

caArrayImportViewer Documentation

Module name: caArrayImportViewer

Description: Exports experiment data from the caArray database and writes it to a

GenePattern gct file

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Summary: The caArrayImportViewer exports experiment data from the caArray database and writes it to a GenePattern gct file.

An experiment in the caArray database generally includes physical, measured, and derived bioassays. The caArrayImportViewer exports only derived bioassays; physical and measured bioassays are not currently used by existing GenePattern modules. Each derived bioassay has multiple data columns (quantitation types) associated with it; for example, signal intensity, absent/present/marginal call, and so on.

In the caArrayImportViewer, you select an experiment, one or more derived bioassays, and a quantitation type. The caArrayImportViewer generates a gct file that contains a column for each bioassay, a row for each feature (gene), and the selected data value (quantitation type) for each feature in each bioassay.

Quantitation Types:

The caArrayImportViewer can create gct files for any quantitation type. However, when you are creating gct files for use with GenePattern, you generally want to use the following quantitation types for cDNA and Affymetrix microarrays:

- For two-color data, common quantitation types have names such as cy5/cy3 ratio, Ratio, Log2Ratio, and LOG_RAT2N_MEDIAN. If your data does not have these quantitation types, look for another 'ratio' named quantitation type. If your data does not include a quantitation type for the ratio, you may need to use external software to calculate it.
- For Affymetrix data, common quantitation types are Avg Diff, RMA normalized value, and Signal.

Usage/Example:

To begin exporting data from the caArray database, specify the caArray server. Once the server is specified, you will see a series of screens that allow you to choose the data to export and the gct file to create. The details of these screens are outlined below.



Step 1: Log into caArray:

- Accept the default caArray server address or enter the address of an alternative caArray server.
- 2. Enter your caArray user name.
- 3. Enter your caArray password.
- 4. Click Next.

The caArrayImportViewer uses National Cancer Institute Center for Bioinformatics (NCICB) protocols to connect and log into the caArray database without storing your login information. It retrieves a list of your experiments and displays the next screen.

Step 2: Select the experiment that you want to export:

- Click the radio button to the left of the experiment.
- 2. Click Next.

The caArrayImportViewer retrieves all derived bioassays for the selected experiment and displays the next screen.

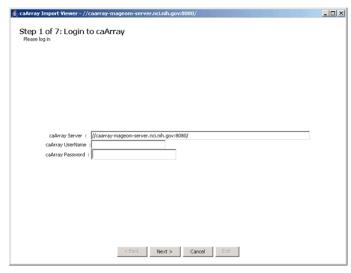
Step 3: Select the derived bioassays that you want to export:

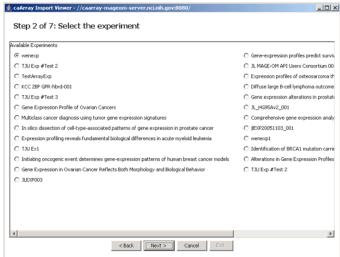
Check the derived bioassays that you want to export.

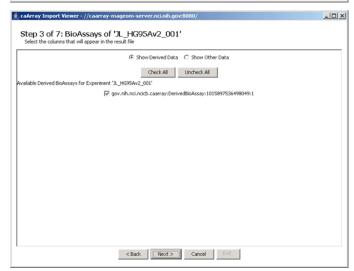
By default, all bioassays are checked. To toggle the check mark for a bioassay, click its check box.

2. Click Next.

The caArrayImportViewer retrieves the quantitation types common to all of the selected bioassays and displays the next screen.









Step 4: Select the data value that you want to export:

- Select the radio button next to the quantitation type that you want to export.
- 2. Click Next.

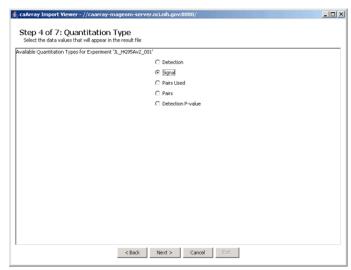
The caArrayImportViewer displays the next screen.

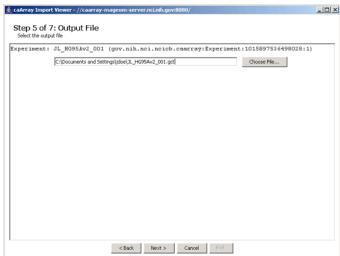
Step 5: Select a name for the Gene Cluster Text (gct) file:

- Accept the default file name supplied by the caArrayImportViewer, or choose an alternative name either by clicking the Choose File button to browse for a file or by entering the full path name of a file. The default file name supplied by the caArrayImportViewer is the experiment name or, if the name is too long, the experiment identifier.
- 2. Click Next.

If the file exists, the caArrayImportViewer displays a message asking if you want to replace it. Click Replace to overwrite the file or Cancel to enter a different file name.

The caArrayImportViewer displays the next screen.





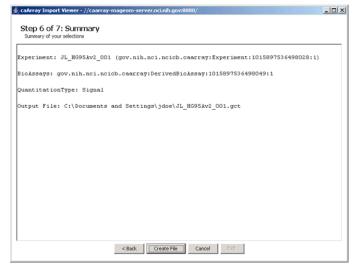


Step 6: Confirm the information that you have provided. If it is correct, click Create File to continue.

The caArrayImportViewer creates the gct file, which may take a few minutes. The file will contain a column for each bioassay, a row for each feature (gene), and the data value of the specified quantitation type for each feature in each bioassay.

After writing the file, the caArrayImportViewer displays a confirmation message on the final screen.

Step 7: Click Exit to exit from the caArrayImportViewer.





Parameters:

Name Description

caArray server Address of the caArray server

Platform dependencies:

Task type: Visualizer

CPU type: any

OS: any

Java JVM level: 1.4

Language: Java