

5th IEEE International Workshop on High Performance Computational Biology

HiCOMB 2006

April 25, 2006

Rhodes Island, Greece

in conjunction with 20th International Parallel and Distributed Processing Symposium

Message from the Workshop Chairs

Welcome to the Fifth International Workshop on High Performance Computational Biology (HiCOMB). Computational Biology is fast emerging as an important discipline for academic research and industrial application. The large size of biological data sets, inherent complexity of biological problems and the ability to deal with error-prone data all result in large run-time and memory requirements. 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 Chau-Wen Tseng and a distinguished program committee consisting of fifteen members from academia, government research institutes, and industry. This year we received fifteen submissions from around the world. Each submission was thoroughly reviewed by at least three program committee members. Based on the reviews, eleven papers were selected for presentation at the workshop and inclusion in the workshop proceedings.

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.

Chau-Wen Tseng, David A. Bader, and Srinivas Aluru

Workshop Organizers

Workshop Co-Chairs

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

Program Chair

Chau-Wen Tseng (University of Maryland)

Program Committee

Michael Cummings (University of Maryland)
Arthur Delcher (University of Maryland)
Nathan Edwards (University of Maryland)
Wu-Chun Feng (Los Alamos National Laboratory)
Guang Gao (University of Delaware)
Attila Gursoy (Koc University)
Sorin Istrail (Brown University)
Luay Nakhleh (Rice University)
Jan Prins (Univ. of North Carolina at Chapel Hill)
Joel Saltz (Ohio State University)
Alejandro A. Schäffer (National Institutes of Health)
Alexandros Stamatakis (ICS-FORTH)
Michela Taufer (University of Texas at El Paso)
Thomas Wu (Genentech)
Albert Y. Zomaya (Univ. of Western Australia)

List of Accepted Papers

Bio-Sequence Database Scanning on a GPU

Weiguo Liu, Bertil Schmidt, Gerrit Voss, Andre Schroder, and Wolfgang Muller-Wittig

Some Initial Results on Hardware BLAST Acceleration with a Reconfigurable Architecture
Euripides Sotiriades, Christos Kozanitis, and Apostolos Dollas

An Experimental Study of Optimizing Bioinformatics Applications

Guangming Tan, Lin Xu, Zhenghua Dai, Shengzhong Feng, and Ninghui Sun

Parallel Implementation of the Replica Exchange Molecular Dynamics Algorithm on Blue Gene/L
M. Eleftheriou, A. Rayshubski, J. W. Pitera, B. Fitch, R. Zhou and R. S. Germain

Application Re-Structuring and Data Management on a GRID Environment: a Case Study for Bioinformatics

G. Ciriello, M. Comin, and C. Guerra

A Method to Improve Structural Modeling Based on Conserved Domain Clusters

Fa Zhang, Lin Xu, and Bo Yuan

Phylospaces: Reconstructing Evolutionary Trees in Tuple Space

Marc L. Smith and Tiffani L. Williams

Parallel Implementation of a Quartet-Based Algorithm for Phylogenetic Analysis

B. B. Zhou, D. Chu, M. Tarawneh, P. Wang, C. Wang, A. Y. Zomaya and R. P. Brent

Phylogenetic Models of Rate Heterogeneity: A High Performance Computing Perspective

Alexandros Stamatakis

Parallel Multiple Sequence Alignment with Local Phylogeny Search by Simulated Annealing

Jaroslaw Zola, Denis Trystram, Andrei Tchernykh, and Carlos Brizuela

MT-ClustalW: Multithreading Multiple Sequence Alignment

Kridsadakorn Chaichoompu, Surin Kittitornkun, and Sissades Tongsim