

GenePro Demo

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Analysis of the genome-scale networks of interacting genes and proteins has become a major focus of systems biology. Currently however, there is a shortage of effective software tools for the interactive analysis and display of such networks. Here we present GenePro, a plugin to Cytoscape (<http://www.cytoscape.org/>) that provides several integrative and interactive visualization and analysis tools for networks of interacting proteins/genes.

GenePro employs a cluster-centric design to display pre-clustered protein-protein interaction (PPI) networks at two levels of resolution. At lower resolution, nodes are gene/protein clusters that are connected to one another on the basis of a derived metric which indicates the strength of the link between nodes. For instance, two nodes can be connected if there are interactions between proteins in each cluster, with the thickness of the edge being proportional to the number of such interactions. This representation positions the protein clusters (or complexes) in the context of global interaction network, revealing which of the clusters is highly connected to other clusters and suggesting the extent to which the predicted complexes may share genes *in vivo*. Some clustering procedures produce clusters that share components (overlapping clusters). For such cases the user can specify edges to represent the number of shared genes between nodes.

To facilitate the validation and analysis of the computed clusters, GenePro offers an additional set of features. Each cluster can be represented as a pie chart where the size and color of wedges represent the fraction of the genes/proteins in each cluster that share identical attributes. The attributes that can be mapped onto the network of clusters include, but are not limited to: 1) functional annotations, 2) subcellular localizations, 3) level of sequence conservation, and 4) groups of co-regulated genes/proteins. Options for mapping mRNA expression data onto individual genes in the network of clusters are also available, as are various options for interactively querying the displayed information.

At higher resolution, GenePro allows analyzing the proteins in individual clusters and their pair-wise interactions. A double click on a given cluster displays a new graph, whose nodes are the proteins within the cluster, as well as their nearest neighbors from other clusters (colored differently from the proteins within the cluster) and the arcs are their interactions in the PPI network. Clicking on a link between two genes displays a table listing the reliability score of the interaction, as well as the raw score of each observation recorded for the interaction in the original proteomics experiments.

The data required to activate the features are loaded into GenePro via tab-delimited text files. SIF files that are required by Cytoscape to create the interaction networks are generated automatically. The various features in the GenePro plugin have been developed in Java. In addition to a user manual, example datasets, tutorial movies and a tutorial document are also available at: <http://genepro.ccb.sickkids.ca>. (We thank the CIHR for support under the Canada Research Chair program and support by the McLaughlin Center for Molecular Medicine is gratefully acknowledged.)