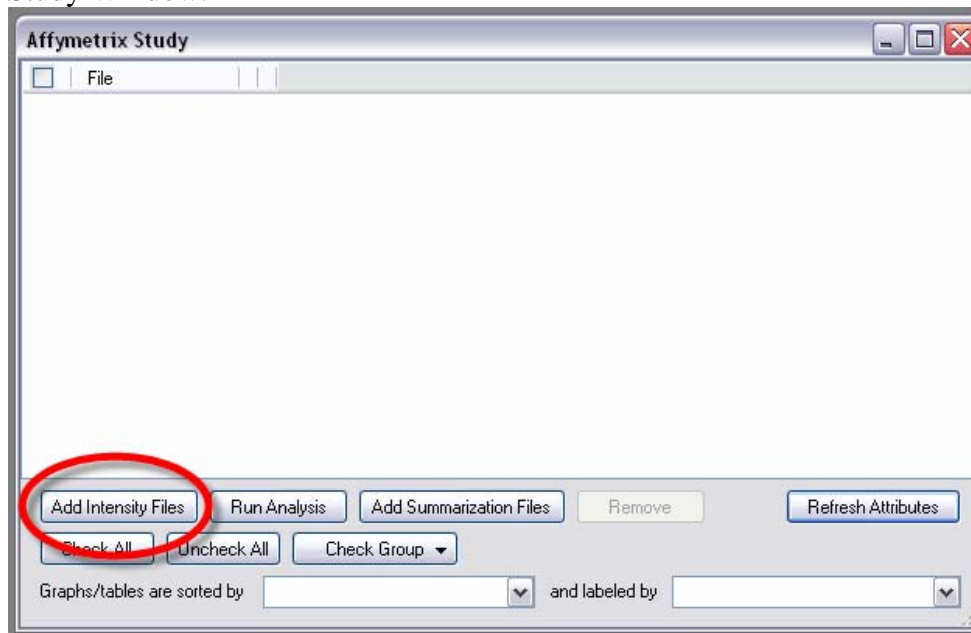


Quick Start Guide for Exon Arrays

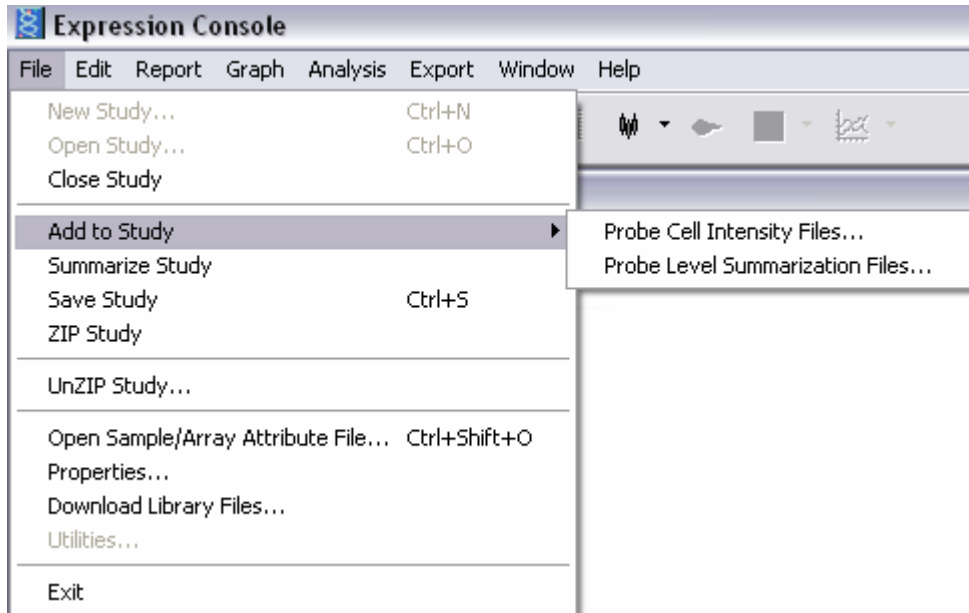
The purpose of the Expression Console™ software application is to enable probe set summarization and initial data quality examination for Affymetrix expression arrays. Expression Console software takes probe cell intensity files (*.CEL) and creates probe level summarization files (*.CHP) using the selected algorithm workflow. Probe level summarization files can then be further analyzed using software applications from Affymetrix GeneChip Compatible partners to identify differentially expressed genes (<http://www.affymetrix.com/products/software/compatible/index.affx>.)

1. Download the necessary library files for analyzing your array type if they are not already in the library file directory.
 - a. Go to the **File** menu and select **Download Library Files**.
 - b. Enter your NetAffx email address and password. If you do not have one you will first need to register at <https://www.affymetrix.com/site/terms.affx?buttons=on&dest=register>
 - c. In the NetAffx Library File window check all probe array types that you will be analyzing now or in the future and click on the **Download** button. You can always come back and add more library files at a later date.
 - d. The download will include the pgf, clf, bgp files and the Affymetrix default meta-probeset files (mps), probe set list files (ps), and control probe set list files (qcc). In addition, an “.exon_analysis_configuration” file that is required to perform any Exon Array analysis within Expression Console will also be downloaded.
 2. Create a New Study by selecting **File ->New Study** or by going to the Study tab of the workflow toolbox and selecting **Create New Study**. A Study consists of a collection of probe cell intensity files (CEL) and probe level summarization files (CHP) of the same array type.
 3. A blank Affymetrix Study window is created. Use the **Add Intensity Files** button at the bottom of the Affymetrix Study window, select **File -> Add to Study-> Probe Cell Intensity Files**, or click on **Add Intensity Files** in the **Toolbox** to add your collection of CEL files to the study.
- Affymetrix Study Window:



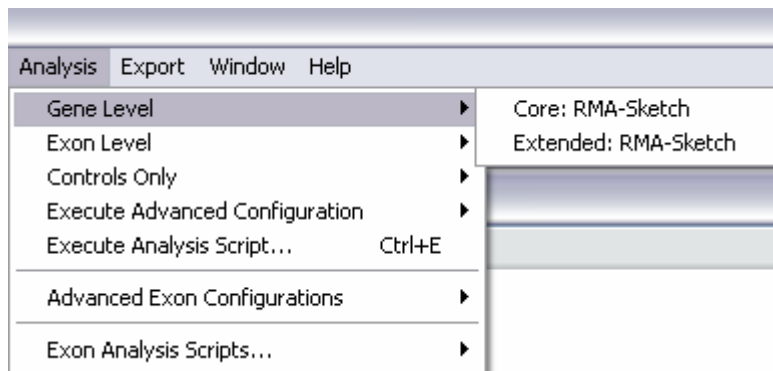
Quick Start Guide for Exon Arrays

File Menu:



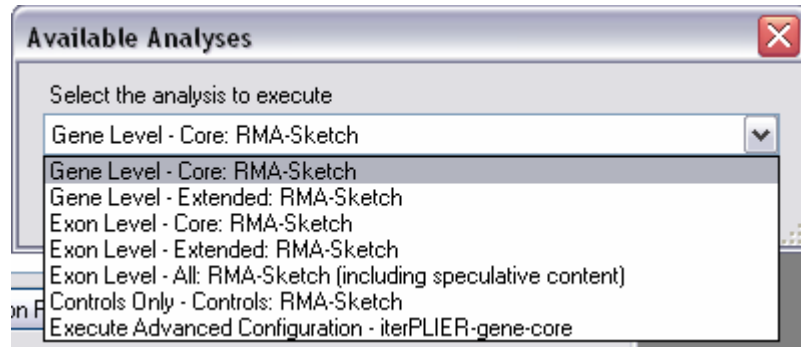
4. Once the appropriate CEL files have been added, use the check boxes to select the files to be analyzed.
5. Select the desired level of analysis from the choices from the **Analysis** menu. Alternatively, clicking the **Run Analysis** button at the bottom of the **Affymetrix Study** window or selecting **Run Analysis** in the **Toolbox**, also enables the algorithm workflow to be selected. Note, advanced configurations can be selected from the **Analysis** menu **Advanced Expression Configurations** or from the drop-down list in the **Available Analyses** window after they have been defined.
 - a. Select the level of the analysis **Gene**, **Exon**, or **Controls Only**.
 - b. Under the selected analysis level, select the confidence level for the probe sets to be reported: **core**, **extended** or **full**. For details on the analysis and confidence levels please refer to the whitepaper entitled “Exon Probeset Annotations and Transcript Groupings” (http://www.affymetrix.com/support/technical/whitepapers/exon_probeset_trans_clust_whitepaper.pdf).

Analysis Menu:

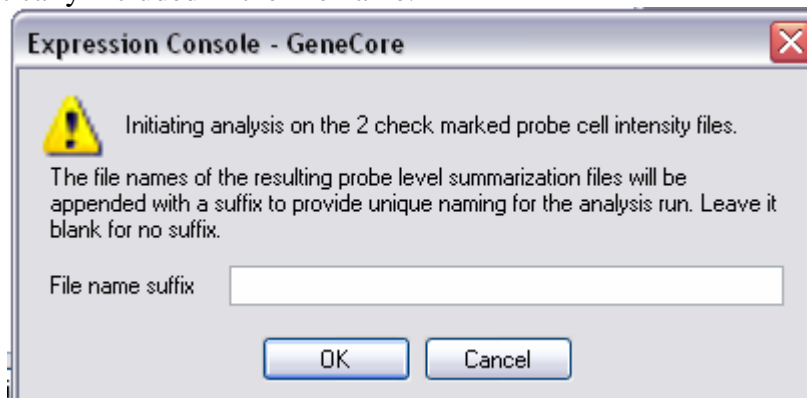


Quick Start Guide for Exon Arrays

Toolbar/Run Analysis button:

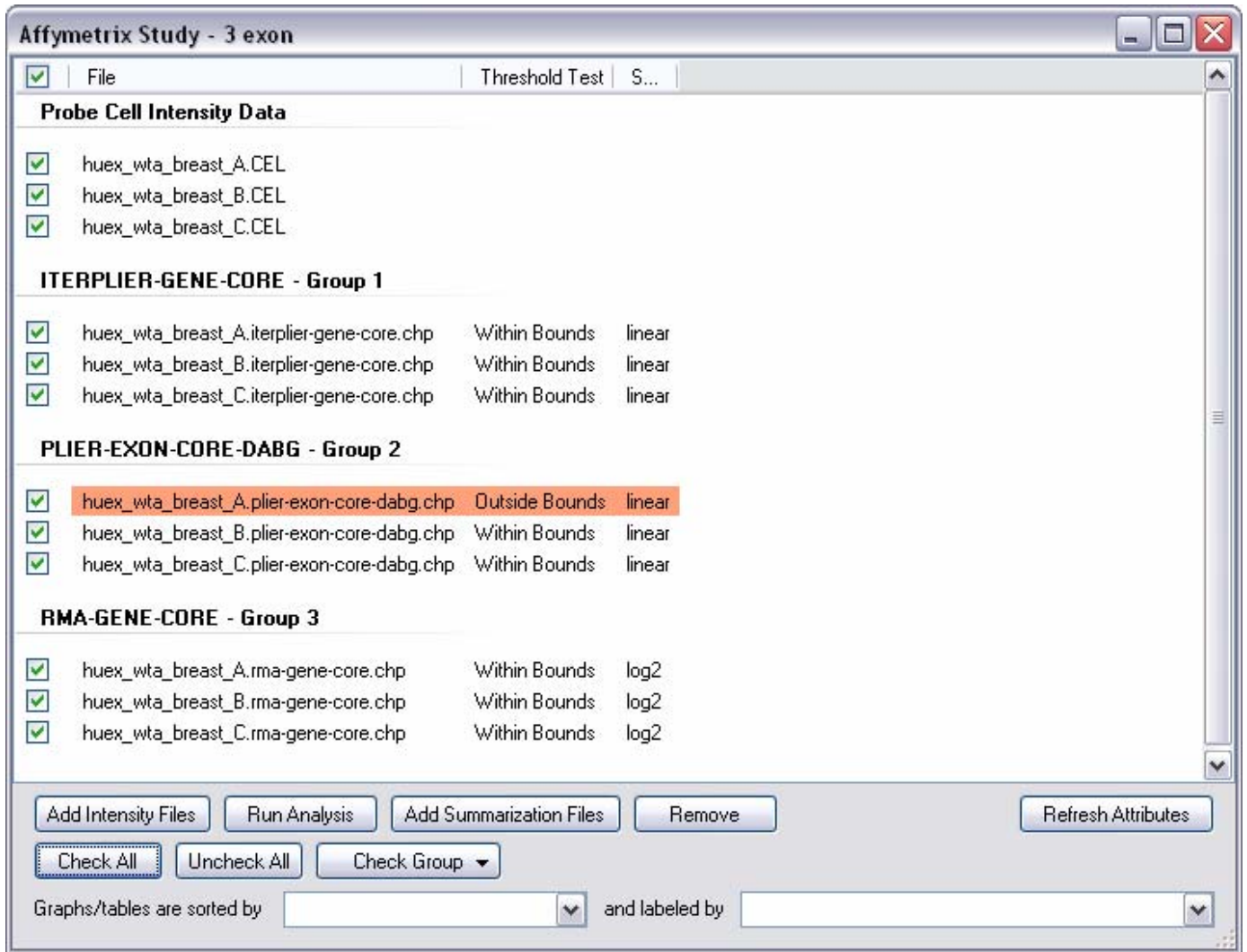



6. The default algorithm workflow for both Gene and Exon level analysis is RMA-Sketch. For more information about gene level analysis please see the whitepaper, “Gene Signal Estimates from Exon arrays” (http://www.affymetrix.com/support/technical/whitepapers/exon_gene_signal_estimate_whitepaper.pdf).
7. If desired enter a suffix to be appended to the file name, then Select **OK**. Note, the summarization method is automatically included in the file name.



8. The processing time for the CEL files depends on a number of factors including, the number of CEL files, level of analysis, confidence level, amount of available RAM, and speed of the computer processor.

9. After summarization is completed the study window will contain a new Group containing your newly generated CHP files.



10. Highlighted rows in the **Affymetrix Study Table** signify CHP files that contain metrics outside of the user defined thresholds .
 - a. There are three ways to display the thresholds. Menu item: **Edit-> Report Thresholds;**
Toolbar: the  button, and the **Toolbox: Configuration-> (4) Specify Report Thresholds.**
11. The newly created CHP files are now ready for QC analysis within the Expression Console software or other software provided by a GeneChip Compatible partner. The CHP files can be found in the same directory as the first CEL files in your input list.