

8.8 Explorative Graph Visualization

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The exploration of graphs for analysis purposes has received increasing interest over the last years. What started out as a socio-mathematical tool for network researchers is nowadays applied to networks in many application domains ranging from homeland security to cell biology. Yet, the larger these graphs grow the more analysis needs to integrate explorative, visual methods alongside computationally complex algorithms. This has not only the benefit of utilizing the extremely efficient visual system of the human analyst, but also of bringing the analyst with her background knowledge and common sense back into the previously more and more automated analysis process. This development falls under the only recently coined term *Visual Analytics* [1].

In the context of the GRK dIEM oSiRiS, Visual Analytics of graphs is employed to gain insight into the time-varying structures of cell biological models. This raises several visualization challenges imposed by the models themselves and by the available associated data including biological experiment results from the wet-lab and simulation experiment data from the dry-lab:

- the models may be of different graph types and on different levels of scale – from small-scale network structures of signalling pathways to large-scale hierarchical structures of agent-based multi-level models,
- the inherently uncertain biological context from which the model parameters have been derived must be communicated – e.g., accuracy and precision of the corresponding lab experiment,
- the large quantity and stochasticity of the resulting data for multiple experiment setups and multiple simulation runs must be handled and visually integrated.

An integrated visual analysis of cell biological model structures generating a synergy, an added analytical benefit of the above aspects, is one of the main aims of the combined visualization efforts in the GRK dIEM oSiRiS.

Depending on the type of the model structure (e.g., hierarchy, network, hypergraph), different integrated visualization approaches have been developed in the GRK. For the coupling between model and simulation data, this includes for example a table-based visualization technique for attributed π -Calculus models, which exhibit a time-varying, bipartite graph structure during simulation. Its table-layout allows for an intuitive exploration of structural relations as well as node attributes at the same time [2]. Time-value

plots enhance the exploration and hint at time points of interest by evaluating a model's structural complexity and other parameters over time [3]. This visualization is used for model debugging and refinement.

For the integration of wet-lab data from the biomedical domain with the model, this includes the utilization of the visual analysis framework Caleydo for the combined exploration of pathways and gene expressions. In this specific case, the focus lies on the co-located, cooperative visual analysis by bringing together domain experts from different fields of biology and medicine and visually guiding them along the exploration process [4]. This is yet another current research topic in Visual Analytics and our GRK is a prime example for the necessity of interdisciplinary, cooperative analysis.

This summarizes some of the research on Visual Graph Exploration in the scope of the GRK diEM oSiRiS. Other research topics within the GRK interlock with this work, as multiple research challenges need to be addressed simultaneously and in close cooperation in order to find a comprehensive solution. One example is the heterogeneity of the data and the visual integration of the multiple available data sources from wet-lab and dry-lab experiments, as well as data from online databases (e.g., pathways) along the lines of the interaction concept developed in [4]. Other research within the GRK more extensively explores time-varying properties of model structures and the integration of visualization into the model validation process.

Bibliography

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