

Computational Structural Bioinformatics Workshop

November 4, 2007, San Jose CA

<http://www.cs.nmsu.edu/~xqin/bioworkshop/bioworkshop.htm>



The Program

10:30-11am	Poster setup
11-12:30am	Session I
Welcome	
"Refinement of Under-determined Loops of Human Prion Protein by Database-Derived Distance Constraints" <i>Feng Cui, Kriti Mukhopadhyay, Wonbin Young, Robert Jernigan, and Zhijun Wu</i>	
"Comparison of Experimental and Computed Protein Anisotropic Temperature Factors" <i>Lei Yang, Guang Song, and Robert Jernigan</i>	
"Non-Quantized Minimum Free Energy in Untranslated Region Exons", <i>Keith Knapp, Ahadur Rahaman, and Phoebe Chen</i>	
"Point to face shortest paths in simple polytopes with applications in structural proteomics" <i>Yam Ki Cheung and Ovidiu Daescu</i>	
12:30 - 1:30pm	Conference lunch break
1:30-3:20pm	Session II
1:30-2:10pm Keynote Speaker: Dr. Vasant Honavar, Dept. of Computer Science, Iowa State University	
"Incorporating Constraints from Low Resolution Density Map in Ab Initio Structure Prediction Using Rosetta" <i>Yonggang Lu, Charlie E. M. Strauss, and Jing He</i>	
"Enhancing the Computation of Approximated Solutions of the Protein Structure Determination Problem Through Global Constraints for Discrete Crystal Lattices", <i>Alessandro Dal Palu, Agostino Dovier, and Enrico Pontelli</i>	
"Structural Characterization of RNA-Binding Sites of Proteins: Preliminary Results" <i>Fadi Towfic, David Gemperline, Cornelia Caragea, Feihong Wu, Drena Dobbs, and Vasant Honavar</i>	
3:20-4:10pm	Poster session & Coffee break
4:10-5:30pm	Session III
"Detecting Constituent Sequences by means of HP Pattern Based Grammars to Synthesize Proteins: inferring sequence-structure-function relationship", <i>Giuseppe Nicosia, Eva Sciacca, and Luca Zammataro</i>	
"Flagellar Proteins Prediction After Sequence-Structure Alignments of Coronin and Arp2/3 Complex in Leishmania spp.", <i>Marcilia Costa, Halisson Ribeiro, Allan Rodrigo Maia, Ana Carolina Pacheco, Daniel Pinheiro, Michel Kamimura, Raimundo Arajo-Filho, and Diana Oliveira</i>	
"PRTAD: A Database for Protein Residue Torsion Angle Distributions" <i>Xiaoyong Sun, Di Wu, Robert Jernigan, and Zhijun Wu</i>	
Closing Remarks	

Poster:

"Protein folding simulation by all-atom CSAW method", Weitao Sun

"An approximate robotics algorithm to assemble a loop between two helices" Jing He, and Kamal Al Nasr

"Alignment meets graph theory" Jarrar, and Brook Milligan

"Targeted data mining of spatial proximity relationships of repetitive regions in genomes" Surya Saha, Daniel G. Peterson, Susan Bridges

PROGRAM CHAIRS

Jing He, New Mexico State University

Jinyan Li, Nanyang Technological University, Singapore

PROGRAM COMMITTEE

Jin Chen, Stanford University

Lin Feng, Nanyang Technological University, Singapore

David Hsu, National University of Singapore

Haiquan Li, Noble Foundation, USA

Suryani Lukman, Institute for Infocomm Research, singapore

Enrico Pontelli, New Mexico State University

Guang Song, Iowa State University

Joe Song, New Mexico State University

Michela Taufer, University of Texas at El Paso

Changhui Yan, Utah State University

Iosif Vaisman, George Mason University

STEERING COMMITTEE

Lydia Kavrakli, Rice University

Desh Ranjan, New Mexico State University

Vasant Honavar, Iowa State University