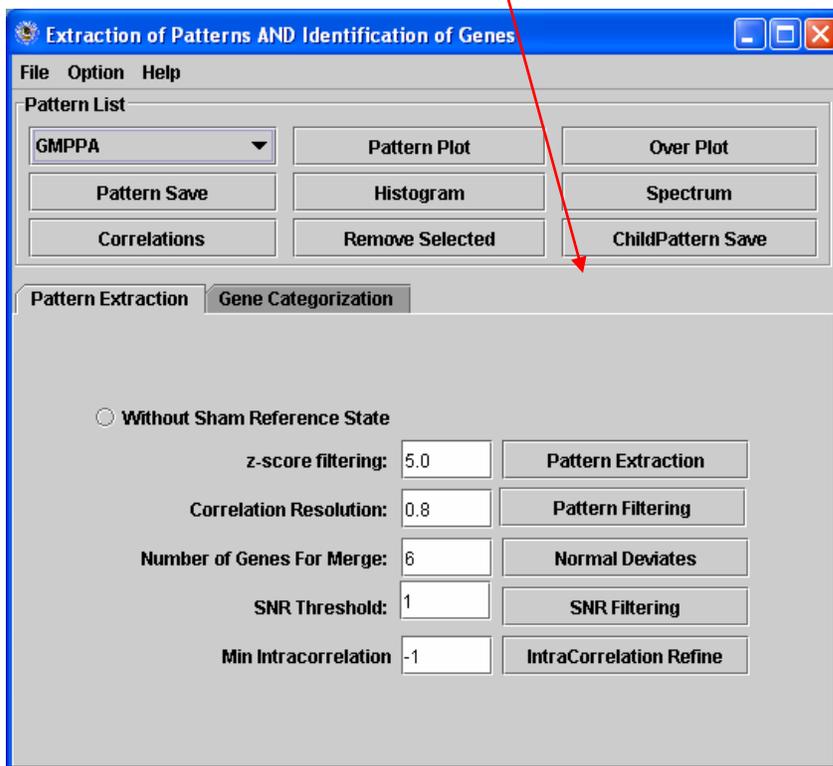


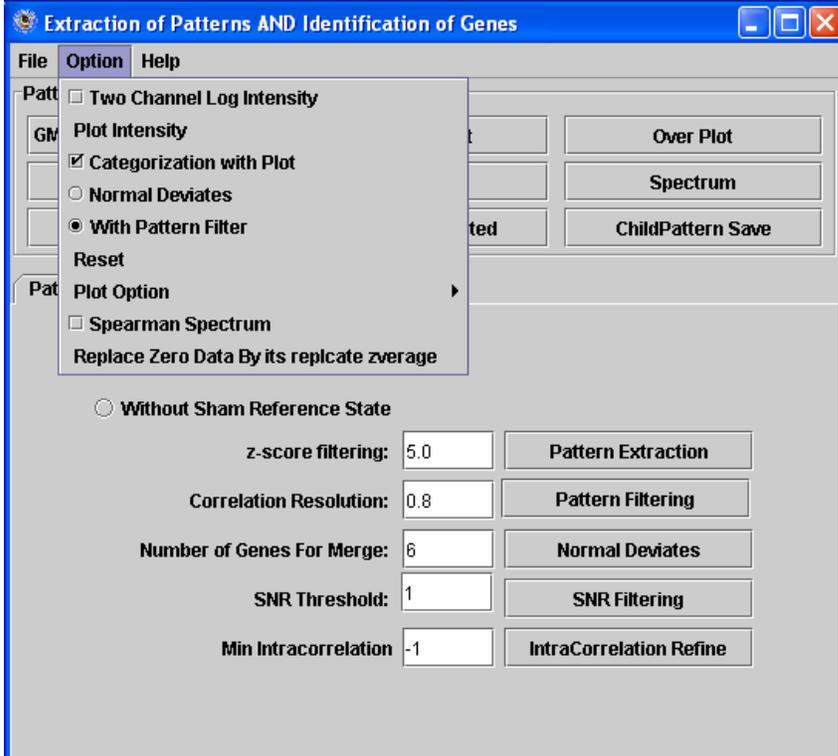
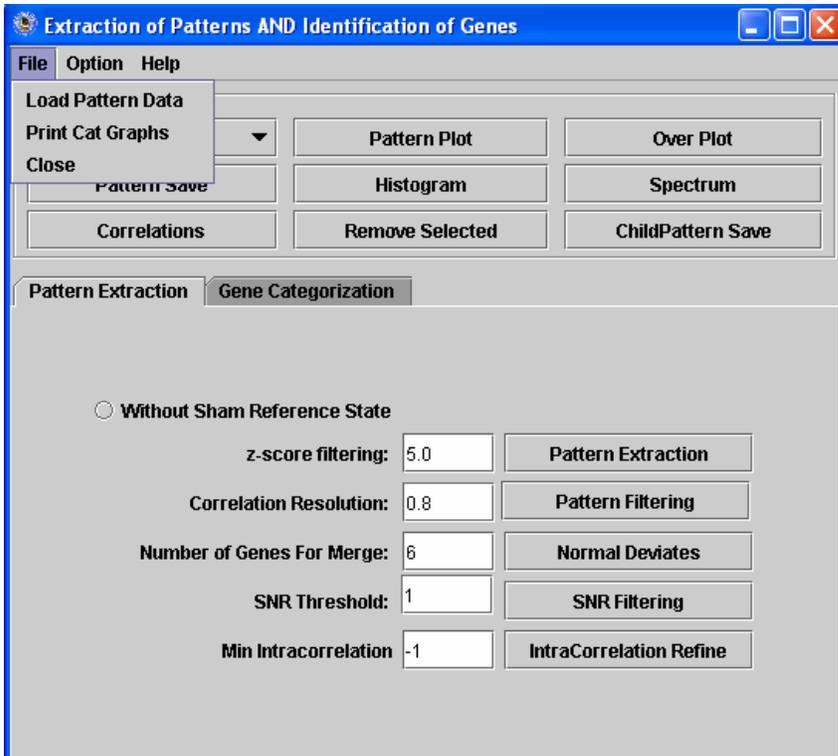
Extraction of Patterns and Identification of Genes (EPIG)

EPIG is an in-house developed microarray gene expression data analysis tool. EPIG consists of two parts. The first part is pattern extraction. The second part is the gene identification.

(1) Extraction of Gene Expression Patterns

User may click Button “Pattern Extraction” to perform pattern extraction. “z-score filtering” will filter those genes which have one or more data points with z-score larger than 5. “Correlation Resolution” is a correlation threshold to filter those profiles with a r-value larger than 0.8 to another profile. “Number of Genes For Merge” gives a number with which number of profiles to be merged. “SNR threshold” filter those profiles which have the SNR less than the given value. (Detail see EPIG manuscript)





Extraction of Patterns AND Identification of Genes

File Option Help

Pattern List

GMPPA

Pattern Plot Over Plot

Pattern Save Histogram Spectrum

Correlations Remove Selected ChildPattern Save

Pattern Extraction Gene Categorization

Categorization S.Pattern display all

SNR Histogram Signal Histogram r-Value Histogram

Magnitude 0.5 p-value 1

SNR 3 ABS(Mag-SNR)

r-Value above: 0.8

below:

AND

Display Selected Category Display All Category