Chordal Graphs in Computational Biology - New Insights and Applications

(Keynote Talk Abstract)

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Recent advances in experimental techniques resulted in accumulation of vast amounts of information, which is often represented by various types of biological networks. Therefore it is not surprising that increasingly more complex graph-theoretical tools are developed to analyze such biological networks and extract biologically meaningful patterns. In this talk I will describe the research done in my group directed towards computational analysis of biological networks.

Graph theoretical representation of biological relationships provides insight into the evolution of biological systems and their function. For example, in order to focus on the properties of multi domain proteins and the relationships between them, we introduced and studied graph theoretical representation of multidomain proteins called domain overlap graph. In the domain overlap graph, the vertices are protein domains and two domains are connected by an edge if there is a protein that contains both domains. We demonstrate how properties of this graph such as chordality and the Helly property can indicate various evolutionary mechanisms [1].

The concept of domain overlap graph can be seen as an example of a more general construction, the construction of character overlap graphs. We show that character overlap graphs for characters that are appropriate to use in parsimony methods are characterized by significant under-representation of holes, and thus are relatively close to chordal graphs. This characterization explains success in constructing evolutionary trees using parsimony method for some characters (e.g. protein domains) and lack of such success for other characters (e.g. introns). In the latter case, the understanding of mathematical obstacles to applying the parsimony method in a direct way has lead us to a new algorithm that is able to bypass these obstacles [2].

A major challenge in systems biology is to understand the intricate network of interacting molecules. The complexity in biological systems arises not only from various individual protein molecules but also from their organization into systems with numerous interacting partners forming protein complexes and functional modules. We focus on the analysis of protein-protein interaction networks directed towards recovering temporal relation and overlaps between functional groups. We developed a graph-theoretical framework, based on properties of chordal graphs and cographs [3]. We apply our approach to delineate pheromone signaling pathway from the high throughput protein-protein interaction network.

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References

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