

## MAGEMLImportViewer Documentation

**Module name:** MAGEMLImportViewer  
**Description:** A visualizer to import data in MAGE-ML format into GenePattern  
**Author:** Joshua Gould, [gp-help@broad.mit.edu](mailto:gp-help@broad.mit.edu)

**Summary:** The MAGEMLImportViewer imports data in MAGE-ML format into GenePattern. MAGE-ML is a standard for the representation of microarray expression data. See <http://www.mged.org/Workgroups/MAGE/mage-ml.html> for more information about MAGE. This module takes a zip file containing the MAGE-ML files as input. Files containing MAGE data can be downloaded from ArrayExpress (<http://www.ebi.ac.uk/arrayexpress/>).

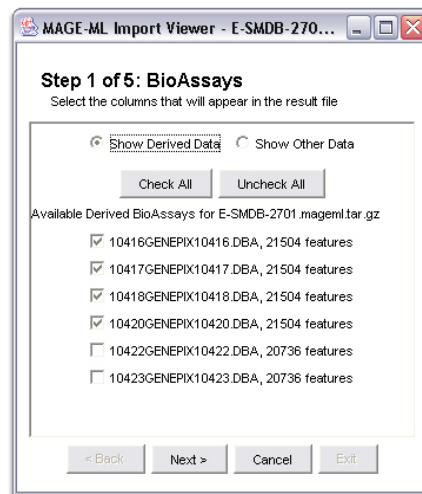
Although this module will create a gct file with any quantitation type you select, there are typical quantitation types for cDNA and Affymetrix microarrays which you will most likely want to use. Common quantitation types for two-color data have names such as cy5/cy3 ratio, Ratio, Log2Ratio, and LOG\_RAT2N\_MEDIAN. If none of these quantitation types is listed for your data, you should look for a quantitation type that contains the text 'ratio'. In some cases, a quantitation type for the ratio is not included, and you will need to use external software to calculate it. For Affymetrix data, common quantitation types are Avg Diff, RMA normalized value, and Signal.

### Usage/Example:

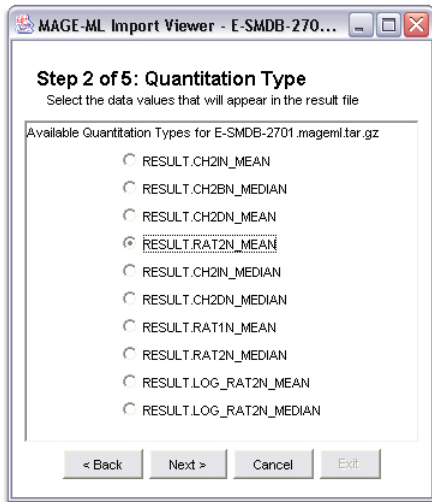
Once the data file is specified and parsed you will see a series of screens that allow you to choose how your MAGE-ML file will be handled. The details of these screens are outlined below.

#### Step 1 - BioAssays:

This screen allows you to select the BioAssays to use in the output file. We distinguish between derived data, which includes expression values and other data, which includes raw probe intensity values. Check the desired BioAssays and click Next.



# GenePattern

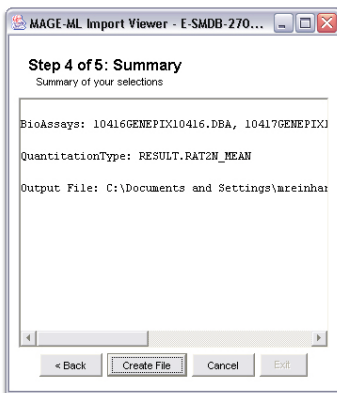
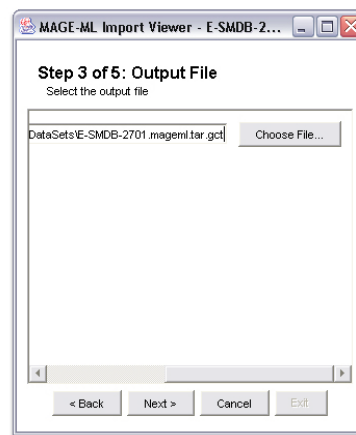


## Step 2 - Quantitation Type:

This window lets you select the data values that will appear in the result file. Select the desired quantitation type and click Next.

## Step 3 - Output File:

Here you choose the path and filename of the output file in .gct format. Use the default filename or specify your own in the text box and click Next.

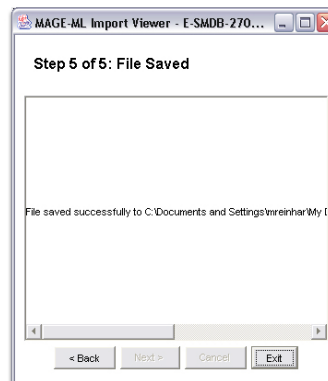


## Step 4 - Summary:

Shows a summary of your selections. Click Back if you would like to change any of the values or click Create File to continue.

## Step 5 - File Saved:

This window indicates that you have successfully imported your MAGE-ML file. Click Exit to close the viewer module.



# GenePattern

## Parameters:

<b>Name</b>	<b>Description</b>
input.filename	The archive file containing the MAGE-ML files - .tar, .tgz, .tar.gz, .zip, .gz

## Platform dependencies:

<b>Task type:</b>	Visualizer
<b>CPU type:</b>	any
<b>OS:</b>	any
<b>Java JVM level:</b>	1.4
<b>Language:</b>	Java