

MyBioNet: interactively visualize, edit and merge biological networks on the Web

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ABSTRACT

Summary: MyBioNet is a web-based application for biological network analysis, which provides user-friendly web interfaces to visualize, edit and merge biological networks. In addition, MyBioNet integrated KEGG metabolic network data from 1366 organisms and allows users to search and navigate interesting networks.

Availability and Implementation: All KEGG metabolic network data are organized and stored in the MySQL database. MyBioNet is implemented in Flex/Actionscript and PHP languages and deployed on an Apache web server. MyBioNet is accessible through all the Flash-embedded browsers at <http://bis.zju.edu.cn/mybionet/>.

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1 INTRODUCTION

Owing to the emergence and rapid proliferation of new high-throughput sequencing technologies, more and more biological data are produced and are used to infer underlying networks by means of various methods in systems biology. Network visualization can map different sorts of biological information onto the graph, giving researchers new biological insight. In this respect, network visualization is becoming increasingly important for analyzing large amounts of data.

Developed network visualizations can be roughly classified as either web-based or stand-alone (Gehlenborg *et al.*, 2010). Traditional web-based visualization tools, e.g. VisANT (Hu *et al.*, 2009), are mostly implemented as Java applets, whereas a few web-based visualization tools have been developed using the Flash platform that is browser independent and more flexible for users to design their custom templates. Cytoscape Web (Lopes *et al.*, 2010) is a web-based visualization tool based on the Cytoscape algorithm, using the Flash platform as a client component to visualize network data on websites. Another visualization tool, STRING (Jensen *et al.*, 2009), utilizes the Flash platform to visualize protein–protein interactions data on a web server. Both

these applications do not allow users to edit and update a network. yWorks developed a commercial web application yFiles Flex, which integrates complicated graph visualization and editing functionality with an internet application relying on Flash player (http://www.yworks.com/en/products_yfilesflex_about.html).

However, this is a canonical network tool, not particularly tailored for analyzing biological networks, and in addition it is commercial software.

In this article, we have developed a Web application, MyBioNet, on a Flash platform. MyBioNet is designed to be a lightweight, easy to use, web-based tool for analyzing biological networks. It has important features for biological network operations, including visualization, editing and merging networks. KEGG (Kanehisa *et al.*, 2008) metabolic networks are integrated into MyBioNet, allowing users to search and navigate the KEGG data conveniently.

2 IMPLEMENTATION

MyBioNet is developed using Adobe Flex Builder 3. The visualization part of it is based on the secondary development of Ravis library (<http://code.google.com/p/birdeye/wiki/RaVis>), an open source Flex library for data visualization of relational datasets. MyBioNet can be readily used with Adobe Flash Player installed in the user's personal computer.

Biological network data can be imported and exported through MyBioNet's predefined XML format. We have also developed a converter to transform a network file in a tab-delimited format into a network file in a predefined XML format.

MyBioNet visualizes a subnetwork which is based on a specific node named as 'root node'. The subnetwork visualization is centered around the root node, which is marked in yellow color and can be easily changed to another node. All surrounding nodes related to the root node are also shown. The relativity called 'visible distance' can be customized freely by users. Visualized subnetwork can be exported as image files with the extension 'jpg' or 'gif'

3 FEATURES

Network visualizing: MyBioNet focuses on the visualization of subnetworks. It enables users to visualize and check different

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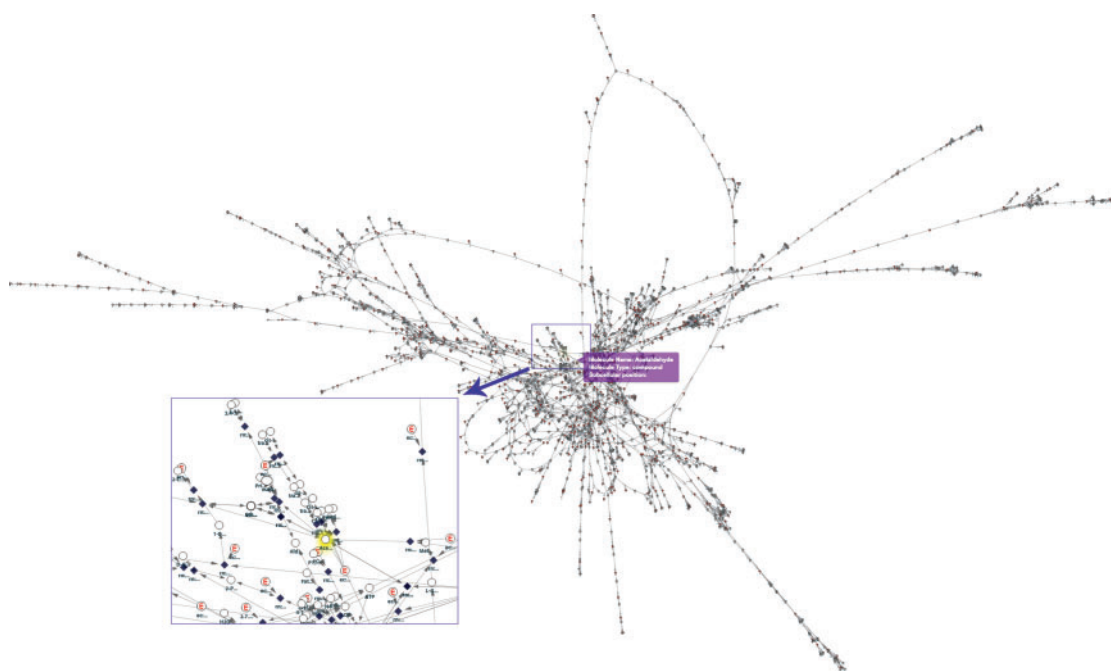


Fig. 1. The core metabolic network of *Oryza sativa japonica* includes 3035 nodes, 5774 edges; layout algorithm is force directed with the root node of acetaldehyde.

subnetwork in a large and whole network by setting different node as root node or taking various visible distances to control the subnetwork scales. MyBioNet has the basic network visualization features, which are typically used to map biological information to nodes and edges. In MyBioNet, node colors show subcellular locations, node shapes show various types of biological entities and edge shapes show types of reactions. The features of highlighting and tooltips of nodes and edges facilitate the navigation of the visualized network. The highlighted nodes or edges will have specific views, e.g. the root node glows yellow. The tooltips show the biological attributes of nodes or edges.

Network editing: we provided a network editor to enable users to examine their network data after new experiments or prediction processing. It is accessible for readily editing networks, including adding, updating and deleting network items (nodes and edges). With the editor, new networks can be conveniently created. Furthermore, users can also edit their networks interactively both in files and in the visualized network image.

Network merging: two networks with common nodes or edges can be merged when it is verified that these networks share functional modules. Common nodes are defined as items having the same names and common edges are defined as items connecting common nodes. Common nodes and edges will be labeled with the updated properties from the second network. Network merging can assist users to find the relationship between nodes in respective networks.

Navigate metabolic networks of KEGG: we integrated KEGG metabolic network data into MyBioNet through KGML files downloaded from KEGG. The KEGG data can be queried either by molecule names or by KEGG IDs among 1366 organisms. Figure 1 shows the metabolic network of *Oryza sativa japonica* in KEGG. The search result of KEGG networks can be visualized and exported as XML files. Users are allowed to access the detailed information of the network nodes or edges during navigations. Users can also try to do network merging between their network data and the KEGG data to complete the biological networks of particular species.

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Conflicts of Interest: none declared.

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