

BiNoM I/O

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Import BioPAX Document from file: imports a BioPAX file from a local folder and creates three BioPAX interfaces (Reaction Network (RN), Pathway Structure (PS) and Protein-Protein interactions (PP)).

Import BioPAX Document from URL: imports BioPAX interfaces from a web address.

BioPAX Property Editor: reviews all the available information about a protein, a gene, a pathway, contained in BioPAX.

BioPAX Class Tree: shows all instances of BioPAX classes (proteins, complexes, conversions,

catalyses, etc.) with possibility to call the editor and create new instances.

Using Name Service Names / Using URI Names: changes the way species is named: from names generated by BiNoM Naming Service to URIs (Uniform Resource Identifier) and vice versa.

Save whole associated BioPAX as: saves the whole BioPAX object associated with the current interface.

Synchronize networks with BioPAX: updates all interfaces according to changes made in their common BioPAX object.

Import CellDesigner Document from file: imports a CellDesigner file (with .xml extension) from a local folder.

Import CellDesigner Document from URL: imports a CellDesigner file (with .xml extension) from a web address.

Export current network to BioPAX: saves the network (interface) into a BioPAX format (with .owl extension) provided that it is associated to an existing BioPAX file. Only visible part of information is exported.

Export current network to CellDesigner: saves the network into a CellDesigner format (with .owl extension) provided that it is associated to an existing CellDesigner file. Only visible part of information is exported.

Export current network to SBML: saves the Reaction Network interface into an SBML format.

Associate BioPAX Source: associates the Cytoscape network with an existing BioPAX object (or file).

Associate CellDesigner Source: associates the current network an existing CellDesigner document.

BiNoM Analysis

Get Connected Components...
Get Strongly Connected Components...
Prune graph...
Get Material Components...
Get Cycle Decomposition...
Path analysis...
Generate modular view...
Cluster networks...

Get Connected Components: isolates from the rest of the network all the connected components

Get Strongly Connected Components: isolates a sub-network with the property that there exists an undirected path from one node to another.

Prune graph: separates the graph into three sub-networks: incoming flux (what comes in), outgoing flux (what goes out) and the cyclic part (containing strongly connected components).

Get Material Components: separates the network into sub-networks describing the life cycle of each entity (protein, small molecule, etc.).

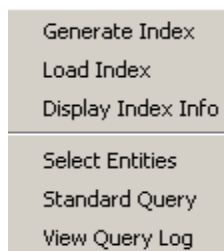
Get Cycle Decomposition: decomposes the network into minimal cycles.

Path Analysis: highlights shortest, sub-optimal or all paths from a species to another. Select some nodes first.

Generate Modular View: creates a graph in which nodes represent other selected sub-networks or modules of an initial network linked together according to the number of common interactions, or nodes.

Cluster networks: lumps together sub-networks or modules that share a certain proportion of nodes, given a specified percentage of overlap.

BiNoM BioPAX Query



Generate Index: generates a full attributed graph representation of BioPAX (*index*) creating an .xgmml format from an .owl file (maps BioPAX onto a labelled graph).

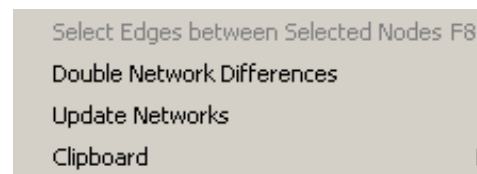
Load Index: loads the full attributed graph representation of BioPAX.

Display Index Info: lists the names of the index and of the index file, the accession number table file (when available), number of all types of objects in the index.

Select entities from the index: finds entities specified by names or accession numbers in the BioPAX index loaded

Standard Query: given a BioPAX interface, extends it from the BioPAX index loaded (adds complexes, chemical species, reactions, or publications).

BiNoM Utilities

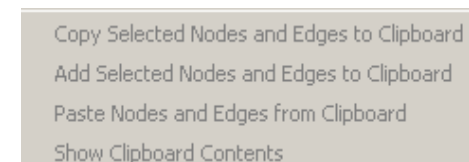


Select Edges between selected nodes: selects all the edges that connect selected nodes.

Double Network Differences: compares two networks A and B by computing first $A-A \cap B$ and then $B-A \cap B$.

Update Networks: updates specified Cytoscape networks related to some base network according to the modifications made in that network (for example, used to propagates changes on sub-networks).

Clipboard



Clipboard: computes several clipboard operations such as: copying and pasting selected nodes and edges, adding selected nodes and edges to clipboard and showing the content of the clipboard.