

Speaker: Allen Holder
Department of Mathematics
Rose-Hulman Institute of Technology

Title: Efficient Protein Alignment

Abstract: Computational Biology is a burgeoning field of study that applies mathematics and computer science to answer questions in biology. One of the primary studies lies with identifying protein structure and function, and one way to assess a protein's function is to associate it with similar proteins whose function is already known. We develop a model for pairwise comparisons using fundamental topics in linear algebra. We show that we can solve our optimization model in polynomial time with a single application of dynamic programming. Recent computational results show that our mathematical model is stable with regards to data perturbations due to experimental errors or protein dynamics.