Tutorial:Assorted Cytoscape Plugins

Cytoscape Plugins

Importing public pathways

Using Cytoscape plugins, you can directly connect to external public databases and import network and annotation data. The program supports many standard network and annotation formats, and also imports from delimited text files and MS Excel Workbook.

Pathway Commons

As a pathway source, Pathway Commons provides a convenient point of access to biological pathway information collected form public pathway databases, which you can browse or search.

WikiPathways

WikiPathways, a community pathway curation, is a wiki model for biological databases. The plugin provides a single, intuitive interface for submission, updating, organizing, and access. WikiPathways allows the community to participate in curation process and keep up with the influx of new data. The output to Cytoscape is via GPML format, and users can cut and paste between systems.

MiMI Plugin

MiMI integrates data from multiple well-known protein interaction databases using an intelligent deep-merging approach. The Cytoscape MiMI plugin retrieves molecular interactions and interaction attributes from MiMI and displays interaction networks and attributes using Cytoscape. The plugin integrates with a biology natural language processing database (BioNLP) and a multi-document summarization system, MEAD, provides users literature information associated with interactions. In addition, the MiMI plugin also integrates with a graph matching tool (SAGA) for chosen networks graphic match against biological pathways.

Agilent Literature Search

The Agilent Literature Search plugin extracts biomolecular associations from the scientific literature. You can integrate with experimental data via inference of Cytoscape network, gather evidence to support interactions in existing networks, and expand an existing network with associations from literature.

CytoProphet

The CytoProphet plugin allows prediction and visualization of protein and domain interaction networks. It implements three algorithms that predict new potential physical interactions using the domain composition of proteins and experimental assays:

1. maximum likelihood estimation (MLE) using expectation maximization (EM)
2. the set cover approach maximum specificity set cover (MSSC)
3. the sum-product algorithm (SPA)

CytoProphet takes an input set of proteins with Uniprot ID/Accession numbers and a selected prediction algorithm. The plugin also draws a network of potential interactions with probability scores and GO distances as edge attributes. A network of domain interactions between the domains of the initial protein list can also be generated.

Expression Correlation Plugin

The Expression Correlation plugin computes a similarity network from either the genes or conditions in an expression matrix. Nodes in a similarity network represents genes or conditions. Links represent similarity between vectors of the expression levels of genes across all given conditions (gene correlation network) or the similarity between vectors of the expression levels of all genes in a single condition (condition correlation network). The Similarity Matrix is computed using the Pearson Correlation Coefficient. A histogram tool is available for choosing a similarity strength threshold, in order to ease creation of a reasonable sized network.

DomainGraph

The DomainGraph plugin allows for integrative analysis and visualization of protein and domain interactions together with exon expression data. The plugin also enables users to decompose any user-imported protein interaction network into underlying domain-domain interactions, as well as the integration of exon array expression data for highlighting protein domains and their interactions affected by alternative slicing events. The plugin can also create a graphical representation of the protein domain architectures, the underlying exon structures, probeset annotations, and GO and OMIM annotations. So, users can easily detect occurrences of alternative splicing and investigate their effect on the protein and domain network.

Network Analyzer

The Network Analyzer plugin computes and displays a comprehensive set of topological parameters and centrality measures for undirected and directed networks. These parameters include the number of nodes, edges, and connected components, the network diameter, radius, density, centralization, heterogeneity, clustering coefficient, and the characteristic path length. Users can also chart the distribution of node degrees, neighborhood connectivities, average clustering coefficients, and shortest path lengths. The Network Analyzer can also construct the intersection or union of two networks.

OmicsViz

Using the OmicsViz plugin, users can map and visualize large-scale *"omics"* data sets across species, including those with many-to-many mappings between homologs. The plugin can map data onto pathways of related model organisms and map schemas across species or different experimental protocols. In addition, users can comparatively analyze the *l"omics"* data, and visualize data in parallel-coordinate plots.

BiNGO- functional enrichment

BiNGO determines which Gene Ontology (GO) categories are statistically overrepresented in a set of genes or a subgraph of a biological network. The plugin maps the predominant functional themes of a given set on the GO hierarchy, and outputs this mapping as a Cytoscape graph. The main advantage of BiNGO over other GO tools is the fact that it can be used directly and interactively on molecular interaction graphs. BiNGO allows users to carry out hypergeometric or binomial tests for overrepresentation, as well as multiple testing correction using Bonferroni (FWER) or Benjamini&Hochberg (FDR) correction.

MCode: molecular complex detection

Clusters created by the MCode plugin can mean complexes, pathways, or families (in similarity networks). A greedy algorithm scores nodes by connectivity. The highest-score nodes accrues neighbors by rules and thresholds, next highest unclustered node continues the process. There are many parameters to tweak, and new directions. Users can:

- show clusters by GO category
- exclude by size threshold
- augmented clustering - use other attributes to help cluster network
- simplification with group nodes (aggregation)
- automated BiNGO validation using GO categories

UCSF ClusterMaker Plugin

ClusterMaker unifies a number of different clustering techniques and visualizations in a single interface. Current clustering algorithms include:

- Hierarchical and K-Means for clustering expression or genetic data, and
- MCL and FORCE for clustering similarity networks to look for protein families

Hierarchical clusters may be visualized as hierarchical groups or using the familiar TreeView heat map. K-means clusters may also be visualized either as groups or as heat maps. MCL and FORCE both create collapsible "meta nodes" to allow interactive exploration of the putative family associations with the Cytoscape network.

GLAY: Normalizing Visualization with Hierarchical Community Structure

The GLAY plugin allows users to find community structures in large biological networks, which may infer protein complexes and biological pathways. It utilizes the community structure information to improve visualization of later interaction networks. Users can partition the graph to maximize intra-cluster edge density and minimize inter-cluster edge density w.r.t. to a random graph.

- Measure: Modularity Q put forward by Mark Newman. For an Erdoa Renya random graph, q is usually <0.3. For real world graph with high quality community structure, q > 0.7.
- Algorithm implemented Greedy Algorithm, A. Clauset et. al, Greedy w/consolidation ratio, K. Wakita et. al.

jActiveModules

jActiveModules output with the second pathway shown selected and displayed as a separate child network. The plugin finds a connected network of differentially regulated genes, as shows by the red nodes in the child network.

Agilent VistaClara plugin for Cytoscape

VistaClara provides a highly interactive exploratory environment for analyzing gene expression data. The plugin extends the traditional heat map views into dynamic interactive permutation, and allows users to incorporate meta-data about genes and conditions as well as gene expression data. Users can explore methods of joint expression/meta-data analysis

- Gene ontology enrichment
- Pathway membership enrichment
- Similarly matching to condition meta-data

PowerGraph (CyOog)

Power Graph Analysis is a lossless transformation of biological networks into a compact, less redundant representation, exploting the abundance of cliques and bicliques as elementary topological motifs. The plugin clusters edges rather than nodes.

Cerebral

The cerebral plugin uses subcellular localization annotation to create a layered view of a cell, placing nodes in the region of the screen corresponding to the appropriate localization. Small multiple views enable a user to see expression data from 2 or more conditions overlaid on a network. A difference view allows two conditions to be selected and a new view is colored based on the changes between the selected conditions. The interactive k-means clustering tool also allows users to cluster their data, using a slider to adjust the number of desired clusters, and quickly select nodes based on cluster membership.

BubbleRouter

BubbleRouter allows users to layout a network incrementally and in a semi-automated way. It arranges specific nodes in user-drawn regions based on a selected attribute value, such as GO cellular compartment.

SFLDLoader

This plugin allows users to browze the enzyme superfamilies in the UCSF Structure Function Linkage Database. Users can create similarity networks from the precomputed pairwise BLAST data stored in the database, and view the structure via the *StructureViz* plugin.

UCSF StructureViz plugin

StructureViz links Cytoscape visualization of biological networks with UCSF Chimera visualization and analysis of molecular structures and sequences. Users can open structures in UCSF Chimera and align them using Chimera's Sequence/Structure tools. Structures may be PDB identifiers, ModBase identifiers, or SMILES strings. Users can select by chemistry (Ligand, Ions, Solvent, Secondary Structures, and in the model context menu, Functional Residues).

Cheminformatics Plugin

This plugin integrates 2D chemical visualization into Cytoscape, and provides linkouts to chemical resources that focuses on biological activities of small molecules, such as PubChem, MACiE, and ChEBl. Cheminformatics provides a clustering algorithm for molecules in a network based upon calculation of Tanimoto similarity between molecules.

DrugViz

DrugViz allows users to visualize and analyze small molecules within the framework of the interactome, and import drug-target network information in an extended SIF file format to Cytoscape. Users can display the 2D structures of small molecules and identify the small molecule nodes by isomorphism, substructure and fingerprint-based similarity searches. The two-side clustering analysis on drugs and targets provides detailed analysis of the active compounds in the network, and elucidates relationships between drugs and targets.

Article Sources and Contributors

Tutorial:Assorted Cytoscape Plugins *Source*: http://labrador.library.ucsf.edu/opentutorials/index.php?oldid=327 *Contributors*: AnnaKuchinsky

License