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SEMINAR

HPD Model for Protein Structure Simulation

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Abstract: The protein folding problem is a fundamental problem in computational molecular biology. Various methods have been applied to solve protein folding problem. We represent the protein like a sequence over 3 letter alphabet according the specific functions of amino acids (hydrophobic, polar or destructor). After that the folding problem is defined like optimization problem. Our protein model is multifunctional. It can be used to predict the 3D structure of the protein from its amino acid sequence. The model can predict the changes in the protein folding when several amino acids are mutated. By it can be constructed a protein with needed 3D folding.

Bio: Stefka Fidanova was born in Stara Zagora, Bulgaria in February 14 1964. She received her master and PhD degrees from Sofia University, Bulgaria in 1988 and 1999 respectively. Since 1993 she works in the Institute of Information and Communication Technologies (former Institute of Parallel Processing) at Bulgarian Academy of Science. Her main fields of research are stochastic methods for combinatorial optimization, parallel algorithms, mathematical modeling. She has several long stays in foreign universities as: 1995, 6 months at Institute of Applied Mathematics and IMAG - Centre National de Recherche Scientifique - LMC, Grenoble, France; 1999, 1 year Post.Doc at Institute National de Recherche en Informatique et en Automatique, Sophia-Antipolis, France; 2000-2002, 2 years Marie Curie Fellow of EC at IRIDIA Universite Libre de Bruxelles, Belgium; 2007, 3 months invited professor University of Malaga, Spain. She has more than 110 publications including 10 books and book chapters. Her results are cited more than 320 times.

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