Visualizing gene expression in transcription regulation and metabolic networks

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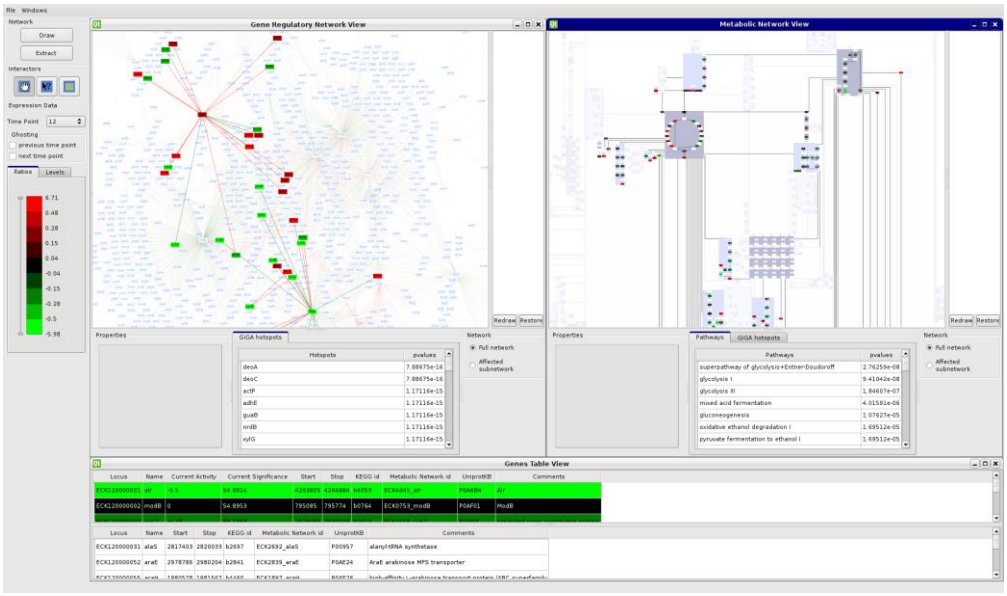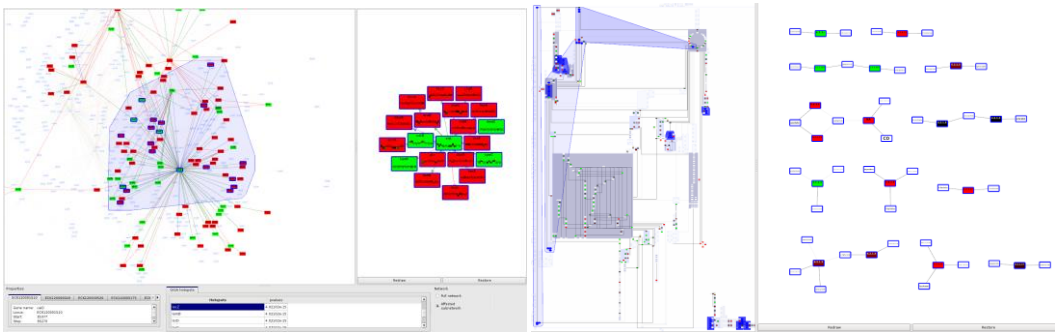
GENeVis is an application for integrated visualization of genome expression and network dynamics in regulatory and metabolic networks. Integration of these two levels of cellular processes is necessary, as it provides the link between the measurements at the transcriptional level and the phenotype at the functional and behavioral level. The integration requires visualization approaches besides traditional clustering and statistical analysis methods. GENeVis is an interactive tool, and has features that are currently lacking in many existing tools, such as mapping of expression value and corresponding p-value (or other statistic) to a single visual attribute and multiple time point visualization. In addition to time series visualization, GENeVis supports identification and visualization of affected subnetworks based on the expression data. The nodes of a subnetwork are highlighted in both the regulatory network and metabolic network. This can reveal quickly whether two independent regulatory subnetworks are connected at the metabolic level by a metabolite, or, conversely, whether two independent metabolic subnetworks are connected at the regulatory level by a shared regulator.