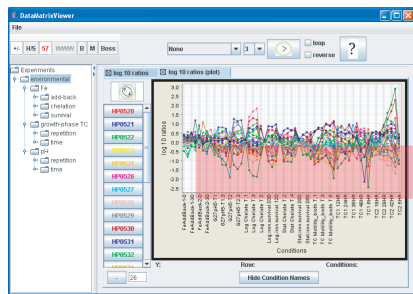
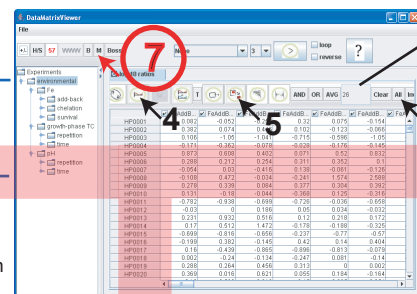


DataMatrixViewer (DMV)

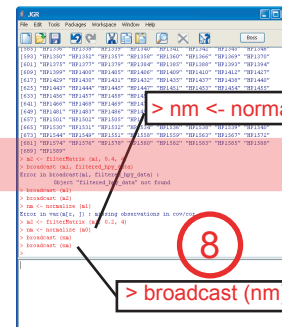


Experiment Tree
4 Plot expression profiles



26 genes selected
6

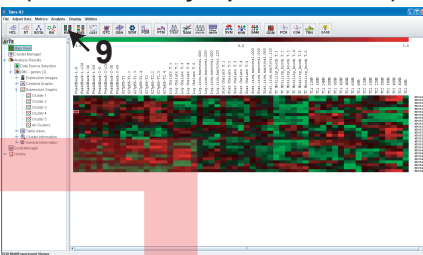
JGR (Java GUI for R Statistical Environment)



7 26 genes with matrix (m1)

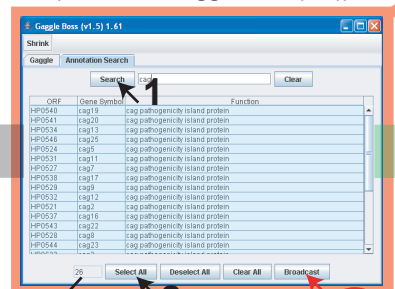
8 normalized matrix

TMeV (TIGR Microarray expression Viewer)



9 (K-means clustering)

Function Annotation Database (within the GaggieBoss (GB))

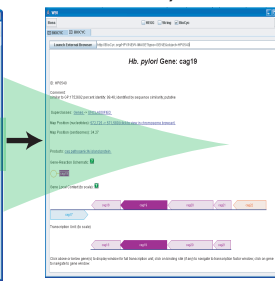
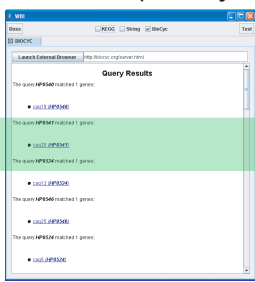


26 genes selected

3 26 selected genes

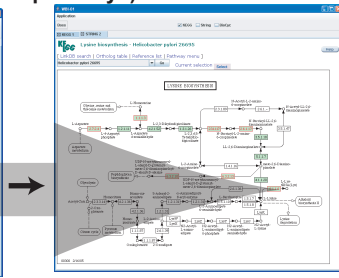
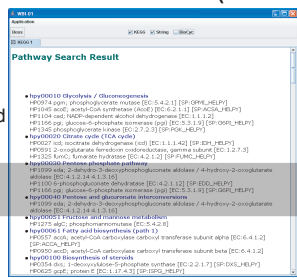
START HERE

BioCyc (Pathway/Genome Database)

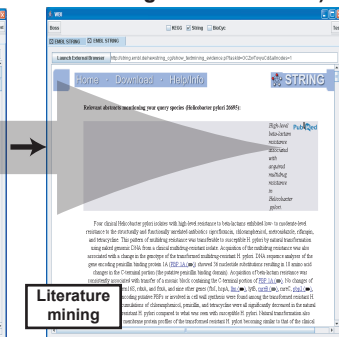
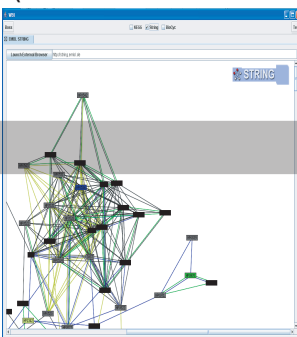


Although some *cag* genes are correlated over all conditions, most are correlated only over a subset emphasizing a need for biclustering (go back to Step 3 and follow link to InferelaterView)

KEGG (Metabolic pathways)



STRING (Search Tool for the Retrieval of Interacting Genes/Proteins)

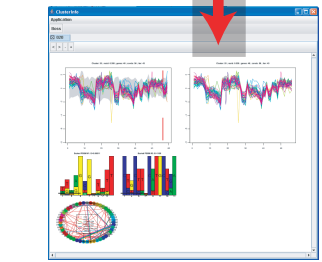


Cytoscape (Prolinks Network)

263 genes selected

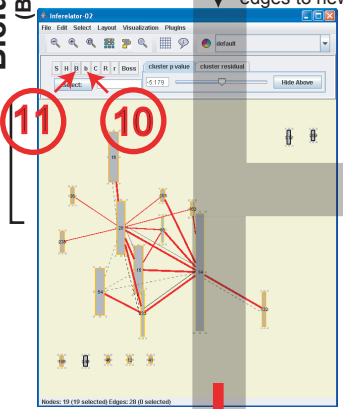
12 263 selected genes

ClusterInfo (expression profile, motifs, etc.)



DATA INTEGRATION IN GAGGLE

BiclusterView (Biclusters)



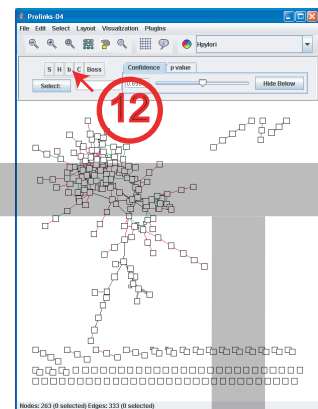
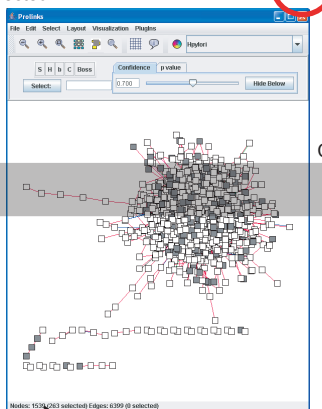
bicluster node name

Ctrl + N (selected nodes and edges to new window)

11

selected bicluster genes and environmental conditions

Ctrl + N



12 263 selected genes