Exploring the Use of 3D Layouts to Analyze Disease-Gene Networks

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Abstract

While several network visualization applications provide the ability to lay out networks in three dimensions (3D), few studies have analyzed their usefulness for biological networks. Using a case study approach, we used a 3D network to analyze a dataset of 7 renal diseases and 747 implicated genes. Our initial results pinpoint the challenges in using 3D network layouts, and provide insights on how those challenges might be overcome by viewing a 3D network in a 3D immersive environment.

Introduction

Numerous network visualization applications such as Pajek provide the functionality to lay out networks in 3D. However, while bioinformaticians have widely adopted network analysis, the networks themselves have been visualized and analyzed mainly in two dimensions (2D). Using a case study approach we posed the question: *Can 3D network layouts reveal novel regularities in biological networks?* Here we present initial qualitative results suggesting how 3D layouts can be effective in analyzing networks.

Method

We used the Fruchterman-Reingold [1] force-directed 3D layout algorithm in Pajek version 1.23 to lay out a bipartite network of 747 genes significantly regulated in 7 renal diseases. The resulting layout was viewed in the Pajek viewer, which enables the network to be dynamically rotated horizontally and vertically around the central axes. The 3D layout was compared to a 2D layout of the same data published in a previous study [2].

Results and Discussion

Figures 1a and 1b show the 2D and 3D network layouts of the same data. As shown by the arrows, the 3D layout expanded a dense collection of genes close to the center of the network verifying our earlier observation that four diseases close to the center had mostly down-regulated genes. However, our interaction with the 3D network revealed two difficulties. (1) Several of the nodes (e.g., SLE to the far left) were occluded by edges that were in front of them, and their labels were not visible. (2) Horizontal and vertical rotation of the network enabled us to view the above occluded nodes, but it was difficult to comprehend the network as the node labels were moving across the screen causing us to get disoriented. The 3D network, viewed on a 2D screen therefore helped to verify previous results, but did not lead to any new insights due to the occlusions, and disorientation caused by the rotations.

Our ongoing investigations suggest that the above limitations can be addressed by viewing the network in an immersive 3D environment, where the viewer can traverse a magnified network without occlusion. Such studies should reveal if 3D networks viewed in 3D immersive environments can help to reveal novel insights in biological networks.

References

1. Fruchterman T, Reingold E. *Software: Practice and Experience* 1991; 21:1129-1164.
2. Bhavnani SK, Eichinger F, Martini S, et al. *BMC Bioinformatics,* 2009; 10:S3.

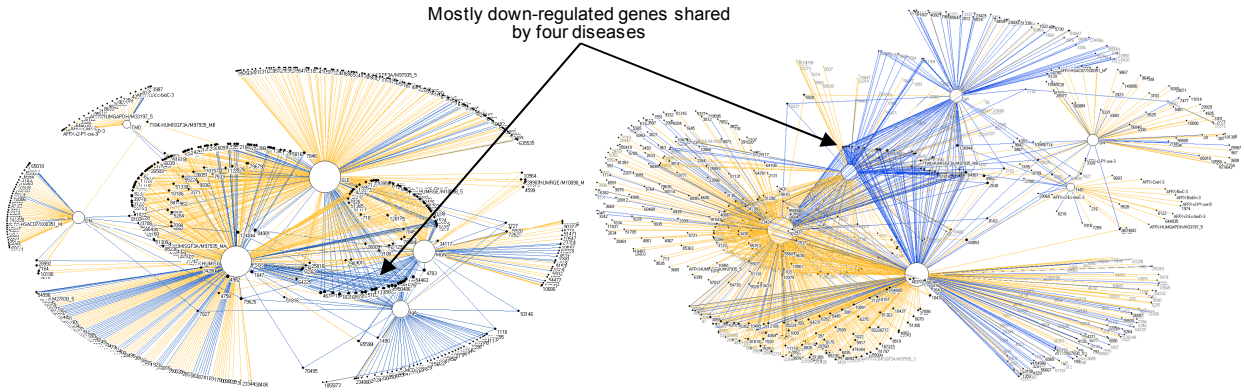

Figure 1. The renal bipartite network laid out by the Fruchterman-Reingold [1] algorithm in 2D (a), and in 3D (b). The white and black nodes represent renal diseases and implicated genes respectively, and the yellow and blue edges represent up and down regulation respectively.