

Development of a Cytoscape plugin for analysis of biological time series data.

Backgrounds

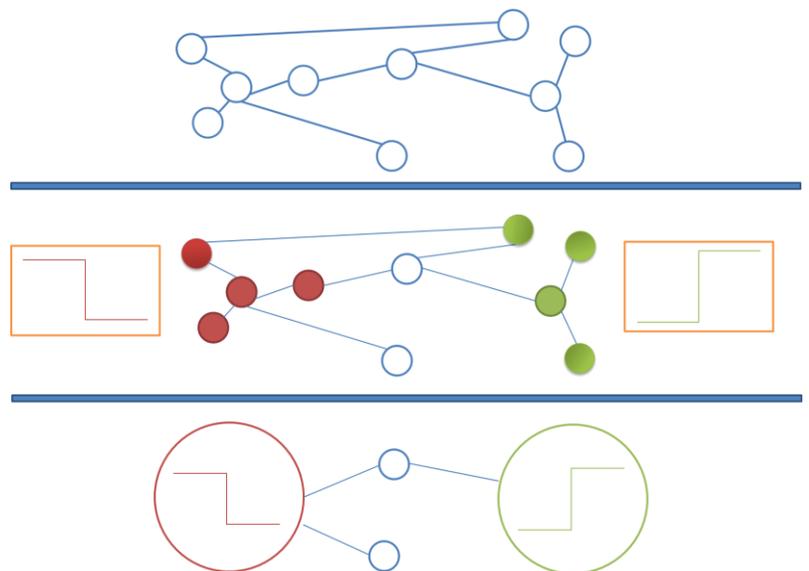
Network visualization is often the first step of a network analysis. However, the visualization of biological time-series data still poses a major challenge: such visualization has to preserve information about the network's topology as well as its changes over time as best as possible. This easily leads to high complexity and reduces interpretability.

To reduce this visual complexity, one can partition the given network into subgraphs which exhibit similar behavior over time. Because each subgraph can be represented by a prototype-node the resulting visualizations are easier to interpret. Clustering methods can be used to identify such subgraphs, where nodes of a single subgraph show a predefined time-series expression profile. Entities sharing the same profile might exhibit similar cellular functions and can give clues about the global behavior of the biological system in the given time points. We want to develop a Java plugin which extends the widely used network analysis platform Cytoscape with such visualizations.

Aims

The aim of this project is to design and implement a Cytoscape plugin which visualizes groups of entities that follow predefined time series pattern in the context of known biological networks. The plugin should be able to:

- (1) map the time-series data and clustering of entities to the biological network
- (2) provide a simplified visualization of the whole biological network, which highlights the groups of nodes that follow the same time-series pattern.



Conclusion

Nowadays, many large scale biological projects measure time series data. Solutions to represent this data are of high importance. This project will provide the applicant with experience in working with biological data and with the commonly used network analysis software Cytoscape. It will challenge your programming skills, expand data visualization experiences, and further offers the chance to contribute to an important and challenging problem in the bioinformatics/systems biology field.