

Quick Start Guide for the Human Gene 1.0 ST Array

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 (*e.g.*, HuGene-1_0-st-1 library files). You can always come back and add more library files at a later date.
- 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 or click on **Add Intensity Files** in the toolbox to add your collection of CEL files to the study.

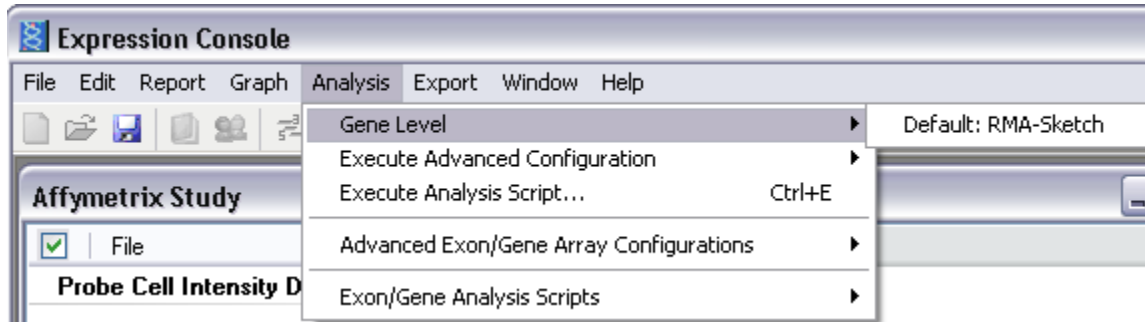


- 4) Once the appropriate CEL files have been added, use the check boxes to select the CEL files to be summarized.

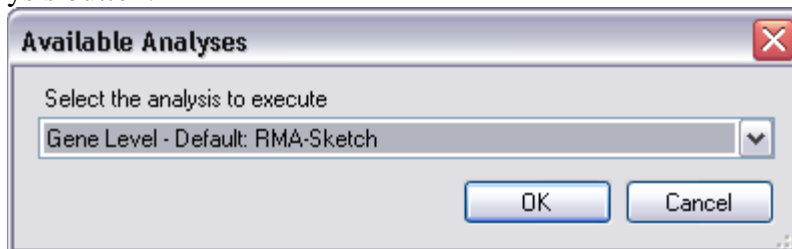
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- 5) Under **Analysis-> Gene Level**, select **Default: RMA-Sketch** as the probe summarization method. Alternatively, clicking the **Run Analysis** button at the bottom of the **Affymetrix Study** window or selecting **Run Analysis** in the **Toolbox**, also allows the **RMA-Sketch** workflow to be selected.

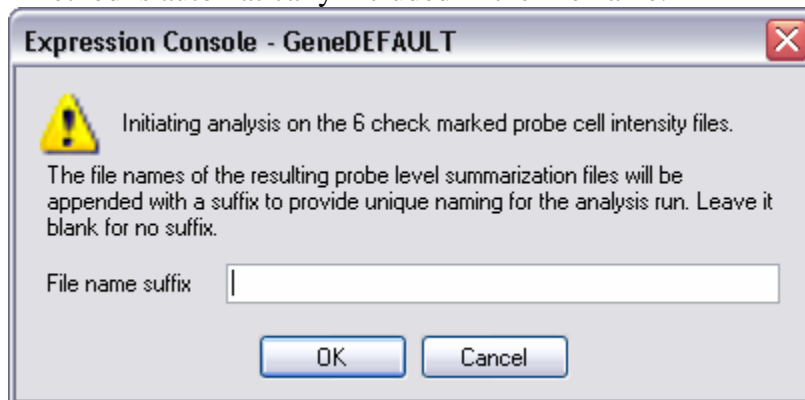
Analysis Menu:



Toolbar/Run Analysis button:

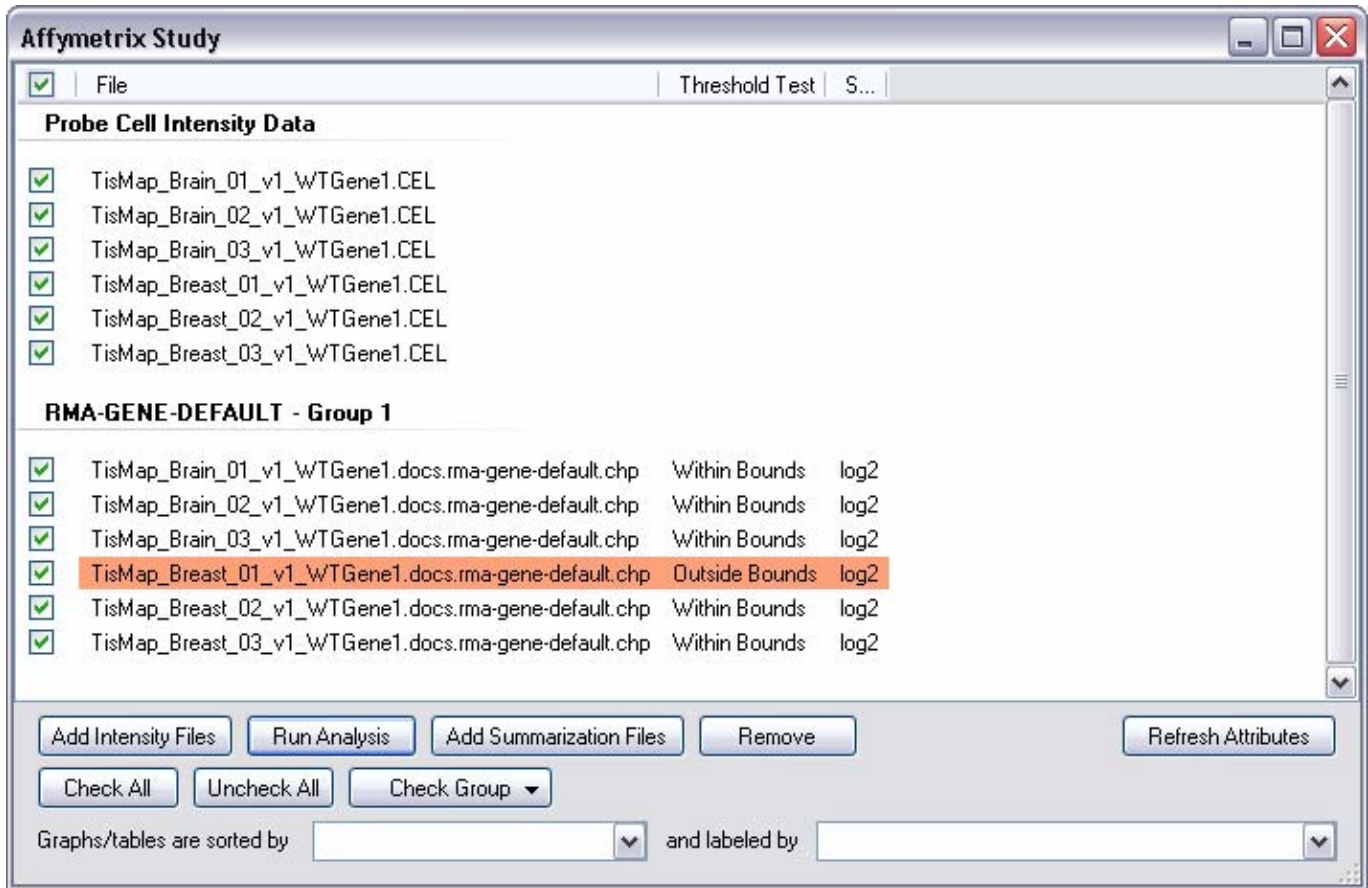



- 6) If desired, enter a suffix to be appended to the file name, and then Select **OK**. Note, the summarization method is automatically included in the file name.



- 7) Depending on the number of arrays selected, several minutes may be required for processing. Once processing is complete the newly summarized data (CHP files) will appear in a new group in the Study window. The title of the new group will be "**RMA-GENE-DEFAULT – Group 1**". If other analysis runs have been completed already the group number will be incremented.

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- 8) 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.**
- 9) 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 your original input CEL files.
- 10) To Export a data table containing the probe set summarized values and annotation please see the Quick Start guide entitled "How to Export Signal Values with Annotation Information".