The 2009 Computational Structural Bioinformatics Workshop

November 1, Washington D.C.

The Program

8 - 8:15am   Poster Setup
8:15 - 10am   Session 1 (Cabinet/Judiciary Room, Each speaker: 18-minute talk + 2-minute questions)
Brief Welcome   8:15 - 8:20am
1. "An Efficient Geometric Build-up Algorithm for Protein Structure Determination with Sparse Exact Distance Data"   *Robert Davis, Claus Ernst, and Di Wu*
2. "Tracing Conformational Changes in Proteins"   *Nurit Haspel, Mark Moll, Matthew Baker, Wah Chiu, and Lydia Kavraki*
3. "Prediction of Protein Long-Range Contacts Using GaMC Approach with Sequence Profile Centers"   *Peng Chen and Jinyan Li*
4. "Generalized Spring Tensor Models for Protein Fluctuation Dynamics and Conformation Changes"   *Tu-Liang Lin and Guang Song*
5. "An artificial backbone of hydrogens for finding the conformation of protein molecules"   *Carlile Lavor, Antonio Mucherino, Leo Liberti, and Nelson Maculan*
10:00 - 10:15am   Coffee Break
10:15 - 12:15pm   Session 2 (Cabinet/Judiciary Room, Each speaker: 18-minute talk + 2-minute questions)
6. "Effect of sidechain anisotropy on residue contact determination"   *Weitao Sun and Jing He*
7. "Computational Testing of Protein-Protein Interactions"   *Ataur Katebi, Andrzej Kloczkowski, and Robert Jernigan*
8. "Discrimination of Thermophilic and Mesophilic Proteins"   *Todd Taylor*
9. "Sequence-based B-cell epitope prediction by using associations in antibody-antigen structural complexes"   *Liang Zhao and Jinyan Li*
10. "Matching Observed Alpha Helix Lengths to Predicted Secondary Structure"   *Brian Cloteaux and Nadezhda Serova*
11. "How does the periodicity associated with nucleosomal DNA reflect on its intrinsic curvature?"   *Murlidharan Nair*
12:15-1:15pm   Lunch Break
1:15-2:15pm   Poster Session
2:15 - 3:55pm   Session 3 (Cabinet/Judiciary Room, 20 minutes each)
12. "Polynomial-Time Disulfide Bond Determination Using Mass Spectrometry Data"   *William Murad, Rahul Singh, and Ten-Yang Yen*
13. "Density-Based Classification of Protein Structures Using Iterative TM-score"   *David Hoksza and Jakub Galgonek*
14. "A global optimization algorithm for protein surface alignment"   *Paola Bertolazzi, Concettina Guerra, and Giampaolo Liuzzi*
15. "Upper Bounds for Foldings in the FCC-HP Protein Model"   *Abu Dayem Ullah and Kathleen Steinhofel*
16. "Node Degree Distribution in Amino Acid Interaction Networks"   *Omar GACI and Stefan BALEV*
3:55pm   Closing Remarks

Posters :

Paper 1-16 and additionally following two posters:

"Fast database search for similar and flexible structures based on TOPS++FATCAT", *Mallika Veeramalai and Adam Godzik*

"Structure Prediction for Helical Skeletons from Low Resolution Protein Density Map", *Kamal Al Nasr, Jing He*

PROGRAM CHAIRS	Leela Rakesh, Central Michigan University
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Jing He, Old Dominion University	Joe Song, New Mexico State University
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PROGRAM COMMITTEE	
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