Computational Methods for Data-Driven Study of Protein Structure and Function

High-throughput sequencing has been producing a large amount of protein sequences, but many of them are missing solved structures and functional annotations, which are essential to the understanding of life processes and diseases and also have tremendous implications to drug discovery and design. This talk will focus on protein homology detection and knowledge-based structure prediction, which are widely used for the elucidation of protein structure and function as well as protein evolutionary relationships. In particular, this talk will demonstrate how statistical machine learning (e.g., probabilistic graphical models) and optimization methods can be applied to address some fundamental challenges facing protein homology detection and protein folding by taking advantage of high-throughput sequencing.

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