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Title: Computational Network Biology for systems-level functional annotation of proteins and proteomes

Abstract:

Computational Systems Biology aims to develop and apply efficient algorithms to address critical scientific questions through computer simulations and theoretical modeling. The system-wide level modeling is particularly relevant in modern biological sciences, where the key challenge has shifted from the study of single molecules to the exhaustive exploration of molecular interactions and biological processes at the level of complete proteomes. Understanding how complex living systems work can help find treatments for disorders of poorly understood etiology, such as cancer and neurodegenerative disorders. The major focus of our group is the design and development of novel tools for the modeling and analysis of biological networks using Computational Systems Biology. We are interested in applying various Computational Systems Biology tools to study the evolution and organization of pathways into biological networks with the primary application in modern drug discovery and design.