# Developing adaptive data analysis approaches for protein research

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The biological activities and functional specificities of proteins depend on their native three-dimensional structures, which are defined by the corresponding chemical compositions or sequences. Statistics on the structures suggests that, there are universal geometric factors as constraints on native conformations, while the combinations of properties of amino acids in sequences lead to diversity of functions. In this seminar, I will introduce our recent works on structure, stability, and dynamics of biomolecules based on adaptive data analysis approaches which are developed to reconcile two concepts. Application of the idea to the analysis of intrinsically disordered proteins will also be discussed.