

**ProViz: protein interaction visualization and exploration**

Florian Iragne, Macha Nikolski, Bertrand Mathieu, David Auber and David Sherman

LaBRI UMR 5800, Université Bordeaux 1, 351 cours de la Libération, 33405 Talence Cedex, France

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**ABSTRACT**

Summary: ProViz is a tool for the visualization of protein–protein interaction networks, developed by the IntAct European project. It provides facilities for navigating in large graphs and exploring biologically relevant features, and adopts emerging standards such as GO and PSI-MI.

Availability: ProViz is available under the GPL and may be freely downloaded. Source code and binaries are available at http://cbi.labri.fr/eng/proviz.htm.

Contact: david.sherman@labri.fr

**INTRODUCTION**

Analysis of protein–protein interaction (PPI) networks requires a combination of algorithmic and visualization tools, ideally integrated within a software platform that is itself integrated with access to local and distant data banks. We present a software tool called ProViz that provides highly interactive visualization of large networks of interactions, integrated with the IntAct data model (Hermjakob et al., 2004a). ProViz is similar in purpose to PIMrider (Legrain et al., 2001), Osprey (Breitkreutz et al., 2003), and other visualization or analysis tools (Tucker et al., 2001; Lappe et al., 2001; Koike and Rzhetsky, 2000; Shannon et al., 2003).

**OVERVIEW OF ProViz**

Graph drawing and interactive graph exploration are active domains in computer science and many tools are available for this task. Adaptation of these tools and techniques to the specific needs of biologists exploring PPI networks is a current effort in bioinformatics. The challenge is to add valuable information and functions that enable the user to discover interesting biological relations hidden within the data.

ProViz improves over existing work by providing a fast, scalable, open tool with extensive plugins, that integrates emerging standards for representing biological knowledge in a biologist-oriented interface.

*To whom correspondence should be addressed.*

**Intended use.** ProViz is designed with an understanding of the ways that biologists prefer to work. It may be used for exploring large graphs in order to identify proteins and interactions of interest, either through keyword search or through analysis of the combinatorial structure of the network; for comparing graphs from different strains or species over orthologous sets of genes; for extracting views and subgraphs for further analysis; and for clustering related proteins and interactions (see examples in Supplementary Material). ProViz is highly interactive, providing screen updates within 50 ms on standard workstations while manipulating graphs with a million elements.

ProViz can be a content-type helper for interaction database query results in PSI-MI format (Hermjakob et al., 2004b). Name-based or sequence-based queries to the IntAct federated database of protein–protein interactions produce networks that ‘link out’ to ProViz for detailed study, and protein nodes and interaction edges link back in to IntAct web services.

**User interface.** The ProViz screen is intentionally uncluttered (Fig. 1). The right half of the screen displays the current view of the current graph; the different views available are selected through the use of tabs above the window. Above this window in the tool bar are buttons for changing the layout of the current view. The mouse can be used to select elements or to move elements, and the mouse wheel can be used to zoom in or out and to pan the image. Below are buttons for cloning and for closing the view. Four tabs are available on the left: Views, for information about existing views; Node Ontology, for selecting proteins based on GO terms; Edge Ontology, for selecting interactions based on controlled vocabularies; and Properties, for viewing the complete set of properties associated with a node or edge element.

**Views.** Subgraphs produced by selection, filtering or clustering are automatically organized into views that can be manipulated independently and used to produce subsequent views. Each view has its own layout and zoom, and views can be used to compare different analyses of the same interaction network. Views are organized in a tree, a quotient graph whose nodes are individual subgraphs.
Fig. 1. View of a spoke-model PPI graph for yeast. (a) Protein properties. (b) Protein selection using GO terms. (c) Main window showing part of current view (right) and the cluster tree (left).

**Layout algorithms.** Of the dozens of layout algorithms in the plugin library, three were chosen for direct use based on their capacity to highlight biologically pertinent information. GEM (Frick et al., 1994) is an efficient directed force-based graph drawing algorithm. It groups related nodes and can be used to quickly identify proteins with a given role, or for visualizing protein complexes. Hierarchical layout (Messinger et al., 1991) reveals ancestral relationships between nodes and is useful when looking for cascade-type interactions or comparison to metabolic pathway data. Circular layout is a neutral choice that does not attribute any semantics to edge relations.

**Integrating controlled vocabularies.** ProViz uses GO and PSI-MI controlled vocabularies for describing proteins and interactions. Users employ these vocabularies when building views of interaction networks by manual filtering or through the use of clustering plug-ins. In Figure 1, we see the property list for the node corresponding to yeast Rad16 (nucleotide excision repair protein), including GO evidence, gene names and external links.

**Tulip development platform.** ProViz development is based on the Tulip platform (Auber, 2003), designed for management and three-dimensional display of large graphs. It provides a rich set of operations on graphs: metric computation, node and edge layout, selection, extraction of view and subgraphs, and labeling of nodes and edges with arbitrary sets of attributes. Operations specific to the application domain are provided by means of software plugins. Any program using Tulip can add to the core features by providing its own domain-specific plugins. Tulip is written in C++ and uses Qt and OpenGL for enhanced portability.

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**REFERENCES**


