CALIFORNIA STATE SCIENCE FAIR
2017 PROJECT SUMMARY

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Project Title

New Link Grouping Network Visualization Technique for Social Network Analysis and Biological Network Alignment

Abstract

Objectives/Goals

Traditional node-link diagrams for visualizing networks do not scale as networks become larger and are nicknamed "hairballs". To address the need for the visualization of large networks, the Institute for Systems Biology, Seattle, developed BioFabric, a software tool that depicts nodes as horizontal lines and edges as vertical lines. However, the BioFabric default layout does not utilize link relations. My objective is to develop link grouping network visualization that allows the user of BioFabric to closely analyze link relations, as well as network connectivity and biological network alignments.

Methods/Materials

I implemented the link grouping network visualization within the existing open-source BioFabric Java code base. I developed the link grouping algorithm that places edges of the same link relation adjacent to each other forming link groups. I tested the link grouping layout on a Facebook social network and the alignment of the protein-protein interaction (PPI) networks of mouse and plant.

Results

The link grouping layout displays each social circle in the Facebook social network in organized fashion that amplifies similarities and differences in connectivity. Social circles with high connectivity are easily distinguishable due to the similar shape of the edges laid out on each node-line. The link grouping layout displays the network alignment of the mouse and plant PPI networks with its aligned edges and unaligned edges placed in separate link groups. Based on the relative width of each link group, one can see how topologically similar these networks are, thus allowing the transfer of biological data between the mouse and plant PPI networks.

Conclusions/Discussion

I developed a novel method to visualize large and complex networks that provides several advantages over traditional node-link diagrams and the BioFabric default layout. This method gives researchers a powerful tool to analyze link relations, network connectivity, and network alignments through simple inspection.

Summary Statement

I developed a software tool based on link grouping that allows researchers to visualize and analyze large and complex networks through simple inspection.

Help Received

Mr. Longabaugh at Institute for Systems Biology, Seattle, and Prof. Hayes at UC Irvine provided guidance and valuable comments.