

Licentiate Thesis in Computer Science

Towards the Visualization of Multivariate Biochemical Networks

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Abstract Many open challenges exist when dealing with different biological networks. They are crucial for the understanding of living beings. Complete drawings of these typically large networks usually suffer from clutter and visual overload. In order to overcome this issue, the networks are divided into single, hierarchically structured pathways. However, this subdivision makes it harder to navigate and understand the connections between pathways. Another challenge is to visualize ontologies and hierarchical clusterings, which are important tools to study high-throughput data that are automatically generated nowadays. Both of these methods produce different types of large graphs. Although these methods are used to explore the same data set, they are usually considered independently. Therefore, a combined view showing the results of both methods is desired. Additionally, real life data sets, including biological networks, usually have additional attributes related to the considered network. Investigating means to visualize such multivariate data together with the network drawing is also one of the ongoing challenges in biology, but also in other fields.

The aim of this thesis is to lay out the foundations towards defining techniques for the visualization of multivariate biochemical networks. An overall understanding of the problems related to biochemical networks should be acquired to achieve this aim. More importantly, a contribution to the aforementioned challenges is necessary. Two research goals have been defined to accomplish our aim: for the first goal, we should improve shortcomings of the approach of dividing larger biological networks into smaller pieces and contribute to the problem of a visualization of different types of interconnected biological networks. The second goal is a contribution for the visualization of multivariate biological networks.

Initially, a brief survey on techniques to visualize multivariate networks is presented in this thesis. Then, various visualization and interaction techniques are presented that address the challenges in biochemical network analysis. Three different software tools were implemented to demonstrate our research efforts. We discuss all features of our systems in detail, describe the visualization and interaction techniques as well as disadvantages and scalability issues if present.