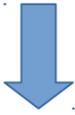


Dataset



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.