**ProLiVis: Protein-Protein Interaction Literature Visualization System**

**Abstract**

**Summary:** We provide a visualization model that targets the visualization of Protein-Protein Interactions (PPI) and combines it with a super view based on publications and methods to extract interactions. Although there are several existing tools, our model considers the existing literature and is capable to demonstrate all interactions for the selected organisms. In our model, we propose a three-level visualization concept for the PPI networks with the current state-of-the-art studies based on several organisms. And, we abstract of overall network based on two perspectives; "experimental method types of each interaction" and "ownership with the publication". We claim that it is more efficient to work on our proposed layout rather than parsing text files or databases. For that way, we plan to support the existing visuals with complementary outsourced information from the existing knowledge base.

**Availability:** ProLiVis is available under the MIT License. Source code is available under Github and binaries are implemented using OGDF and cross-platform QT Framework

https://github.com/melihsozdinler/CenterLayout

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**Keywords** PPI Networks · Information Retrieval · Literature Preview

1 Introduction

Visualization of biological data is a key and important task for research teams. This is because there has been already a data explosion and it is hard to distinguish extract expected know-how from text files without visualization and analysis. In some cases, biological data converges to large networks and it is more attractive to use some tools to observe hidden outcomes. Protein-Protein Interaction (PPI) networks are one of the kinds that require meaningful visualizations and layout methods. Unfortunately, these networks may converge to hundred of thousands of interactions with more than several thousand nodes. Recently, the statistics of well-known PPI database, BioGRID Stark et al. [2006], has reached more than 2,290,000 raw interactions at the 4.4.203 version. And, raw interactions was 830,000 at the 3.2.106 version. As a result, the visualization of all such interactions is not possible and yields congested layouts. As a result, researchers require using new layout models or some abstraction layer for further analysis rather than visualizing all interactions. Currently, there are several visualization tools aimed to visualize these networks. These are ProViz [Iragne et al. [2005], Osprey [Breitkreuz et al. [2003], Medusa [Hooper and Bork [2005], PIVOT [Orlev et al. [2004], Robinviz [Aladag et al. [2010]. For more information, refer to the review paper of Pavlopoulos et al. [2008]. Our motivation is to approach from a different perspective for the visualization of these networks. Using natural clustering identities such as Experimental Methods to extract an Interaction and Published Literature Papers can support our motivation to do abstraction layer. With that motivation, we can contain all interactions in one unique layout with the appropriate abstraction model. This unique layout is also supported with sub-layouts to increase the efficiency of information extraction.

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Figure 1: a) Conceptual First Level Visualization of *Rattus Norvegicus*; b) Second Level Visualization or PPI View; c) Outsourced information tab for the selected protein SNAP25 in (b); d) *Mus Musculus* Literature View example from the current ProLiVis Software

2 Method Overview

Our visualization model contains three levels of hierarchy. The first level represents the overall visualization. The overall visualization contains different types of nodes and semantic edges. Nodes differ according to two semantic identities; "Experimental Methodology of an Interaction" as *type I node*, and "Published Literature Papers and First Author Name" as *type II node*. Among these, *type I node* identity allows us to filter the whole network with "Experimental Methods". Additionally, *type II node* lets us to filter the "Literature" for the specific organisms supported by BioGRID database. Using the *type II node* node identity, the contribution of any publication is ready for the visualization. The amount of contribution can also be validated with the size of nodes. When the node size grows, this means its publication source is contributed more. We also propose the third level. Even, in terms of publication number, there could be thousands of *type I node* entities. We limit the first level hierarchy when there are less contribution of interactions and we add a new type of node that collects these nodes into the third layout for each *type II nodes*. This allows us to simplify the first level into one apparent node and to form a third level for these nodes. The edges in the first and third level represented as *semantic edges* meaning that if a *type I node* is connected *type II node*, we infer that publication under
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**Visualization Tool**

*type I node* use the experimental methodology of *type II node*. In addition to all these, We use the format and data of BioGRID [Stark et al. 2006]. BioGRID allow us to form three-level layouts for the supported organisms.

In Figure 1(a), we provide the conceptual visualization of the first level layout of *Rattus Norvegicus*. Adjacent nodes like *FRET*, *Co-Crystal Structure*, *Protein-Peptide* are *type I node* and leaf nodes show us the third and they represent literature nodes and we also call *type III node*. In Figure 1(b), we provide second-level visualization of *type III nodes*. This visualization is currently supported with Force Directed Layout. And, large networks can be considered as future work. In Figure 1(c), we select *SNAP25* protein from Figure 1(b) and inside the tool, we will provide access to online databases such as BioGRID, UniProt, and Gene Ontology Amigo. In Figure 1(d), we give the view current development version of ProLiVis and the concept mentioned in Figures 1(a,b,c) are expected to be finalized as future work.

There are also several unique properties of our visualization tool.

- **Literature Overview**: We can see all publications in three-level layouts. The first level and third level give the literature overview of a specific organism. For each node, tool-tips and labels can be seen. Each label has author information and a unique PubMed ID. The layout is also interactive with zoom-in and zoom-out.

- **PPI View**: PPI view is the part of all *type I node* identities. It is based on Force Directed Layout of OGDF library [Gutwenger et al. 2001] and allow users to see the whole PPI the network formed within its publication. Each protein nodes in PPI View have an option to reach the corresponding familiar websites using QT Webkit.

- **Local Computation**: Our main concern is to provide an instant view to users about the current literature of the PPI network. When a user needs to visualize interactions of any publications, that will be obtained from the local indexed database. That way users can continue using the visualization part without the Internet connection. As a future plan, users can also download new DB files when the BioGRID releases a new snapshot. Retrieval of DB files and update procedure is not implemented yet.

### 3 Conclusion

ProLiVis differs from other tools with its interactive level-by-level hierarchy. Similar interactivity is also proposed in Robinviz [Aladağ et al. 2010]. Rather than using theoretical clustering methodologies, ProLiVis use natural clusters and propose end-users efficiently without disturbing the overall layout. For the new enhancements and future work, we plan to extend the existing first-level hierarchy. We can add new node types to increase the information extraction such as publication year. Also, we will write some plugins to post the specific graphs to the other visualization tools for further analyses.

BioGRID also offers Cytoscape [Otasek et al. 2019] plugin(https://wiki.thebiogrid.org/doku.php/biogridplugin2), however this plugin directly focus on PPI network visualization. There is no combined high-level view for an organism like we offered in Figure 1(d).

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