

## BiNoM REFERENCE CARD

### BiNoM I/O

*Import BioPAX Document from file:* imports a BioPAX file (with .owl extension) 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.

*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 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 the 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 the 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).

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

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

### BiNoM Analysis

*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 the nodes are sub-networks (or modules) of an initial network. The modules are 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.

*Mono-molecular reactions to edges:* transforms a BioPAX network into an influence graph

*Extract reaction network:* cleans up the diagram from all extra edges and nodes such as publications, entities, etc. and only keeps the reaction network.

### BiNoM BioPAX Utils

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

*BioPAX Class Tree:* shows all instances of BioPAX classes (proteins, complexes, conversions, catalyses, etc.) with the possibility to call the editor and create new instances.

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

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

### BiNoM BioPAX Query

*Generate Index:* generates a full attributed graph representation of BioPAX (*index*) creating a file with 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).

*Index Path Analysis:* finds the directed or non-directed, shortest, optimal or suboptimal, non intersecting paths with a pre-defined number of intermediaries in an index file. Select species on the graph before this query.

*View query log:* recapitulates all the queries done during the session.

## 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 propagate 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.