinations.
8) Retain only features meeting the scoring thresholds for these statistics (splicing score, splicing t-test p, permutation p, MiDAS p – see Section 3.2).
9) Import feature-protein, feature-domain and feature-miRNA associations pre-built local from flat files (see Section 6).
10) For the remaining features, import all protein domain and miR-BS to all pre-built feature associations (see Section 3.3 for details). Import all feature-domain and –miR-BS associations for all genes to calculate an over-representation z-score for all domains and miR-BS's along with a non-adjusted and adjusted p-value. Export the resulting statistics and annotations to tab-delimited files in the "AltResults/AlternativeOutput" folder in the user-defined output directory.
11) ***(Junction Analysis Only)*** Import splicing and exon annotations for regulated exons corresponding to each set of reciprocal junctions (e.g. for E1-E3 compared to E1-E2, E2 is the regulated exon). These annotation files are the same as those for exon arrays, except that the probe set is replaced by the exon predicted to be regulated by the reciprocal junction-pair (see Section 6.2).

12) For protein domain and miR-BS annotations, reformat the direction/inclusion status of the annotation. For example, if a kinase domain is only found in a protein that aligns to a exon, junction or probe set, but was down-regulated, then the annotation is listed as (-) kinase domain, but if up-regulated is listed as (+) kinase domain.
13) Export the results from this analysis to the "AltResults/AlternativeOutput" folder in the user-defined output directory.
14) Summarize the probe set or reciprocal junction data at the level of genes and export these results (along with Gene Ontology/Pathway annotations).
15) Export overall statistics from this run (e.g. number of genes regulated, splicing events).
16) ***(Junction Analysis Only)*** Combine and export the exported feature and gene files for each comparison analyzed, to compare and contrast differences.

Result File Types

When finished AltAnalyze will have generated five files.

1) name-scoringmethod-exon-inclusion-GENE-results.txt
2) name-scoringmethod-exon-inclusion-results.txt
3) name-scoringmethod-ft-domain-zscores.txt
4) name-scoringmethod-miRNA-zscores.txt
5) name-scoringmethod-DomainGraph.txt

Here, "name" indicates the comparison file name from ExpressionBuilder, composed of the species + platform_name + comparison_name (e.g. Hs_Exon_H9-CS-d40_vs_H9-ESC-d0), "scoringmethod" is the type of algorithm used (e.g. SI) and the suffix indicates the type of file.

The annotation files used by AltAnalyze are pre-built using other modules with this application (see Section 6). Although the user should not need to re-build these files on their own, advanced users may wish to modify these tables manually or with programs provided (see Section 6.7).

For protein-level functional annotations (e.g., domain changes), this software assumes that if an exon is up-regulated in a certain condition, that the protein domain is also up-regulated and indicates it as such. For example, for exon array data, if a probe set is up-regulated (relative to gene constitutive expression) in an experimental group and this domain is found in the protein aligning to this probe set, in the results file this will be annotated as (+) domain. If the probe set were down-regulated (and aligns as indicated), this would be annotated as (-) domain.

Section 6 – Building AltAnalyze Annotation Files

6.1 Splicing Annotations and Protein Associations

A number of annotation files are built prior to running AltAnalyze that are necessary for:

1) Organizing exons and introns from discrete transcripts into consistently ordered sequence blocks (`UCSCImport.py` and `EnsemblImport.py`).
2) Identifying which exons and introns align to alternative annotations (`alignToKnownAlt.py` and `EnsemblImport.py`).
3) Identifying exons and junctions with likely constitutive annotations (`EnsemblImport.py`).
4) Identifying which probe sets align to which exons and introns (`ExonArrayEnsemblRules.py`).
5) Extracting out protein sequences with functional annotations (`ExtractUniProtFunctAnnot.py` and `EnsemblSQL.py`).
6) Identifying features that overlap with microRNA binding sites (`MatchMiRTargetPredictions.py` and `ExonSeqModule.py`).
7) Matching feature genomic coordinates to cDNA exon coordinates and identify the optimal matching and non-matching mRNA/protein for each feature (`IdentifyAltIsoforms.py`).
8) Identifying features that overlap with protein domains and UniProt motifs (`ExonAnalyze_module.py, FeatureAlignment.py`)

These annotation files are necessary for all exon and junction analyses. Junction analyses further require:

9) Matching reciprocal junctions to annotated exons or introns (`JunctionArray.py`, `EnsemblImport.py` and `JunctionArrayEnsemblRules.py`), creating a file analogous to (4) above.

10) Matching reciprocal junction sequence to microRNA binding sites (`JunctionSeqSearch.py`), creating a file analogous to (6) above.

11) Matching junction sequence to cDNA sequences (`mRNASeqAlign.py`), prior to identification of optimal matching and non-matching mRNA/proteins (`IdentifyAltIsoforms.py`).

With the creation/update of these files, the user is ready to perform alternative exon analyses for the selected species and platform. Since many of these analyses utilize genomic coordinate alignment as opposed to direct sequence comparison, it is import to ensure that all files were derived from the same genomic assembly.

Note: Although all necessary files are available with the AltAnalyze program at installation and some files can be updated automatically from the AltAnalyze server, users can use these programs to adjust the content of these files, use the output for alternative analyses, or create custom databases for currently unsupported species.

6.2 Building Ensembl-Feature Associations

Exon and Gene Arrays

The Affymetrix Exon 1.0 ST and Gene 1.0 ST arrays are provided with probe set sequence, transcript cluster and probe set genomic location from Affymetrix. Each of these annotations is used by AltAnalyze to provide gene, transcript and exon associations. Although transcript clusters represent putative genes, the AltAnalyze pipeline derives new gene associations to Ensembl genes, so that each probe set aligns to a single gene from a single gene database. This annotation schema further allows AltAnalyze to determine which probe sets align to defined exons regions (with external exon annotations), introns, and untranslated regions (UTR).

To begin this process, Ensembl exons (each with a unique ID) and their genomic location and transcript associations are downloaded for the most recent genomic assembly using the AltAnalyze `EnsemblSQL.py` module, which parses various files on the Ensembl FTP SQL

database server to assemble the required fields. This file is saved to the directory "AltDatabase/ensembl/*species*/" with the filename "*species*_Ensembl_transcript-annotations.txt". Since Ensembl transcript associations are typically conservative, transcript associations are further augmented with exon-transcript structure data from the UCSC genome database, from the file "all_mrna.txt" (Downloads/*species*/Annotation database/all_mrna.txt.gz). This file encodes genomic coordinates for exons in each transcript similar to Ensembl. Transcript genomic coordinates and genomic strand data from UCSC is matched to Ensembl gene coordinates to identify genes that specifically overlap with Ensembl genes with the Python program `UCSCImport.py`. Unique transcripts, with distinct exon structures from Ensembl, are exported to the folder "AltDatabase/ucsc/*species* "*species*_UCSC_transcript_structure_filtered_mrna.txt", with the same structure as the Ensembl_transcript-annotations file.

Once both transcript-structure files have been saved to the appropriate directory, `ExonArrayAffyRules.py` calls the program `EnsemblImport.py` to perform the following steps:

1) Imports these two files, stores exon-transcript associations identify exon regions to exclude from further annotations. These are exons that signify intron-retention (overlapping with two adjacent spliced exons) and thus are excluded as valid exon IDs. These regions are also flagged as intron-retention regions for later probe set annotations.
2) Assembles exons from all transcripts for a gene into discrete exon clusters. If an exon cluster contains multiple exons with distinct boundaries, the exon cluster is divided into regions that represent putative alternative splice sites (Text S1 Figure 1). These splice sites are explicitly annotated downstream. Each exon cluster is ordered and number from the first to the last exon cluster (e.g., E1, E2, E3, E4, E5), composed of one or more regions. These exon cluster/region coordinates and annotations are stored in memory for downstream probe set alignment in the module `ExonArrayAffyRules.py`.
3) Identifies alternative splicing events (cassette-exon inclusion, alternative 3' or 5' splice sites, alternative N-terminal and C-terminal exons, and combinations there in) for all

Ensembl and UCSC transcripts by comparing exon cluster and region numbers for all pairs of exons in each transcript (see proceeding sections for more information). Alternative exons/exon-regions and corresponding exon-junctions are stored in memory for later probe set annotation and exported to summary files for creation of databases for the Cytoscape exon structure viewer, SubgeneViewer (currently in development).

4) Constitutive exon regions are defined by counting the number of unique Ensembl and UCSC mRNA transcripts (based on structure) associated with each unique exon region. If multiple exon regions have the same number of transcript associations, then these are grouped. The grouped exon regions that contained the most transcripts for the gene are defined as constitutive exon regions. If only one exon region is considered constitutive then the grouped exon regions with the second highest ranking (based on number of associated transcripts) are included as constitutive (when there at least 3 ranks) (Figure 3.1).

Upon completion, `ExonArrayAffyRules.py`:

1) Imports Affymetrix Exon 1.0 ST probe sets genomic locations and transcript cluster annotations from the Affymetrix probeset.csv annotation file (e.g., HuEx-1_0-st-v2.na23.hg18.probeset.csv). Note: prior to AltAnalzye 1.14, mRNA alignment count numbers were also downloaded from this file to deduce constitutive probe sets. Although transcript clusters will be disregarded at the end of the analysis, these are used initially to group probe sets.
2) Transcript cluster genomic locations are matched to Ensembl genes genomic locations (gene start and stop) to identify single transcript clusters that align to only one Ensembl gene for the respective genomic strand. For transcript clusters aligning to more than one Ensembl gene, coordinates for each individual probe set are matched to aligning Ensembl genes, to identify unique matches. If multiple transcript clusters align to a single Ensembl gene, only probe sets with an Affymetrix annotated annotation corresponding to that Ensembl gene from the probeset.csv file, are stored as proper relationships. This ensures that if other genes, not annotated by Ensembl exist in the same genomic

interval, that they will not be inaccurately combined with a nearby Ensembl gene. If multiple associations or other inconsistencies are found, probe set coordinates are matched directly to the exon cluster locations derived in `EnsemblImport.py`.

3) Each probe sets is then aligned to exon clusters, regions, retained introns, constitutive exon regions and splicing annotations for that gene. In addition to splicing annotations from `EnsemblImport.py`, splicing annotations from the UCSC genome annotation file "knownAlt.txt" (found in the same server directory at UCSC as "all_mRNA.txt") using the program `alignToKnownAlt.py`, are aligned to these probe sets. If a probe set does not align to an `Ensemblmport.py` defined exon or intron and is upstream of the first exon or downstream of the last exon, the probe set is assigned a UTR annotation (e.g., U1.1). All aligning probe sets are annotated based on the exon cluster number and the relative position of that probe set in the exon cluster, based on relative 5' genomic start (e.g., E2.1). This can mean that probe set E2.1 actually aligns to the second exon cluster in that gene in any of the exon regions (not necessarily the first exon region), if it is the most 5' aligning.
4) These probe set annotations are exported to the directory "AltDatabase/*species*/exon" with the filename "*species* _Ensembl_probesets.txt". Exon block and region annotations for each probe set are designated in the AltAnalyze result file.

Junction Arrays

For the exon-junction AltMouse array, the same process is applied to the highlighted critical exon(s) from all pre-determined reciprocal junction-pairs, exported by the program `ExonAnnotate_module.py`. A highlighted critical exon is an exon that is predicted to be regulated as the result of two alternative junctions. For example, if examining the exon-junctions E1-E2 and E1-E3, E2 would be the highlighted critical exon. Alternatively, for the mutually-exclusive splicing event E2-E4 and E1-E3, E2 and E3 would be considered to be the highlighted critical exons. To obtain the genomic locations of these exons, sequences for each are obtained from a static build of the mouse AltMerge program (March 2002)

(ExonAnalyze_module.py) and searched for in FASTA formatted sequence obtained from BioMart for all Ensembl genes with an additional 2 kb upstream and downstream sequence (JunctionArray.py and EnsemblImport.py). For both the AltMouse and junction array, gene to Ensembl ID associations are obtained by comparing gene symbol names and assigned accession numbers (GenBank for AltMouse and Ensembl for JAY/Glue) in common, as opposed to coordinate comparisons.

For the later generation HJAY, HTA2.0 and MJAY junction arrays, a similar strategy is employed to the AltMouse to obtain genomic coordinates. First, probe set sequences are extracted (exons and junctions) and searched for in the same FASTA formatted sequence file downloaded for AltMouse probe set mapping. The same methods are employed for AltMouse, Glue and JAY array to obtain probeset genomic coordinates. This allows for the export of an exon-coordinate file analogous to the exon probeset.csv file. As with the Affymetrix exon array coordinate file, these genomic positions are aligned to AltAnalyze annotated exon regions and annotations. For junction probe sets, the two exons that compose the junction are individually mapped to exon regions (Figure 3.1). For exon-junction alignments, if the 5' junction exon aligns perfectly to the last few base pairs of the exon and the 3' junction exon aligns perfectly to the first few bases, then the match is considered to be to the predicted junction. If the match is not perfect, then new exon IDs are assigned to the corresponding exons, reflecting the mismatching alignment genomic position.

Reciprocal probe sets for the hGlue, HJAY, HTA2.0 and MJAY arrays are determine using two approaches; 1) AltAnalyze determined junction comparisons for all Ensembl and UCSC mRNA isoforms (Figure 3.1), 2) comparison of Affymetrix assigned junctions exon cluster ID annotations to find junction ends with common exon cluster IDs. Approach 1 is computed using the function "getJunctionComparisonsFromExport" from JunctionArrayEnsemblRules.py and approach 2 is computed using the function "identifyJunctionComps" from JunctionArray.py. The resulting relationships are stored in "AltDatabase/EnsMart55/Mm/junction/Mm_junction_comps_updated.txt" (or relevant species and database version). This approach allows us to capture known alternative splicing events,

based on mRNA evidence (approach 1) and putative alternative splicing events predicted by Affymetrix (approach 2). This does not currently capture all alternative splicing events and alternative exons, since some junctions do not share an exon cluster ID, but do reflect alternative modes of transcript regulation. To further detect such events, all exon and junction data is also stored for later individual probeset analysis using algorithms previously reserved for the exon and gene arrays (e.g., splicing-index, MiDAS, FIRMA).

Constitutive exon-junction probe sets are for the hGlue, HJAY, HTA2.0 and MJAY arrays are currently determined by two methods; 1) determine if both of the exons in the junction are annotated as constitutive and 2) determine if the junction is annotated as a putative 'alternative' probe set according to the manufacturer annotation file (e.g., mjay.r2.annotation_map). If both lines of evidence indicate the probeset is constitutive, then the probeset is annotated accordingly. Probe set annotations are provided in "AltDatabase/EnsMart55/Hs/junction/Hs_Ensembl_probesets.txt" (modify based on species and Ensembl version). This functionality is executed in the `JunctionArray.py` function "identifyJunctionComps" and the `JunctionArrayEnsemblRules.py` function "importAndReformatEnsemblJunctionAnnotations".

The highlighted critical exons associated with reciprocal junctions are used for annotation of the associated reciprocal exon(s). In fact, these critical exons are the ones examined for assigning an alternative exon annotation to reciprocal junctions (e.g, alternative cassette-exon), Ensembl genomic domain overlap and microRNA binding site targets. For Ensembl genomic domain overlap (`FeatureAlignment.py`), the exon genomic coordinates are used as opposed to the junction coordinates. When aligning identified miRNA target sequences, all Ensembl and UCSC identified exon sequences, identified during the database build procedure discussed in previous sections, are extracted from Ensembl chromosome FASTA files using the function getFullGeneSequences() in the module `EnsemblSQL.py`, stored in a temporary file and used as surrogates for exon array probe set sequences in `JunctionSeqSearch.py`.

RNA-Seq Analyses

The AltAnalyze gene database for RNASeq database is built using many of the same modules as those used for junction arrays. Instead of initially aligning known features to exons and junctions, as with the junction microarrays, all known Ensembl/UCSC extracted exons, junctions, reciprocal junctions, alternative exons, constitutive exons are exported by `EnsemblImport.py`. and stored in the format as probe set aligned annotations. For example, instead of the file Hs_Ensembl_probesets.txt, the files Hs_Ensembl_exons.txt and Hs_Ensembl_junctions.txt are exported to the RNASeq database directory. Rather than unique probe set identifiers, unique IDs for each exon and junction are stored in the format Ensembl-gene:ExonID and Ensembl-gene:5primeExonID-3primeExonID, respectively. The exon IDs are the exon region IDs in the format E1.3-E2.1. Associated Ensembl/UCSC exon annotations and genomic coordinates are stored with each exon and junction ID. These identifiers are treated the same as junction array probe set IDs and analyzed using the same modules outlined above for mRNA isoform alignment (`mRNASeqAlign.py`), optimal reciprocal protein isoform identification (`IdentifyAltIsoforms.py`), alternative domain (`ExonAnalyze_module.py`, `FeatureAlignment.py`) and miRNA binding site identification (`MatchMiRTargetPredictions.py`, `JunctionSeqSearch.py`). Just as with junction arrays, AltAnalyze exon region sequence and genomic locations, for the critical exons associated with reciprocal junctions, are used to identify overlapping miRNA targets and genomic overlapping InterPro domains. For single-junction analyses (e.g., splicing-index and MiDAS), these annotations are built separately using the same pipeline for individual junctions rather than reciprocal junctions, in a similar manner to junction arrays. These single junction annotations are stored to the sub-folder “junction” in the RNASeq directory.

When a users begins an AltAnalyze analysis on their experimental RNA-Seq input files, some of the above analyses are repeated to build an augmented, experiment specific set of AltAnalyze databases that include *de novo* identified junctions, exons, reciprocal junction-pairs and alternative exon annotations. Several files normally found in the AltAnalyze program directory, AltDatabase/EnsMart<version>/<species>/RNASeq folder are stored to this same path, in the user designated output directory. Thus, analyses can be easily repeated at any step

using these compiled dataset specific annotations. Only identified exon and junction annotations are included in these databases to maximize performance. These analyses are directed by the module `RNASeq.py`. In this module, the function alignExonsAndJunctionsToEnsembl() extracts genomic locations of the identified junction splice sites (5' and 3') and exons, aligns these to Ensembl junctions, genes, exons and introns and known splice sites. If both junction splice-sites are found in the AltAnalyze database, those junction and associated exon entries are migrated to the user database. If the junctions or splice-sites are novel, new identifiers are created indicating which exon/intron region the splice-site is found in with the splice-site genomic location indicated in the exon/junction name (e.g., ENSMUSG00000019715:I2.1_29554605). If the two junction splice-sites align to two different genes, the junction is annotated as trans-splicing. For any novel identified exon junctions, reciprocal junction analysis is re-performed using the function compareJunctions() in `EnsemblImport.py` to identify novel reciprocal junctions to be used during ASPIRE or Linear Regression analyses. The number of novel junctions and trans-splicing events is reported during BED file import. When an exon coordinates and read counts are present, these coordinates are aligned to Ensembl genes, exon regions and introns. Novel exons that overlap with an Ensembl gene are included.

6.3 Extracting UniProt Protein Domain Annotations Overview

The UniProt protein database is a highly curated protein database that provides annotations for whole proteins as well as protein segments (protein motifs or domains). These protein motif annotations correspond to specific amino acid (AA) sequences that are annotated using a common vocabulary, including a class (uniprot feature key) and detailed description field. An example is the TCF7L1 protein (http://www.uniprot.org/uniprot/Q9HCS4), which has five annotated motif regions, ranging in size from 7 to 210 AA. One of these regions has the feature key annotation "DNA binding" and the description "HMG box". To utilize these annotations in AltAnalyze, these functional tags are extracted along with full protein sequence, and external annotations for each protein (e.g., Ensembl gene) from the "uniprot_sprot_*taxonomy*.dat" file using the `ExtractUniProtFunctAnnot.py` program. FTP file locations for the UniProt database file can be found in the file "Config/Default-file.csv"

for each supported species. To improve Ensembl-UniProt annotations, these relationships are also downloaded from BioMart and stored in the folder “AltDatabase/uniprot/*species*” as “*species*_Ensembl-UniProt.txt”, which are gathered at `ExtractUniProtFunctAnnot.py` runtime to include in the UniProt sequence annotation file. These files are saved to “AltDatabase/uniprot/*species*” as “uniprot_feature_file.txt” and “uniprot_sequence.txt”.

6.4 Extracting Ensembl Protein Domain Annotations Overview

In addition to protein domains/features extracted from UniProt, protein features associated with specific Ensembl transcripts are extracted from the Ensembl database. One advantage of these annotations over UniProt, is that alternative exon changes that alter the sequence of a feature but not its inclusion will be reported as a gain and loss of the same feature, as opposed to just one with UniProt. This is because protein feature annotations in UniProt only typically exist for one isoform of a gene and thus, alteration of this feature in any way will result in this feature being called regulated. Although an Ensembl annotated feature with a reported gain and loss can be considered not changed at all, functional differences can exist do to a minor feature sequence change that would not be predicted if the gain and loss of the feature were not reported.

Three separate annotation files are built to provide feature sequences and descriptions, “Ensembl_Protein”, “Protein”, and “ProteinFeatures” files (“AltDatabase/ensembl/*species*”). The “ProteinFeatures” contains relative AA positions for protein features for all Ensembl protein IDs, genomic start and end locations along with InterPro annotations and IDs. Only those InterPro domains/features with an alignment e-score < 1 are stored for alignment to regulated exons. The “Protein” file contains AA sequences for each Ensembl protein. The “Ensembl_Protein " provides Ensembl gene, transcript and protein ID associations. Data for these files are downloaded and extracted using the previously mentioned `EnsemblSQL.py` module. The feature annotation source in these files is InterPro, which provides a description similar to UniProt. As an example, see:

http://ensembl.genomics.org.cn/Homo_sapiens/protview?db=core;peptide=ENSP00000282111, which has similar feature descriptions to UniProt for the same gene, TCF7L1.

6.5 Extracting microRNA Binding Annotations Overview

To examine the potential gain or loss of microRNA bindings sites as the direct result of exon-inclusion or exclusion, AltAnalyze requires putative microRNA sequences from multiple prediction algorithms. These binding site annotations are extracted from the following flat files:

- miRNAMap predictions from multiple algorithms (TargetScan, RNAhybrid and miRanda) are downloaded from the miRNAMap ftp server for all species present (http://mirnamap.mbc.nctu.edu.tw/html/about.html). Target sequences from this database are linked to Ensembl transcript IDs.
- TargetScan conserved predicted targets (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_50). UTR sequences (UTR_Sequences.txt) are matched to corresponding miRNA target coordinates (Predicted_Targets_Info.txt) for each species based on the taxonomic identifer. The primary gene ID, gene-symbol, is linked to Ensembl based on gene-symbol to Ensembl gene annotations (from several Ensembl builds – outdated symbols are often used).
- miRanda human centric with multi-species alignment information was obtained from target predictions organized by Ensembl gene ID (http://cbio.mskcc.org/research/sander/data/miRNA2003/mammalian/index.html). A larger set of associations was also pulled from species-specific files (http://www.microrna.org/microrna/getDownloads.do), where gene symbol was related to Ensembl gene. Both files provided target microRNA sequence.
- Sanger center (miRBase) sequence was provided as a custom (requested) dump of their version 5 target predictions (http://microrna.sanger.ac.uk/targets/v5/), containing Ensembl gene IDs, microRNA names, and putative target sequences, specific for either mouse or human. Currently, rat has not been obtained.

- PicTar conserved predicted targets (from Dog to Human) were provided as supplementary data (Supplementary Table 3) at http://www.nature.com/ng/journal/v37/n5/suppinfo/ng1536_S1.html, with conservation in human, chimp, mouse, rat, and dog for a set of 168 microRNAs. For mouse, human gene symbols were searched for in the BioMart derived "Mm_ Ensembl_annotation.txt" table after converting these IDs to a mouse compatible format (e.g., TCF7L1 to Tcf7l1). The same was used for aligning to PicTar. The same strategy is used for rat.

Ensembl gene to microRNA name and sequence are stored for all prediction algorithm flat files and directly compared to find genes with one or more lines of microRNA binding site evidence using the program `MatchMiRTargetPredictions.py`. The flat file produced from this program ("combined_gene-target-sequences.txt") was used by the program `ExonSeqSearch.py` to search for these putative microRNA binding site sequences among all probe sets from the "*species*_Ensembl_probeset.txt" file built by `ExonArrayEnsemblRules.py` and probe set sequence from the Affymetrix 1.0 ST probe set FASTA sequence file (Affymetrix) or the reciprocal junction critical exon sequence file (see section 6.2). For gene arrays, NetAffx currently only provides probe sequences, thus, probe set sequences from the exon array are used for probe set found to overlap in genomic space. Two resulting files, one with any binding site predictions and another required to have evidence from at least two algorithms, are saved to "AltDatabase/*species*/*array_type*/" as "*species*_probe set_microRNAs_any.txt" and "*species*_probe set_microRNAs_multiple.txt", respectively.

6.6 Inferring Protein-Feature Associations Overview

To obtain associations between specific exons, junctions or probe sets to proteins, the programs `IdentifyAltIsoforms.py` (exon and junction platforms) and `ExonSeqModule.py` (junction platforms only) were written. The program `IdentifyAltIsoforms.py` grabs all gene mRNA transcripts and associated exon genomic coordinates from Ensembl and UCSC and compares these to probe set coordinates (or critical

exon for junction-sensitive platforms) to find pairs of transcripts (one containing the probe set or critical exon and the other not) that have the least number of differing exons (see Section 3.4). These transcript pairs are thus most likely to be similar with exception to the region containing the probe set or critical exon. Once these best matches are identified, corresponding protein sequences for each mRNA are downloaded from Ensembl using `EnsemblSQL.py` or are downloaded using NCBI webservices via BioPython's `Entrez` function.

If protein sequences are unavailable for an mRNA accession, the mRNA sequence for that identifier is downloaded (using the above mentioned services) and translated using the custom `IdentifyAltIsoforms.py` function "BuildInSilicoTranslations", which uses functions from the BioPython module to translate an mRNA based on all possible start and stop sites to identify the longest putative translation that also shares either the first or last 5 AA of its sequence with the N-terminus or C-terminus (respectfully) of a UniProt protein.

While this same protocol is used for junction-sensitive platforms, prior to this analysis reciprocal junctions are mapped to all possible aligning and non-aligning transcripts through direct junction sequence comparison via `mRNASeqAlign.py`. This module takes the junction sequence for all reciprocal junction-pairs and searches for a match among mRNA transcript FASTA formatted sequences from Ensembl and UCSC mRNAs that correspond to that gene. Only a 100% sequence match is allowed, (matches may not occur do to polymorphisms between sequence sources and genomic assemblies). These associations are then used by `IdentifyAltIsoforms.py`, as described above.

At this point, only two mRNAs are matched to each exon, junction, probe set or junction-pair, matching and non-matching mRNAs. Next, differences in protein feature composition between these two proteins, alternative N or C-terminal sequences, coding sequence and protein length are assessed using `ExonAnalyze_module.py` and exported to text files (associations and protein sequences) for import when AltAnalyze is run. These two files have the suffix "exoncomp.txt". Two analogous files with the suffix "seqcomp.txt", are derived by identifying the best matching and non-matching mRNAs based on comparison of protein sequence as compared exon composition (e.g. least differences in protein domain composition),

but are currently used only for internal analyses (contact the authors for the seqcomp files to replace exoncomp). The genomic locations of critical exons associated with these reciprocal junctions are used to identify direct and indirect overlapping InterPro domains from Ensembl in the function `FeatureAlignment.py`.

6.7 Required Files for Manual Update

For advanced users and developers that wish to build databases outside of AltAnalyze's normal release cycle or build custom database installations, several built-in, automated tools are available to build AltAnalyze databases. These functions are accessible from command-line flags in AltAnalyze. In AltAnalyze 2.0, we have tried to increase ease and consistency in which these databases are built, by building new methods to automatically download and extract necessary external databases from resource FTP and HTTP servers, where accessible. Although several external databases are required for the above build strategies, AltAnalyze should be able to automatically download these during the automated build processes from our web servers. The exception to this rule is Affymetrix annotation files, once a genome build for that species is updated, which cannot be downloaded without logging into the Affymetrix support site and downloading these manually. These files consist of the Affymetrix probeset.csv annotation files, however, if the genome build is the same, then no manual downloads are needed. Current and details on updating and customizing the AltAnalyze databases can be found at:
http://code.google.com/p/altanalyze/wiki/BuildingDatabases

Section 7 – Evaluation of AltAnalyze Predictions

To assess AltAnalyze exon array analysis performance relative to other published approaches, we analyzed published experimental confirmation results for a dataset of splicing factor knockdown (mouse polypyrimidine tract binding protein (PTB) short-hairpin RNA (shRNA)). From two independent analyses (12, 13), alternative splicing (AS) for 109 probe sets was assessed in the mouse PTB shRNA dataset by RT-PCR (Supplemental Tables 1,2 and 4 from the referenced study) (13). Among these, 25 were false positives, one was a true negative, one undetermined and 81 were true positives.

Summary of Published MADS Results

In the analysis by Xing et al., alternative exons discovered by multiple splicing array platforms and RT-PCR were examined using a new algorithm named microarray analysis of differential splicing or MADS. MADS implements a modification of the splicing index method on gene expression values obtained using multiple scripts from GeneBase and filtering of probes predicted to hybridize to multiple genomic targets. Using this algorithm, the authors were able to verify AS detected by RT-PCR of mouse Affymetrix Exon 1.0 array data as well as predict and validate 27 novel splicing events by RT-PCR. Using the microarray CEL files posted by Xing and colleagues, we ran AltAnalyze using default options (same as used in the corresponding primary report), which includes quantile normalization via RMA-sketch using AltAnalyze's interface to Affymetrix Power Tools.

AltAnalyze Results

Of the 109 probe sets linked to splicing events characterized by RT-PCR, 78 were analyzed by AltAnalyze (version 1.13, EnsMart49). Those probe sets not analyzed by AltAnalyze were either not apart of the AltAnalyze "core" probe sets or were excluded due to high detection p-value or low expression thresholds. A breakdown of the number of RT-PCR true positive, false positive, undetermined and false negative (out of the 81 documented true positives) is shown for various AltAnalyze filters (Table 7.1).

Of the 78 analyzed probe sets, 26 were called by AltAnalyze to be alternatively regulated (using default parameters), out of 194 probe sets called by AltAnalyze as alternatively regulated. All 26 probe sets were annotated as true positives according to the published RT-PCR data. Although 17 probe sets were RT-PCR false positives among the 78 probe sets with RT-PCR data, only one false positive was considered to be alternative regulated by AltAnalyze with any of the AltAnalyze filters alone (splicing-index $p<0.05$ alone without additional default options). The MADS algorithm was able to validate AS for 27 novel splice events corresponding to 41 probe sets. Of these 41 probe sets, 33 were examined by AltAnalyze and 23 were considered alternatively regulated.

Conclusions

This analysis suggests that AltAnalyze analysis using default parameters produces conservative results with high specificity (100% true positives in this analysis) with reasonable sensitivity (~42% that of MADS). For smaller datasets, such as the PTB knock-down comparison, the decreased sensitivity results will have a significant impact on the number of true splicing events detected, however, for larger datasets with thousands of regulated probe sets, AltAnalyze is likely to reduce the number of false positives and reduction in overall noise. It is important to note however, for the MADS analysis only a p-value threshold was used and for AltAnalyze, both a MiDAS and splicing-index p-value in addition to splicing-index fold change thresholds were used. For these analyses, we have not filtered probe sets based on association with annotated splicing events (see Materials and Methods for description), which should further decrease false positives. If probe sets with annotated splicing events are filtered out, 20 versus 26 true positives will remain.

Although a false positive rate of up-to 50% has been reported with the conventional splicing-index implementation (e.g., using the Affymetrix ExACT software) (13), AltAnalyze's analysis differs in several ways. First, in this analysis RMA-sketch was used as the method for quantile normalization. After obtaining expression values for probe sets (no low level filtering currently implemented), probe sets for each of the two biological groups are filtered based on

two main parameters: DABG p-value and mean expression filters. Any probe set with a DABG p-value > 0.05 in both biological groups or mean expression < 70 are excluded.

Additional AltAnalyze specific parameters relate to how probe set to gene associations are obtained, which probe sets are selected for analysis and how probe sets are selected for calculation of gene expression. Unlike ExACT, probe set to gene association are via genomic coordinate alignment to Ensmebl/UCSC mRNA transcripts for unique Ensembl genes rather than to Affymetrix transcript clusters. This process ensures that a probe set only aligns to one Ensembl gene. Probe sets can align to an exon, intron or UTR of a gene. Any probe set aligning to an analyzed mRNA is used for analysis in the AltAnalyze "core" set along with any Affymetrix annotated "core" probe set. To determine gene expression from the exon-level a two-step method is employed. First, probe sets that are most over-represented among mRNAs or mRNAs and ESTs (associations from Affymetrix probe set annotation file) are selected as constitutive. Next if constitutive probe set is "expressed" in both biological groups (using the DABG and mean expression filters listed above), the probe set is retained for constitutive expression calculation. If more than one "expressed" constitutive probe set is present, the mean expression of all constitutive probe sets for each array is calculated. As a final step, probe sets with an associated gene expression difference between the two array groups greater than 3 are not reported. These analysis steps result in a unique splicing-index, splicing-index *t* test p-value and MiDAS p-value calculation from other analysis methods.

Since this validation set provides a limited test case for analysis of type I (false positive) and type II (false negative) errors, the AltAnalyze algorithms will continue to be assessed as additional validation data is made available. Future implementations will likely include "low-level" analyses that reduce the occurrence of type I errors (e.g., elimination of expression data for specific probes that introduce additional noise). However, this data supports the concept that AltAnalyze produces conservative results with a level of confidence.

				AltAnalyze RMA Analysis				
	All	**MADS p<0.05**	**MADS p<0.01**	**All**	**SF>2**	**SP <0.05**	**SP|MP <0.05**	**SF>2, GEF<3, SP|MP <0.05**
TP	81	62	55	60	30	36	32	26
FP	25	6	2	17	0	1	0	0
UD	1	1	1	1	0	1	1	0
FN	0	19	26	21	51	45	49	55

Table 7.1 - Analysis of PTB shRNA verified splicing events with AltAnalyze. The number of probe sets matched to different RT-PCR absence or presence calls for AS from an analysis of mouse PTB shRNA knockdown of a neuroblastoma cell line compared to empty vector shRNA knockdown using the Affymetrix Mouse 1.0 Exon array [12]. Results are shown for all probe sets (All), MADS p<0.05 or p<0.01 (after removing cross-hybridizing probes), AltAnalyze "core" probe sets (All) analyzed by RT-PCR, splicing-index fold change >2, splicing-index t-test p (SP) <0.05, MiDAS p (MP) <0.05 or combination of all three options (SF>2 & SP & MP <0.05 – default option) along with gene expression filtering (GEF) of < 3 fold, for true positive (TP), false positive (FP), un-determined (UD), and false negative (FN) RT-PCR results. False negative probe set counts are relative to all original true positives experimentally identified, independent of whether they were considered by AltAnalyze.

Section 8 - Analysis of AltAnalyze Results DomainGraph

Once alternative probe sets have been identified from an AltAnalyze exon array analysis, you can easily load this data in the Cytoscape plugin DomainGraph (http://domaingraph.bioinf.mpi-inf.mpg.de/) to:

1) View prioritized AltAnalyze highlighted alternative exons and annotations.
2) Assess which probe sets overlap with a set of loaded genes and which specific protein domains at a high-level (protein/domain/miRNA binding stie network/pathway) and low-level (domain/exon/probe set view).
3) View alternative probe set data in the context of WikiPathways and Reactome gene networks.

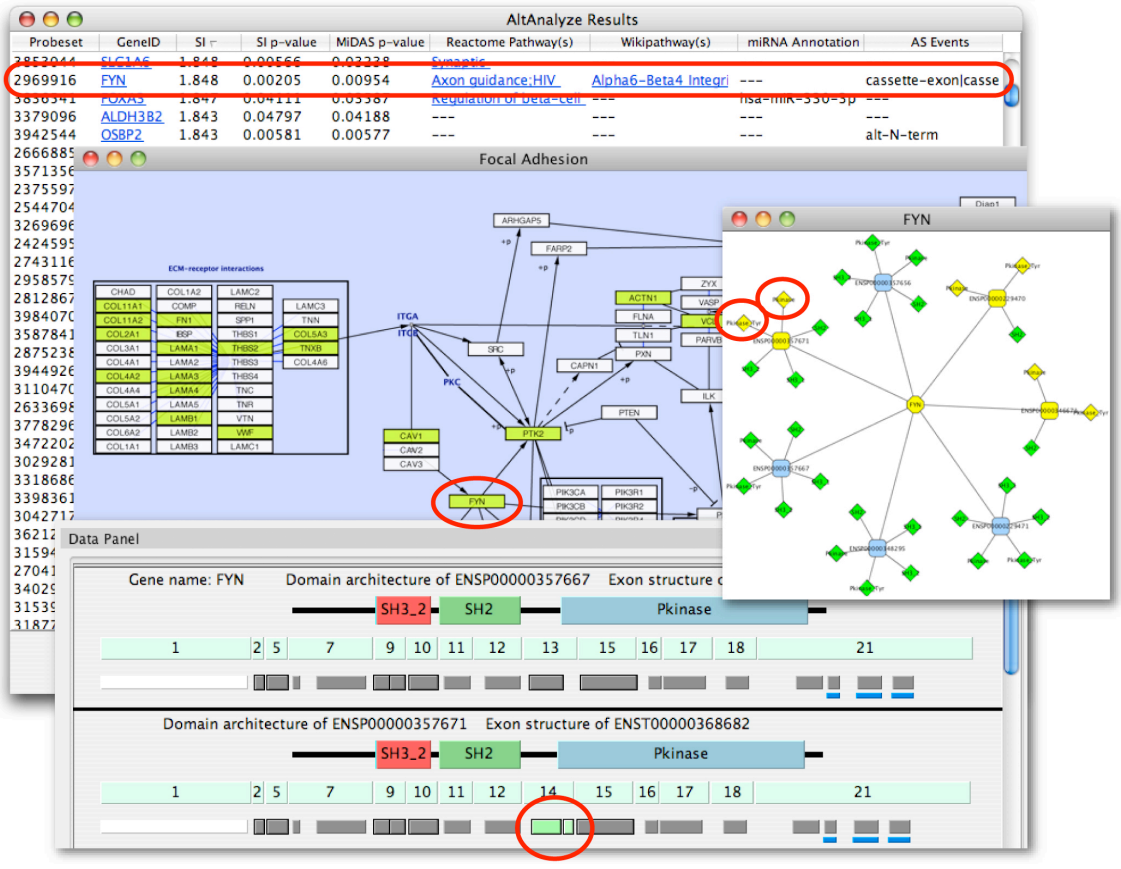


Figure 8.1. Visualization of AltAnalyze regulated probe sets along

exons and protein domains. In the top panel, a loaded Cytoscape DomainGraph network is shown for the gene FYN, with relevant protein domain interactions shown between two alternative isoforms of each gene. Rounded boxes represent gene nodes and diamonds, protein domains and other functional elements. Greenish yellow nodes represent those containing AltAnalyze regulated probe sets, whereas green do not overlap with an AltAnalyze regulated probe set. The gene FYN has been selected in the main network that creates a domain architecture and exon structure view for the select FYN isoform in the Cytoscape "Data Panel". Domains (top), exons (middle) and probe sets (bottom) are shown that correspond to the FYN isoforms ENSP00000229470 and ENSP00000229471, with AltAnalyze down-regulated probe sets in green. Probe sets with a solid black border are associated with an alternative splicing (alternative cassette exon) or alternative promoter annotation. In this example, the probe set with an alternatively splicing annotation overlaps with exon 8 and the Protein Kinase domain of the protein. Probe sets with a blue bar beneath them overlap with predicted microRNA binding sites. Details about each domain, exon, probe set and microRNA binding site, including AltAnalyze statistics and functional annotations are accessible by mousing-over the respective feature and by left-clicking the object to link-out to resources on the web.

Installing DomainGraph with AltAnalyze

- Simply download and extract AltAnalyze 1.15 (or higher) from the compressed installation file and Cytoscape, DomainGraph and the GPML puglin will be ready to use. This plugin can be updated through the Cytoscape plugin manager.
- Start Cytoscape directly from AltAnalyze after the alternative exon results are produced. Alternatively, open Cytoscape manually (AltAnalyze_v1release/Cytoscape).

- Download the species gene database of interest (required for the first use – see below)

Running DomainGraph

Detailed instructions on running DomainGraph can be found here:

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

and at:

http://domaingraph.bioinf.mpi-inf.mpg.de/

or in the AltAnalyze application folder:

AltAnalyze_v1release/Documentation/domain_graph.pdf

Platform Compatibility

The DomainGraph database is designed to specifically work with Affymetrix Exon 1.0 arrays, however, AltAnalyze exports files for the Affymetrix Gene 1.0, hGlue, HJAY, HTA2.0 and MJAY arrays as well as human, mouse and rat RNA-Seq results that allow for visualization of these results as well. In order to accomplish this, non-exon array probe set IDs are converted to exon array probe set IDs. This translation is performed by matching the optimally aligning exons, junctions or probe sets using the AltAnalyze exon block/region annotations and probe set genomic positions. For reciprocal probeset junction array analyses (ASPIRE or Linear Regression), matching is to the predicted alternative exon rather than the reciprocal junctions.

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