A Java applet for visualizing protein–protein interaction

Ralf Mrowka

Johannes-Müller-Institut für Physiologie, Charité, Humboldt-Universität zu Berlin, Tucholsky Str. 2, D-10117 Berlin, Germany

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ABSTRACT

Summary: A web applet for browsing protein–protein interactions was implemented. It enables the display of interaction relationships, based upon neighboring distance and biological function.

Availability: The Java applet is available at http://www.charite.de/bioinformatics

Contact: Mrowka@rz.hu-berlin.de

With the advances in the proteomics technology huge data-sets of protein–protein interactions emerge (Uetz et al., 2000). An interactive Java applet was devised which allows visualizing these interactions based on function and neighboring distances.

The challenge is to visualize these interactions, in order to find possible new genes of interest. Conventional tree visualization techniques, like file system directory representation may not be used, since there is no hierarchical structure in the data, i.e. there are circular relationships, but no root. It was decided to use a relaxation technique for this task, which maximizes the distances of the proteins in the 2D graphical representation, but constrains interacting proteins to a predefined distance. The code for the application was implemented as a Java applet, thus allowing a broad community to share and browse experimental data.

The applet is based on the GraphJava applet distributed in the Java development distribution of SUN Microsystems Inc.

Fig. 1. Java applet for visualization of protein–protein interactions.
The algorithm for finding an optimal representation of the protein is based on a relaxation technique. Two commercial products PimRider and MyriadPronet use a relaxation technique for their interaction visualization modules. Finding nth-level neighbors was implemented with a tree-scan algorithm.

The applet was tested with data of protein–protein interactions discovered by the yeast-two-hybrid technique. All 958 interactions, which occur among ~6000 open reading frames of *Saccharomyces cerevisiae* have been included. The current browsing tool (PathCalling® at http://www.portal.curagen.com) for this data-set is restricted to show up to two levels of neighboring distance. The interaction visualization modules of PathCalling, PimRider, and MyriadPronet do not allow selection of functional groups within the visualization. The devised applet provides a cost effective, easy-to-implement, and platform independent solution.

The data are fed to the applet via the applet arguments in the html source, thus other data may be visualized easily. Functions of known genes are also arguments for the applet, allowing selection of certain cellular roles.

The user may interact with the representation of the proteins using the computer mouse. This allows selection of movement and extraction of proteins (and their neighbors) of interest. Since the relaxed state is of interest, turning off the display mode will speed up the relaxation process. The number of interactions that may be visualized within the applet is limited by the size of the screen, the computational power of the computer system, and the optimization of the implementation of the virtual-Java-machine of the web-browser. The description of the algorithms applied, the usage of the program and how to implement a custom data-set can be found at http://www.charite.de/bioinformatics.

REFERENCES