

## Dataset



## Meta-Analysis



## Filtering

**runMetaAnalysis(metaObject)**  
Run the meta analysis pipeline

**filterGenes(metaObject, ...)**  
Filter the genes returned by analysis.

## Validation

**summarizeFilterResults(metaObject, FilterLabel)**  
Display key information returned by the filter.

**calculateScore(filterObject, datasetObject)**  
For each sample, calculate its similarity to the filter results.

## Visualization

**forestPlot(metaObject, geneName)**  
Gene expression across studies.

**violinPlot(filterObject, datasetObject)**  
Compare groups in a study.

**rocPlot(filterObject, datasetObject)**  
Classification accuracy in a study.

## Search

**forwardSearch(metaObject, filterObject)**  
Identify most important genes by adding one at a time.

**backwardSearch(metaObject, filterObject)**  
Identify most important genes by removing one at a time.

## Helper Functions

**checkDataObject(object, objectType, objectStage)**  
Validate data object format.

**getMostRecentFilter(metaObject)**  
Get the name of the most recent filter.

**calculateROC(labels, predictions)**  
Calculate ROC statistics.