

GenePattern

Express Matrix Documentation

Module Name: ExpressMatrix

Description: Comparative display of expression values between microarray samples in a dataset.

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SUMMARY: ExpressMatrix displays a matrix of expression/expression plots and calculates the correlation coefficients for all samples in a microarray dataset (GCT file). Users have to ability to zoom in on selected plots for closer examination. The zoom window plot can highlight and tally all genes that have a fold change greater than or equal to a specified cutoff value (+/-). Both the overall matrix and individual plots can be exported as JPG/PNG image files.

Specifications





<u>PARAMETERS</u>	<u>Name</u>	<u>Description</u>	<u>Optional</u>
	Input file name	The name/location of a microarray dataset (GCT file).	No
PLATFORM	Task Type:	Visualizer	
	CPU Type:	Any	
	OS:	Any	
	Language:	JAVA (1.6+)	

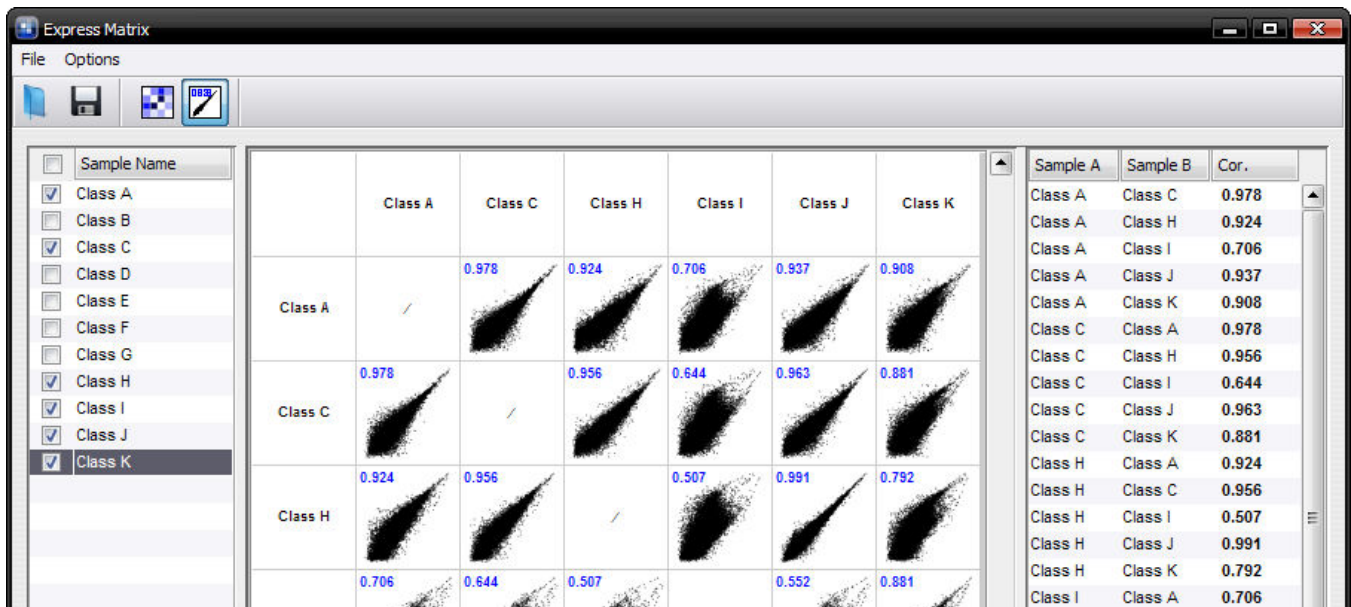
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Overview of ExpressMatrix Functionality

The ExpressMatrix user interface is relatively straightforward. The left panel lists all of the samples within a given GCT file. The center panel contains the expression/expression plots and the correlation heatmap. And the right panel contains the correlation coefficients for the various comparisons. Clicking on a plot will open the Zoom window which allows for closer inspection. The plot matrix may be saved to a JPG file either by clicking the corresponding icon, or by selecting **File | Save plot as images...** from the menu. Additionally, a new GCT file may be loaded from within the program itself (as opposed to launching from GenePattern) by clicking the corresponding icon or selecting **File | Open GCT File...** from the menu.

Tool Bar Icons

	Open File	Opens a new GCT file.
	Export	Export matrix & plot images to PNG format.
	Toggle heatmap	Switches between showing the expression/expression plots and a heatmap of correlation values.
	Toggle correlation values	Toggles the display of the correlation values in the top-left of each plot.



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Correlation Heatmap

The correlation heatmap view can be customized by going through **Options | Define heatmap palette...** There, the user has the option of defining the color gradient used to illustrate relative correlation levels, as well as define a saturation point below which all values are colored the same. Typically, this is done to enhance the contrast of a heatmap due to the fact that correlation values rarely drop below 0.5.

The screenshot shows the GenePattern interface with a correlation heatmap and a 'Define correlation gradient' dialog box. The heatmap displays correlation values between classes A through K. The dialog box allows users to define a color gradient and a saturation limit. Callouts provide instructions on how to interact with these elements.

Define correlation gradient dialog box:

- Slider: 0.0 to 1.0, with a current value of 0.39.
- Buttons: Cancel, OK.
- Color selection: A red color is selected.

Callouts:

- Select **Options | Define heatmap palette.**
- Drag the slider to define saturation limit.
- Click on a color to bring up a color selection dialog.

Heatmap Data (Approximate values):

	Class A	Class C	Class H	Class I	Class J	Class K
Class A	1.0					
Class C	0.978	1.0				
Class H	0.924	0.956	1.0			
Class I	0.706	0.644	0.507	1.0		
Class J	0.937	0.963	0.991	0.552	1.0	
Class K	0.908	0.881	0.792	0.881	0.823	1.0

Color Selection Dialog (Approximate values):

Class X	Class Y	Cor.
Class C	Class A	0.978
Class C	Class H	0.956
Class C	Class I	0.644
Class C	Class J	0.963
Class C	Class K	0.881
Class H	Class A	0.924
Class H	Class C	0.956
Class H	Class I	0.507
Class H	Class J	0.991
Class H	Class K	0.792
Class I	Class A	0.706
Class I	Class C	0.644
Class I	Class H	0.507
Class I	Class J	0.552
Class I	Class K	0.881
Class J	Class A	0.937
Class J	Class C	0.963
Class J	Class H	0.991
Class J	Class I	0.552
Class J	Class K	0.823
Class K	Class A	0.908
Class K	Class C	0.881

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Zoom Window

The Zoom window allows for closer inspection of each plot. The plot can be customized by toggling the display of a diagonal axis line and the highlighting of genes above the fold change criteria. The APPLY button must be pressed in order to update any changes to the fold change value that the user makes. Right-clicking the mouse over the graph brings up a context menu with some additional options, illustrated below. Going into the Properties menu gives the user even more flexibility in customizing the display of each plot.

