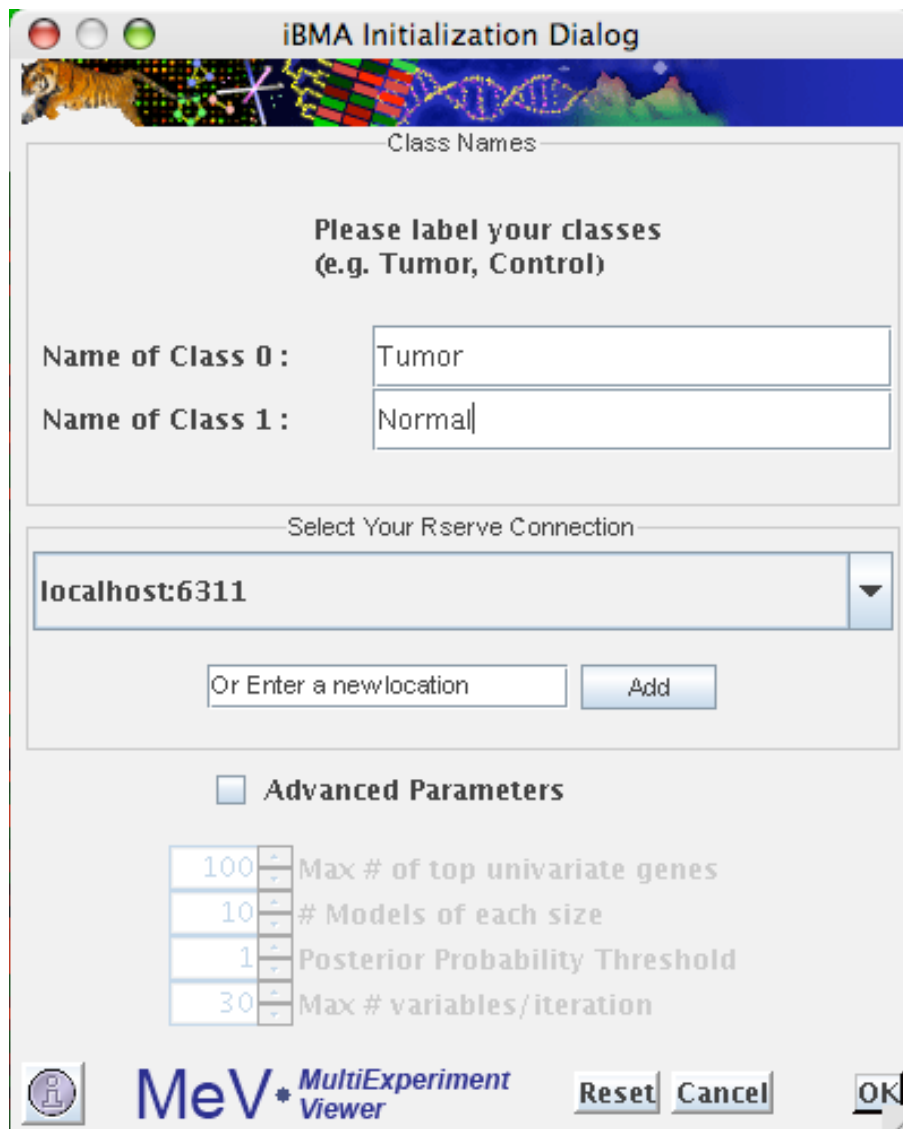


## iBMA: Iterative Bayesian Model Averaging (Yeung et al. 2005)

Gene Selection and Classification of microarray data. This package can be used with both cDNA microarrays and Affymetrix chips, however, is limited to data in which there are two classes, and the number of variables is greater than the number of responses.

The iterativeBMA algorithm is a multivariate technique for gene selection and classification of microarray data. Bayesian Model Averaging (BMA) takes model uncertainty into consideration by averaging over the posterior distributions of predicted probabilities based on multiple models, weighted by their posterior model probabilities. In the training data, the classes (or labels) of the samples are used to select a small number of genes to predict the classes (or labels) of the samples in the test set.

The initialization dialog shown below (1.1.1) allows the user to label the classes of the loaded data. Default is Class 0 and Class 1.

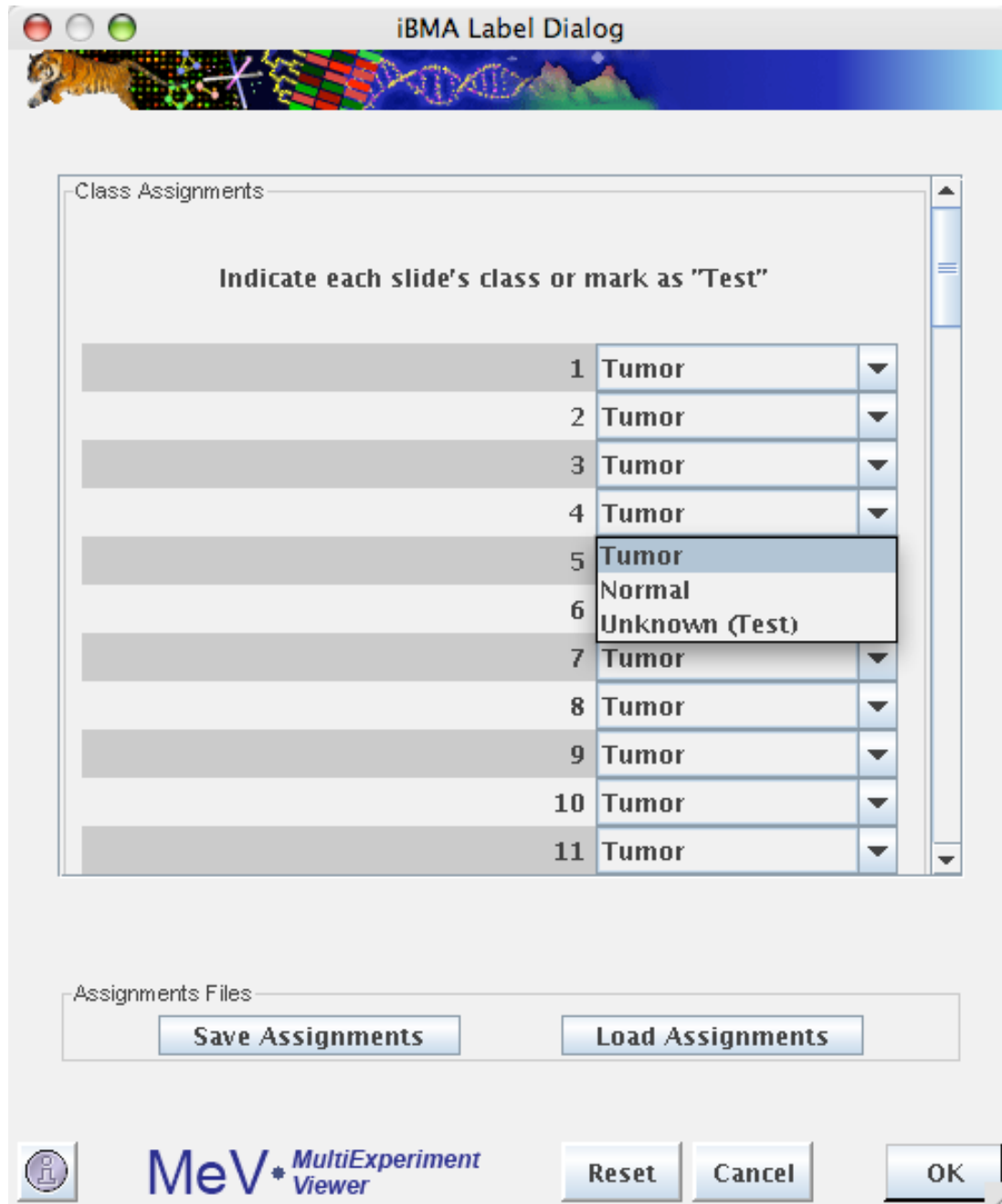


The image shows a software dialog box titled "iBMA Initialization Dialog". The window has a decorative header with a tiger, a star, a DNA helix, and a mountain range. The main content area is titled "Class Names" and contains the instruction "Please label your classes (e.g. Tumor, Control)". There are two text input fields: "Name of Class 0:" with the value "Tumor" and "Name of Class 1:" with the value "Normal". Below this is a section titled "Select Your Rserve Connection" with a dropdown menu showing "localhost:6311" and a button labeled "Add". There is also a text input field "Or Enter a new location". At the bottom, there is a checkbox for "Advanced Parameters" which is unchecked. Below the checkbox are four spinners with labels: "100" for "Max # of top univariate genes", "10" for "# Models of each size", "1" for "Posterior Probability Threshold", and "30" for "Max # variables/iteration". At the very bottom, there is a logo for "MeV MultiExperiment Viewer" and three buttons: "Reset", "Cancel", and "OK".

## Rserve Connection

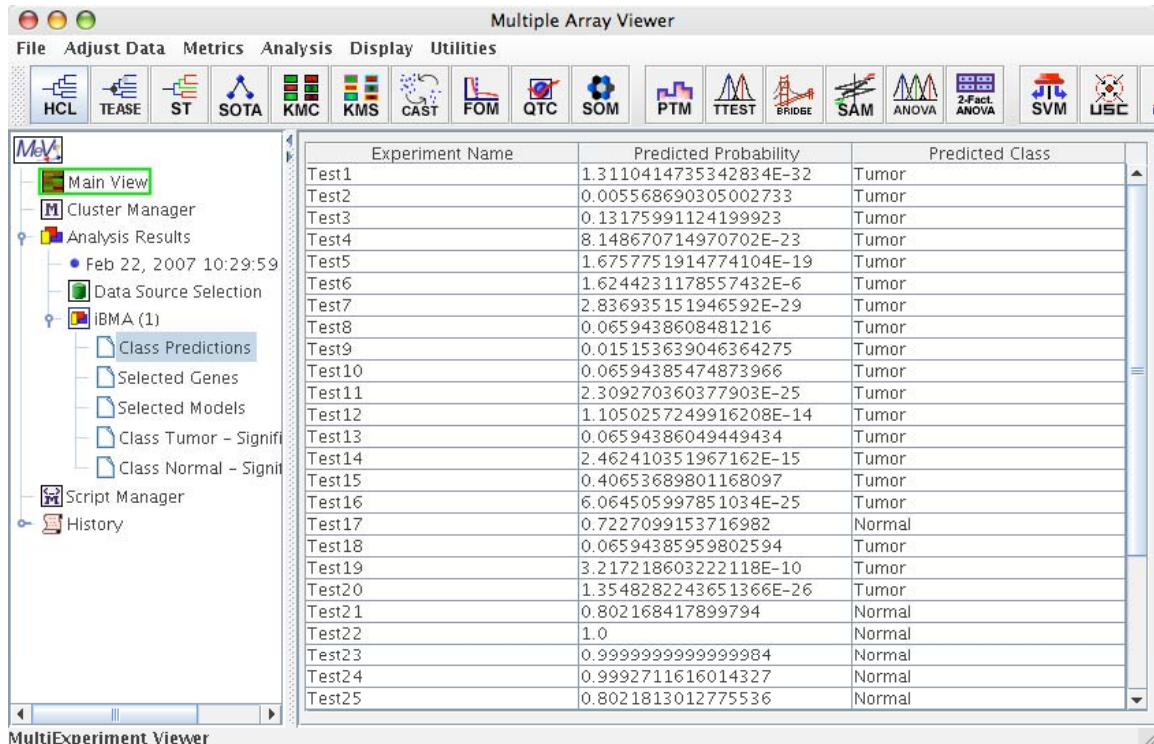
By default, Bridge will look on the local machine for an Rserve server. However, since Rserve is a TCP/IP server, theoretically it could be running anywhere. The user need only enter an IP address and port number separated by a : in the Text Field “Enter a new location”. By clicking “Add”, the new location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

### 1.1 iBMA Initialization Dialog



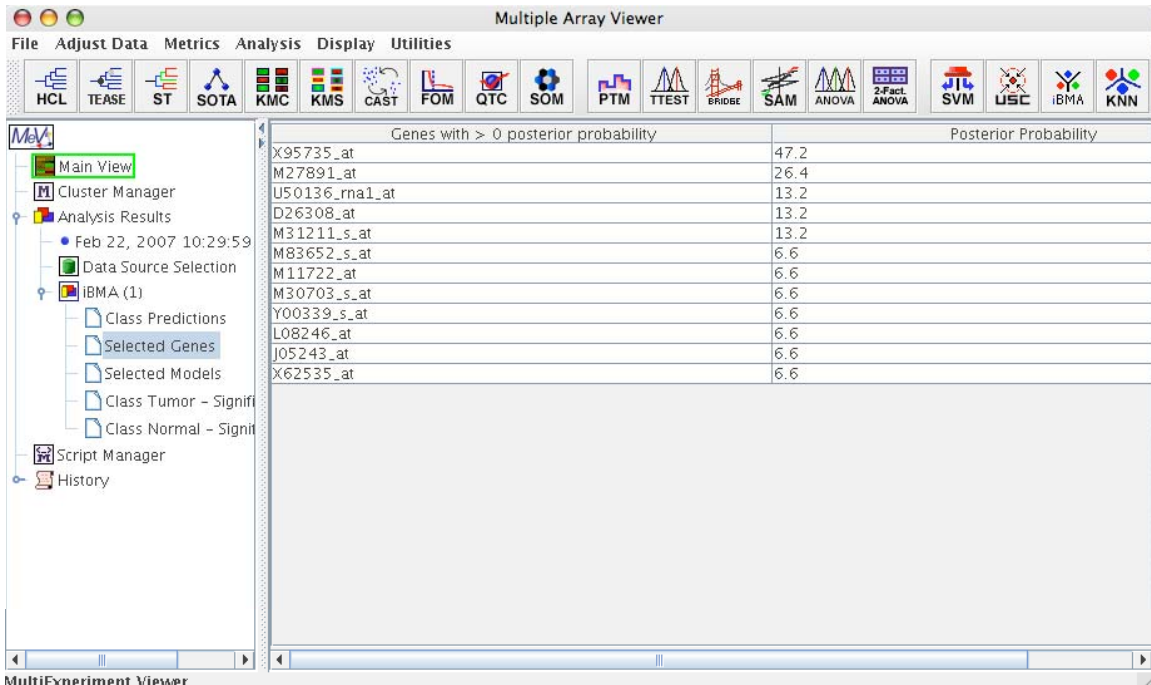
### 1.2 iBMA Label Dialog

The iBMA Label Dialog allows users to assign each loaded sample's status. For the known samples, the user may assign the class to which it belongs. For unknown samples, "Unknown (Test)" should be chosen. Additionally, users may wish to save these assignments to a file for later use.



### 1.3 iBMA Class Predictions View

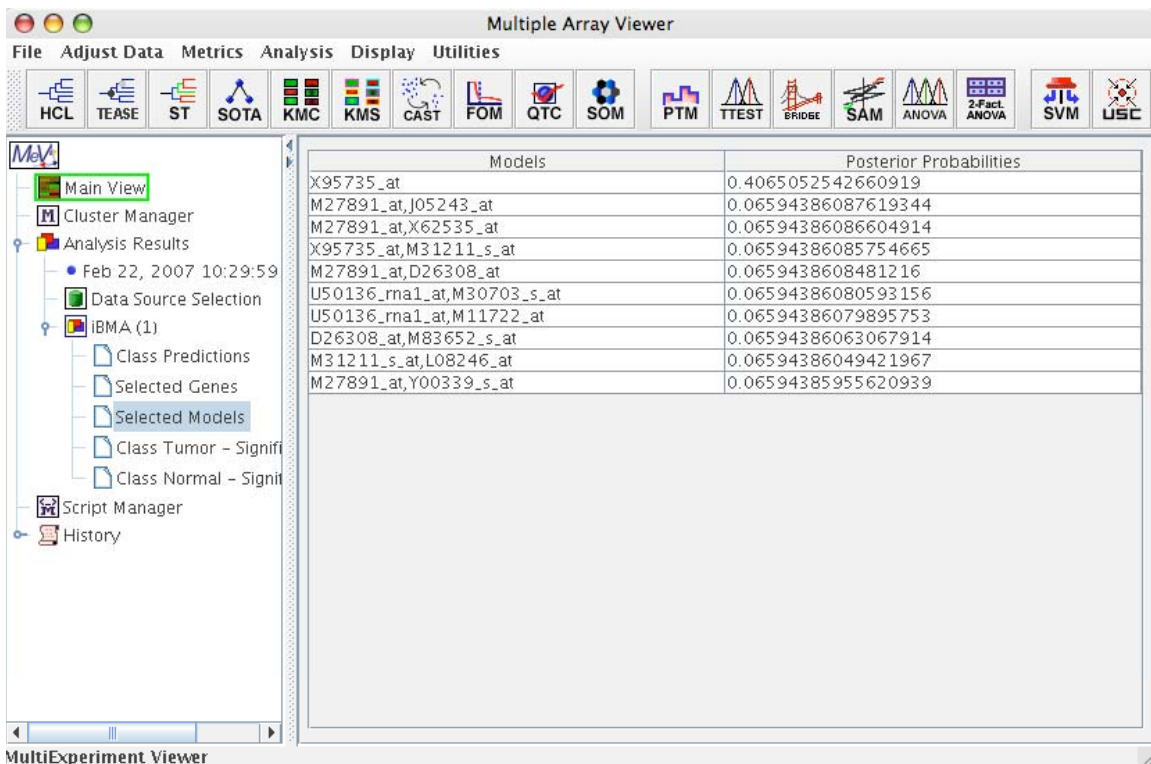
The Class Predictions view shows the predicted posterior probability and class for each test sample with unknown class. When the predicted posterior probability is less than 0.5, the predicted class is 0. Otherwise, the predicted class is 1.



MultiExperiment Viewer

#### 1.4 iBMA Selected Genes View

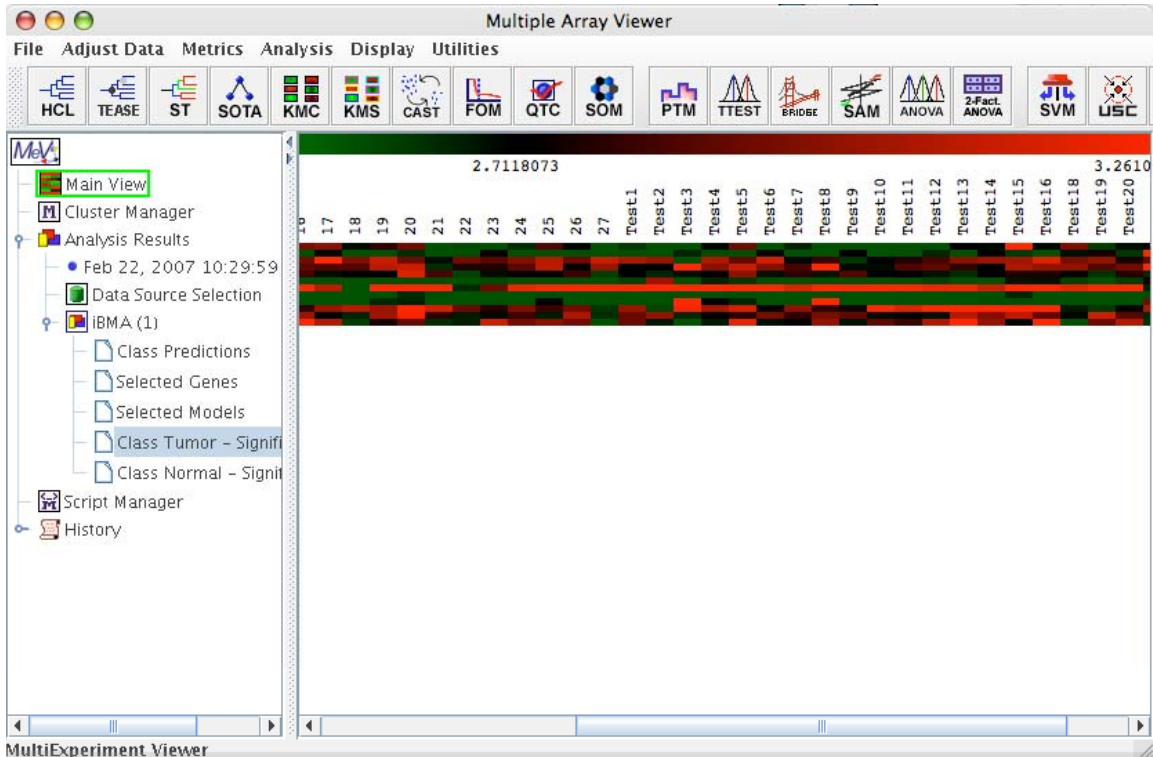
The selected genes view shows the selected genes (variables) with posterior probabilities greater than zero, sorted in descending order of posterior probabilities.



MultiExperiment Viewer

#### 1.5 iBMA Selected Models View

The selected models view shows the selected models and their corresponding posterior probabilities. Note that the model posterior probabilities for all the models a given gene is involved in should sum up to the gene's posterior probability shown in the selected genes view.



### 1.6 iBMA Class 0 – Significant Genes View

This view shows the heatmap of the selected genes with non-zero posterior probabilities for all samples that are assigned to or are predicted to belong to class 0.