

**"Beyond Sequence Alignment": An Optimization Framework for
the Inference of Nontrivial Protein Domain Architecture and Ancient Homology"**

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ABSTRACT

Sequence alignment is at the root of bioinformatics. However, in the post-genomics era, new problem formulations and techniques are needed to meet the challenge of real-world complex biological problems. In this talk we discuss two problems: (i) aligning multiple sequences with shuffled and repeated domains; and (ii) discriminative classification of homologous proteins from structurally analogous proteins. I will show that both problems can be formulated as an optimization problem over the network of aligned residues. Different techniques for solving these problems will also be discussed.