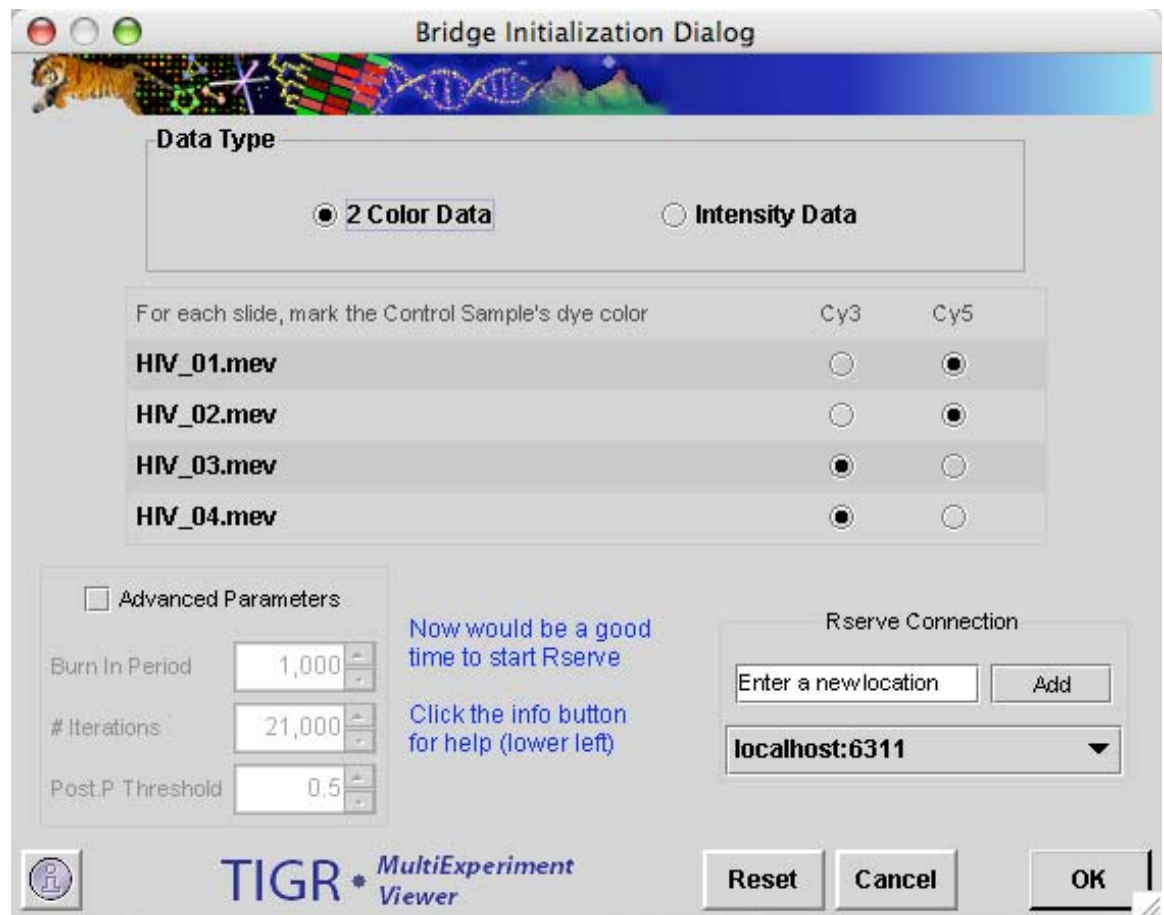


1.1. bridge: Bayesian Robust Inference for Differential Gene Expression (Gottardo *et al.* 2005)

Test for differentially expressed genes with microarray data. This package can be used with both cDNA microarrays or Affymetrix chips. The package fits a robust Bayesian hierarchical model for testing for differential expression. Outliers are modeled explicitly using a t-distribution. The model includes an exchangeable prior for the variances which allow different variances for the genes but still shrink extreme empirical variances. Parameter estimation is carried out using a novel version of Markov Chain Monte Carlo that is appropriate when the model puts mass on subspaces of the full parameter space.

The initialization dialog shown below (11.27.1) allows the user to indicate whether the loaded dataset is 1 or 2-color and to denote the dye labeling scheme used in the experiment. If the data is Intensity, it instead asks the user to denote if the loaded slide is “Treatment” or “Control”.

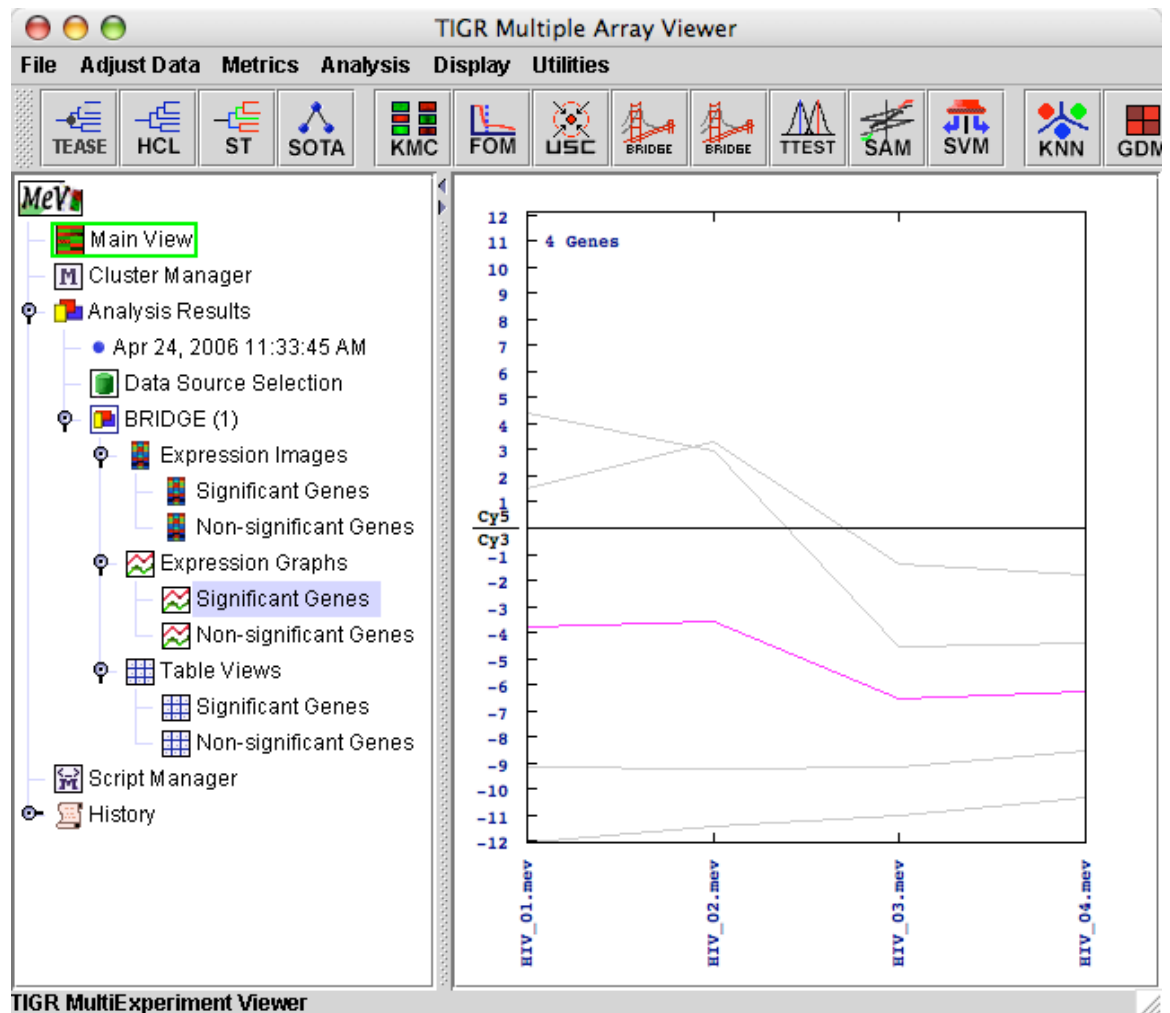


11.27.1. Bridge Initialization Dialog

Rserve Connection

By default, Bridge will look on the local machine for an Rserve server. However, since Rserve is a TCP/IP server, theoretically it could be running anywhere. The user need only enter an IP address and port number separated by a : in the Text Field “Enter a new location”. By clicking “Add”, the new location will populate the pull down menu. It will be saved to the user’s config file and be available for later use.

Sample output from this module is shown below (11.27.2)



11.27.2. Bridge Results: Expression Graph of Significant Genes.