

Protein Network Visualization with JDIP

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ABSTRACT

Recent advances in genome-wide experimental techniques has lead to rapid acquisition of large amounts of experimental data on various aspects of protein function such as protein expression levels[1] and protein-protein interactions [2,3]. However, genome-wide visualization and analysis if this data remains difficult as the currently available database infrastructure provides access to the information centered on a single protein at a time.

JDIP addresses this limitation by providing means of protein-network oriented data retrieval, visualization and analysis. Designed originally as enhanced interface to the Database of Interacting Proteins (DIP; <http://dip.doe-mbi.ucla.edu> [3]), JDIP is a stand-alone Java application that provides a generic framework for integration of diverse data from other biological databases. Additionally, after installation as a browser 'helper' application, JDIP can be fully integrated with the DIP Web interface by providing two-directional queries between the DIP server and JDIP.

Information exchange between the DIP database and JDIP is realized through XML files using JIN (Java Interaction Network)

syntax specified as an XML schema [4]. Besides specifying the structure of the protein network, JIN file format provides a means of attaching an arbitrary list of node and edge attributes together with a set of graphical rendering rules. As JIN does not strive to impose any constraints on the attached attributes, it is in principle possible to map into a corresponding attribute any information obtained from a source external to the DIP database and then render it according to a set of rules specified by the end-user.

REFERENCES

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