

Ph.D. in Information Technology: Thesis Defense

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Computational methods for data-driven predictions and understanding of biological interactions

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Abstract:

Eukaryotic cells are complex biological systems in which complex phenomena take place, including molecular interactions. Mechanisms of cell regulation, differentiation and development derive from such complexity, and they can be explored through system biology, i.e., a common approach for studying molecular interactions involved in specific functions within a cell. Complex networks provide a generalizable method to represent object associations and to understand the overall structure of complex systems. Network-based approaches allow a global vision of each node's contribution, providing insights that other methods based on single node analyses cannot give. Indeed, they are able to significantly improve our knowledge of biological systems and shed light on pathological disruptions occurring in the cell. Moreover, one of their main features is their ability to easily integrate data from various sources. During the last decade, massive efforts were made to build public databases of biological data; among them, next-generation sequencing (NGS) and drug-related data are the ones used for this project. Complex networks are the perfect paradigm to answer to several different biological questions using a vast amount of heterogeneous data due to their reductionist approach. This Thesis focuses on three main steps of network biology: network inference, link prediction and network feature extraction; for each of them it innovatively describes state-of-the-art computational methods and novel computational approaches applied to answer a specific key biological question in a considered case study, obtaining relevant results. My work offers a broad picture regarding what complex networks may accomplish in biology and contributes to delivering advances in this field. From the computational perspective, I developed novel approaches to build, predict and analyze complex networks, whereas, from a biological standpoint, the achieved results have a significant impact on the considered case studies.

PhD Committee

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