

BiNoM: a Cytoscape plugin for using and analyzing biological networks

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BiNoM (BIological NetWOrk Manager) is a Cytoscape plugin, developed to facilitate the manipulation of biological networks represented in standard systems biology formats and to carry out studies on the network structure. BiNoM provides the user with a complete interface for the analysis of biological networks in Cytoscape environment. BiNoM plugin with documentation, API and source code is available for download at: <http://bioinfo-out.curie.fr/projects/binom/>

Motivation

In an effort to exchange and curate pathway database knowledge, several standard formats have been developed (SBML, BioPAX [1] and others). Many softwares, which are centered around the description and representation of biological pathways, adopted these standards. CellDesigner [2] and Cytoscape [3], for instance, allow the visualization and manipulation of networks but meet some limitations. BiNoM was designed to facilitate the use of systems biology standards, the extraction and organization of information from pathway databases through BioPAX interface.

BiNoM Content

BiNoM concentrates on the following aspects: the import and export of BioPAX and (CellDesigner) SBML files and the conversion between them; the structural analysis of biological networks including decomposition of networks into modules, path analysis, etc.; the BioPAX query engine which provides the extraction of information from huge BioPAX files such as whole pathway databases; and various operations on graphs not offered by Cytoscape such as clipboard operations and comparison of networks.

Among the many features of BiNoM, a particularly useful one concerns working and representing the BioPAX object hierarchies. BiNoM provides access to several aspects of BioPAX such as representing the reaction network, the pathway structure and protein-protein interactions. Moreover, BiNoM allows the exploitation (with BioPAX dump) of pathway databases such as Reactome [5]. BiNoM provides tools to visualize, edit, and extract parts of BioPAX files through BioPAX property editor and BioPAX Class tree dialog (see Fig. 1).

Application: example of RB/E2F pathway

The retinoblastoma tumor suppressor protein (RB/RB1) negatively regulates the transcription of cell cycle genes by sequestering major transcription factors, the E2Fs. Based on the literature, a comprehensive map of RB/E2F regulation was built using CellDesigner [4]. The resulting diagram contains 78 proteins, 215 chemical species, 530 reactions and 176 genes. To exploit this map, a decomposition into modules was proposed using BiNoM functionalities.

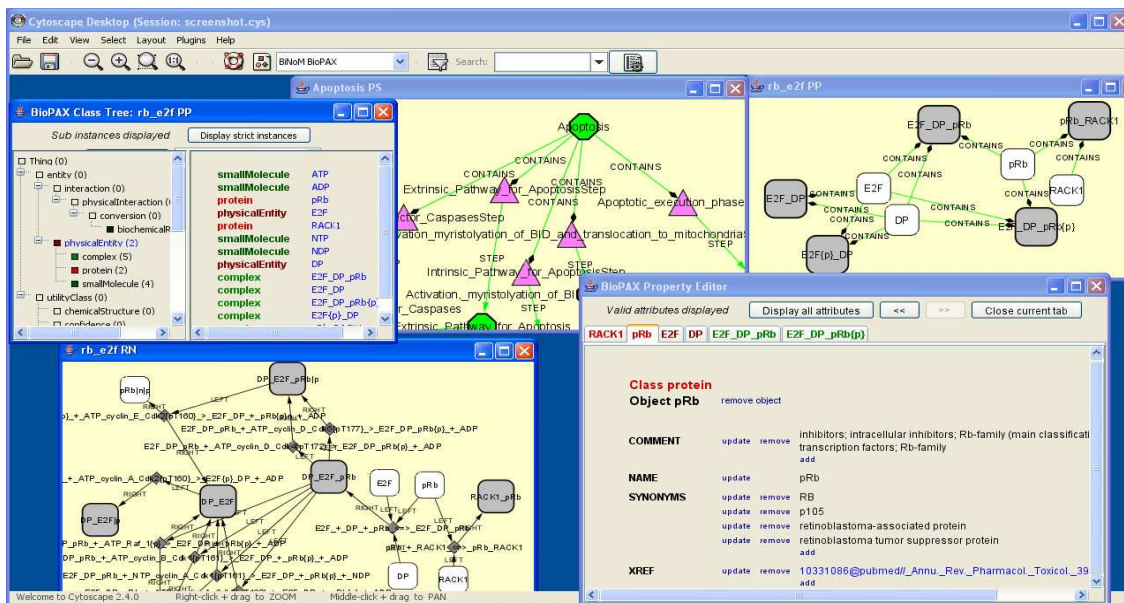


Figure 1: Screenshot of BiNoM interface in Cytoscape environment

With this modular view, a more intuitive understanding of the network can be provided and real biological questions might be addressed.

Once the map was imported from CellDesigner to Cytoscape, the division into modules was done using a curated structural analysis method developed in BiNoM. The result of this analysis and the different steps leading to the modularization of the network can be found at the following address: <http://bioinfo-out.curie.fr/projects/rbpathway/>.

In this study, BiNoM proved to be useful in disentangling and understanding a complex biological network *a priori* difficult to exploit.

References

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- [4] Calzone L. et al. (2007) A Comprehensive Modular Map of Molecular Interactions in RB/E2F Pathway. *Manuscript submitted*. See <http://bioinfo.curie.fr/projects/rbpathway>
- [5] Joshi-Tope G. et al. (2005). Reactome: a knowledgebase of biological pathways. *Nucleic Acids Res* **33**, D428-432.