LETTERS

HiVis: A portable, scalable tool for hierarchical visualization and analysis of biological networks

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Abstract

It is very important to analyze the network structure of interacting genes, proteins, RNAs, etc. in large scale biological networks which represent complex biological systems. Many tools have been made for this purpose. However, they are either unable to display the hierarchically structured view of the networks or not easy to build in cross-platforms. Here we present a navigation tool called HiVis for biological network visualization. HiVis provides a hierarchical view of the networks through a zoom-in or zoom-out function powered by k-means and fast approximate spectral clustering algorithms. It is a cross-platform, portable, fast desktop application to large scale networks.

Keywords: hierarchical visualization; cross-platform; clustering algorithms

Content

Text and results for this section, as per the individual journal's instructions for authors. [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13]

Section title

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If we assume that sensitive cells follow a deterministic decay $Z_0(t) = xe^{\lambda_0 t}$ and approximate their extinction time as $T_x \approx -\frac{1}{\lambda_0} \log x$, then we can heuristically estimate the expected value as

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Figures

Figure 1 Sample figure title. A short description of the figure content should go here.

Figure 2 Sample figure title. Figure legend text.