

6th IEEE International Workshop on High Performance Computational Biology

HiCOMB 2007

March 26, 2007

Renaissance Long Beach Hotel, Long Beach, CA

in conjunction with 21st International Parallel and Distributed Processing Symposium

Message from the Workshop Chairs

Welcome to the Sixth International Workshop on High Performance Computational Biology (HiCOMB). Computational Biology is fast emerging as an important discipline for academic research and industrial application. The inherent complexity of biological systems, the error-prone and incomplete nature of data collection mechanisms, and the large size of biological datasets motivate novel algorithms with significant memory and computational requirements. The goal of this workshop is to provide a forum for discussion of latest research in developing high-performance computing solutions to problems in biology.

The technical program was put together by Program Co-Chairs Ananth Grama and Shankar Subramaniam and thirteen members of a distinguished program committee. This year we received fourteen submissions from around the world. Each submission was thoroughly reviewed by at least three program committee members. Based on the reviews, six papers were selected for presentation at the workshop and inclusion in the workshop proceedings. Four additional papers were invited to provide additional coverage of topics from leading researchers in the community.

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.

Ananth Grama, Shankar Subramaniam, Srinivas Aluru, and David A. Bader

Workshop Organizers

Workshop Co-Chairs:

Srinivas Aluru (Iowa State University)
David A. Bader (Georgia Institute of Technology)

Program Co-Chairs:

Shankar Subramaniam (University of California at San Diego)
Ananth Grama (Purdue University)

Program Committee:

Alberto Apostolico (Accademia dei Lincei & Georgia Tech)
Joel Bader (Johns Hopkins University)
Vineet Bafna (University of California at San Diego)
Jesus Izaguirre (University of Notre Dame)
George Karypis (University of Minnesota)
Daisuke Kihara (Purdue University)
Vipin Kumar (University of Minnesota)
Satoru Miyano (HGC, University of Tokyo)
Ben Raphael (Brown University)
Naren Ramakrishnan (Virginia Tech)
Joel Saltz (Ohio State University)
Mona Singh (Princeton University)
Tandy Warnow (University of Texas at Austin)

List of Accepted Papers

On the path to enable multi-scale biomolecular simulations on Petaflop supercomputer with multi-core processors

S. Alam, P. Agarwal

Analysis of a Computational Biology Simulation Technique on Emerging Processing Architectures

S. Alam, J. Meredith, J.S. Vetter

A Graph-Theoretic Analysis of the Human Protein-Interaction Network Using Multi-core Parallel Algorithms

D.A. Bader, K. Madduri

Biomolecular Path Sampling Enabled by Processing in Network Storage

P. Brenner, J. Wozniak, J. Izaguirre, A. Striegel, D. Thain, J. Peng

Preliminary results in accelerating profile HMM search on FPGAs

A. Jacob, J. Lancaster, J. Buhler, R. Chamberlain

High Performance Database Searching with HMMer on FPGAs

T. Oliver, L.Y. Yeow, B. Schmidt

Exploring the viability of the Cell Broadband Engine for bioinformatics applications

V. Sachdeva, M. Kistler, W.E. Speight, T.-H. K. Tzeng

Data-Driven Time-Parallelization in the AFM Simulation of Proteins

A. Srinivasan, L. Ji, H. Nymeyer, Y. Yu

RNAVLab: A unified environment for computational RNA structure analysis based on grid computing technology

M. Taufer, M.-Y. Leung, K.L. Johnson, A. Licon

An Automated Data Processing Pipeline for Virus Structure Determination at High Resolution

C. Yu, D.C. Marinescu, J.P. Morrison, B.C. Clayton, D.A. Power