

Third IEEE International Workshop on High Performance Computational Biology (HiCOMB)

April 26, 2004

Eldorado Hotel, Santa Fe, NM

in conjunction with 18th International Parallel and Distributed Processing Symposium

Message from the Workshop Organizers

Welcome to the Third International Workshop on High Performance Computational Biology. With the explosion of biological data and the compute-intensive nature of many biological applications, the use of high performance computing will become increasingly important in furthering biological knowledge. The goal of this workshop is to provide a forum for discussion of latest research in developing high-performance computing solutions to problems arising from molecular biology.

The technical program was put together by Program Chair Dan C. Marinescu with the help of a distinguished program committee. Each submission was thoroughly reviewed by at least three expert reviewers. Manuscripts submitted by program committee members are subjected to a more stringent review. This year, the submissions to the workshop were of high quality and from the broader international community; we received 22 submissions from 5 countries. Based on the reviews, twelve submissions have been selected for presentation at the workshop and inclusion in the workshop proceedings. In addition, an invited keynote talk by Timothy S. Baker will be presented on the three-dimensional reconstruction of viruses.

We are grateful to the program committee members for submitting timely and thoughtful reviews. We wish to thank all the authors who submitted manuscripts to this workshop, without which this high-quality technical program would not have been possible. We plan to continue this workshop in the forthcoming years and look forward to your continuing support in this endeavor.

Dan C. Marinescu, David A. Bader, and Srinivas Aluru

Workshop Organizers

WORKSHOP CO-CHAIRS:

David A. Bader, University of New Mexico

Srinivas Aluru, Iowa State University

PROGRAM CHAIR:

Dan C. Marinescu, University of Central Florida

PROGRAM COMMITTEE:

Alberto Apostolico, Purdue University

Concettina Guerra, Universita'di Padova

Wojciech Szpankowski, Purdue University

List of Accepted Papers

- HICOMB-01 Three-dimensional reconstruction of viruses: challenges and strategies (Invited Paper)
Timothy S. Baker; Purdue University
- HICOMB-02 Study of a Highly Accurate and Fast-Protein Ligand Docking Algorithm Based Upon Molecular Dynamics
M. Taufer, M. Crowley, D. Price, A.A. Chien, and C. L. Brooks III
- HICOMB-03 Parallel Protein Folding with STAPL
S. Thomas and N. Amato
- HICOMB-04 A Hypergraph Model for the Yeast Protein Complex Network
E. Ramadan, A. Tarafdar, and A. Pothen
- HICOMB-05 Dynamic Programming for LR-PCR Segmentation of Bacterium Genomes
R. Andonov, D. Lavenier, N. Yanev, and P. Veber
- HICOMB-06 Parallel RNA Sequence-Structure Alignment
T. Liu and B. Schmidt
- HICOMB-07 Constrained De Novo Peptide Identification via Multiobjective Optimization
J.M. Mallard, A. Heredia-Langner, D.J. Baxter, K.H. Jarman, and W. R. Cannon
- HICOMB-08 Identification of Mycobacterium Species Using Curated Custom Databases
D. Kuyper, H. Ali, A.M. Mohamed, and S.H. Hinrichs
- HICOMB-09 High Performance Computational Tools for Motif Discovery
N.E. Baldwin, R.L. Collins, M. A. Langston, M.R. Leuze, C.T. Symons, and B. H. Voy
- HICOMB-10 High Performance Biosequence Database Scanning on Reconfigurable Platforms
T. Oliver and B. Schmidt
- HICOMB-11 New Fast and Accurate Heuristics for Inference of Large Phylogenetic Trees
A.P. Stamatakis, T. Ludwig, and H. Meier
- HICOMB-12 Large-Scale Simulation of Eukaryotic Cell Signaling Processes
J.H. Miller and F. Zheng
- HICOMB-13 Particle Swarm Optimization and Neural Network Application for QSAR
Z. Wang, G.L. Durst, R.C. Eberhart, D.B. Boyd, and Z. Ben Miled