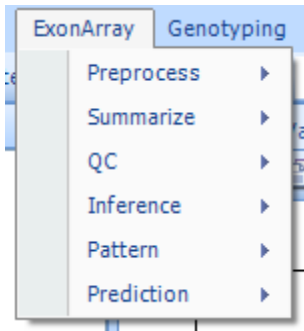


Array Studio 3.2 provides several major improvements on Array Studio 3.0, and fixed more than 30 minor bugs in Array Studio 3.0. This version is assumed to be more stable than 3.0, and will be stabilized for at least 6 months (we expect to release Array Studio 4.0 in 2010 Q1). This document describes the major improvements. To see a complete list of bug fix and improvements/changes, go to *Help / View Change Log* in Array Studio.

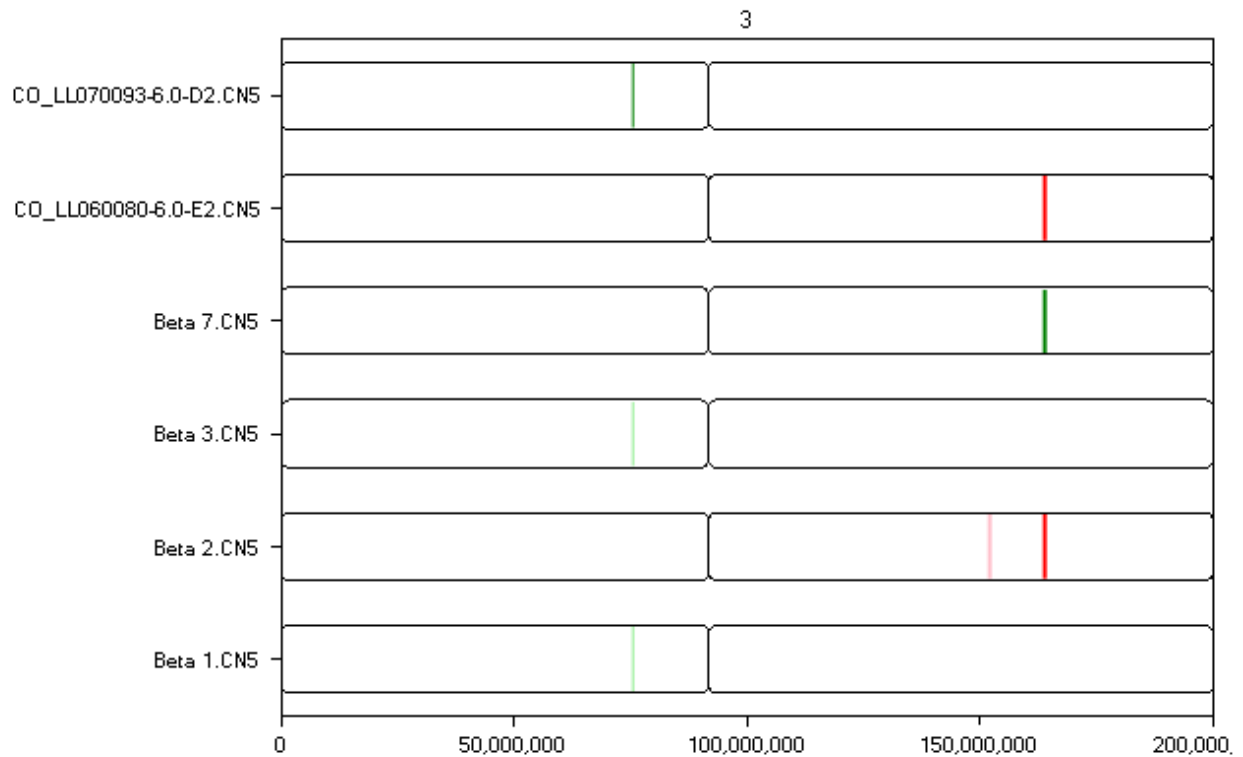
COMPLETE EXON ARRAY SUPPORT

AS 3.2 provides all the necessary tools to process, visualize and analyze Affymetrix Exon array chips. There is a separate menu and a separate workflow for ExonArray analysis. The ExonArray tutorial is also available on the Help menu as well as from the website.



IMPROVED CNV SUPPORT

Array Studio 3.2 refined the CNV views and the segmentation algorithm. It also introduced a new view “SegmentObservationView”. Drag and drop was also supported in the genome view to allow users to refine the segment boundaries.



COLUMN TRANSFORMATION AND SUMMARIZATION

For table data (e.g. design tables), the user is now able to create new columns from column transformation or summarization. Binary operations between two columns are also supported.

Column Transformation X

I time

Add a constant

Multiply a constant

Censor if value <

Censor if value >

Divide time

Transformation method

NoTransformation

Log2

Exp2

SExp2

Log10

NLog10

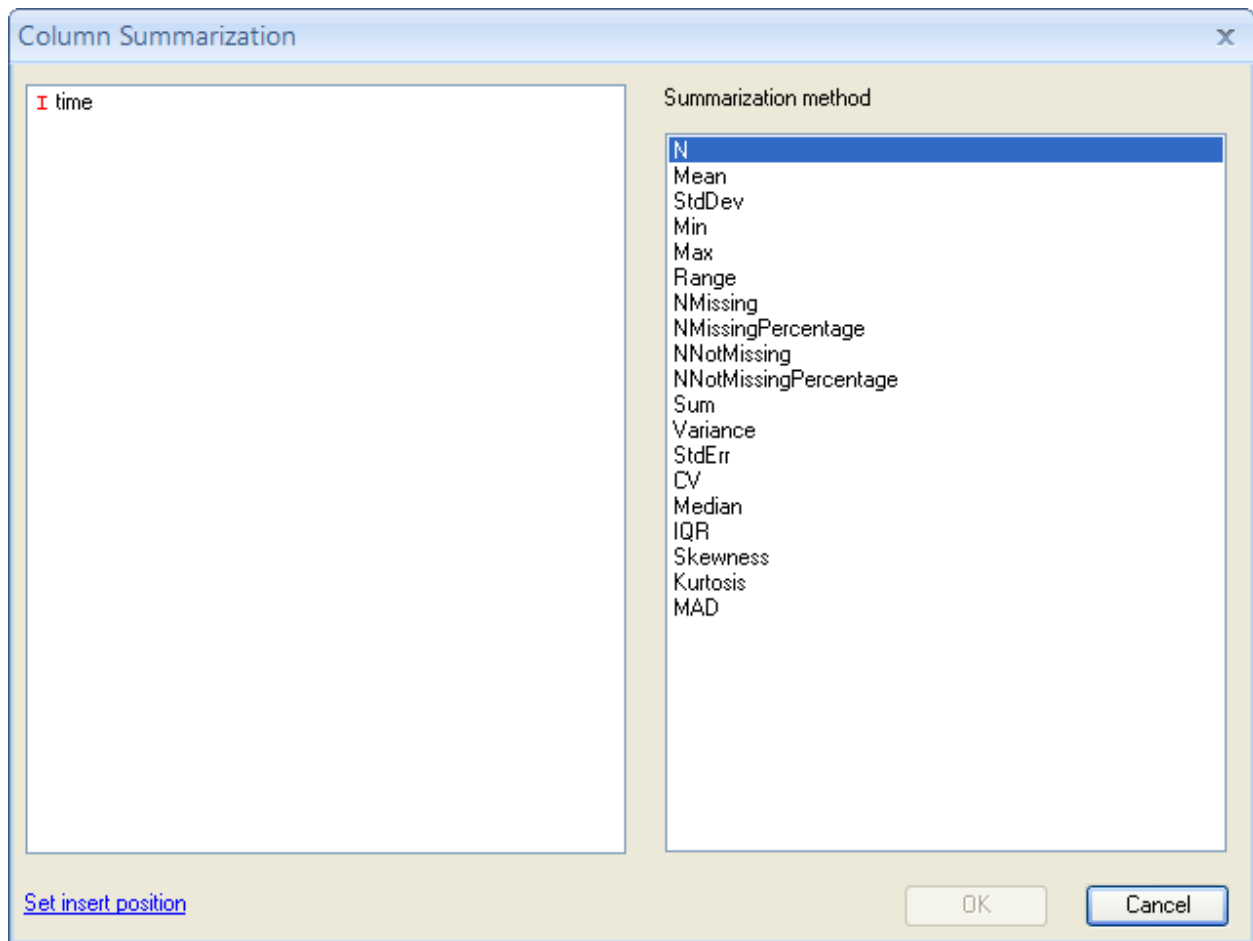
Exp10

Log

Exp

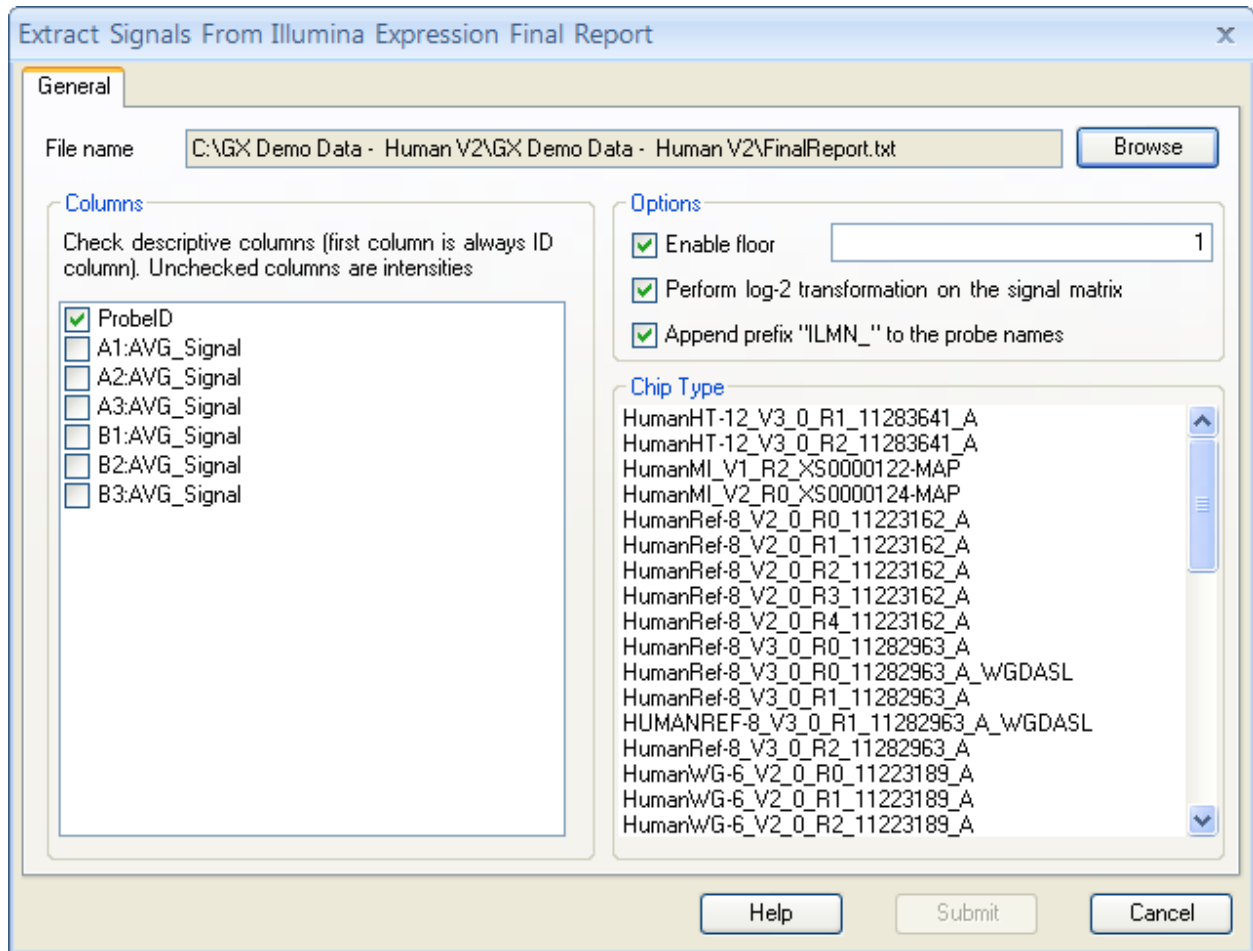
Rank

[Set insert position](#)



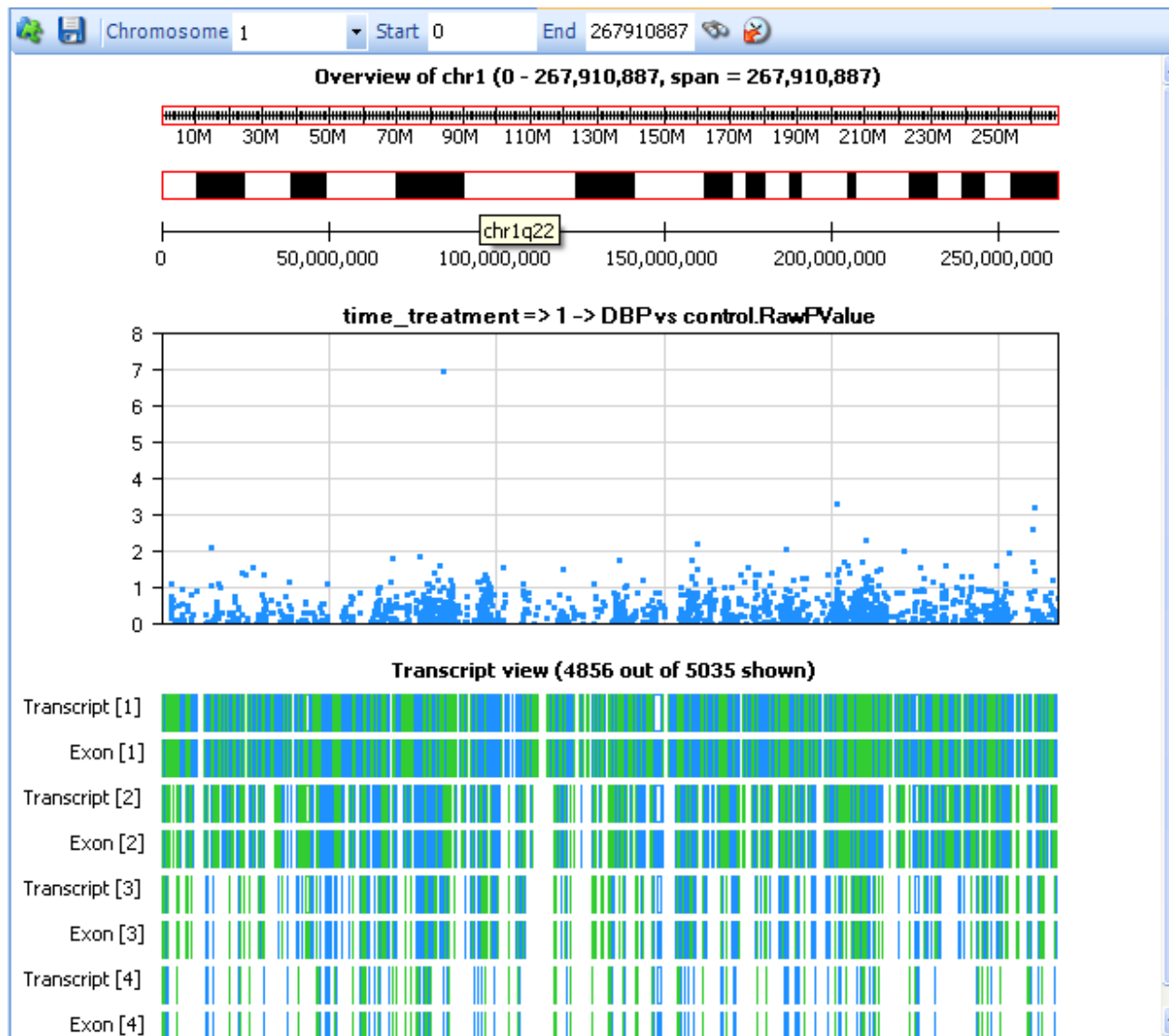
DATA IMPORTING

Illumina expression/miRNA and Agilent expression/miRNA data are now fully supported. For Illumina, we support the final report from BeadStudio/GenomeStudio. For Agilent, we support the Agilent text files. For both platforms, annotations can be automatically attached by selecting the chip type.



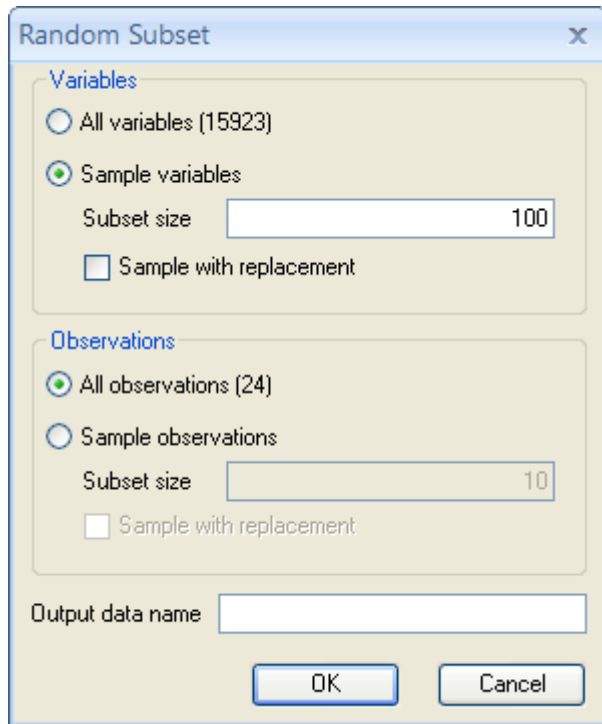
REGION VIEW FOR EXPRESSION DATA

We added the region view support for Affymetrix 3'IVT inference report.



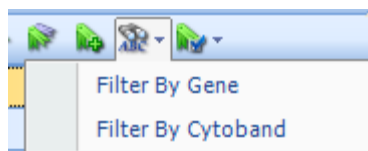
RANDOM DATA GENERATION

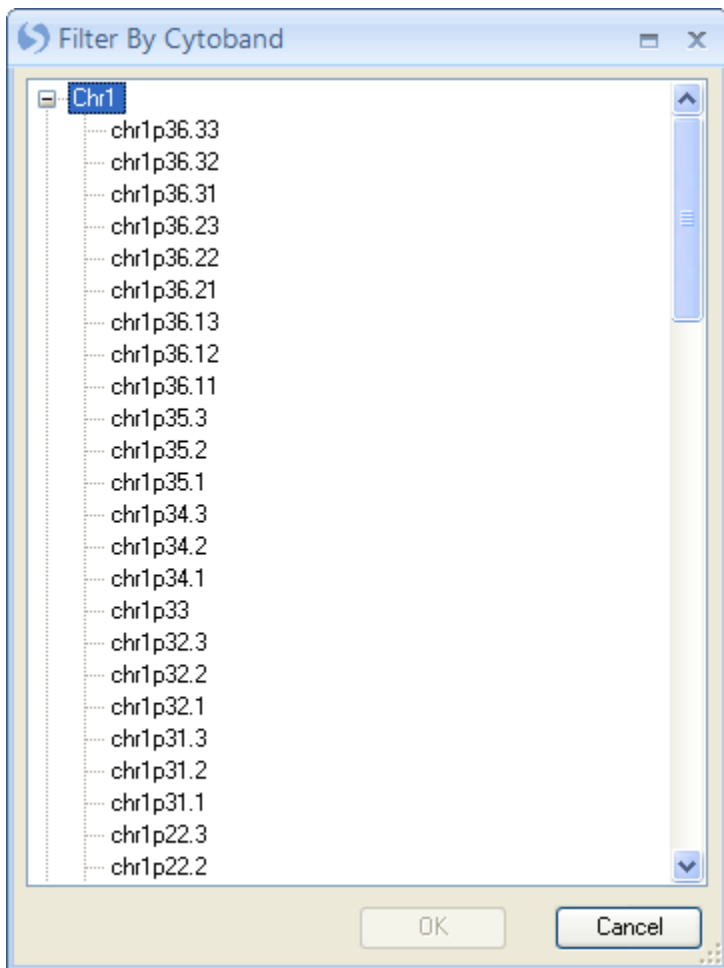
For all data types, the user now can generate a random subset of variables and/or observations.

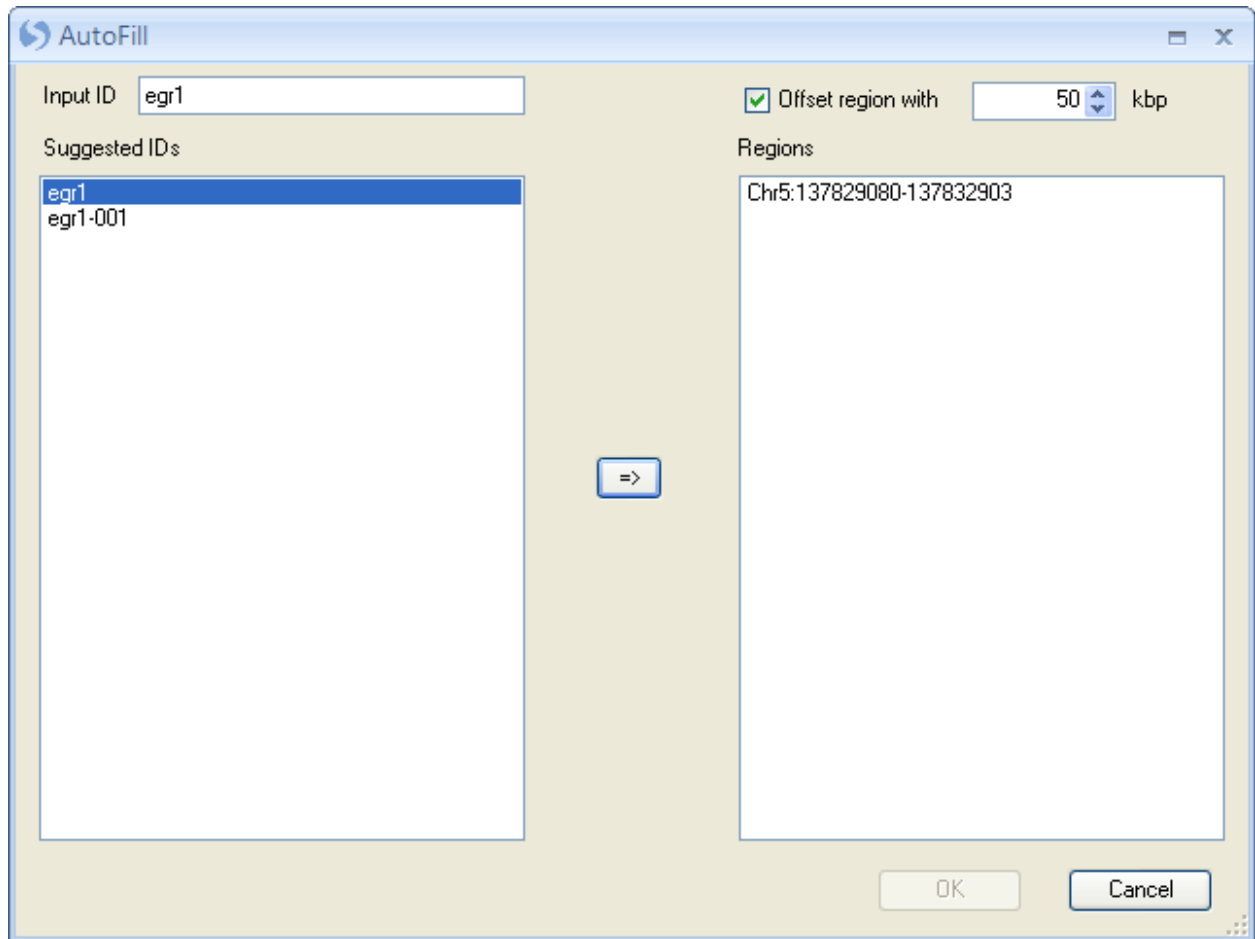


FILTER BY GENE OR CYTOBAND

For SNP/CNV/ExonArray datasets, the filtering toolbox now has a menu to allow users to filter variables by a gene name or a cytoband.

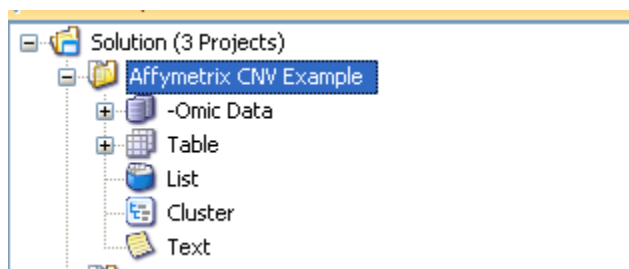


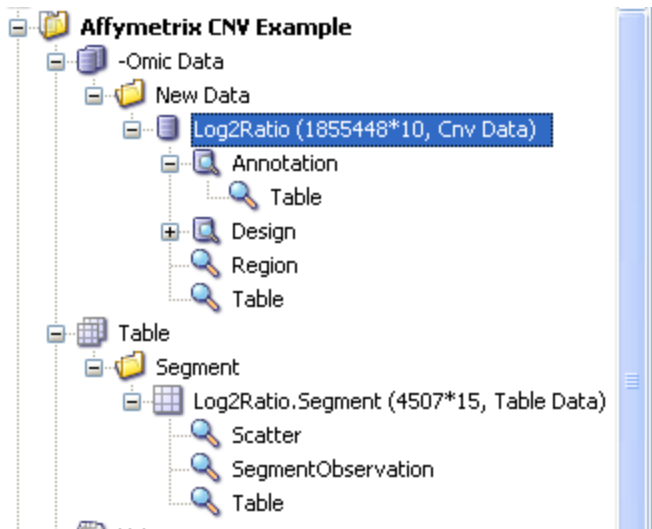




NEW ORGANIZATION IN SOLUTION EXPLORER

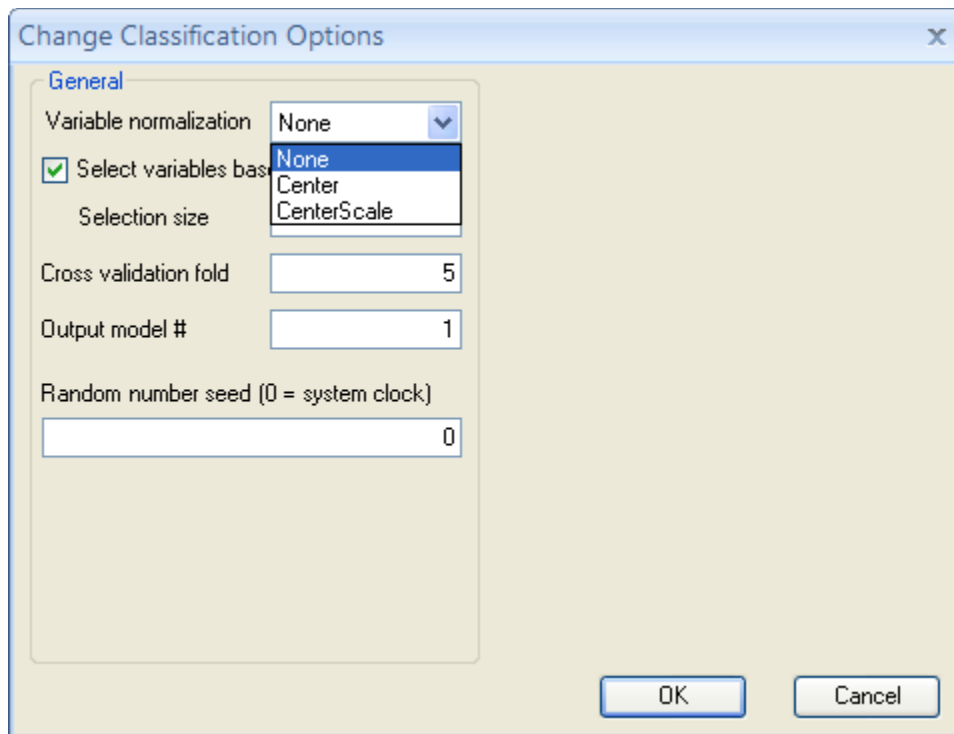
The Solution Explorer now has a new organization structure. For each project, it is separated into two main categories: -Omic Data and Table. Each category allows any number of organizational folders. By default, Array Studio will create a folder structure in each category, as tables and new datasets are created (for instance, inference tables will be automatically placed in an "Inference" folder in the Table category).





CLASSIFICATION/REGRESSION

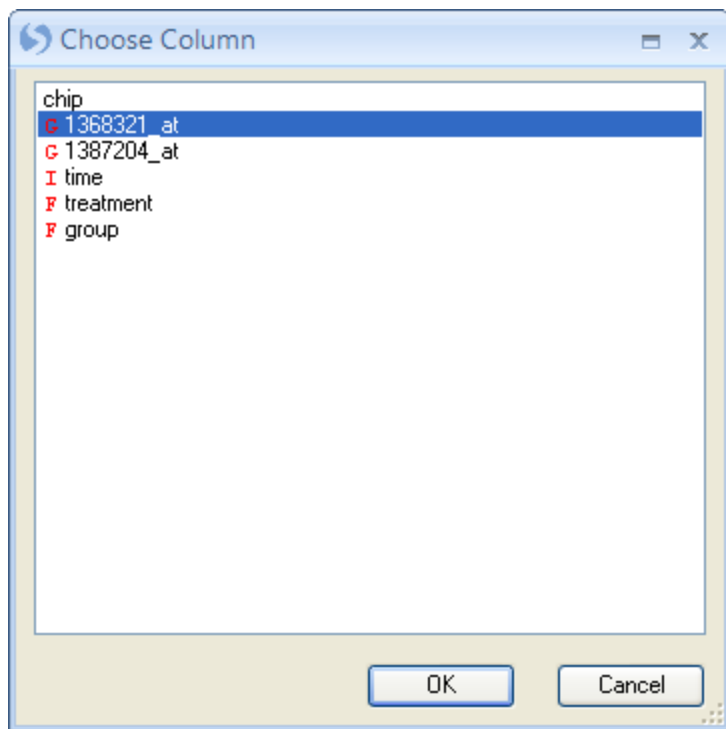
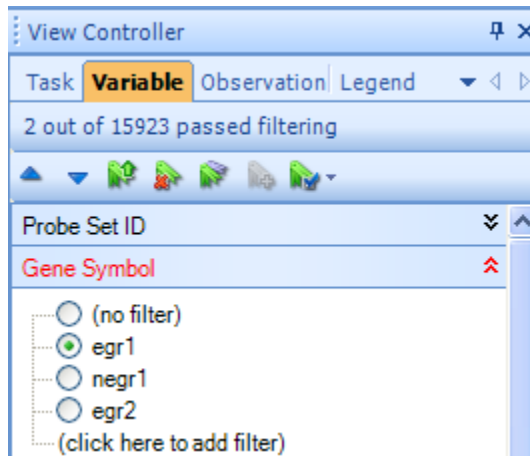
In the Options sections of the Regression and Classification modules, the user now has the option of normalizing variables (None, Center, and CenterScale). This is useful for comparing vastly different datasets with different normalizations.



IMPROVED VARIABLE SCATTER VIEW

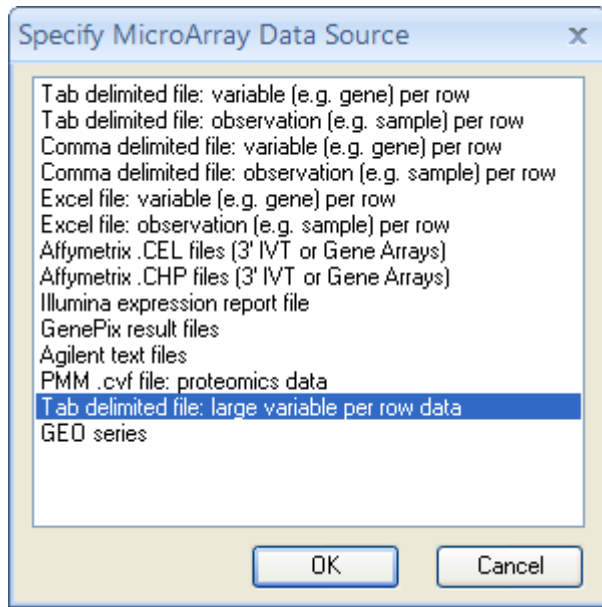
For the variable scatter view, it is now possible to filter by both variables and observations. Previously, it was only possible to filter by observations. Specifying X column and Y column

commands in the task tab will now only show those variables that have been filtered by the Variable filter.



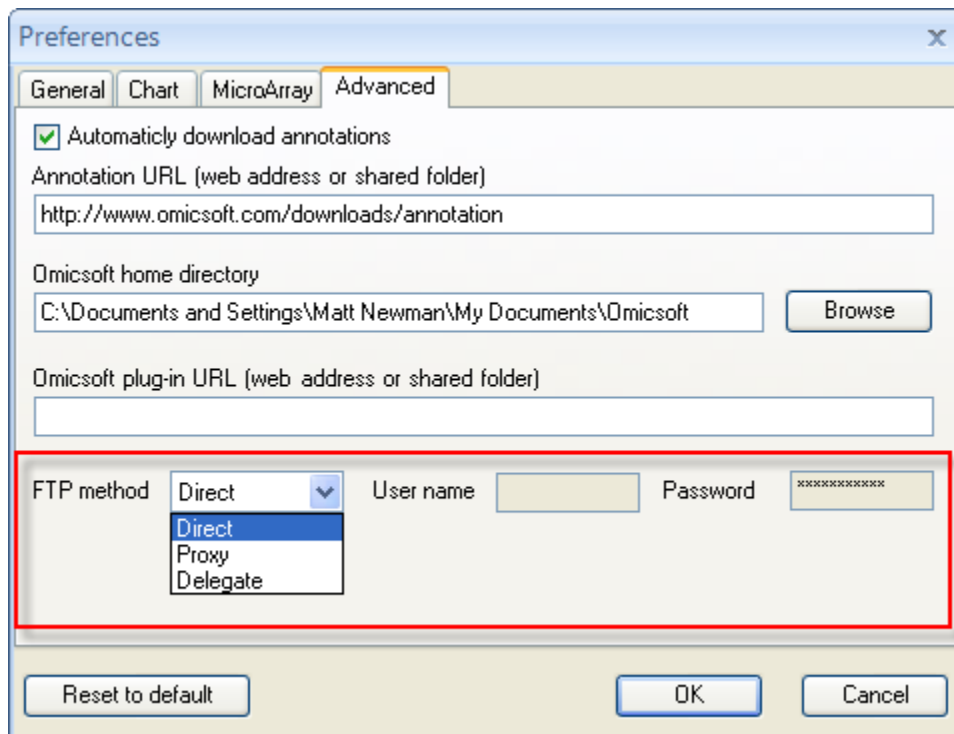
LARGE MICROARRAY DATA SUPPORT

Array Studio now supports extremely large microarray datasets (>1 million variables and >200 samples) using the new large variable per row text format. Not all modules are currently applicable to this data type.



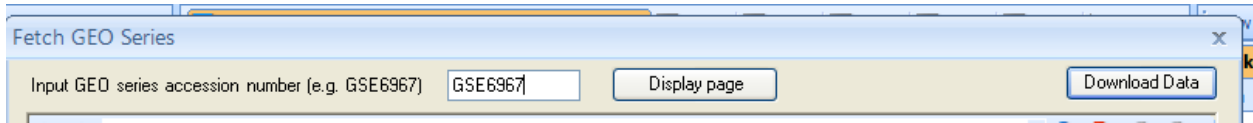
FTP DOWNLOAD

Some corporate users have difficulties accessing GEO data for download. Array Studio now allows three different options for downloading (Direct, Proxy, and Delegate). For proxy, the user can set the user and password for the proxy server. Delegate uses www.arrayserver.com as a delegate, and the downloading goes through Omicsoft's server first, and then from there to the user (this is slower than the other methods).



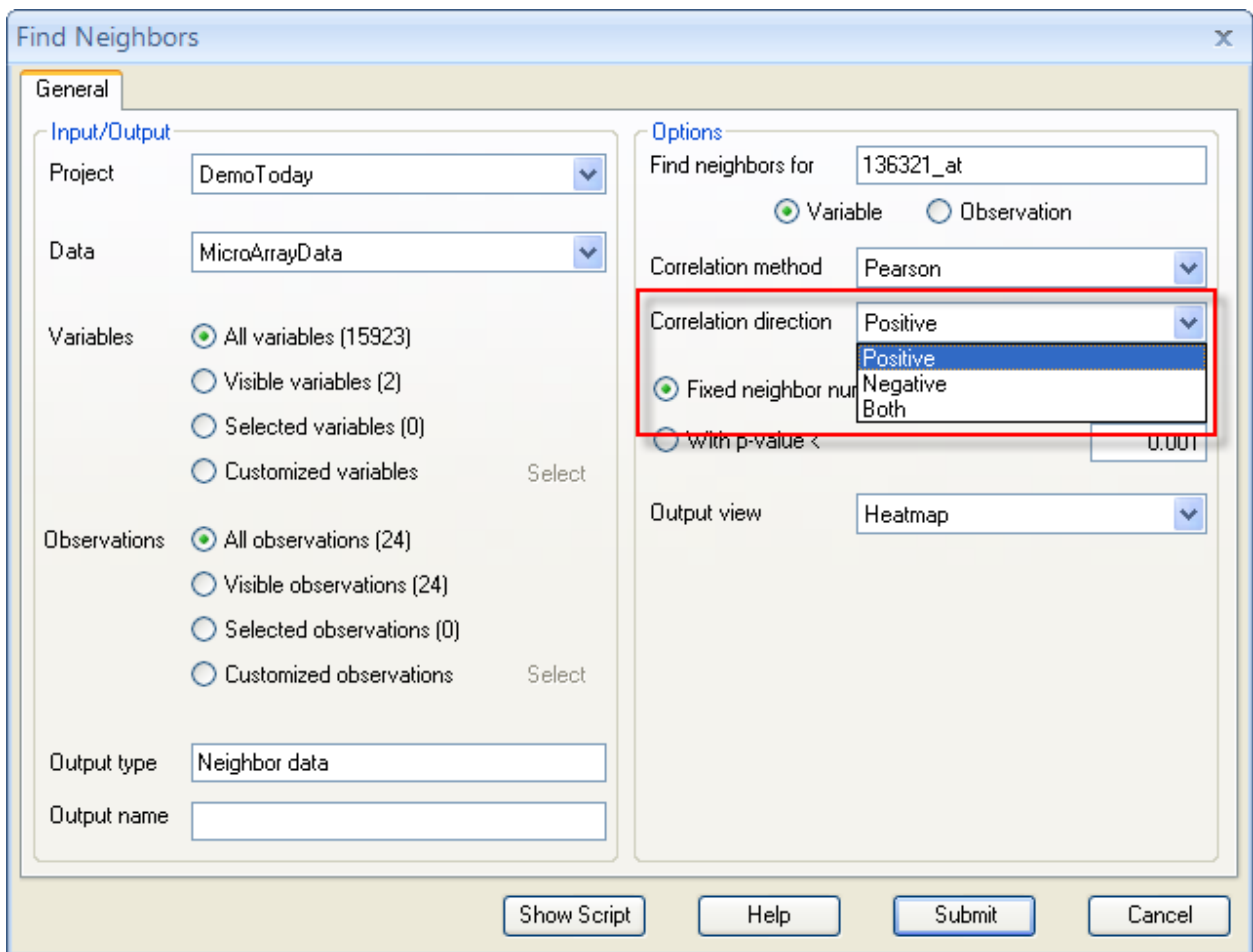
GEO DOWNLOAD

Previously, GEO data download was based on the Series Matrix format, which had many errors. Data is now downloaded using the Minimal Format.



FIND NEIGHBORS

The Find Neighbors module now allows the user to specify the correlation direction (positive correlations, negative correlations, or both directions).



MAS5 SUPPORT FOR PM ONLY CHIP

Array Studio now supports MAS5 normalization for the new PM-only chip. Instead of PM-MM, MM is considered to be 0, and only PM is used.

VARIABLEVIEW

For visualizing data with missing values, a new option in the Task tab is now available for connecting broken lines.

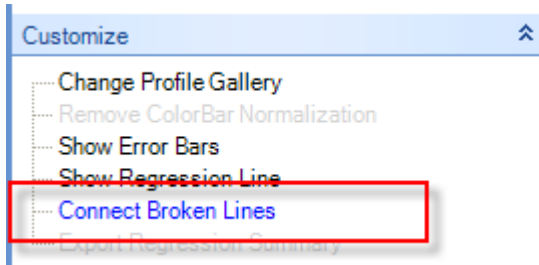
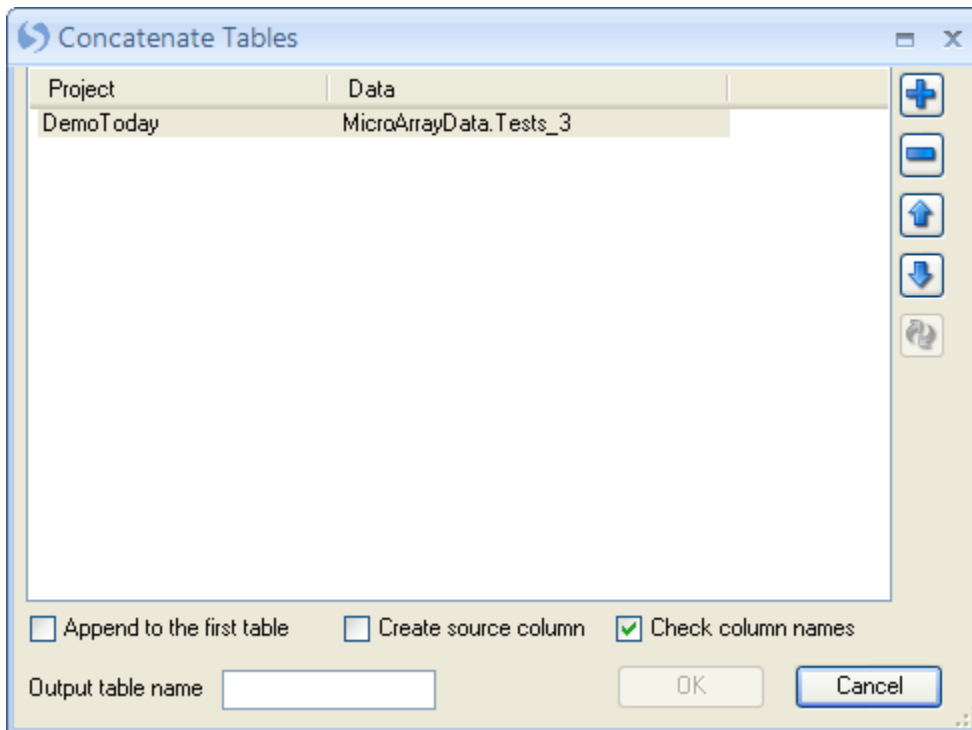


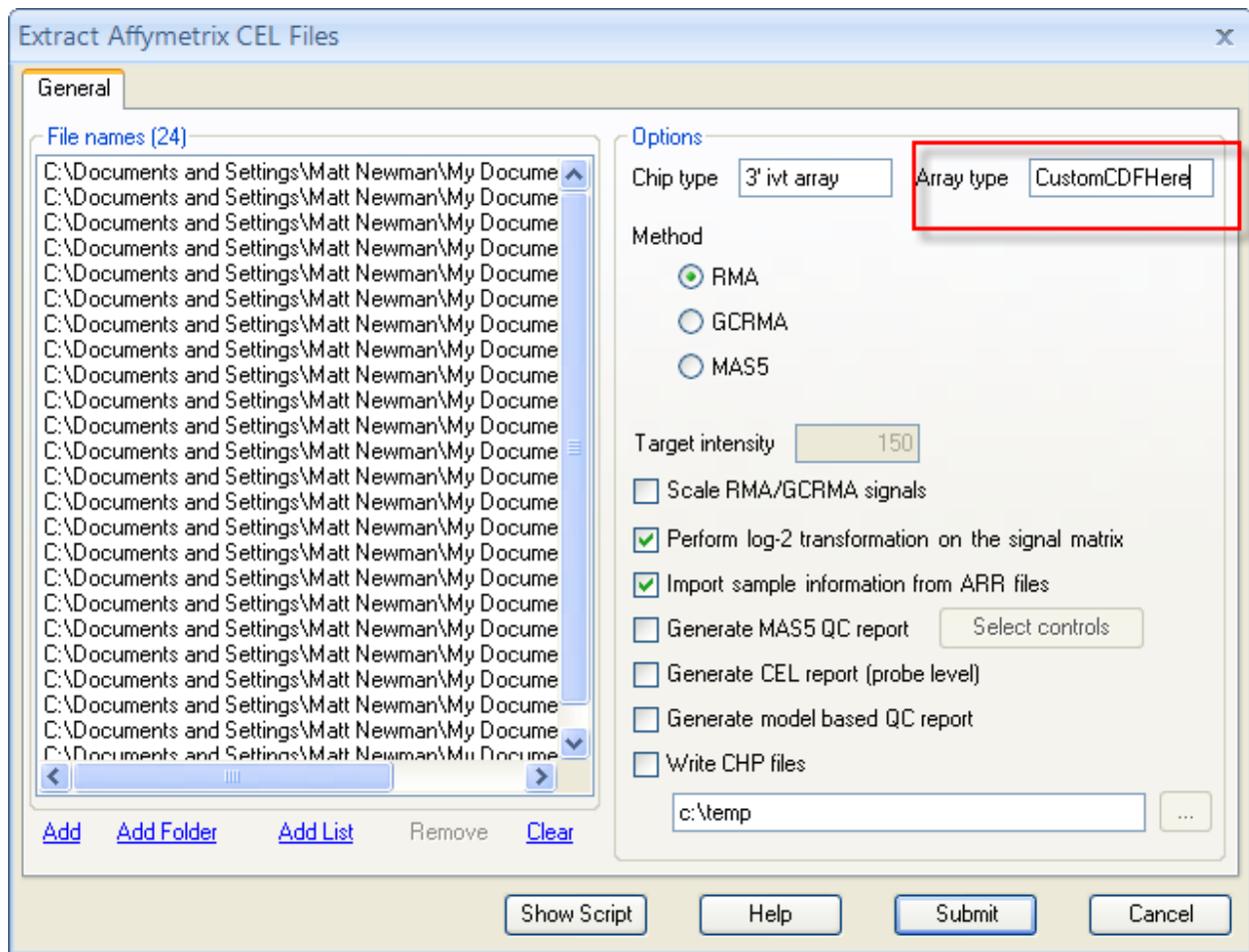
TABLE CONCATENATION

Concatenation of multiple tables is now allowed using the Table Concatenation function found under the Table Menu.



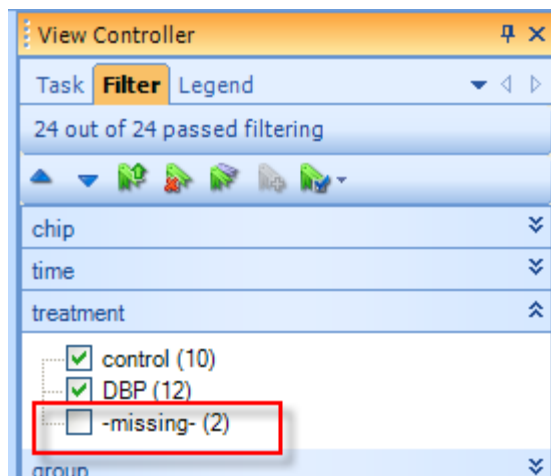
ALTERNATIVE CDF

When importing CEL files, the user can now choose an alternative CDF file to use. This is useful for using CDFs generated outside of Affymetrix (i.e AffyProbeMiner)



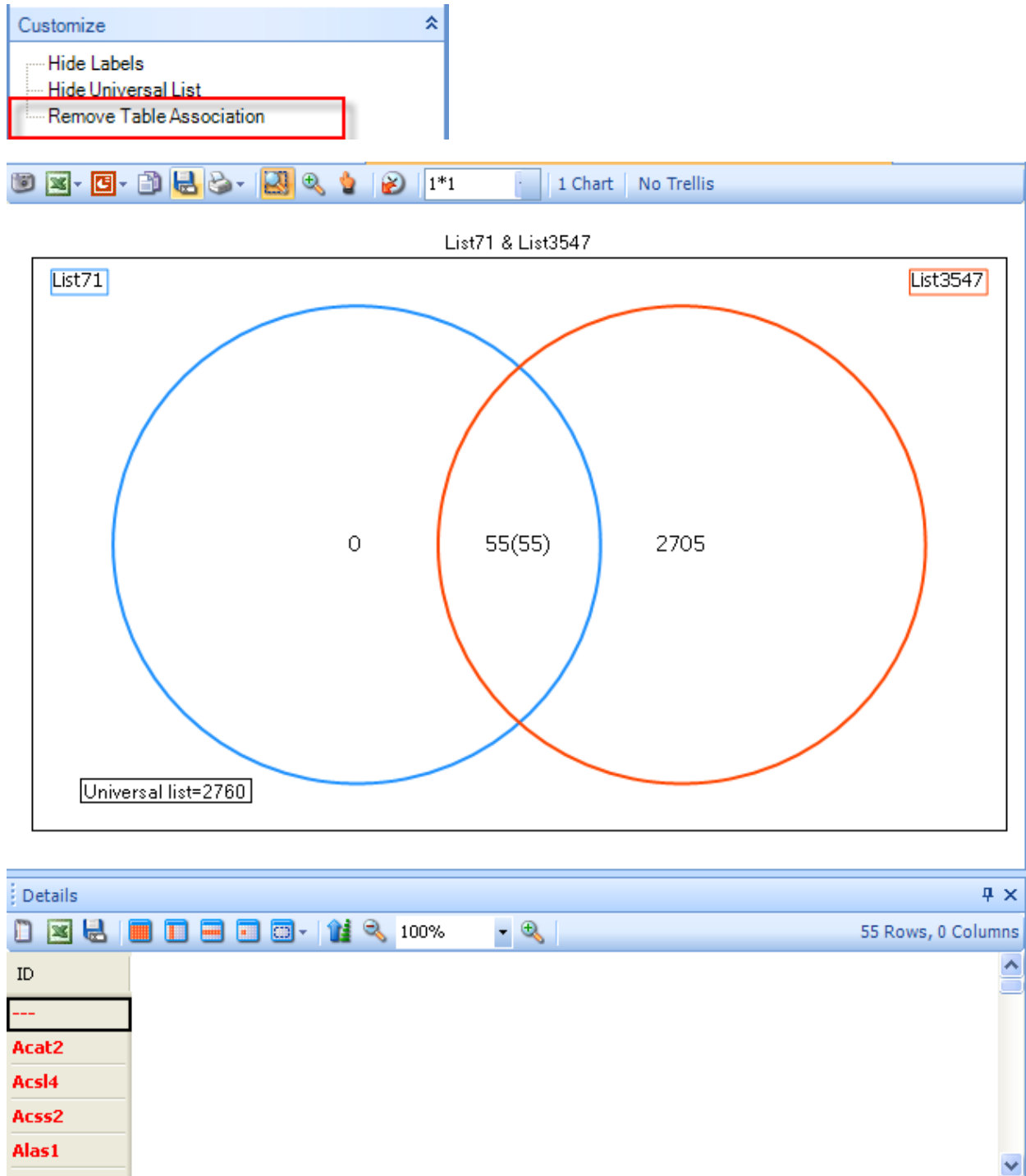
MISSING FACTOR LEVELS

For filtering factor columns with missing levels, a “-missing” radio box and check box is now available.



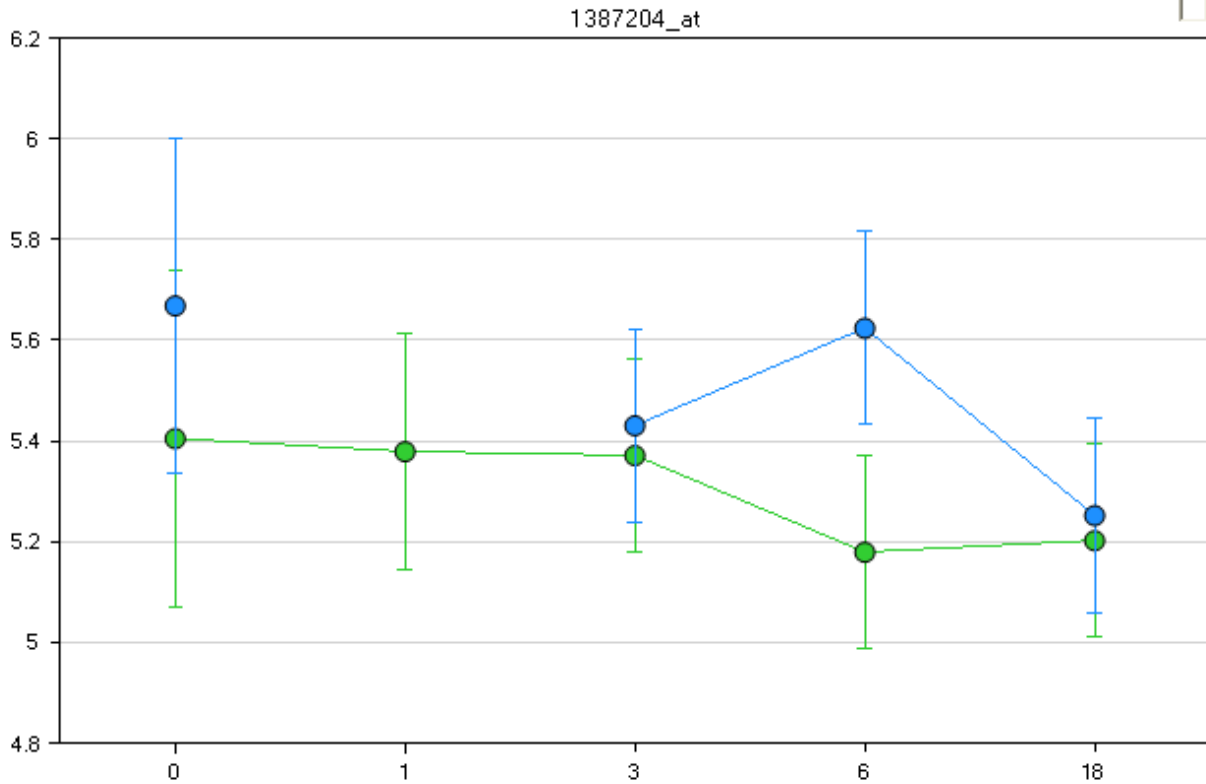
VENN DIAGRAM VIEW

Allows Venn Diagram views for lists that are not associated with a particular table. Previously, Venn Diagrams could only be created using the “ID” column of a table, but now any type of ID can be used to compare.



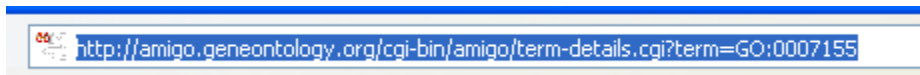
SMART LSMEAN INTERACTION

When doing a One-Way or Two-Way ANOVA, and adding LSMean data, a “smart” interaction plot will be created.



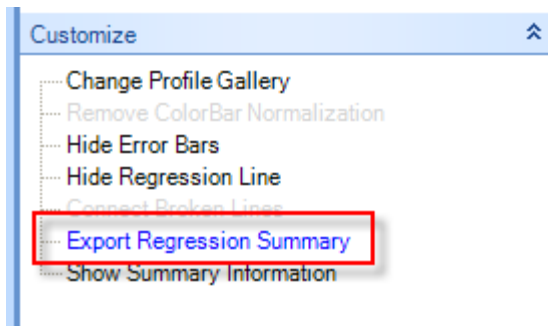
GENE ONTOLOGY URL

The Gene Ontology URL now uses AmiGo as its URL.



EXPORT REGRESSION SUMMARY

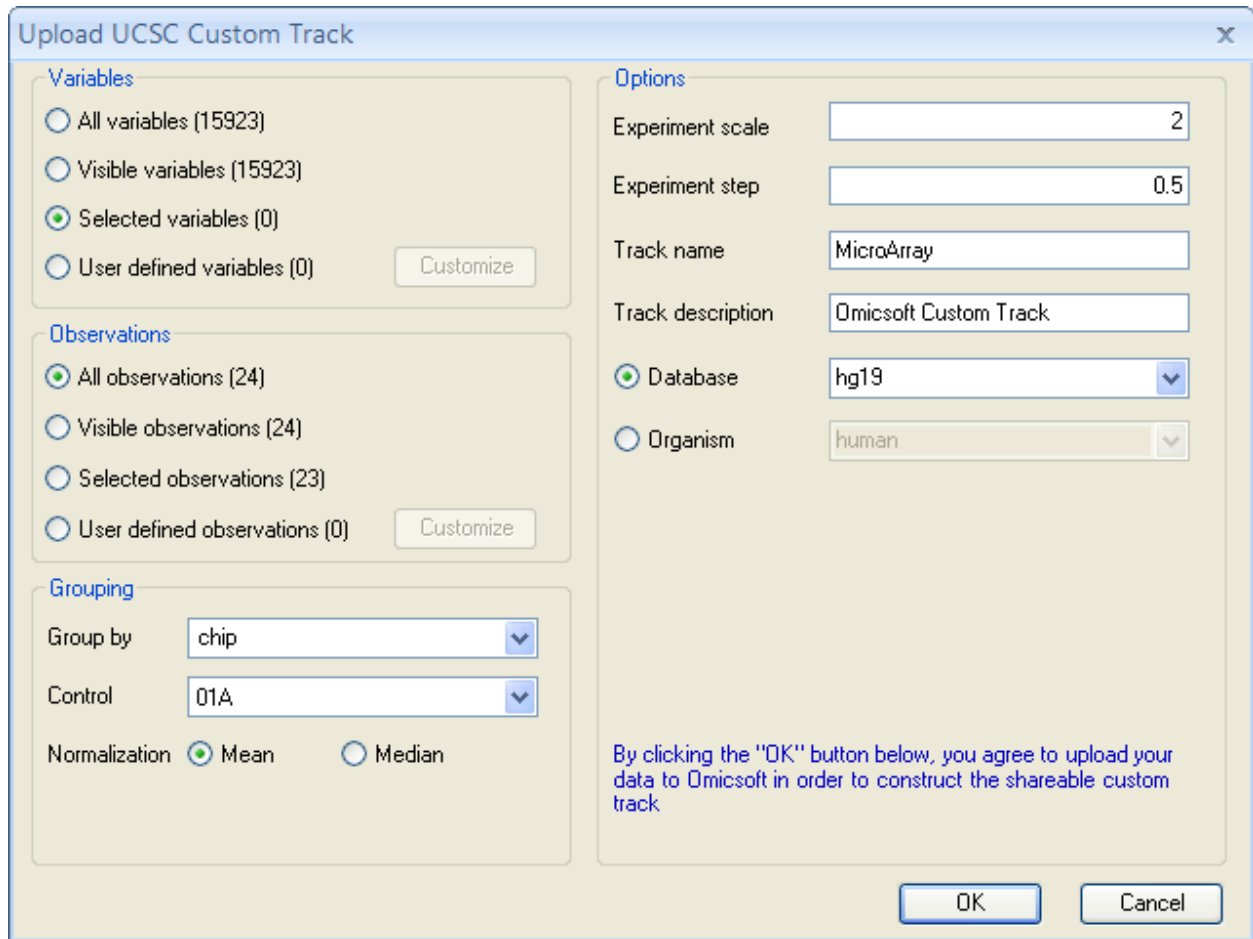
If the profile column for a variable view is numeric, this command (available in the Task tab) will export a summary of the regressions for each of the variables.



	A	B	C	D	E	F	G
1	ID	N	Intercept	Slope	Correlatio	CorrelationPValue	
2	Zzef1, Zinc	24	62.2758	0.6789	0.5207	0.0091	
3	Zzef1, Zinc	24	20.378	0.5523	0.6139	0.0014	
4	Zzef1, zinc	24	15.3039	0.1541	0.3592	0.0847	
5	Zyx, zyxin	24	454.8124	-12.292	-0.4619	0.0231	
6	Zwint, ZW	24	3862.514	-29.6251	-0.5148	0.0101	
7	Zw10, ZW	24	329.0941	-2.8262	-0.6066	0.0017	
8	Zufsp, zinc	24	124.2384	-0.0613	-0.0272	0.8994	
9	Zswim1, z	24	93.9751	-1.0855	-0.74	3.58E-05	
10	Zrsr2, zinc	24	71.4184	4.566	0.76	1.64E-05	
11	Zrsr1, zinc	24	16.9237	0.5248	0.766	1.28E-05	
12	Zranb2, zin	24	451.7853	-3.336	-0.3228	0.124	
13	Zranb2, zin	24	178.8683	4.6216	0.6675	0.0004	
14	Zp3, zona	24	20.1306	-0.093	-0.3342	0.1105	
15	Zp2, zona	24	27.3195	1.9273	0.5224	0.0088	
16	Zp1, zona	24	19.3605	0.032	0.0923	0.668	
17	Znrf1, Zinc	24	15.8114	0.1571	0.4871	0.0158	

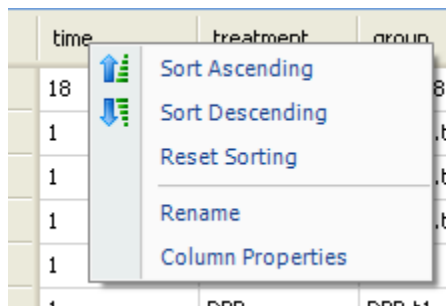
UPLOAD UCSC CUSTOM TRACK

Array Studio now allows the uploading of custom UCSC tracks for microarray and Exon Array data.



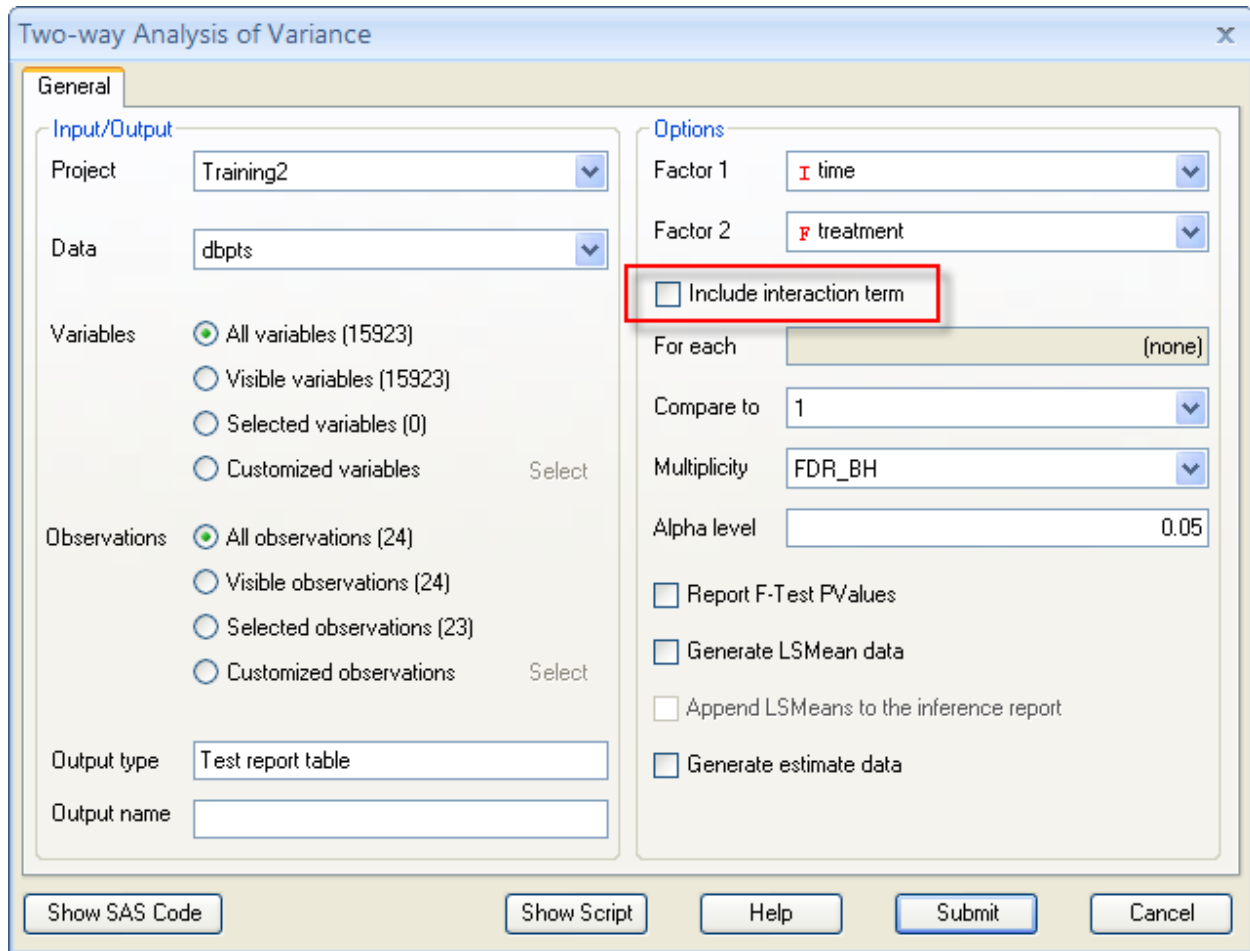
COLUMN NAME/PROPERTIES

Right-clicking a column header now allows quick access to sorting, renaming of columns, and column properties.



TWO-WAY ANOVA

In the two-way ANOVA dialog, it is now possible to remove the interaction term.

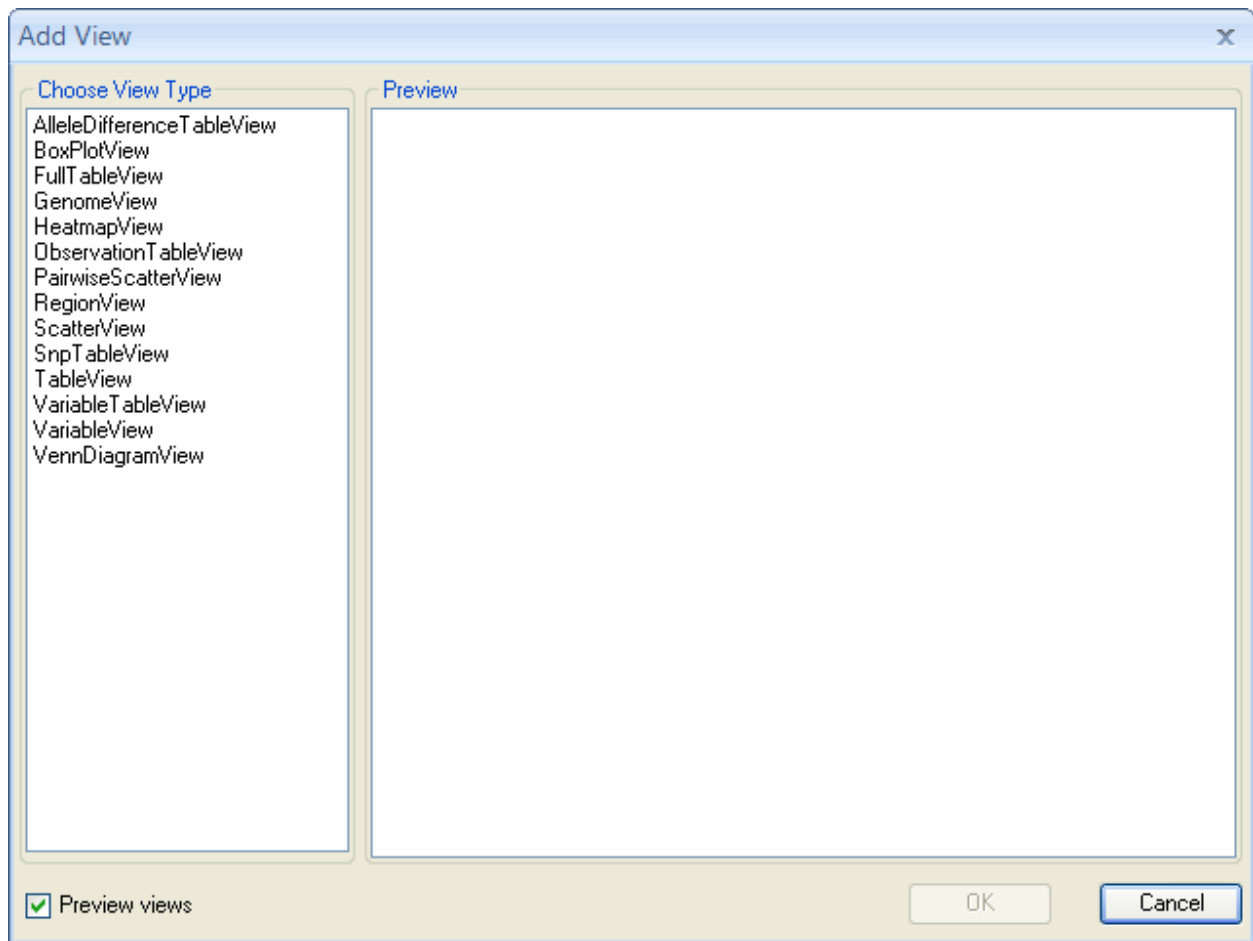


SETTINGS

When upgrading to new versions of Array Studio, previous settings files are automatically upgraded.

ADD VIEW DIALOG

The listing of the views when adding a new view is now alphabetical.

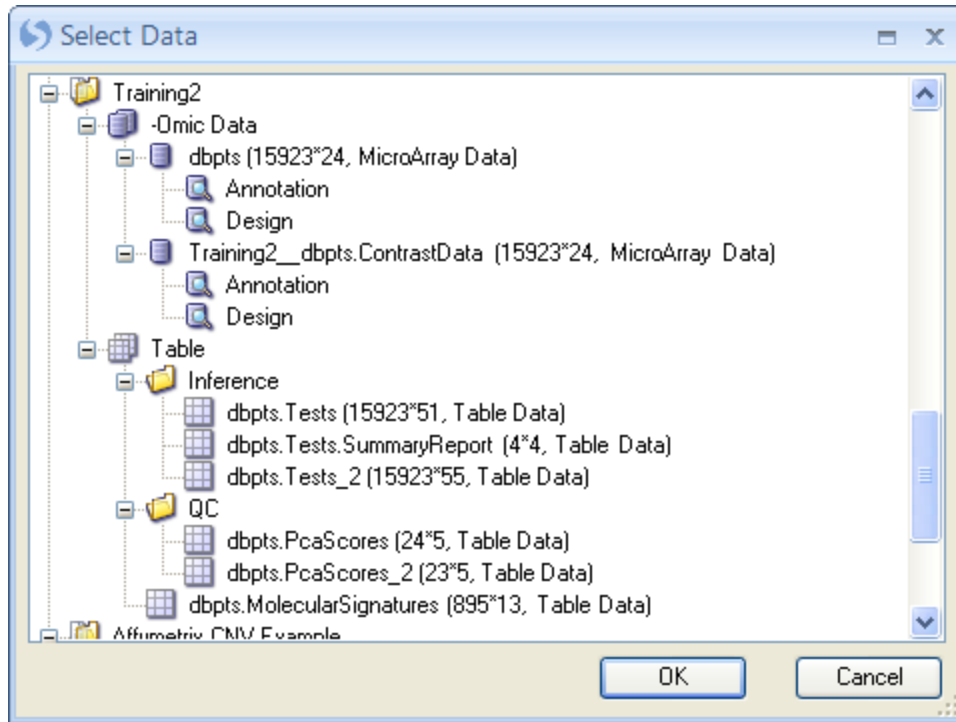


FILTERING

Filtering the original data for some linked tables (i.e Gene Ontology Report, Summarize Inference Report, etc..) will no longer affect the details on demand for that table, in order to avoid confusion.

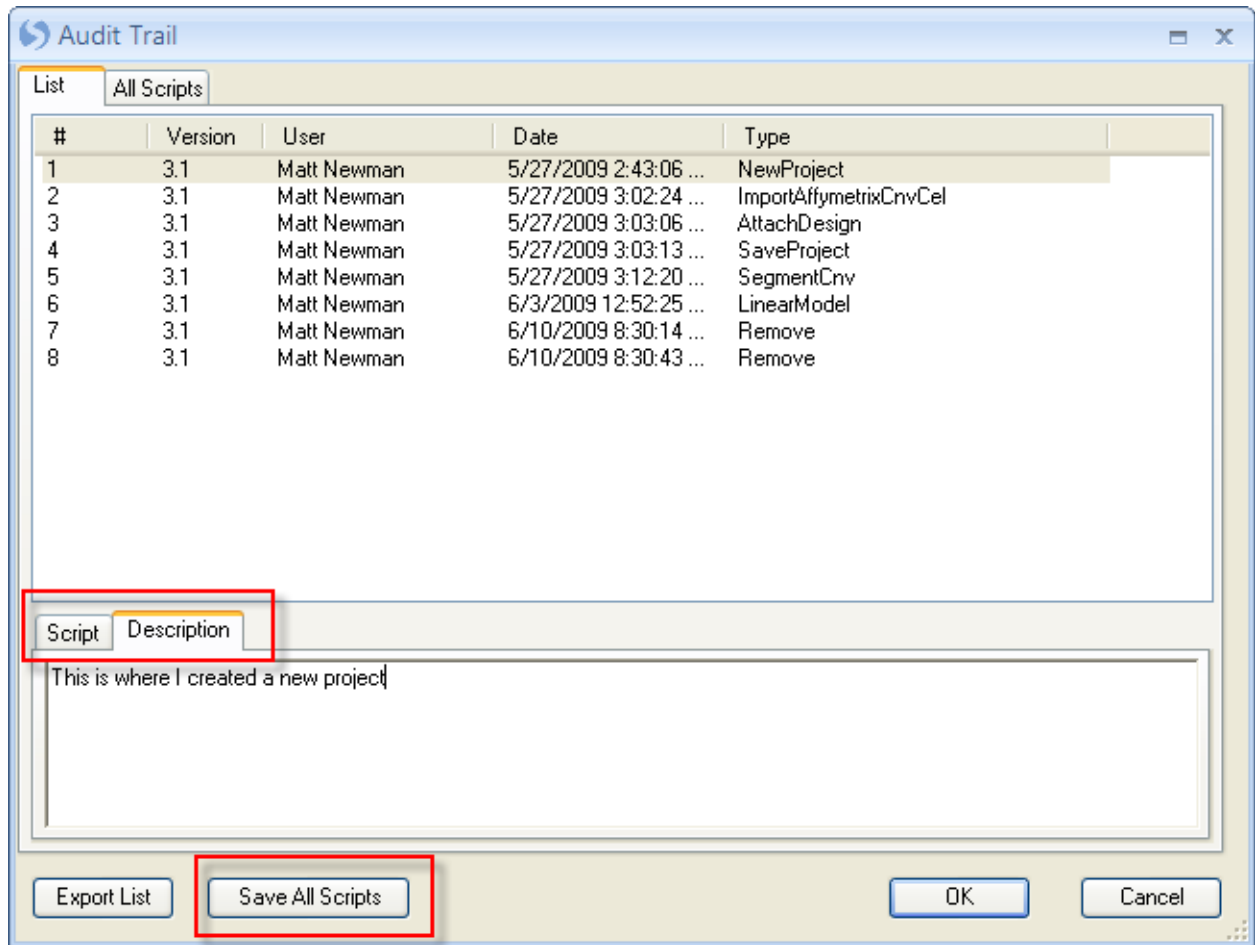
DATA SELECTION

For adding views or using commands from the table menu or data menu, the user now has the ability to select the dataset upon which to run the command (it is no longer dependent on the current view).



AUDIT TRAIL

The Audit trail has been improved, by allowing an editable description for each entry. In addition, there is now a button to save the script as a file, allowing easy saving of scripts.



MAXIMIZE BOX

Any resizable dialog now has the ability to be maximized.

