

PAGE User Manual

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1. Introduction

PAGE is a Java application designed to extract and visualize phase-shifted patterns of gene expression data involving dose, time, and biological responses. To use PAGE, users must first load the gene expression data and then run q-Cluster analysis. This user manual serves as a reference on using PAGE in a step-by-step fashion.

2. Software Requirement

The following software must be installed in order to execute PAGE.

- Java 2 Runtime Environment, Standard Edition 1.4.2 or later

3. Getting Started

- Double click on PAGE.bat

4. Load Experiment

PAGE uses tab-delimited text file as input. This input file contains gene expression data at various dose and time points. The following subsections explain the input file format and the step-by-step description of how to load the input file into PAGE for single and multiple experiments, including how to load and save experiment configuration.

4.1 Input File Format Description

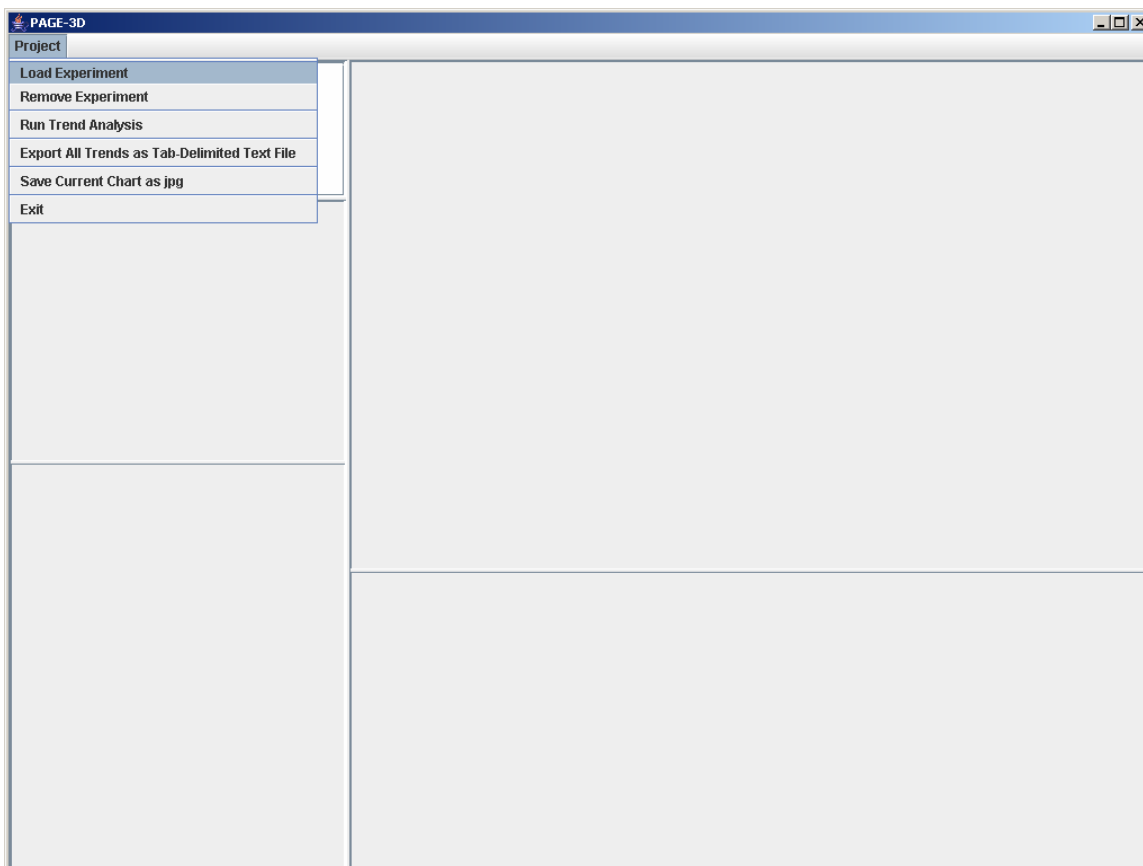
- The input file must be tab-delimited text file.
- The file must not have any empty space between tabs.
- The first row is consisted of header labeling each column as shown in blue.
- The first column contains the unique row identifiers as shown in red.
- The second column contains the gene accession numbers as shown in green.

Probe ID	Gene Accession	Compound1 50mg/kg 48h	Compound1 150mg/kg 48h	Compound1 1500mg/kg 48h
A_43_P001	AA00001	-0.17515	-0.09822	-0.08981
A_43_P002	AA00002	0.05823	-0.03923	-0.12003
A_43_P003	NM_000003	-0.67123	-0.69009	-0.72777

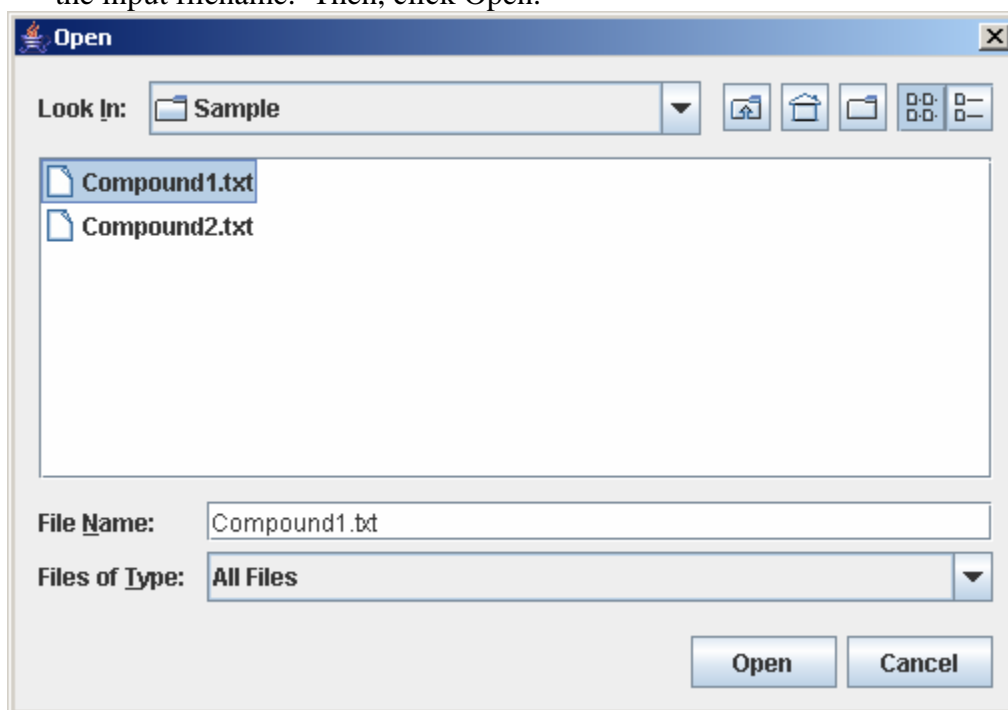
4.2 Load a Single Experiment

To load an experiment from a tab-delimited file:

1. Click on Project and select Load Experiment



1. On the file chooser window, go to the directory containing the input file and enter the input filename. Then, click Open.



2. Enter the number of dose and time points that corresponds to the experiment being loaded. Then, click Submit.

D:\PAGE-3D\Sample\Compound1.txt

Total Dose Points: 3

Total Time Points: 3

Submit Cancel

3. Enter the experiment label in the text field.

Select Array Label for D:\PAGE-3D\Sample\Compound1.txt

Experiment Label:

Row 1	1	2	3
Row 2	4	5	6
Row 3	7	8	9
	Col 1	Col 2	Col 3

OK Cancel Save Load

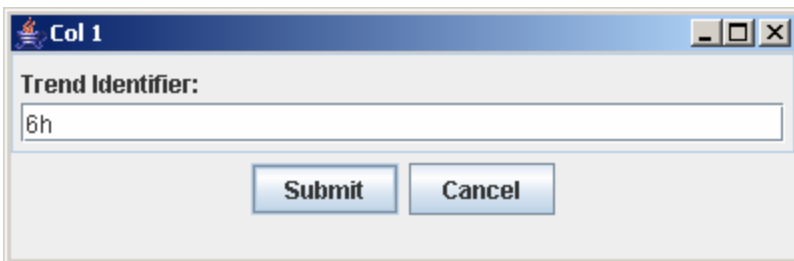
4. Click on the button with “Row #” to label the corresponding row. Enter the trend identifier and click Submit. Repeat this step for each button labeled with “Row #”.

Row 1

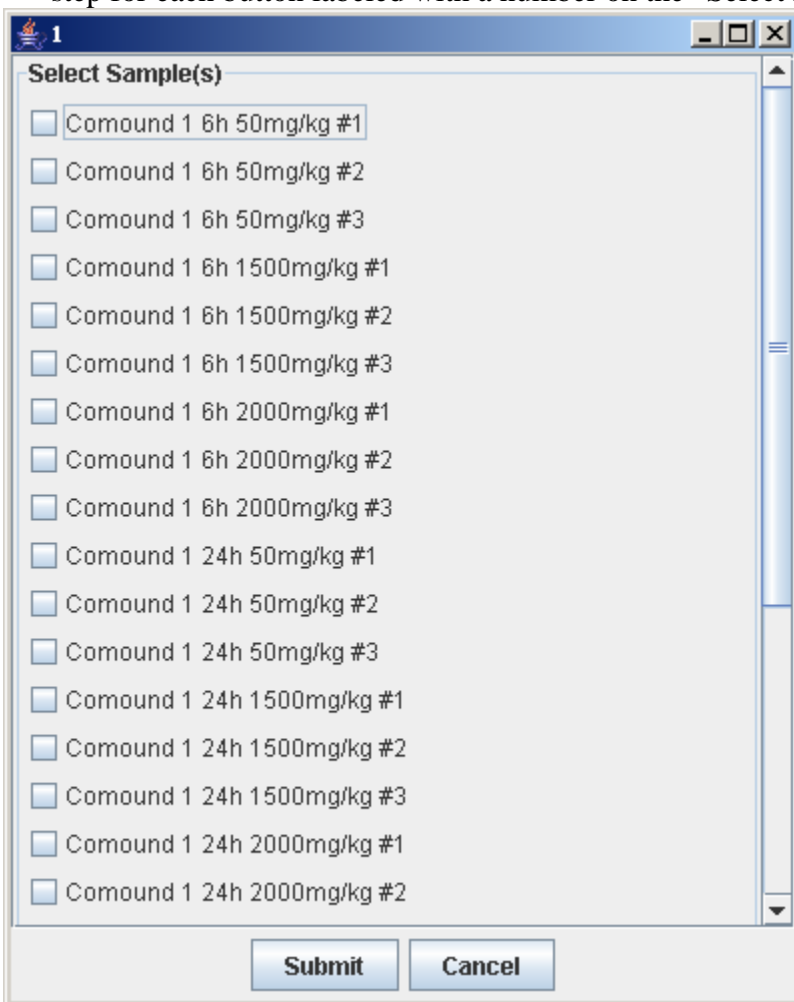
Trend Identifier: 50mg/kg

Submit Cancel

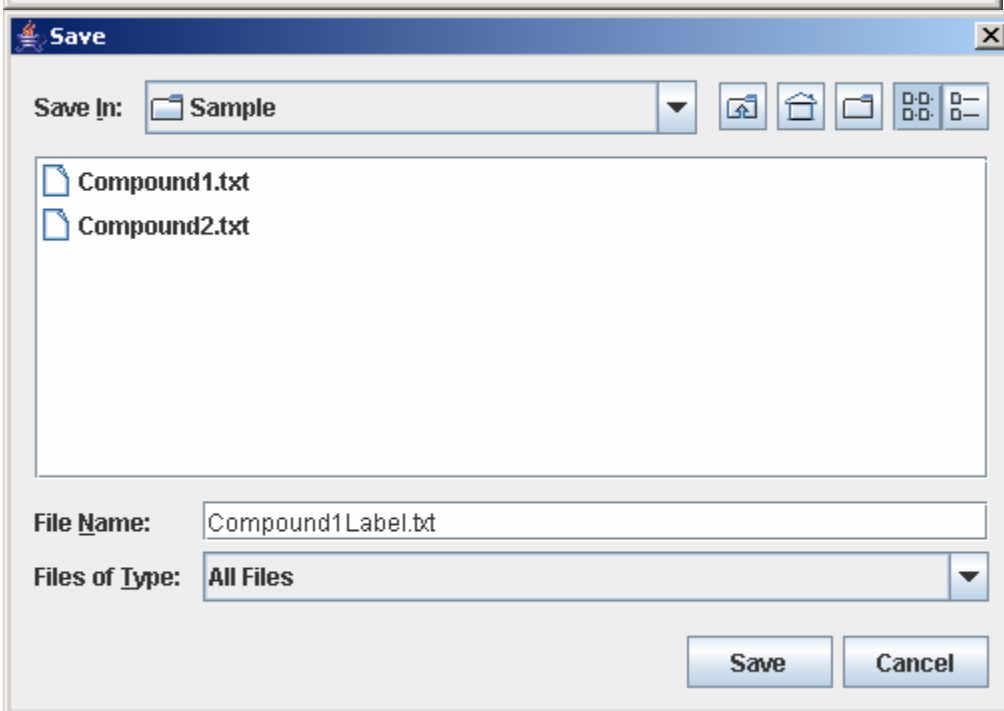
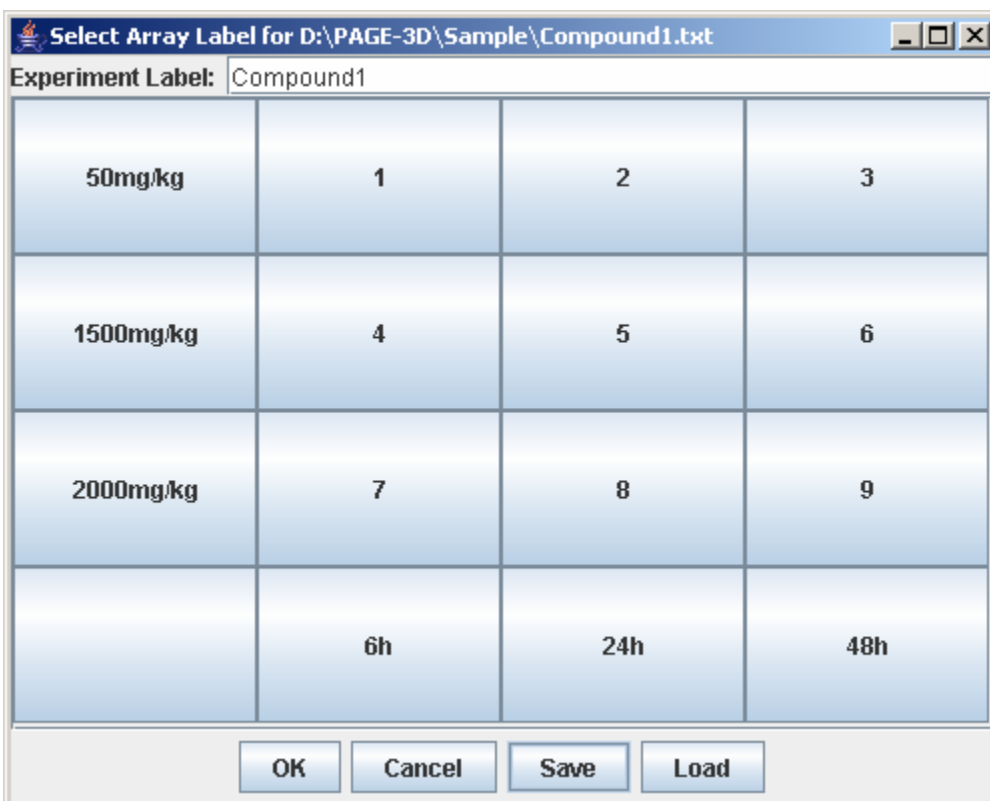
5. Click on the button with “Col #” to label the corresponding column. Enter the trend identifier and click Submit. Repeat this step for each button labeled with “Col #”.



6. Click on the button with a number on the "Select Array Label" panel to select the sample(s) that correspond to the dose and time labels for each row and column. At least one checkbox must be selected. Click Submit when finished. Repeat this step for each button labeled with a number on the "Select Array Label" panel.



7. Click Save to open the file chooser window. Enter the filename and click Save to save the experiment configuration. This step is optional but necessary to avoid repeating the previous steps when the same experiment is being loaded again.



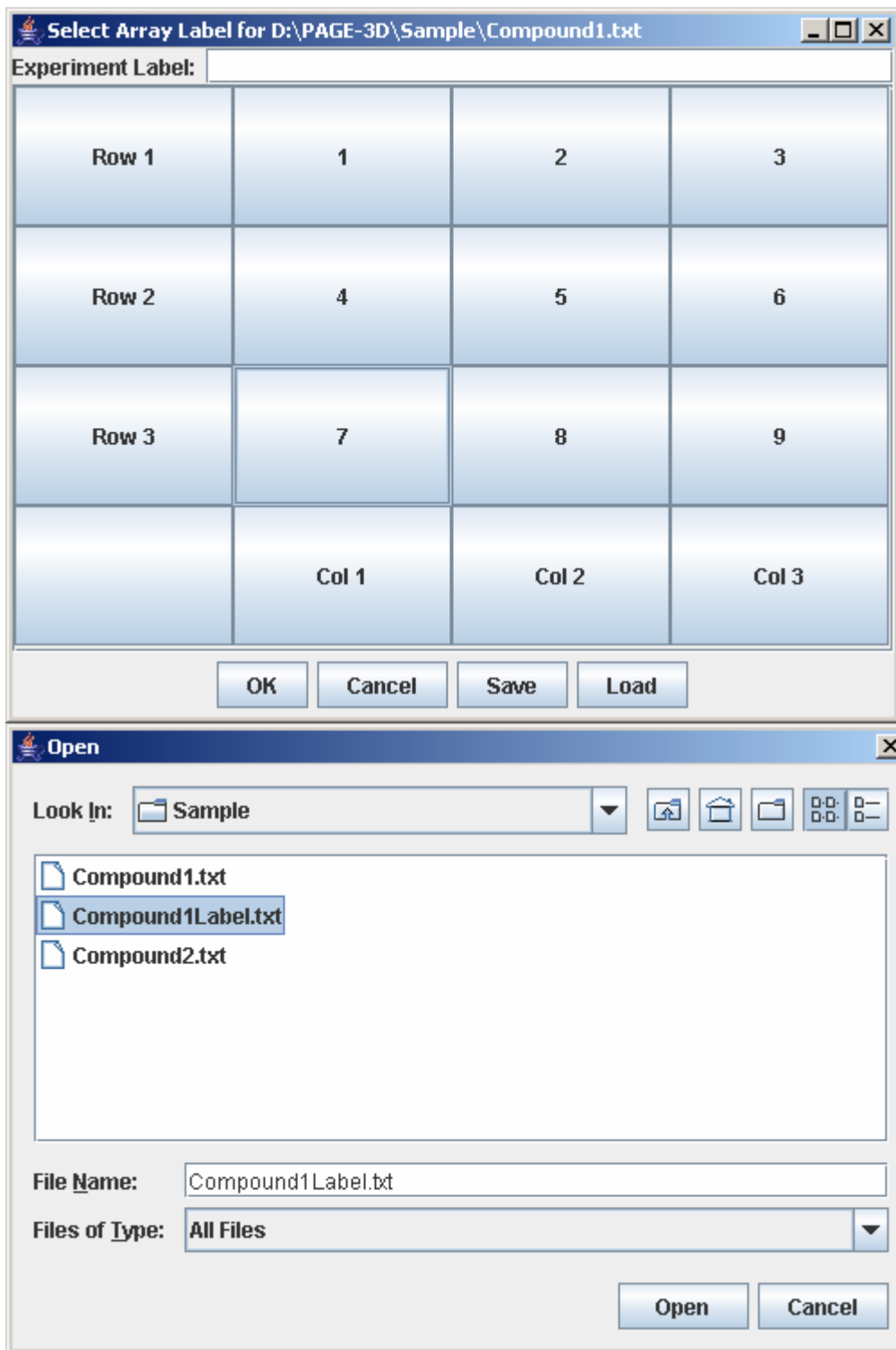
8. Click OK to load the experiment.

4.3 Load Multiple Experiments

- To load multiple experiments onto the same project, repeat steps 1 to 8 in Section 4.2 for each experiment.

4.4 Load Experiment Configuration

To load experiment configuration that have been previously saved, click Load to open the file choose window. Then, select the file containing the experiment configuration and click Open. This step skips steps 4-8 in loading a single experiment.



Select Array Label for D:\PAGE-3D\Sample\Compound1.txt

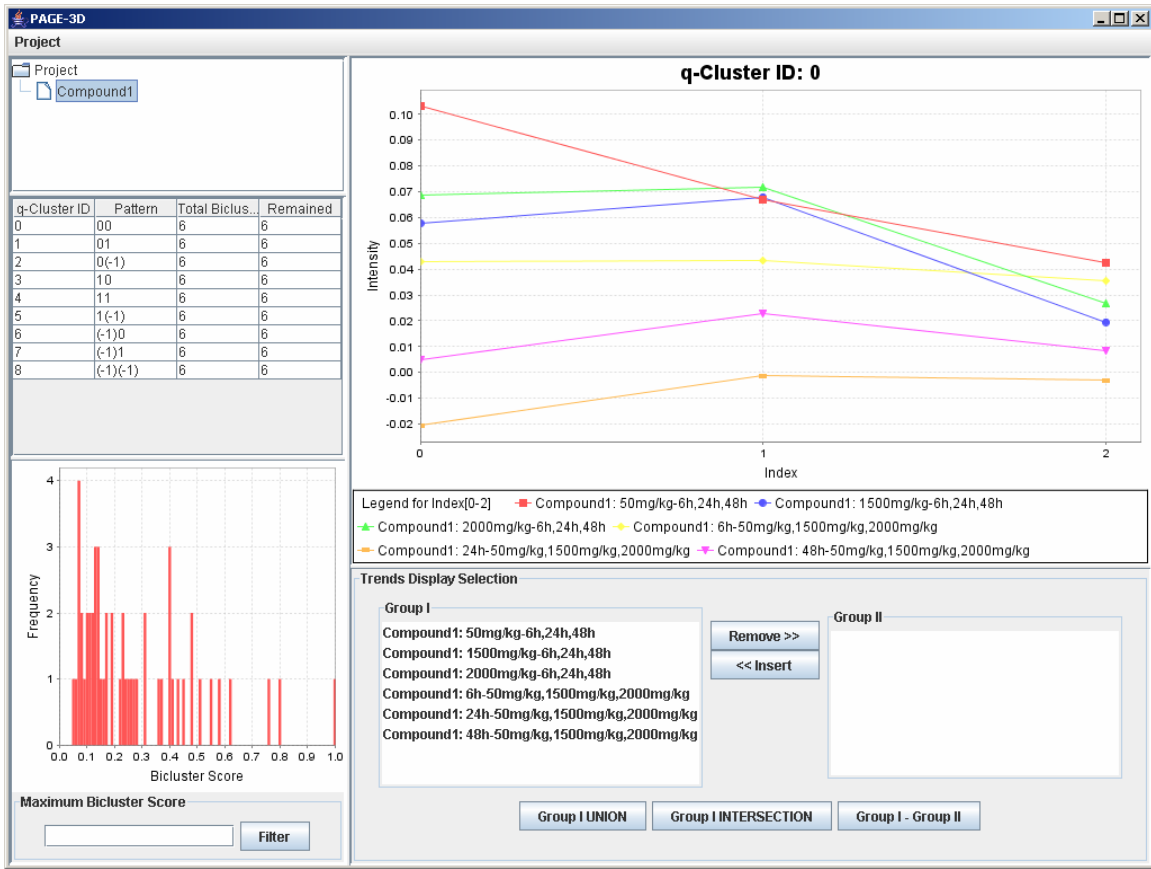
Experiment Label: Compound1

50mg/kg	1	2	3
1500mg/kg	4	5	6
2000mg/kg	7	8	9
	6h	24h	48h

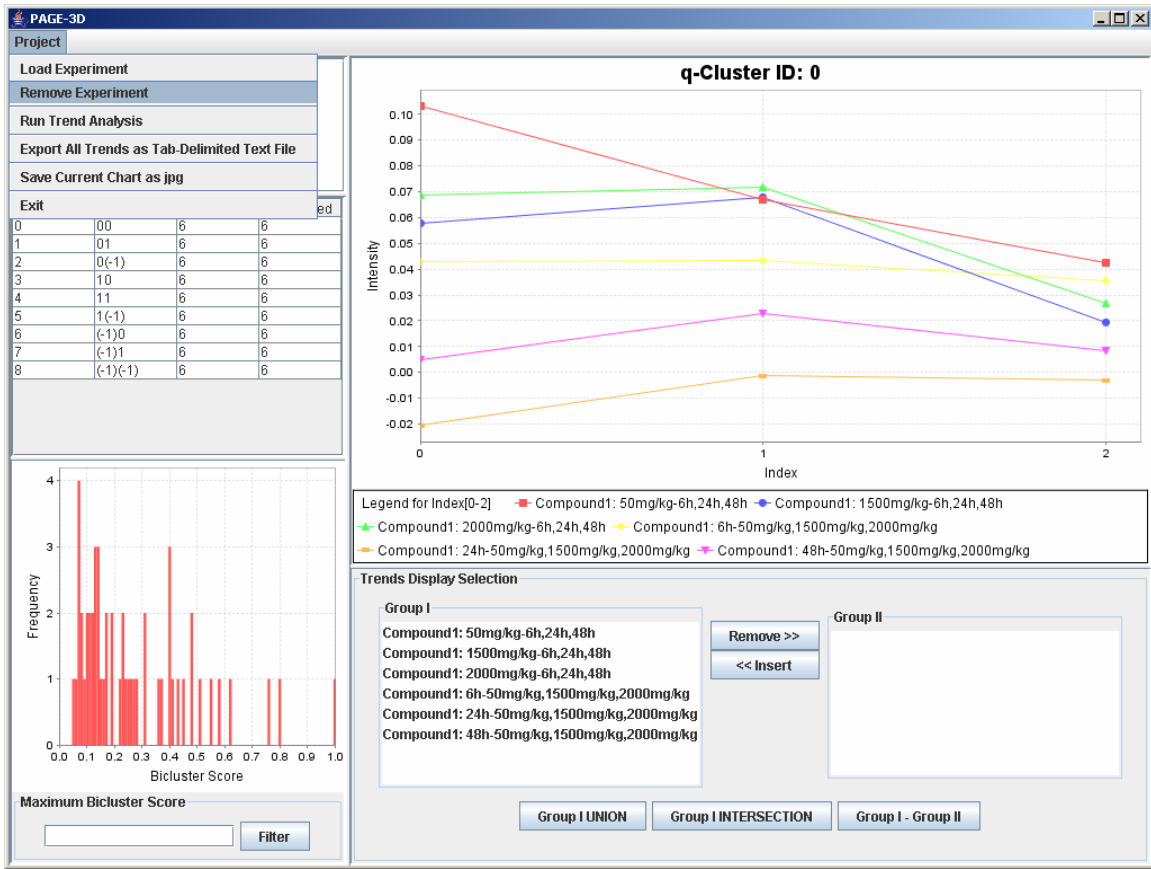
OK Cancel Save Load

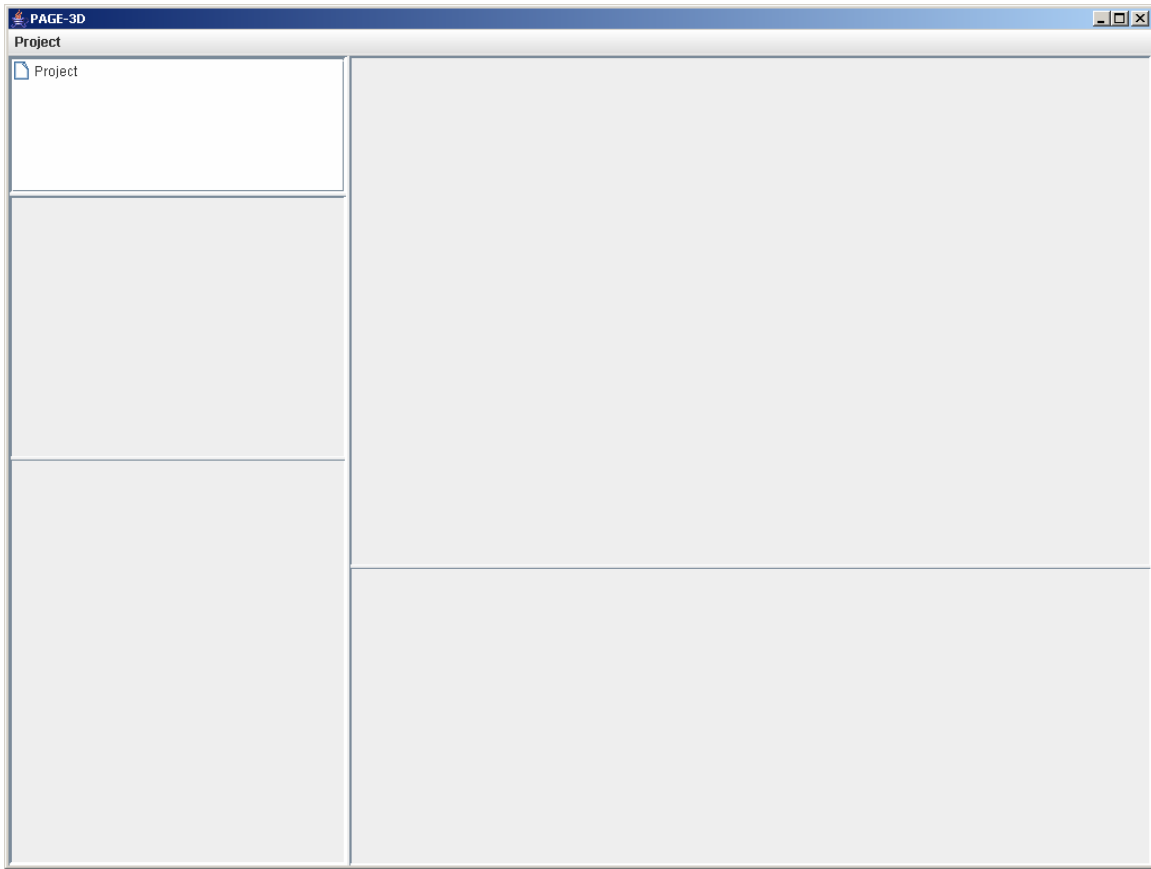
5. Remove Experiment

1. Click on an experiment node from the tree panel.



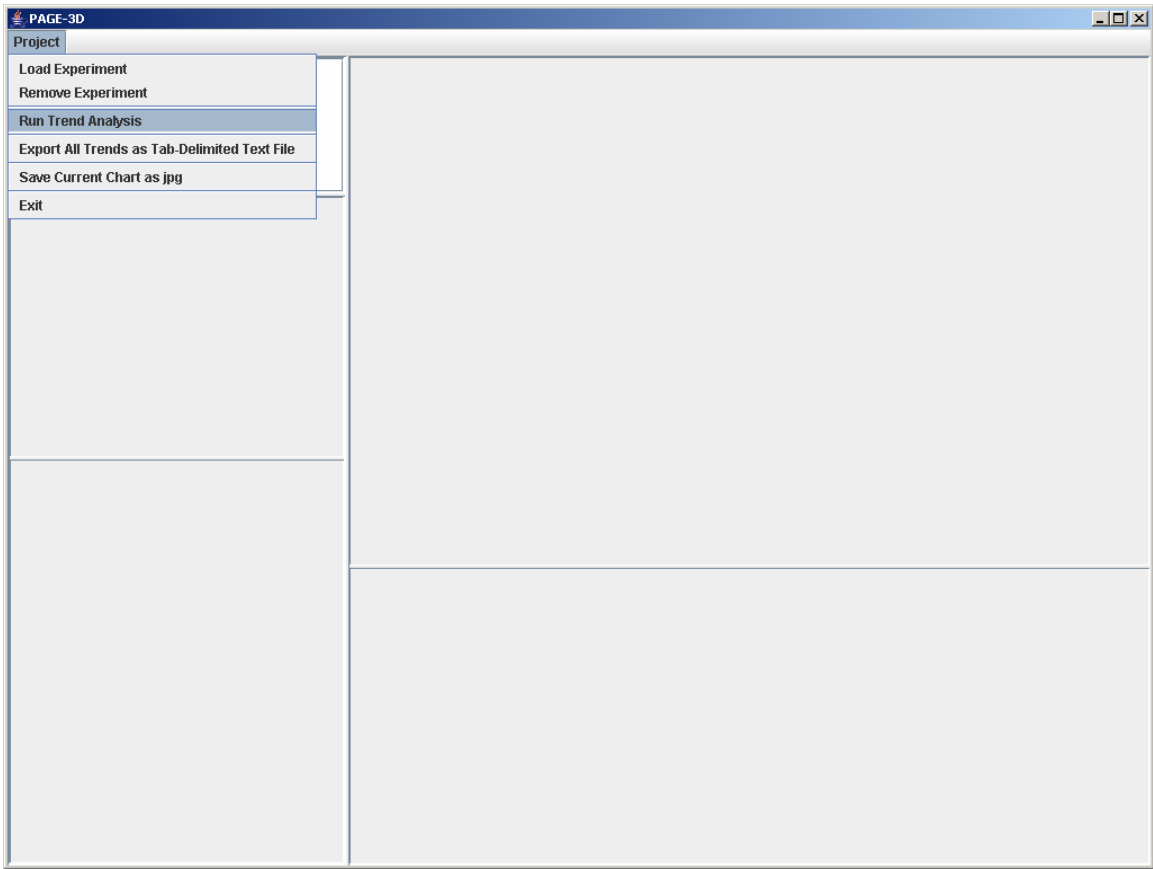
2. Click on Project and select Remove Experiment.



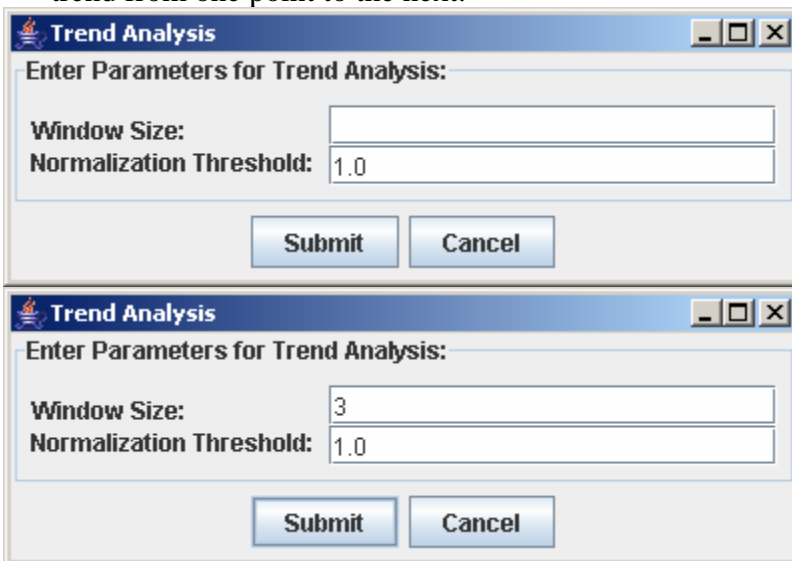


6. Run Trend Analysis

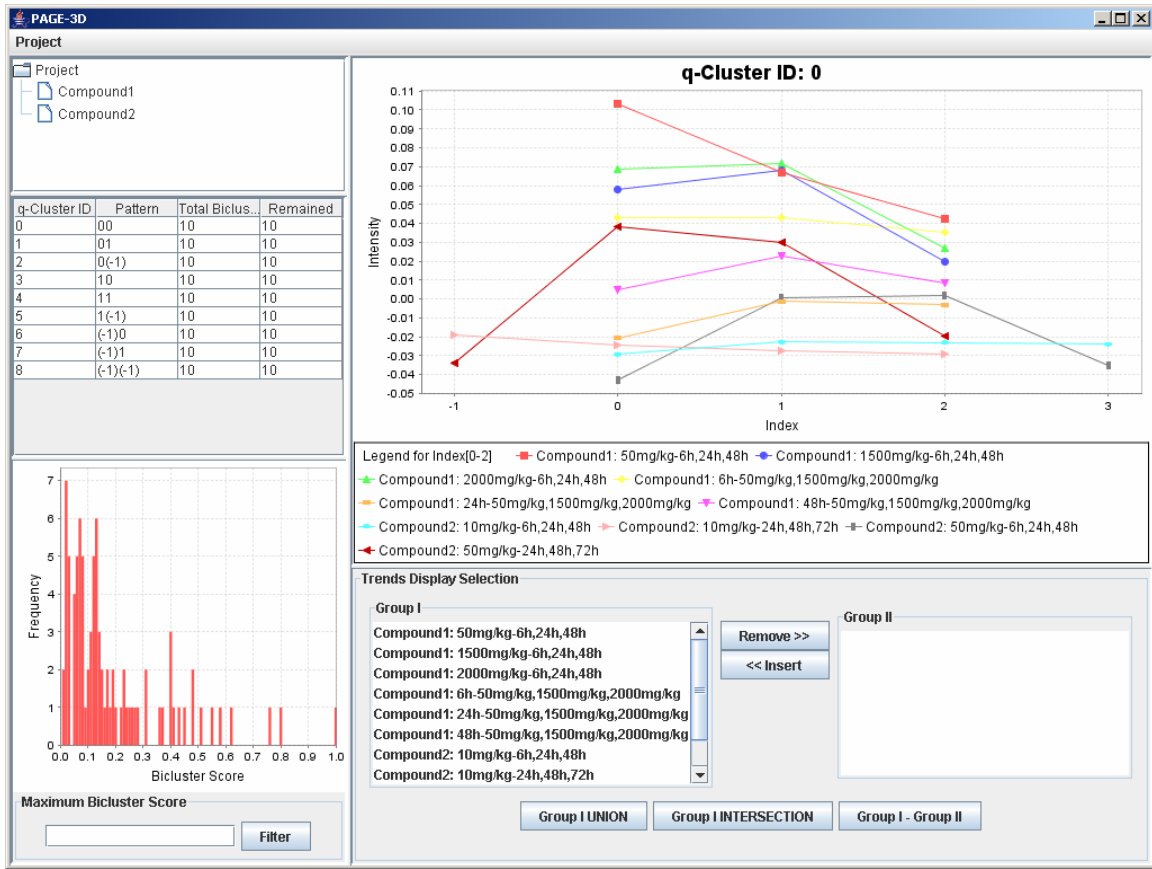
1. Click on File and select Run Trend Analysis



2. Enter the window size and the normalization threshold value. The window size is the number of consecutive points fixed for the trend length. The normalization threshold (default value = 1.0) is the cut-off for defining an upward or downward trend from one point to the next.

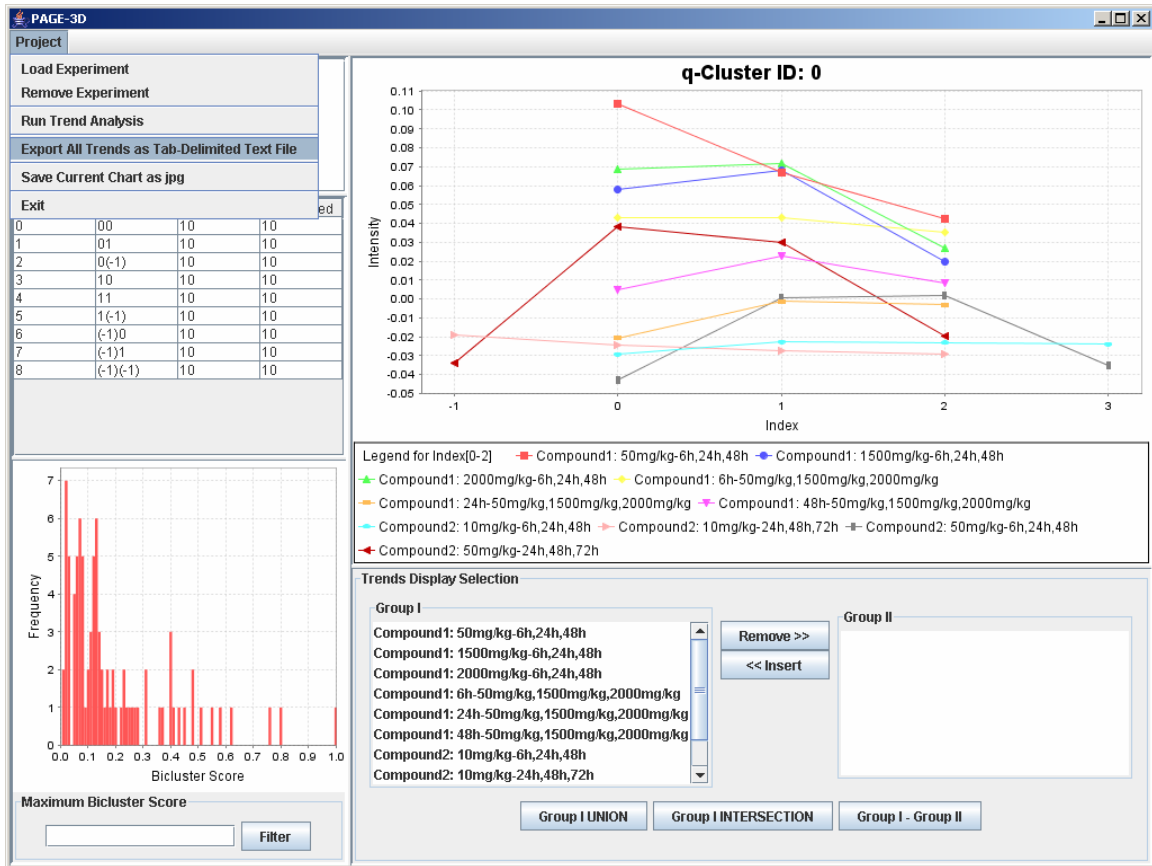


3. Click Submit

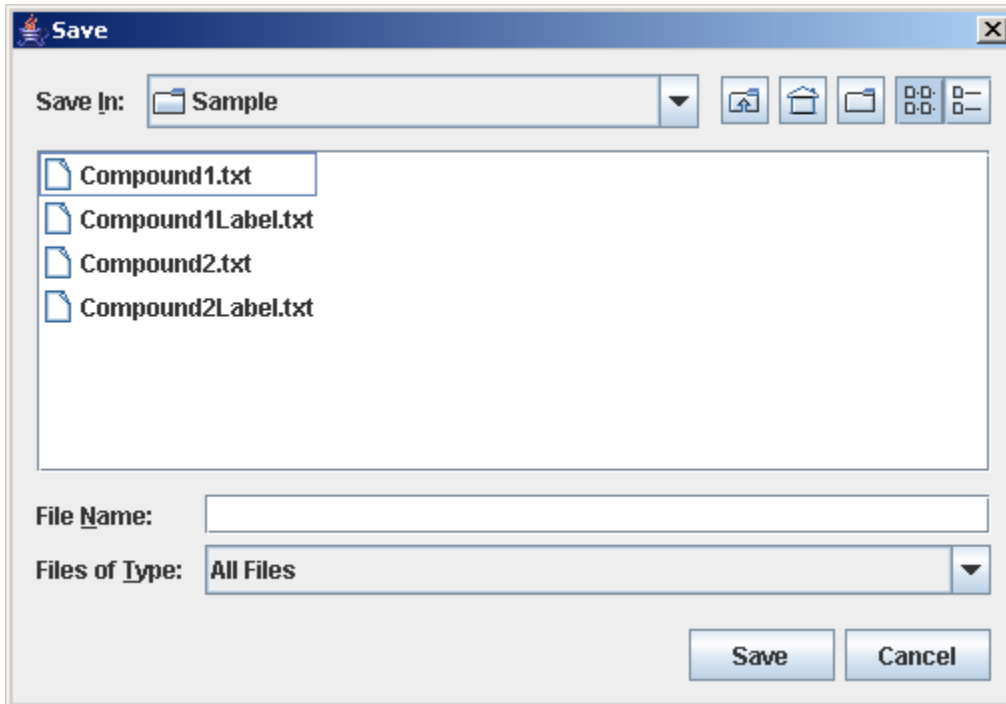


7. Save as Tab-Delimited File

1. Click on Project and select Export All Trends as Tab-Delimited Text File

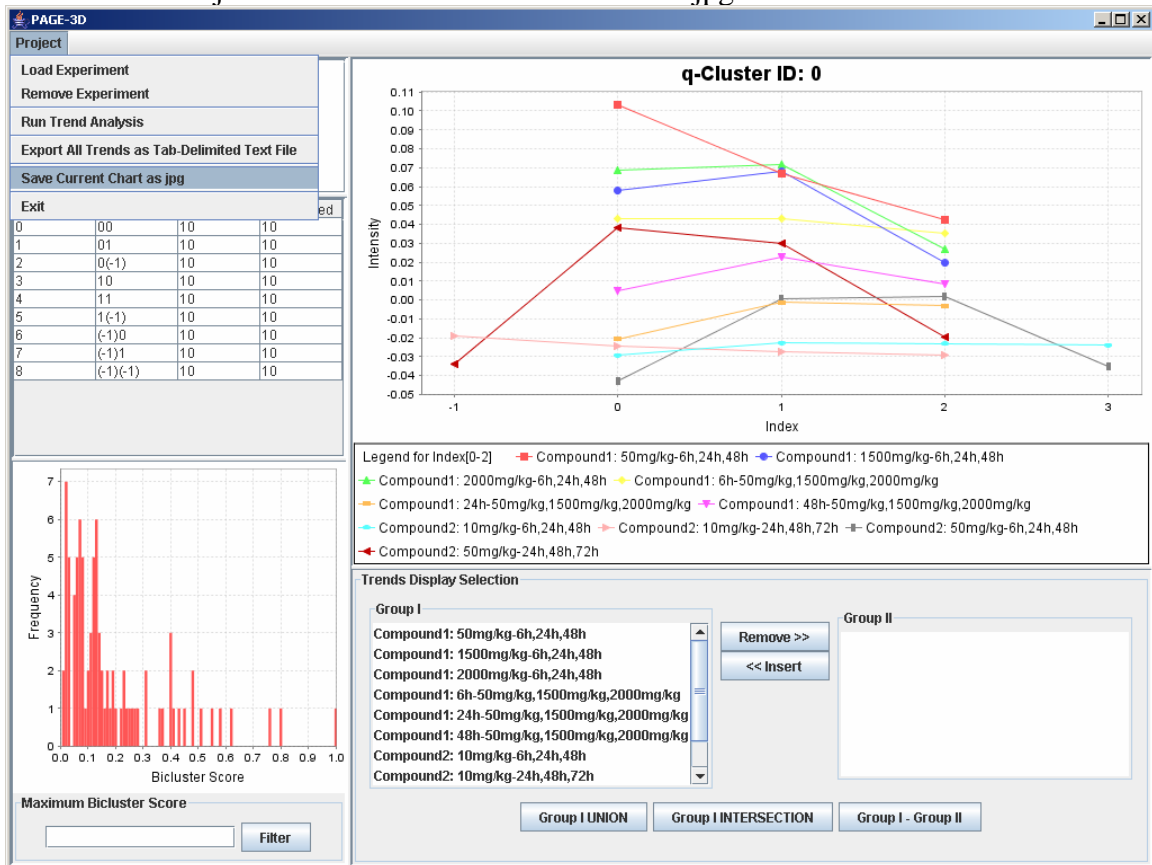


2. Enter the filename and click Save to save the results in a tab-delimited text file.

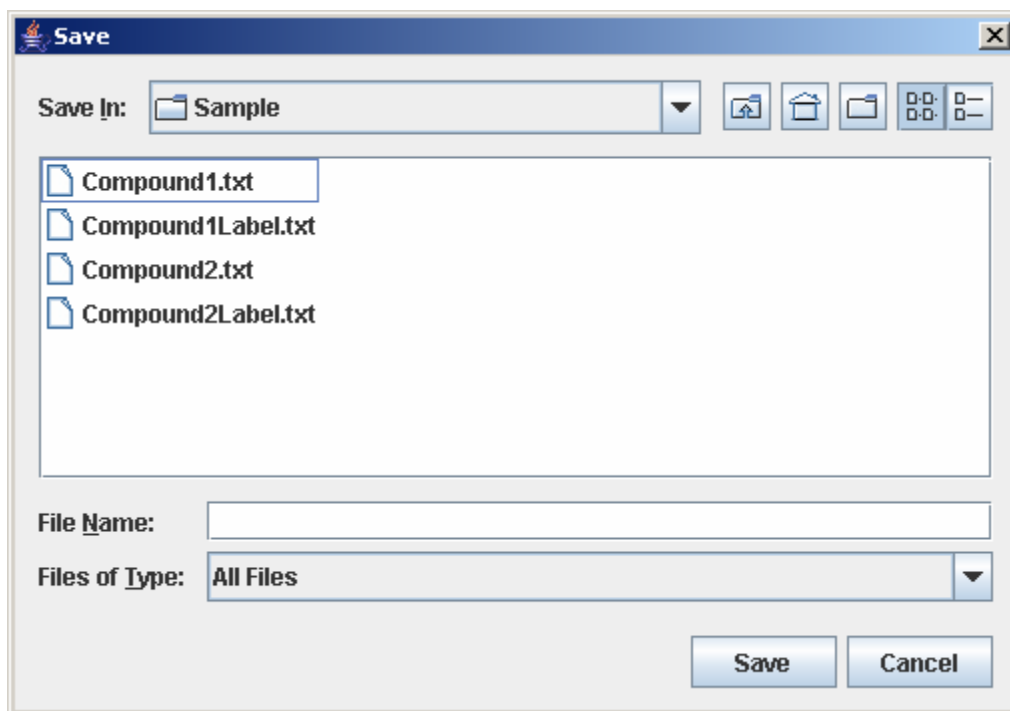


8. Save Current Chart

1. Click on Project and select Save Current Chart as .jpg.



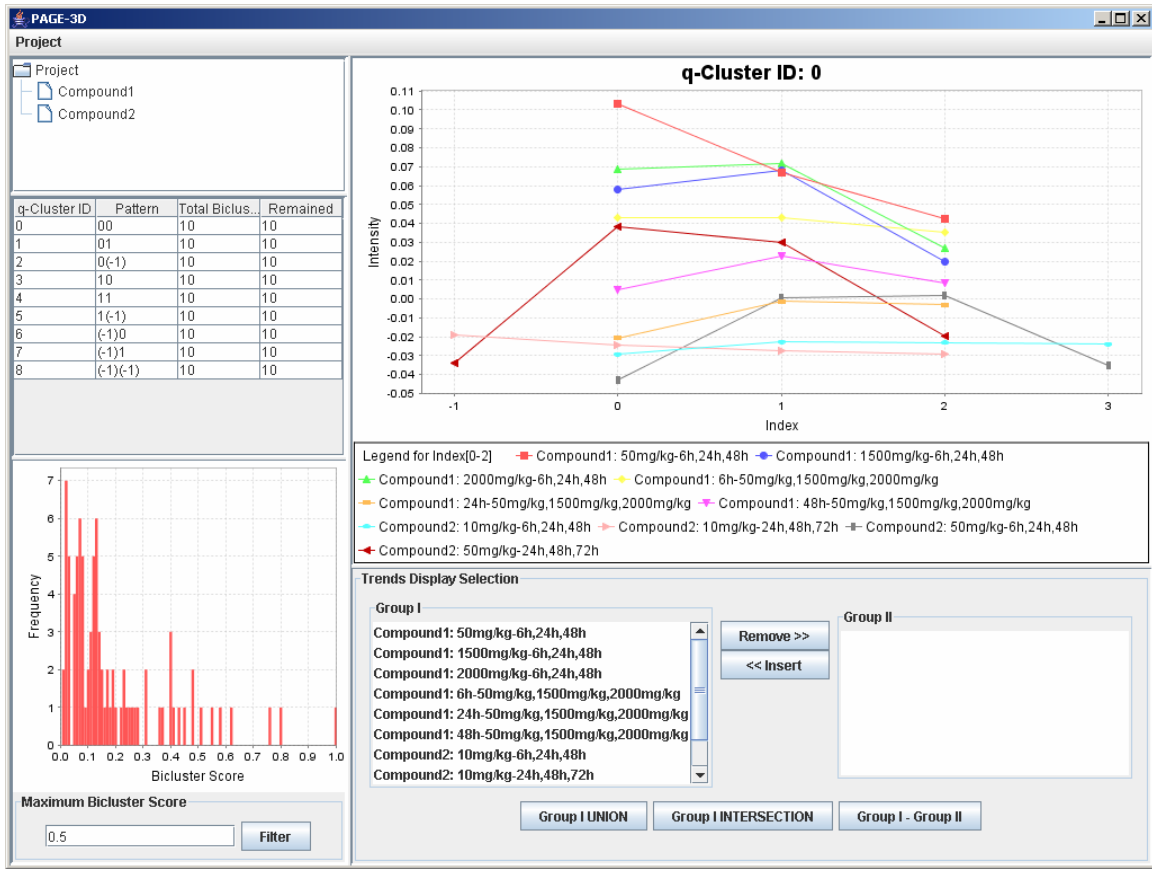
2. Enter the filename and click Save. PAGE will automatically append the .jpg extension to the filename entered by the user.



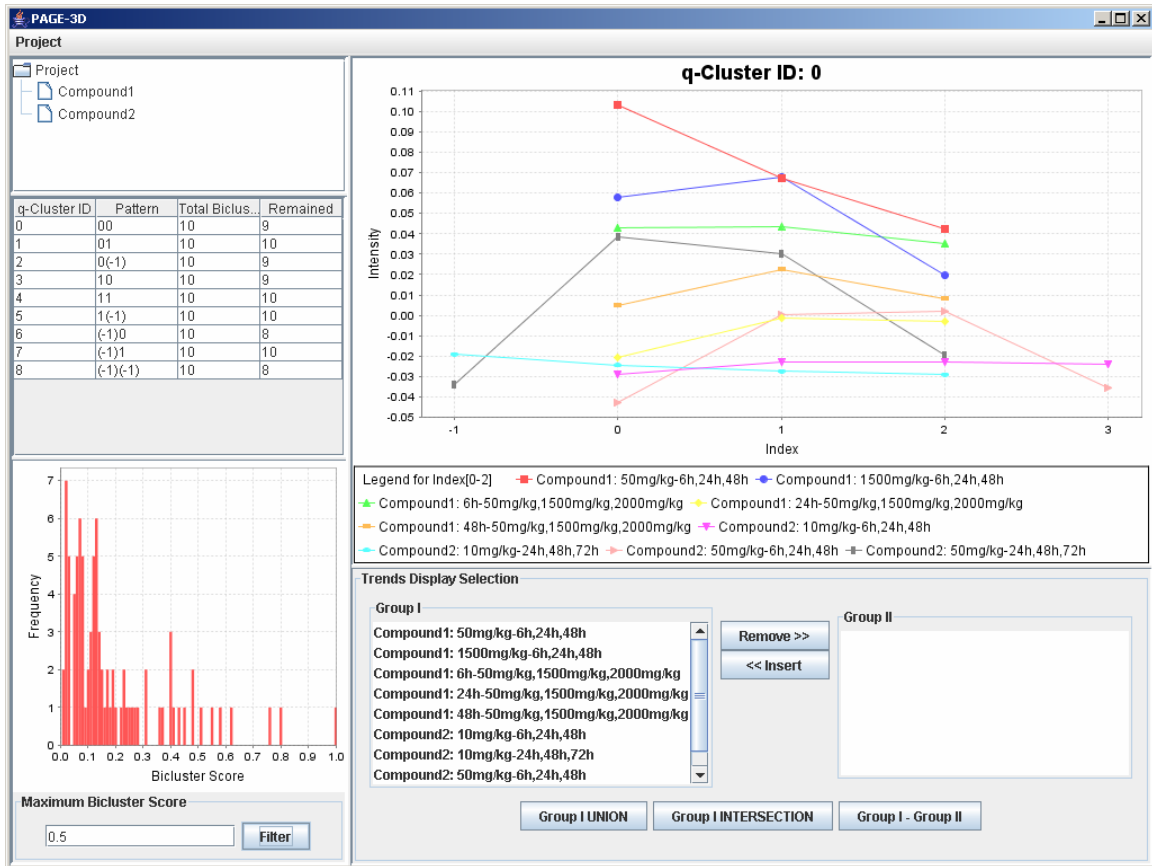
9. View Trend

9.1 *Setting the Maximum Threshold of Biclust*er Score

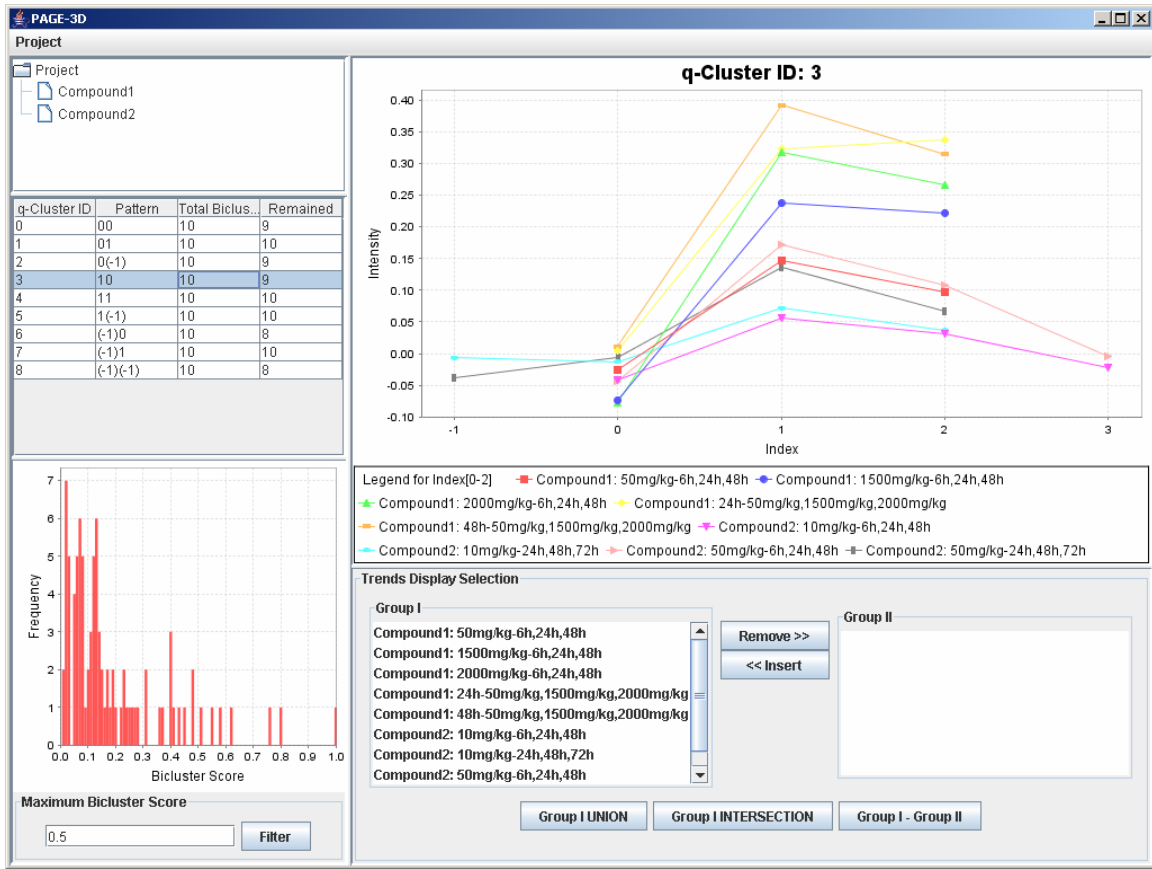
1. Enter a number between 0 and 1 to remove any biclust



2. Click on Filter to apply the bicluster threshold to the analysis.

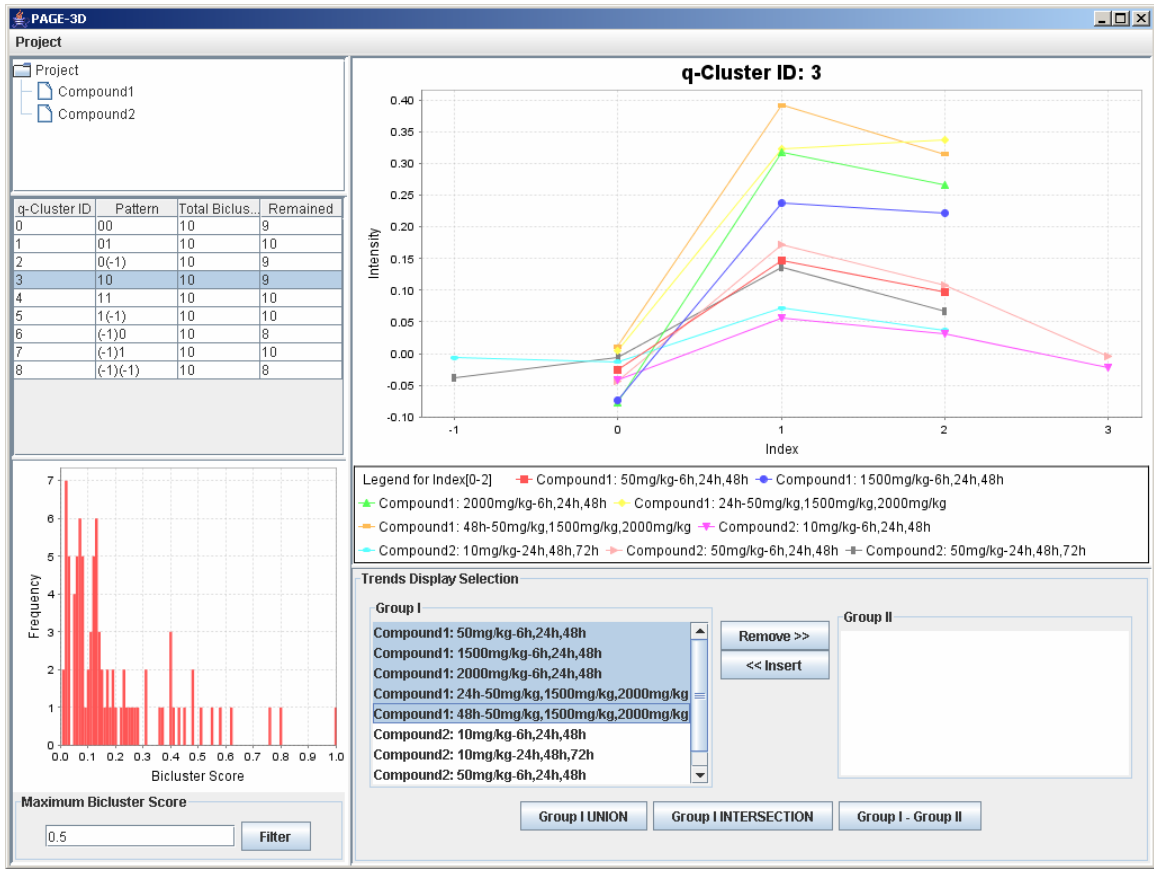


- Click on any row in the table on the left panel to view the corresponding q-Cluster.

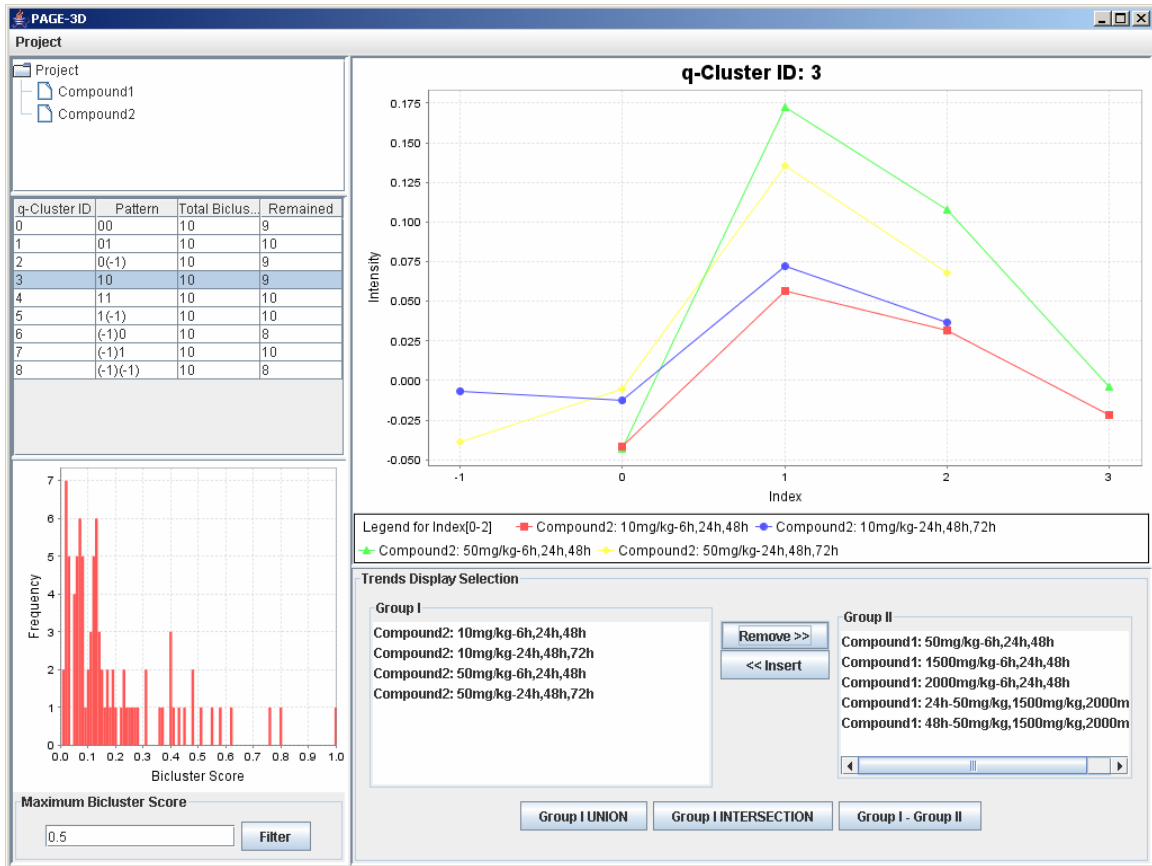


9.2 Selecting Trends

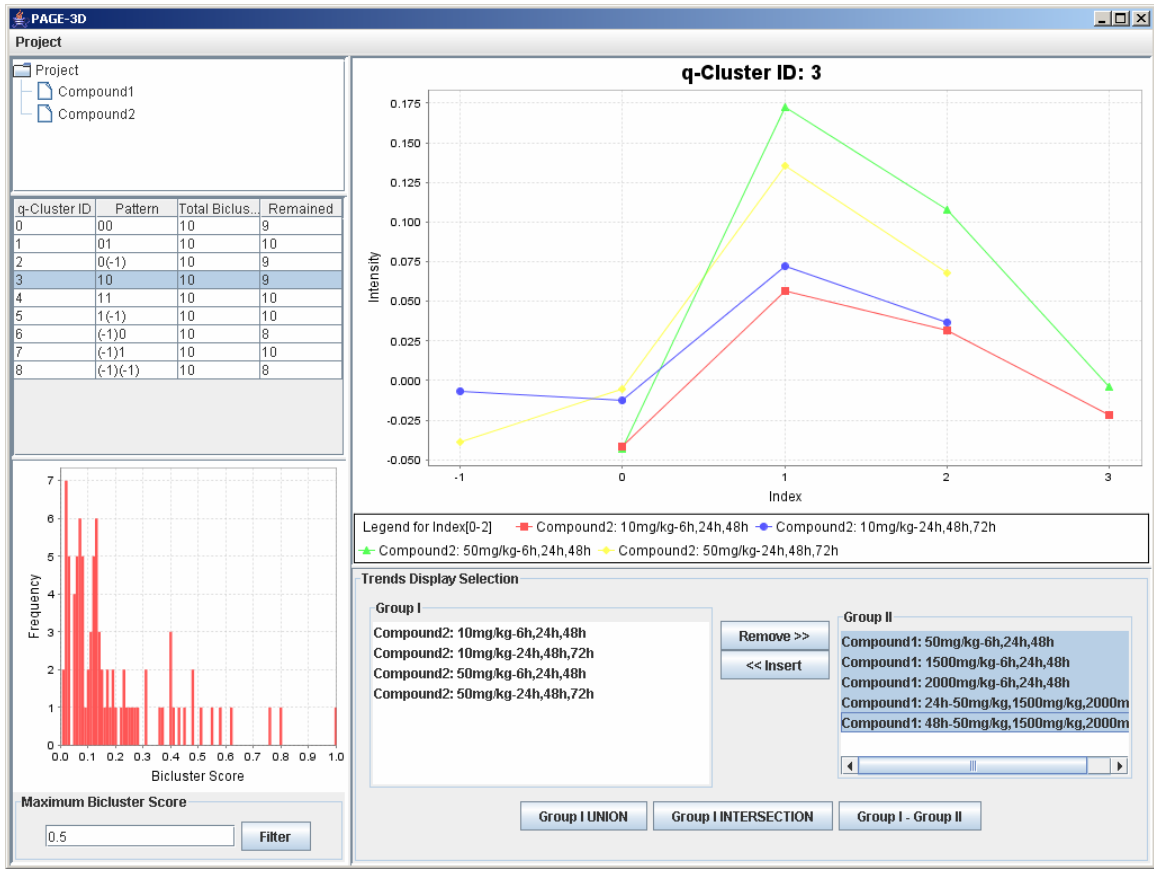
1. To remove any trend in the selected q-Cluster, go to the Trend Display Selection panel and highlight the desired trends in Group I.



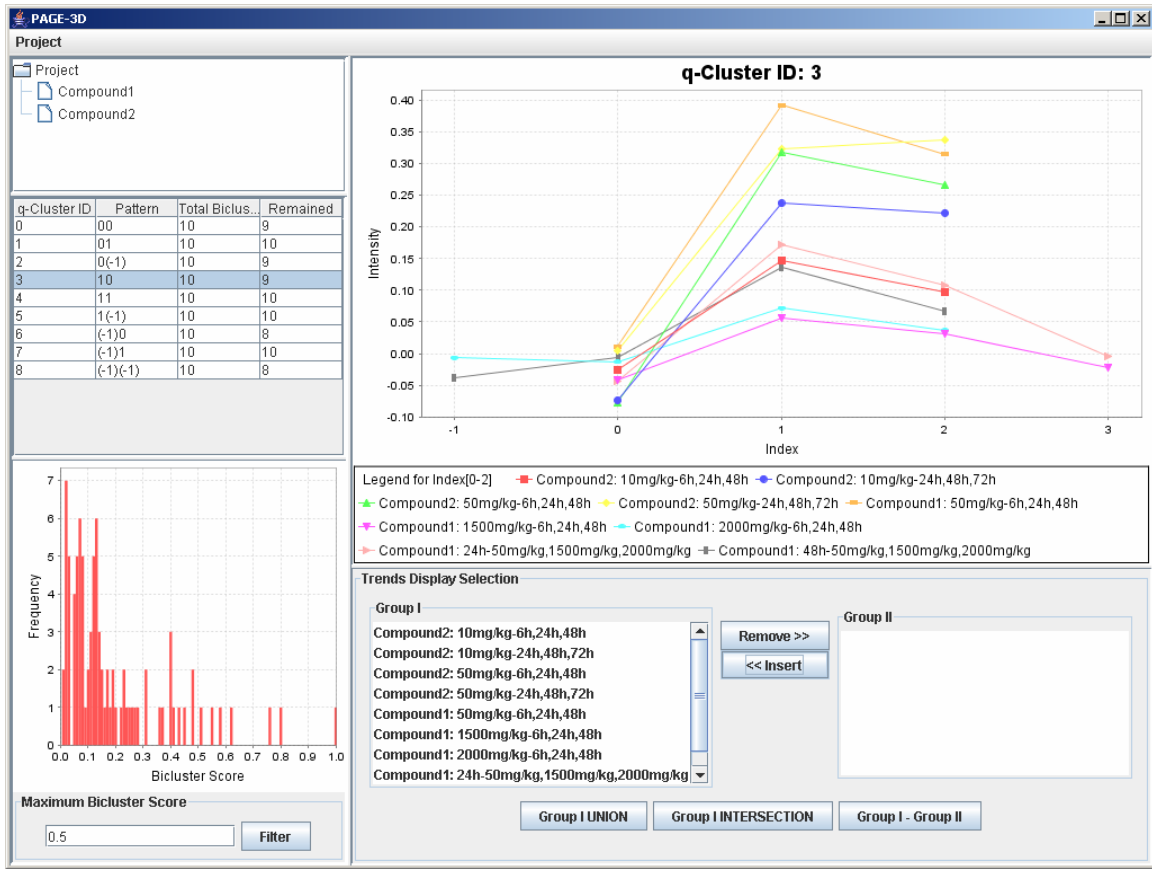
2. Click on the button “Remove >>”



- To insert trends back into the q-Cluster, go to the Trend Display Selection panel and highlight the desired trends in Group II.

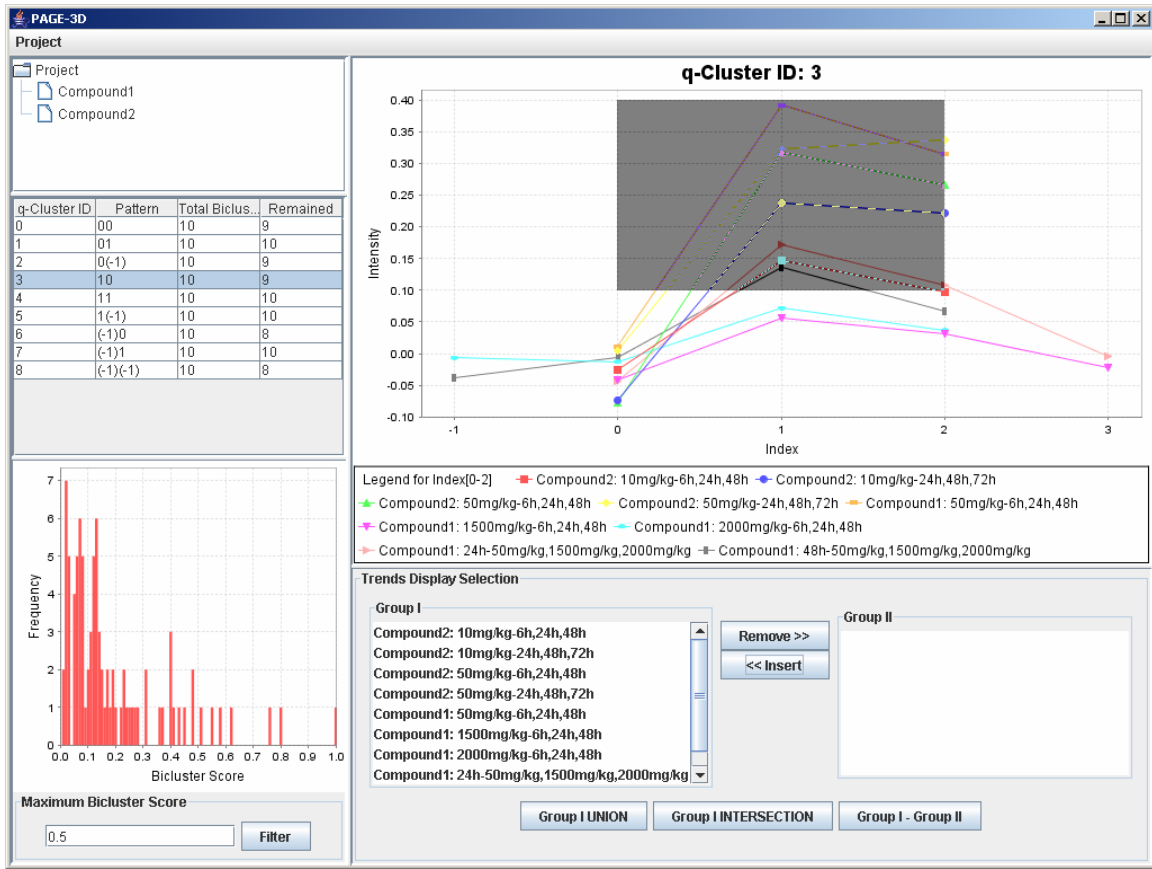


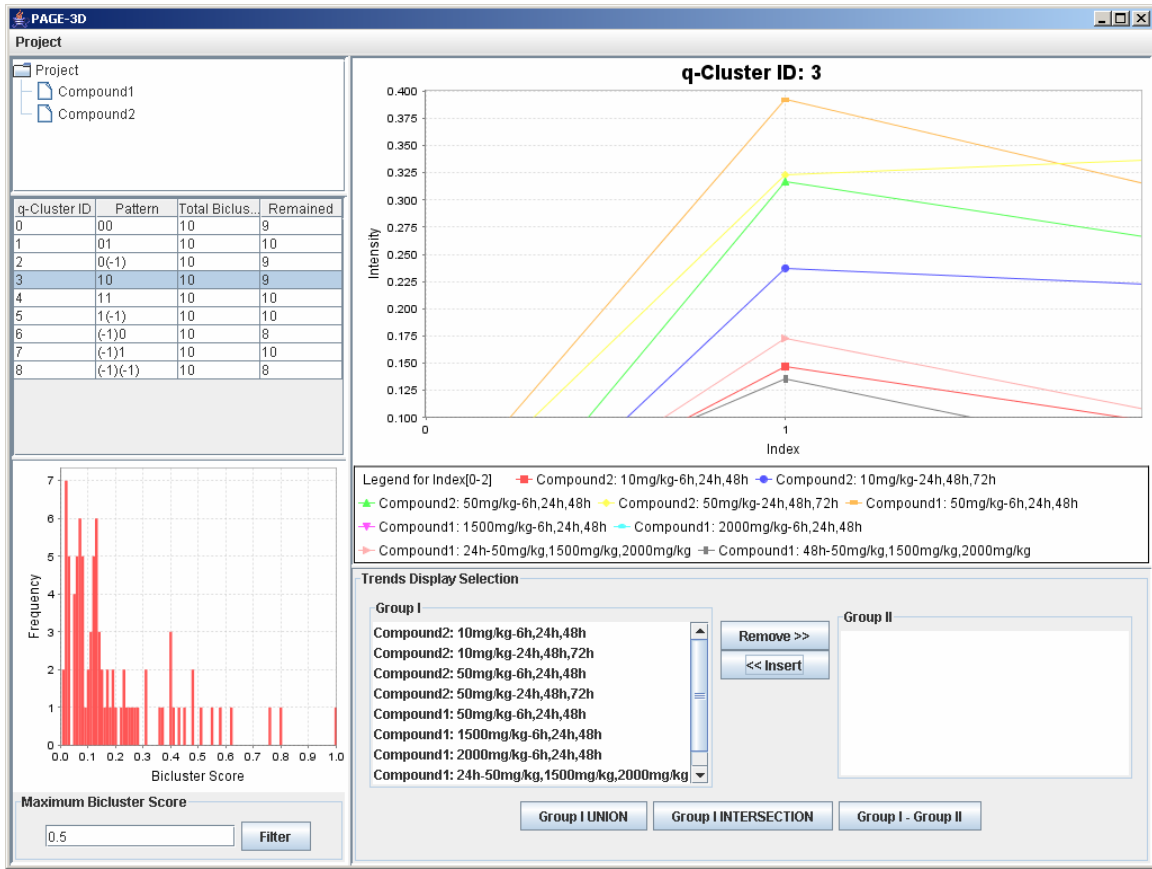
4. Click on button “<< Insert”



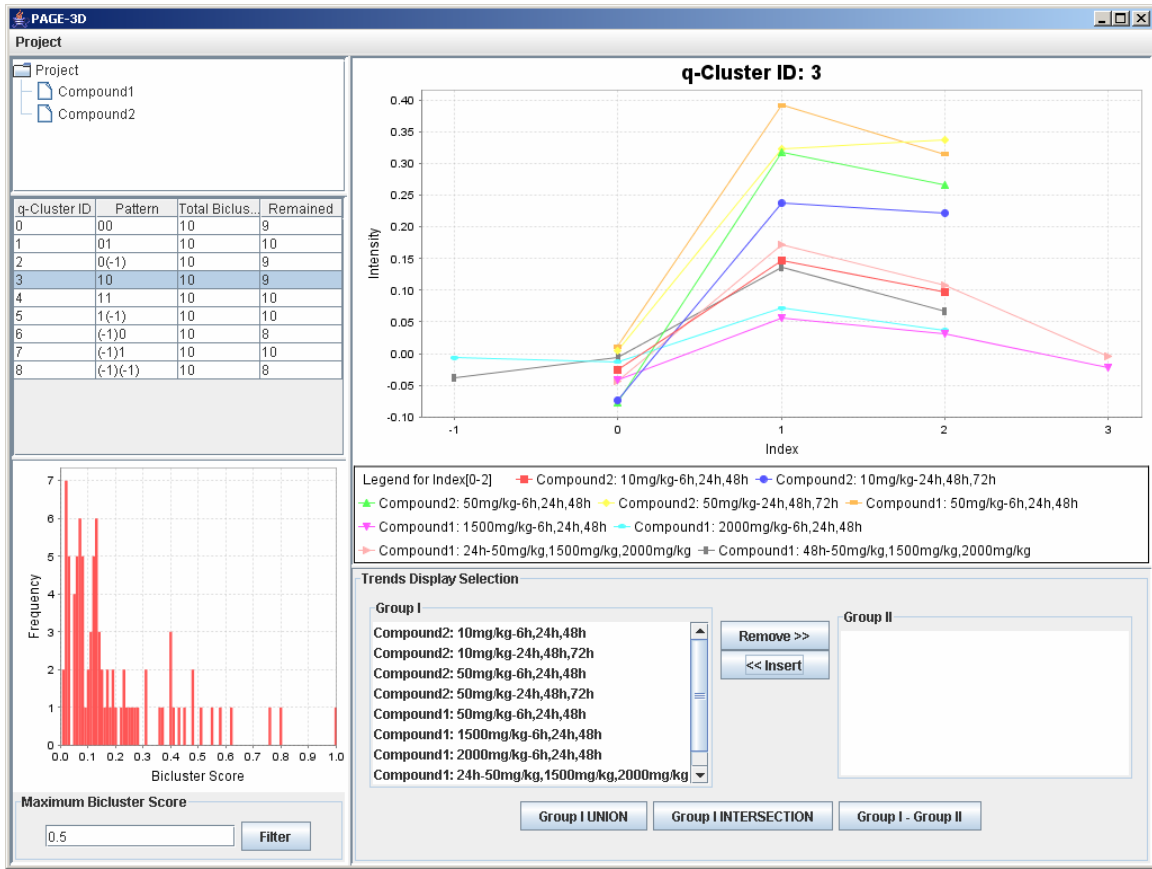
9.3 Zooming

1. Zoom-in: Drag the mouse from the upper left hand corner to the lower right hand corner to highlight the desired zone. Then, release the mouse.





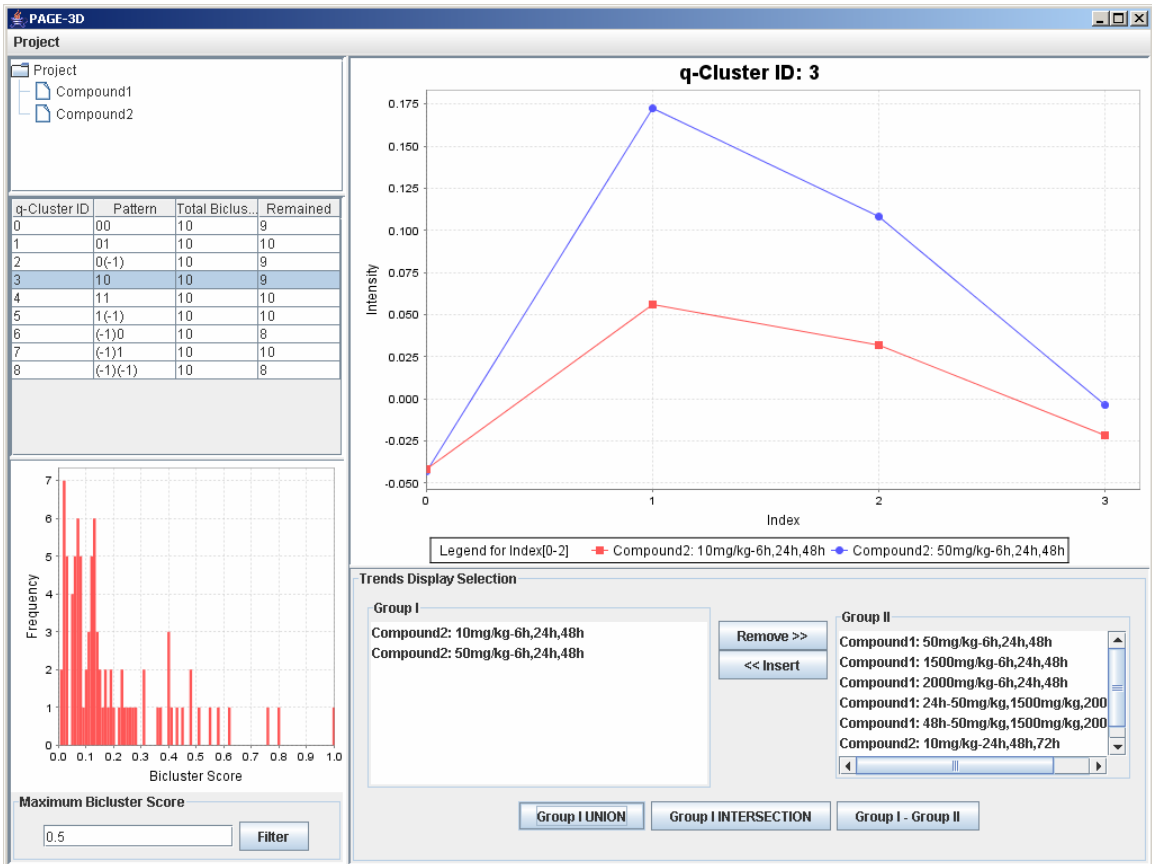
- Zoom-out: Drag the mouse in the opposite direction on the line graph panel and release the mouse.



10. Retrieve Gene List

10.1 Union

1. Click on the button “Group I Union” to generate the union of all the genes from the trends that are being displayed in the line graph panel.



Group I Union

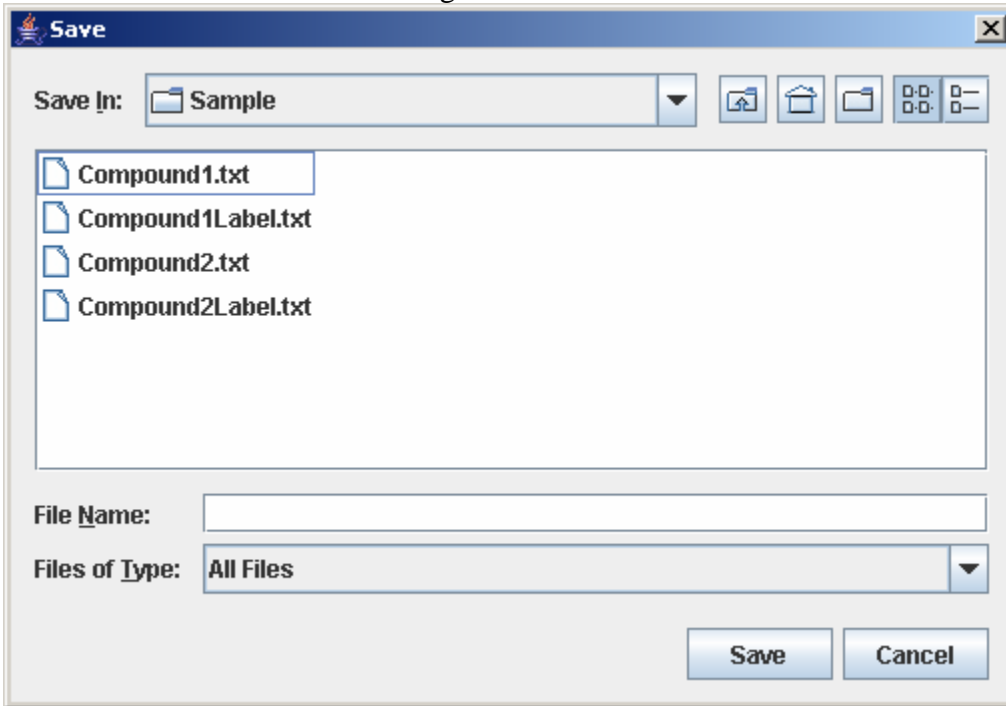
File

Row ID	Gene Accession
15	Gene 15
57	Gene 57
59	Gene 59
60	Gene 60
62	Gene 62
72	Gene 72
88	Gene 88
100	Gene 100
115	Gene 115
116	Gene 116
124	Gene 124
125	Gene 125
151	Gene 151
160	Gene 160
165	Gene 165

2. To save the gene list, click on File and select Save as Tab-Delimited.

	Gene Accession
15	Gene 15
57	Gene 57
59	Gene 59
60	Gene 60
62	Gene 62
72	Gene 72
88	Gene 88
100	Gene 100
115	Gene 115
116	Gene 116
124	Gene 124
125	Gene 125
151	Gene 151
160	Gene 160
165	Gene 165

3. Enter the filename to save the gene list and click Save on the file chooser window.



10.2 Intersection

1. Click on the button “Group I Intersection” to generate the intersection of all the genes from the trends that are being displayed in the line graph panel.

Row ID	Gene Accession
15	Gene 15
88	Gene 88
100	Gene 100
220	Gene 220
223	Gene 223
245	Gene 245
303	Gene 303
388	Gene 388
389	Gene 389

2. To save the gene list, click on File and select Save as Tab-Delimited.
3. Enter the filename to save the gene list and click Save on the file chooser window.

10.3 Difference (Group I – Group II)

1. Click on the button “Group I – Group II” to generate the list of all the genes in Group I but not in Group II.

Row ID	Gene Accession
15	Gene 15
59	Gene 59
62	Gene 62
72	Gene 72
100	Gene 100
160	Gene 160
165	Gene 165
193	Gene 193
303	Gene 303
397	Gene 397
398	Gene 398
399	Gene 399
415	Gene 415
430	Gene 430
440	Gene 440

2. To save the gene list, click on File and select Save as Tab-Delimited.
3. Enter the filename to save the gene list and click Save on the file chooser window.

11. Exit

1. Click on Project and select Exit to exit the program.

