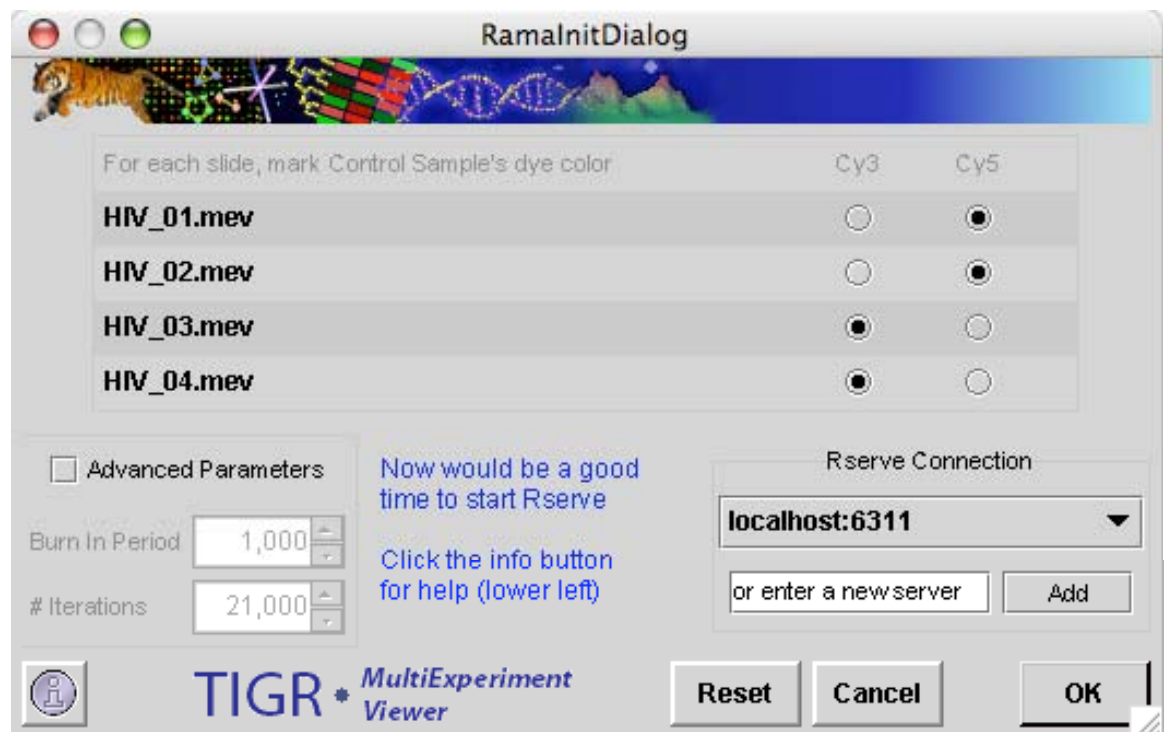


### 1.1. rama: Robust Analysis of MicroArrays (Gottardo *et al.* 2005)

Robust estimation of cDNA microarray intensities with replicates. The package uses a Bayesian hierarchical model for the robust estimation. Outliers are modeled explicitly using a t-distribution, and the model also addresses classical issues such as design effects, normalization, transformation, and nonconstant variance.

The initialization dialog shown below (11.26.1) allows the user to denote the dye labeling scheme used in the experiment.



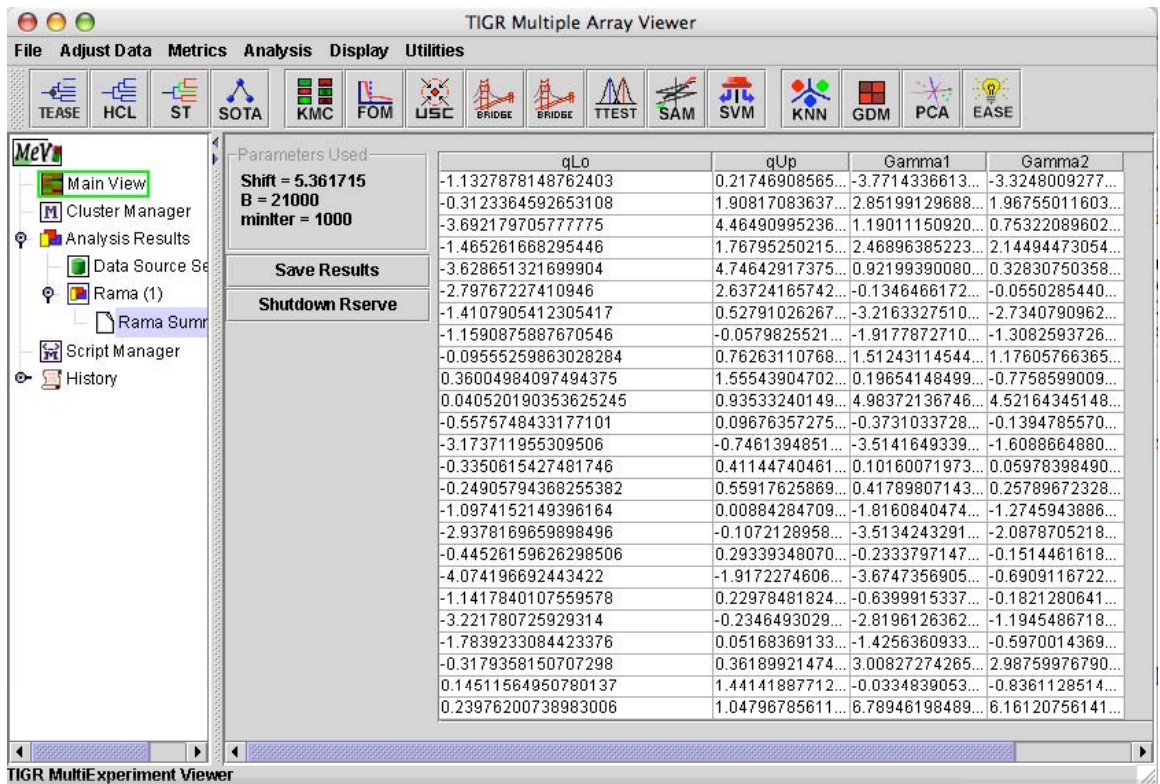
11.26.1. Rama Initialization Dialog

#### 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.

#### Rama Results

Sample output from this module is shown below (11.26.2). Rama estimates intensities based on the data input. The new set of intensities replaces the loaded dataset and is available for further analysis. A table of the results is also made available.



11.26.2. Rama Results: Table of results.