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Identifying a coherent network partition (CNP) together with its related optimization variant

During my Master studies in Computer Engineering I have been become passionately interested in artificial intelligence and machine learning approaches applied to bioinformatics problems. Since data from cellular systems reflect properties of the underlying molecular networks, I would like to gain more understanding of methods which allow reverse engineering of networks based on heterogeneous biological data. As a part of my doctoral work, I will investigate a novel clustering approach which can be applied for mining different biological networks (e.g. protein-protein interaction and gene co-expression networks). Network cluster analysis has already been used to predict gene function, to conduct enrichment analysis with omics data and ontologies. I plan to address the problem of identifying a coherent network partition (CNP) together with its related optimization variant. A coherent partitioning of a graph G allows us to extract clusters which correspond to biclique spanned subgraphs. Some theoretical results about this problem are known (e.g., computational complexity and behavior of special network classes), but its applicability to biological networks has not yet been studied in detail. In addition, connections to seminal approach, such as network modularity, need to be clarified via a comparative study. Exposure to approaches which relate structure of models with their dynamic behavior will provide me with further directions for relating network clusters to underlying biological mechanisms.

Summary

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