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Modeling and Integration of Biological Networks with BiNArr

The investigation of biological networks for their better understanding and making available for practical use is currently an important task in systems biology. The authors developed an integrated environment BiNArr (Biological Network Arranger) aimed to perform a number of practically useful operations on the network data stored in biological databases. Dissimilar to the existing tools like Cytoscape the functionality of our application is rather limited and strictly oriented for transforming structured data from real databases into graphs. This allows its further processing e.g. with use of graph mining algorithms. We proposed the unified graph representation for the structures extracted from original resources and developed the modules for their visualization and edition. Another worthy features are: the automatic coding of the resulting graphs in several formats, the ability to generate graphic files for presentation purposes and an open architecture enabling to cooperate with number of existing biological databases. In order to present capabilities of BiNArr we used the biological structures representing metabolic pathways extracted from KEGG (Kyoto Encyclopedia of Genes and Genomes) as well as protein-protein interactions provided in DIP (Database of Interacting Proteins).