TITLE: From sequences, structures, to interactions of proteins: some recent development.

ABSTARCT:
How proteins fold and bind is a long standing unsolved problem in computational biology. Many tools ranging from machine learning to ab initio structure/ interaction prediction have been developed. In this tutorial, I will discuss several recent development in sequence alignment, sequence-based prediction of structural properties and three-dimensional structures of proteins, and structure-based discovery. In particular, we will discuss in detail the role of profile-profile alignment in multiple sequence alignment, the advancement of accuracy in predicting secondary structures, residue-solvent accessible surface areas and fold recognition, and the impact of a physical reference state in statistical energy function for investigating protein-folding, protein-protein, and protein-ligand interactions.

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