

Tutorial

The GenePattern Tutorial introduces you to GenePattern by providing step-by-step instructions for analyzing gene expression. It takes approximately 40 minutes to complete.

All of the information you need to successfully complete this tutorial is contained in the tutorial. For users who like additional discussion along the way, the tutorial includes pointers to more information in other GenePattern guides. Feel free to follow these links or to ignore them, depending on your learning style.

Introduction

Prerequisites

To follow the hands-on instructions in this tutorial, you must have access to the following:

- A GenePattern server, such as the public GenePattern server available at <http://genepattern.broadinstitute.org/gp/>.
- The server must have the following GenePattern analysis modules installed: `ComparativeMarkerSelection`, `ComparativeMarkerSelectionViewer`, `ExtractComparativeMarkerSelection`, and `HeatMapView`.
- The following example data files: `all_aml_train.res`, `all_aml_train.cls`, `all_aml_test.res`, and `all_aml_test.cls`.

Scientific Scenario

The gene expression dataset used in the tutorial is from Golub and Slonim et al. (1999), which used clustering and prediction algorithms to find genes that distinguish between two subtypes of leukemia, ALL and AML. The dataset consists of 38 bone marrow samples (27 ALL, 11 AML) obtained from acute leukemia patients.

For the purposes of this tutorial, your goal is identify **marker genes** for the two subtypes of leukemia:

1. You use the `ComparativeMarkerSelection` (version 5) analysis to find the genes in the dataset file that are most closely correlated with the two subtypes of leukemia.
2. You use the `ComparativeMarkerSelectionViewer` (version 4) to examine the results of that analysis.
3. You use the `ExtractComparativeResults` (version 3) analysis to create a new dataset that contains the marker genes that you have identified.
4. You use the `HeatMapView` (version 8) to examine the expression levels of the marker genes and to confirm that the marker genes are clearly differentially expressed in the two subtypes of leukemia.

Note: If you are using a different version of any analysis, follow the instructions as closely as possible, but be aware that your results might not match those shown in the tutorial.

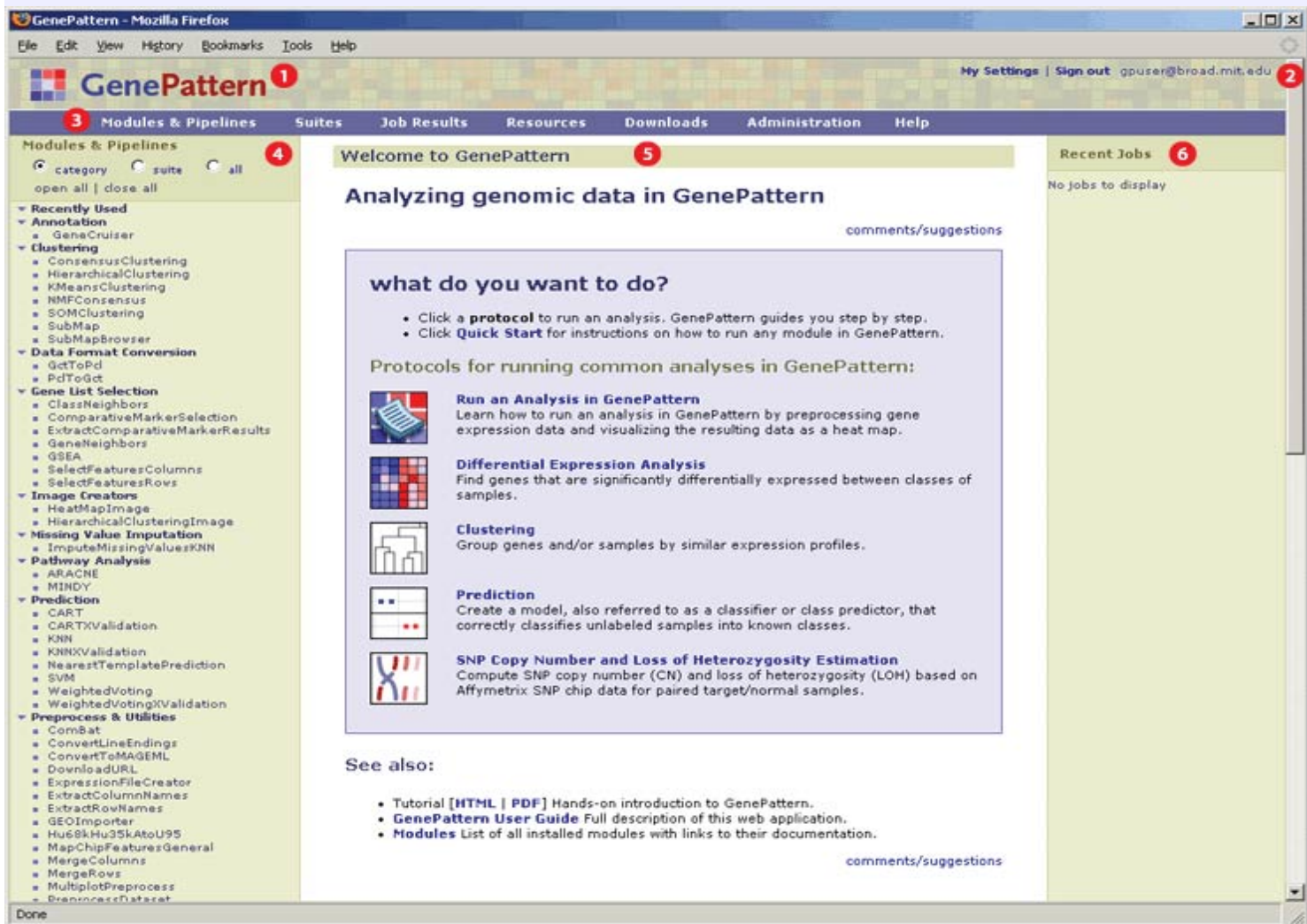
Starting GenePattern

To start GenePattern:

1. Open a web browser, such as Mozilla Firefox, Internet Explorer, or Safari.
2. Enter the URL of the GenePattern server that you want to use. For example, to use the public GenePattern server hosted by the Broad Institute, enter <http://genepattern.broadinstitute.org/gp/>.
The login page appears.
3. Enter your user name and password. If you do not have a GenePattern account, select *Click to register*.
Whether a GenePattern server requires passwords depends on how it is configured. The public GenePattern server requires passwords. By default, a local GenePattern server does not.
4. Click *Sign In*. The GenePattern home page appears.

Note: The pictures in the tutorial show GenePattern running in a Firefox web browser on a Windows PC. If you are using a different web browser or a

different operating system, your screen may look slightly different.



- 1 Click the GenePattern icon to return to this home page at any time.
- 2 The upper right corner shows your user name.
- 3 The navigation bar provides access to other pages.
- 4 The Modules & Pipelines panel lists the analyses that you can run. Click the *all* radio button to list them alphabetically.
- 5 The center pane is the main display pane, which GenePattern uses to display information and to prompt you for input.
- 6 The Recent Jobs panel lists the most recent analyses that you have run and their results files. When you start GenePattern for the first time, this panel is empty.

For more information: see Exploring the User Interface in the *GenePattern User Guide*.

Running Analyses

Now that you have started GenePattern, you are ready to analyze your data. In this section, you learn how to:

- Run the ComparativeMarkerSelection analysis to find marker genes -- the genes in the dataset that are most closely correlated with the two phenotypes (ALL and AML) in the dataset.
- Run the ComparativeMarkerSelectionViewer to examine the ComparativeMarkerSelection analysis results.
- Run the ExtractComparativeResults analysis to create a smaller dataset that contains only the marker genes.
- Run the HeatMapView to examine the expression levels of the marker genes.

Running ComparativeMarkerSelection

Run the ComparativeMarkerSelection analysis to find the genes in the dataset that are most closely correlated with the two phenotypes (ALL and AML) in the dataset. To run the ComparativeMarkerSelection analysis:

1. In the Modules & Pipelines panel, under Gene List Selection, select the ComparativeMarkerSelection analysis. GenePattern displays the ComparativeMarkerSelection parameters.

Show parameter descriptions

ComparativeMarkerSelection version 5

* required field Run Reset [properties](#) | [export](#) | [help](#)

input file* Browse...



Specify URL Upload File



The input file - .res, .gct, .odf type=Dataset

cls file* Browse...


Specify URL Upload File



The class file - .cls


2. For information about the module and its parameters, click *help*.
3. For the *input file* parameter, select all_aml_train.res (ftp://ftp.broadinstitute.org/pub/genepattern/datasets/all_aml/all_aml_train.res).
 - o To use a downloaded copy of the file, click the *Browse* button and select the local file. Leave the *Upload File* radio button selected indicate that you are selecting a file from the file system.
 - o To use the file from the FTP site, select the *Specify URL* radio button and enter the URL of the file.
4. For the *cls filename* parameter, select all_aml_train.cls (ftp://ftp.broadinstitute.org/pub/genepattern/datasets/all_aml/all_aml_train.cls).
5. Click *Run* to start the analysis. GenePattern sends the analysis job to the server and displays the Job Status page. After a minute or two, the status icon changes from running  to complete .


To see options click  icon. For Input Parameters click  icon.



Show Execution Logs

11938.ComparativeMarkerSelection 

 [Edit Sharing...](#)  [Show Input Parameters](#) 

 **input.file:** all_aml_train.res

 **cls.file:** all_aml_train.cls

 **all_aml_train.comp.marker.odf** (1.9 MB)  (Last modified: Tue Jun 02 15:51:56 EDT 2009)

These job results are scheduled to be purged from the server on 6/16/09 4:20 pm

[Return to Modules & Pipelines Start](#)

Analysis results are stored on the GenePattern server. The text shown in red tells you when the analysis results will be deleted. To save your analysis results, copy the files from the GenePattern server to your own directories, as described later in this tutorial.

6. Click *Return to Modules & Pipelines Start* to return to the home page.


Reviewing Result Files

When you return to the GenePattern home page, the Recent Jobs pane shows the analysis job that you ran and the associated analysis results files:

Recent Jobs

 **ComparativeMarkerSelection** 

(11938) Jun 02 03:52:00 PM

all_aml_train.comp.marker.odf 

1. Click the job number. GenePattern redisplay the status page. On the Job Status page, click *Return to Modules & Pipelines Start* to return to the home page.
2. Click the icon next to the analysis job to display commands that you use to work with the job:

Download	Downloads a zip file containing all analysis results files for this job.
Reload	Displays the analysis and its parameters, with the parameters set to the values used for this analysis job.
Delete	Deletes the analysis job and its analysis results files from the GenePattern server.
Info	Displays the parameter values and the analysis results files for this job.
View Java Code	Displays the command line that you would use to run this job in the Java, MATLAB, or R programming environments.
View MATLAB Code	These commands are useful for programmers who want to access GenePattern from one of these programming environments or from their own applications.
View R Code	

3. Click the icon next to an analysis results file to display commands that you use to work with the file:

Delete	Deletes the file from the GenePattern server.
Save	Downloads the file from the GenePattern server.
Create Pipeline	Creates a GenePattern pipeline that reproduces this analysis results file. Pipelines are discussed later in this tutorial.

List of analyses Lists analyses that commonly use this type of file as an input parameter.
 Select an analysis to display its parameters with this results file specified as the first input parameter.

4. Click the analysis results file, **all_aml_train_comp.marker.odf**, to display it in a text viewer. The amount of information it contains makes the file difficult to understand. This file, like most analysis results file, is not intended to be viewed as a text file, but rather intended to be used as input to subsequent analyses.

5. Click the **Back** button in your web browser to return to the home page.

Running the ComparativeMarkerSelectionViewer

After running the ComparativeMarkerSelection analysis, run the ComparativeMarkerSelectionViewer to examine the analysis results. To run the ComparativeMarkerSelectionViewer:

1. In the Recent Jobs pane, click the icon next to your **all_aml_train_comp.marker.odf** results file.
2. Select **ComparativeMarkerSelectionViewer**. GenePattern displays the ComparativeMarkerSelectionViewer parameters. The **comparative marker selection filename** parameter is automatically set to the **all_aml_train_comp.marker.odf** results file.

3. For the **dataset filename** parameter, click **Browse** and select the **all_aml_train.res** file.
4. Click **Run**. GenePattern displays the Job Status page.

Unlike most analyses, viewers run on your desktop PC rather than on the GenePattern server. The first time you run a viewer on your desktop, the following security message may appear.


Warning - Security

The application's digital signature cannot be verified.
Do you want to run the application?

Name: ComparativeMarkerSelectionViewer
Publisher: GenePattern
From: http://genepattern.broad.mit.edu

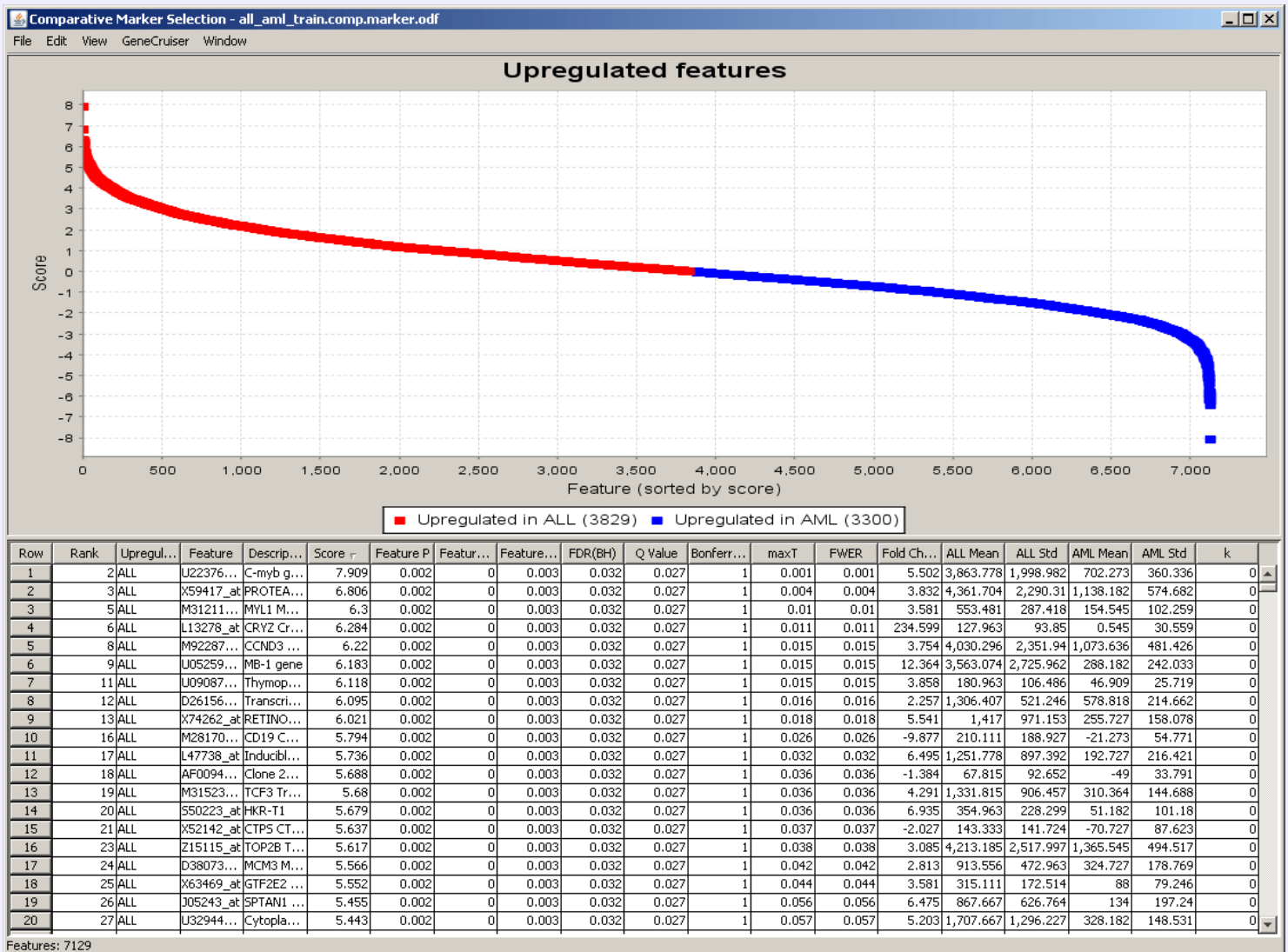
Always trust content from this publisher.

Run **Cancel**

 The digital signature cannot be verified by a trusted source. Only run if you trust the origin of the application. [More Information...](#)

5. If the security message appears, click *Run* to continue.

The ComparativeMarkerSelectionViewer appears:



Tip: To change the width of a column, click and drag the edge of the column heading.

6. In the ComparativeMarkerSelectionViewer:

- o The **Score** column shows the value of the metric used to correlate gene expression and phenotype. A high score indicates correlation with the first phenotype (upregulated in ALL) and a low score indicates correlation with the second phenotype (upregulated in AML).

- o The middle columns, FDR through FWER, provide different ways to measure the significance of the score. The lower the value the more significant the result. For example, you might choose to measure significance using the false discovery rate (FDR) and set a significance cutoff of $FDR < .05$. Using this measure, you would focus on genes with the lowest and highest scores, where the measure of significance for the score was an $FDR < .05$.
7. To close the ComparativeMarkerSelectionViewer, select **File>Exit**.
 8. In GenePattern, click **Return to Modules & Pipelines Start** to return to the home page.

Running ExtractComparativeResults

Now that you have examined the ComparativeMarkerSelection analysis results, you want to create a new dataset that contains only the most promising marker genes from the results file for further analysis. To run the ExtractComparativeResults analysis:

1. In the Recent Jobs pane, click the icon next to the ComparativeMarkerSelection results file, all_aml_train.comp.marker.odf.
2. Select **ExtractComparativeMarkerResults**. GenePattern displays the ExtractComparativeMarkerResults parameters. The *comparative marker selection filename* parameter is automatically set to the all_aml_train.comp.marker.odf results file.
3. For the *dataset filename* parameter, click **Browse** and select the **all_aml_train.res** file.
4. Enter the following parameter values to extract the top 100 features (genes) in the analysis results file:
 - o For the *field* parameter, select Rank.
 - o For the *max* field, enter 100.

Show parameter descriptions

ExtractComparativeMarkerResults version 3

* required field

[properties](#) | [export](#) | [help](#)

comparative marker selection filename*

Specify URL
 Upload File

The results from ComparativeMarkerSelection - .odf

dataset filename*

Specify URL
 Upload File

The dataset file used to select markers - .gct, .res, Dataset

field

The field to filter features on

min

Select features with field >= min

max

Select features with field <= max

number of neighbors

Number of neighbors to select by score in each direction


base output name*

The base name for the output files


[properties](#) | [export](#) | [help](#)

5. Click **Run**. GenePattern displays the Job Status page. After a few seconds, the status icon changes from running to complete and GenePattern displays the analysis results files.

Show Execution Logs

11957.ExtractComparativeMarkerResults 

 Edit Sharing...

 Show Input Parameters 

 **comparative.marker.selection.filename:** all_aml_train.comp.marker.odf

 **dataset.filename:** all_aml_train.res

 all_aml_train.comp.marker.filt.res (38.0 KB)  (Last modified: Wed Jun 03 09:35:15 EDT 2009)

 all_aml_train.comp.marker.filt.bt (2.0 KB)  (Last modified: Wed Jun 03 09:35:15 EDT 2009)

These job results are scheduled to be purged from the server on 6/17/09 4:20 pm

[Return to Modules & Pipelines Start](#)

6. Leave the Job Status page displayed.

Running HeatMapView

The HeatMapView displays expression values in a color-coded heat map. The largest expression values are displayed in red (hot) and the smallest values are displayed in blue (cool). Intermediate values are displayed in different shades of red and blue. The color-coding provides a quick coherent view of gene expression levels.

To display your new dataset in the HeatMapView:

1. On the Job Status page, click the icon next to the results file from the ExtractComparativeMarkerResults analysis, **all_aml_train.comp.marker.filt.res**.
2. Select **HeatMapView**. GenePattern displays the HeatMapView parameters. The *dataset filename* parameter is automatically set to the **all_aml_train.comp.marker.filt.res** results file.

HeatMapView version 8

* required field [properties](#) | [export](#) | [help](#)

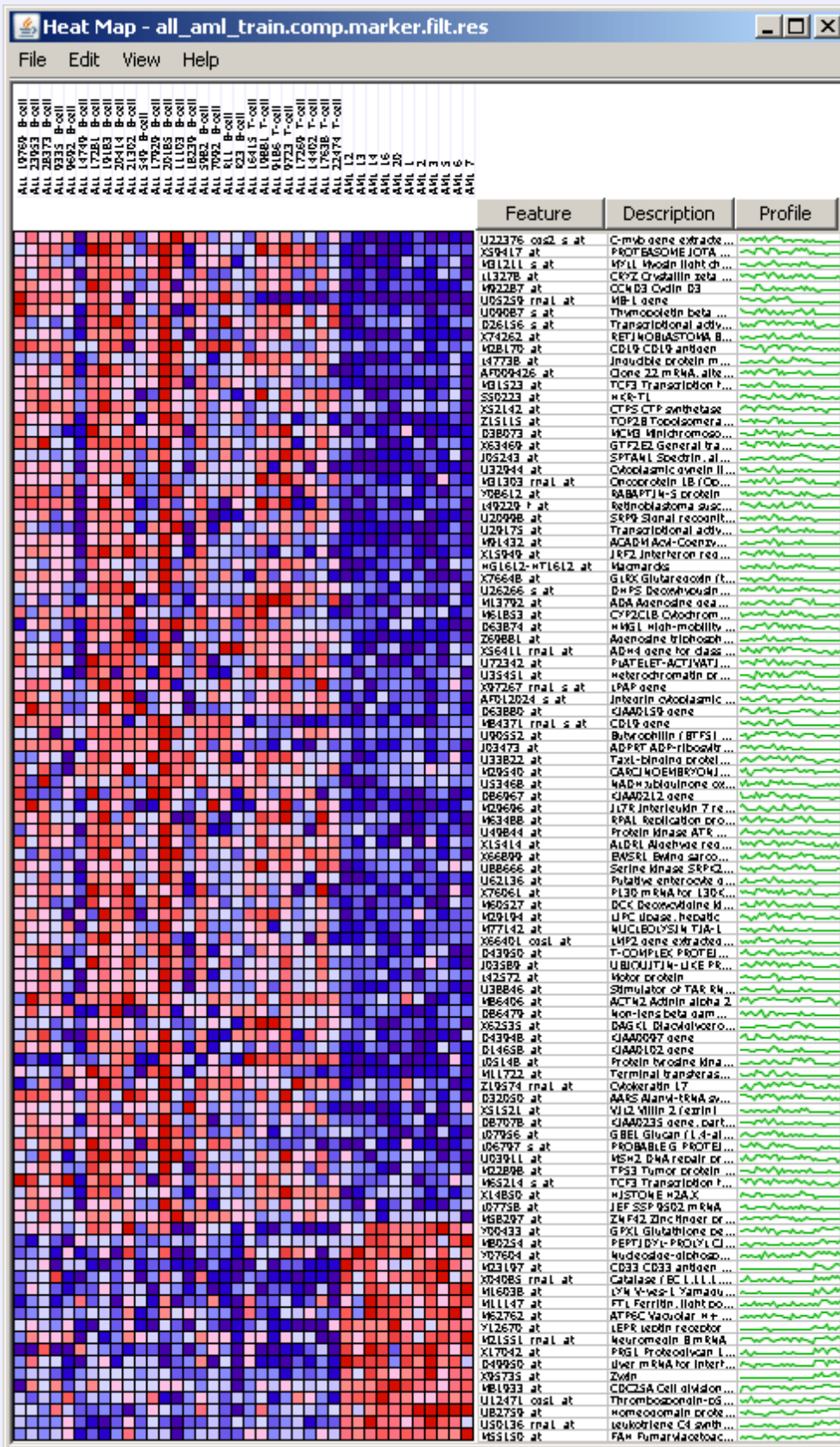
dataset*

Specify URL Upload File

The dataset to display - .gct, .res, odf type=Dataset

[properties](#) | [export](#) | [help](#)

3. Click **Run**. The HeatMapView appears:



4. In the HeatMapView, adjust the grid size for a clearer view of the sample and feature names:

1. Click **View>View Options**.
2. Click-and-drag the **Row Size** or **Column Size** slider to modify the grid size.
3. Close the View Options window.

5. To close the HeatMapView, select **File>Exit**.

6. In GenePattern, click **Return to Modules & Pipelines Start** to return to the home page.

Using Pipelines

As you have seen, GenePattern makes it easy to run individual analyses and to review analysis results. Pipelines take this one step further: they make it easy to

run multiple analyses. You can define a pipeline to run multiple analyses against a single dataset or to run a sequence of analyses, where the output from one analysis becomes the input for a subsequent analysis. Modules run from a pipeline work exactly the same as those run directly from GenePattern.

In this tutorial, you have run two analyses: Comparative Marker Selection and Extract Comparative Marker Results. The analysis results file from the first analysis became the input file for the second analysis. Running these two analyses produced a new dataset that contains the 100 genes in your dataset (`all_aml_train.res`) that are most closely correlated with phenotypes in your class file (`all_aml_train.cls`).

In this section, you will

- Create a pipeline that duplicates your analysis results.
- Edit the pipeline so that it operates on any set of data (`res` and `cls`) files.

For more information: see *Working with Pipelines* in the *GenePattern User Guide*.

Creating a Pipeline Based on Previous Results

You can create a pipeline in one of two ways:

- You can create an empty pipeline and then add to it the analysis modules that you want the pipeline to run.
- You can create a pipeline based on an analysis results file. In this case, GenePattern adds to the pipeline the analysis modules used to create that results file:
 1. It adds the module that created the results file.
 2. It checks the module's input file parameter.
 3. If the input file for the module was the output file of a previous module, the GenePattern adds the previous module and returns to step 2; otherwise, there are no more modules to be added to the pipeline.

To create a pipeline based on the `ExtractComparativeMarkerResults` results file:

1. In the Recent Jobs pane, click the icon next to the results file from the `ExtractComparativeMarkerResults` analysis, `all_aml_train.comp.marker.filt.res`.
2. Select **Create Pipeline**. GenePattern displays the new pipeline.

The new pipeline includes the module that created the results file, `ExtractComparativeMarkerResults`. It also includes the `ComparativeMarkerSelection` analysis because the input file for `ExtractComparativeMarkerResults` was the output file from the `ComparativeMarkerSelection` analysis. The parameters for both analyses are set to the values used to generate the results file. (You will need to scroll to see the entire pipeline.)

Pipeline name*:

Description:

Author: name, affiliation

Privacy:

Version comment:

Documentation:

LSID: urn:lsid:7070.gene patt.node255.broad.mit.edu.gene patternmodules:205:1

1. ComparativeMarkerSelection:

version 5 (latest)

Computes significance values for features using several metrics, including FDR(BH), Q-Value, maxT, FWER, Feature-Specific P-Value, and Bonferroni.

documentation: [ComparativeMarkerSelection.pdf](#)

prompt when run	parameter name	value	description
<input type="checkbox"/>	input file:	<input type="text"/> <input type="button" value="Browse..."/> <GenePatternURL>getFile.jsp?task=<LSID>&file=all_amf_train.res	The input file - .res, .gct, .odf type=Dataset
<input type="checkbox"/>	cls file:	<input type="text"/> <input type="button" value="Browse..."/> <GenePatternURL>getFile.jsp?task=<LSID>&file=all_amf_train.cls	The class file - .cls
<input type="checkbox"/>	confounding variable cls file:	<input type="text"/> <input type="button" value="Browse..."/>	The class file containing the confounding variable.
<input type="checkbox"/>	test direction:	2 Sided	The test to perform
<input type="checkbox"/>	test statistic:	T-Test	The statistic to use
<input type="checkbox"/>	min std:	<input type="text"/>	The minimum standard deviation if test statistic includes min std option
<input type="checkbox"/>	number of permutations:	1000	The number of permutations to perform (use 0 to calculate asymptotic p-values)
<input type="checkbox"/>	complete:	no	Whether to perform all possible permutations
<input type="checkbox"/>	balanced:	no	Whether to perform balanced permutations
<input type="checkbox"/>	random seed:	779948241	The seed of the random number generator used to produce permutations
<input type="checkbox"/>	smooth p values:	yes	Whether to smooth p-values
<input type="checkbox"/>	phenotype test:	one versus all	Tests to perform when cls file has more than two classes (Note: not fully corrected for multiple hypothesis testing)
<input type="checkbox"/>	output filename:	<input.file_basename>.c	The name of the output file

2. ExtractComparativeMarkerResults:

version 3 (latest)

Creates a derived dataset and feature list file from the results of ComparativeMarkerSelection

documentation: [ExtractComparativeMarkerResults.pdf](#)

prompt when run	parameter name	value	description
<input type="checkbox"/>	comparative marker selection filename:	<input type="text"/> <input type="button" value="Browse..."/> or use output from 1. ComparativeMarkerSelection 1st output	The results from ComparativeMarkerSelection - .odf
<input type="checkbox"/>	dataset filename:	<input type="text"/> <input type="button" value="Browse..."/> <GenePatternURL>getFile.jsp?task=<LSID>&file=all_amf_train.res or use output from Choose module	The dataset file used to select markers - .gct, .res, Dataset
<input type="checkbox"/>	field:	Rank	The field to filter features on
<input type="checkbox"/>	min:	<input type="text"/>	Select features with field >= min
<input type="checkbox"/>	max:	100	Select features with field <= max
<input type="checkbox"/>	number of neighbors:	<input type="text"/>	Number of neighbors to select by score in each direction
<input type="checkbox"/>	base output name:	<comparative.marker.sel	The base name for the output files

3. By default, the pipeline name is the job number. Change the pipeline name to MyComparativeMarkerSelection by editing the *Pipeline name* field.

Adding Modules to a Pipeline

The pipeline contains the two analysis modules used to create the analysis results file: Comparative Marker Selection and Extract Comparative Marker Results.

In your original analysis, after creating the analysis results file, you used the Heat Map Viewer to review the results.

To add the Heat Map Viewer module to your pipeline:

1. Scroll to the end of the pipeline definition.
2. Click **Add Another Module** to add a module after the ExtractComparativeMarkerResults analysis. GenePattern prompts you for the module to add:

3. Select **Visualizer** as the category and **HeatMapView** as the module:

GenePattern adds the HeatMapView module to the pipeline:

prompt when run	parameter name	value	description
<input type="checkbox"/>	dataset:	<input type="text"/> Browse...	The dataset to display - .gct, .res, odf type=Dataset
	or use output from <input type="text"/> Choose module		

4. For the *dataset filename* parameter, select the analysis results file from the ExtractComparativeMarkerResults module. To do so: next to *use output from*, choose **ExtractComparativeMarkerResults** as the module and **res** as the output file:

prompt when run	parameter name	value	description
<input type="checkbox"/>	dataset:	<input type="text"/> Browse...	The dataset to display - .gct, .res, odf type=Dataset
	or use output from 2. ExtractComparativeMarkerResults res		

5. Click **Save** to save the pipeline. GenePattern displays a status page.
6. Click **Continue to Modules & Pipelines Start** to return to the home page. GenePattern displays the pipeline and its parameters (if any).

Running the Pipeline




On the home page in the Modules & Pipelines pane, notice that the pipeline names are color-coded; the pipelines you create are displayed in red.

To run the pipeline:




1. Click **Run**. GenePattern displays the Job Status, runs each module, displays the analysis results, and opens the HeatMapView.
2. Close the HeatMapView.
3. In GenePattern, click **Return to Modules & Pipelines Start** to return to the home page.
The Recent Jobs pane shows the pipeline job, which lists each analysis run and its analysis result files.



To review the pipeline results in the HeatMapView:





1. Click the job number to redisplay the Job Status page.



To launch visualizer click  icon. To see options click  icon. For Input Parameters click  icon.







Show Execution Logs



11959.MyComparativeMarkerSelection   Edit Sharing... 



↳ **step 1: ComparativeMarkerSelection [id: 11960]**  Show Input Parameters 

-  **input.file:** [all_aml_train.res](#)
-  **cls.file:** [all_aml_train.cls](#)
-  [all_aml_train.comp.marker.odf](#) (1.9 MB)  (Last modified: Wed Jun 03 10:06:27 EDT 2009)

↳ **step 2: ExtractComparativeMarkerResults [id: 11961]**  Show Input Parameters 

-  **comparative.marker.selection.filename:** [all_aml_train.comp.marker.odf](#)
-  **dataset.filename:** [all_aml_train.res](#)
-  [all_aml_train.comp.marker.filt.res](#) (38.0 KB)  (Last modified: Wed Jun 03 10:06:40 EDT 2009)
-  [all_aml_train.comp.marker.filt.txt](#) (2.0 KB)  (Last modified: Wed Jun 03 10:06:40 EDT 2009)

↳ **step 3: HeatMapView [id: 11962]**  Show Input Parameters 

-  **dataset:** [all_aml_train.comp.marker.filt.res](#)
-  [Open Visualizer](#)

These job results are scheduled to be purged from the server on 6/17/09 4:20 pm

[Return to Modules & Pipelines Start](#)

2. Click the **Open Visualizer** icon. GenePattern opens the HeatMapView.
3. Close the HeatMapView.
4. In GenePattern, click **Return to Modules & Pipelines Start** to return to the home page.

Adding Parameters to a Pipeline


You have created a pipeline that duplicates your original analysis: it runs the Comparative Marker Selection analysis on the `all_aml_train` data (res and cls) files, uses the analysis results as input to the Extract Comparative Marker Results analysis, and then displays the analysis results using the Heat Map Viewer.

You can make the pipeline more generally useful by having it prompt you for the data (res and cls) files to be analyzed, rather than simply analyzing the `all_aml_train` data files.

To edit the pipeline:

1. In the Modules & Pipelines pane, select your pipeline. GenePattern displays the pipeline:

Show parameter descriptions

MyComparativeMarkerSelection version 2 

[Run](#) [Reset](#) [properties](#) | [export](#) | [edit](#) | [help](#)

2. Click **Edit**. GenePattern displays the pipeline definition for editing.

3. The data (res and cls) files to be analyzed are named in the *input file* and *cls file* parameters of the Comparative Marker Selection analysis. Modify the pipeline to have it prompt you for these parameter values:

1. Click on the *Prompt when run* check box next to the *input file* parameter of the Comparative Marker Selection analysis. GenePattern removes the parameter value from the pipeline definition.
2. Click on the *Prompt when run* check box next to the *cls file* parameter of the Comparative Marker Selection analysis. GenePattern removes the parameter value from the pipeline definition.

The screenshot shows the configuration for the '1. ComparativeMarkerSelection' pipeline. It includes a description: 'Computes significance values for features using several metrics, including FDR(BH), Q-value, maxT, FWER, Feature-Specific P-value, and Bonferroni.' and a link to 'ComparativeMarkerSelection.pdf' for documentation. Below this is a table with columns for 'prompt when run', 'parameter name', and 'value'. The 'input file' and 'cls file' parameters have their 'prompt when run' checkboxes checked and their values set to 'set prompt when run display settings...'. The 'confounding variable cls file' parameter has its checkbox unchecked and a 'Browse...' button next to its empty text input field.

prompt when run	parameter name	value
<input checked="" type="checkbox"/>	input file:	set prompt when run display settings...
<input checked="" type="checkbox"/>	cls file:	set prompt when run display settings...
<input type="checkbox"/>	confounding variable cls file:	<input type="text"/> Browse...

3. Optionally, click *set prompt when run display settings* to modify the default text of the prompt.

4. The data (res) files to be analyzed is also named in the *dataset filename* parameter of the Extract Comparative Marker Results analysis. Modify the pipeline to have it prompt you for this parameter value also:

1. Click on the *Prompt when run* check box next to the *dataset filename* parameter of the Extract Comparative Marker Results analysis:

The screenshot shows the configuration for the '2. ExtractComparativeMarkerResults' pipeline. It includes a description: 'Creates a derived dataset and feature list file from the results of ComparativeMarkerSelection' and a link to 'ExtractComparativeMarkerResults.pdf' for documentation. Below this is a table with columns for 'prompt when run', 'parameter name', and 'value'. The 'comparative marker selection filename' parameter has its 'prompt when run' checkbox unchecked and a 'Browse...' button next to its empty text input field. The 'dataset filename' parameter has its 'prompt when run' checkbox checked and its value set to 'set prompt when run display settings...'. Additionally, there is a section for 'or use output from' with a dropdown menu set to '1. ComparativeMarkerSelection' and a text input field containing '1st output'.

prompt when run	parameter name	value
<input type="checkbox"/>	comparative marker selection filename:	<input type="text"/> Browse...
<input checked="" type="checkbox"/>	dataset filename:	set prompt when run display settings...

or use output from

2. Optionally, click *set prompt when run display settings* to modify the default text of the prompt.

5. Scroll to the end of the pipeline definition.

6. Click *Save*. GenePattern displays a message confirming that the pipeline has been saved.

7. Click *Continue to Modules & Pipelines Start* to return to the home page.

Running the Edited Pipeline

When you edit a pipeline and return to the home page, GenePattern displays the pipeline and its parameters:

* required field

Run

Reset

[properties](#) | [export](#) | [edit](#) | [help](#)

input file*

 Browse... Specify URL Upload File

The input file - .res, .gct, .odf type=Dataset

cls file*

 Browse... Specify URL Upload File

The class file - .cls

dataset filename*

 Browse... Specify URL Upload File

The dataset file used to select markers - .gct, .res, Dataset

Run

Reset

[properties](#) | [export](#) | [edit](#) | [help](#)

To run the edited pipeline:

1. For the *input file* parameter, select all_aml_test.res.
2. For the *cls file* parameter, select all_aml_test.cls.
3. For the *dataset filename* parameter, select all_aml_test.res.
4. Click **Run**. The Status page appears and GenePattern runs each module. After a few moments, GenePattern displays the HeatMapView.
5. Close the HeatMapView.
6. In GenePattern, click *Return to Modules & Pipelines Start* to return to the home page.

Saving and Deleting Result Files

As described earlier in the tutorial, analyses are run on the GenePattern server and analysis results files are stored on the server. Server storage is temporary and analysis results files are deleted after they have been on the server for a certain length of time (by default, one week).

To save your analysis results files, you must copy each file from the server to a more permanent location. If you do not need your analysis results, you can delete them at any time.

To save an analysis results file:

1. In the Recent Jobs pane, click the icon next to a results file.
2. Click **Save**.

To delete an analysis results file:

1. In the Recent Jobs pane, click the icon next to a results file.
2. Click **Delete**.

To save or delete a job and all of its analysis results files, click the icon next to the job and click **Download** or **Delete**.

Exiting from GenePattern

To exit from GenePattern, click the *Sign out* link in the top right corner of the title bar and then close the web browser window.

Learning More About GenePattern

Thank you for taking this time to learn about GenePattern!

As you continue to work with GenePattern, please visit <http://genepattern.org>, which provides an overview of the GenePattern analysis modules, as well as links to the GenePattern software and documentation.

We welcome your feedback. If you have suggestions, comments, or questions that are not answered by the documentation, contact the GenePattern help desk ([gp-help \(at\) broadinstitute.org](mailto:gp-help@broadinstitute.org)).