

**Invited Speaker**  
Dr Minghui Jiang  
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***Protein Folding Using the 2D Hexagonal Lattice***

Abstract: Protein folding in the HP model using the 2D hexagonal lattice is a biologically meaningful alternative to the standard square lattice. The hexagonal lattice alleviates the "sharp turn" problem and models certain aspects of the protein secondary structures more realistically. We present a 1/6-approximation and a clustering heuristic for protein folding on the hexagonal lattice. We also implement a Monte Carlo Metropolis algorithm based on the pull moves and a branch-and-bound partial enumeration algorithm, and conduct experiments on simulated data to compare the effectiveness of these algorithms. Finally, we report our on-going work on using the 3D triangular lattice for the study of the RNA secondary structures with pseudo-knots.

Minghui Jiang is an assistant professor of computer science at Utah State University. He received a Ph.D. in computer science from Montana State University in 2005, two M.Sc.s in computer science and physics from Purdue University in 1999, and a B.Sc. in physics from Peking University in 1997. His research interests are the design and analysis of algorithms, discrete and computational geometry, bioinformatics and computational biology, and combinatorial optimization.