

First International Workshop on High Performance Computational Biology (HiCOMB)

April 15, 2002

Fort Lauderdale, Florida, USA

in conjunction with 16th International Parallel and Distributed Processing Symposium

Message from Workshop Chairs

Welcome to the first 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 with the help of a distinguished program committee consisting of 12 members. Each submission was thoroughly reviewed by three to five program committee members. Manuscripts submitted by the workshop organizers were subjected to a more stringent review. Based on the reviews, ten submissions have been 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.

Srinivas Aluru and David A. Bader

Workshop Organizers

WORKSHOP CO-CHAIRS:

Srinivas Aluru, Iowa State University

David A. Bader, University of New Mexico

PROGRAM COMMITTEE:

Suchendra Bhandarkar, University of Georgia

Alok Choudhary, Northwestern University

Bruce Hendrickson, Sandia National Laboratories

Xiaoqiu Huang, Iowa State University

Joseph JáJá, University of Maryland

Suresh Kothari, Iowa State University

Arvind Krishnamurthy, Yale University

Timothy Mattson, Intel Corporation

Quinn Snell, Brigham Young University

Stefan Unger, Sun Microsystems

Honghui Wan, National Center for Genome Resources

Albert Y. Zomaya, University of Western Australia

List of Accepted Papers

- TurboBLAST: A Parallel Implementation of BLAST Based on the TurboHub Architecture for High Performance Bioinformatics
R.D. Bjornson, A.H. Sherman, S.B. Weston, N. Willard, and J. Wing, TurboGenomics, Inc.
- Improving Performance of Multiple Sequence Alignment Analysis in Multi-client Environments
U. Catalyurek, R. Ferreira, T. Kurc, J. Saltz, Ohio State University
- TCS: Estimating Gene Genealogies
M. Clement, Q. Snell, P. Walker, D. Posada and K. A. Crandall, Brigham Young University
- Parallel Genehunter: Implementation of a linkage analysis package for distributed memory architectures
G. Conant and A. Wagner, University of New Mexico
S. Plimpton, Sandia National Laboratories
W. Old and P. Fain, University of Colorado
- Parallel EST Clustering
A. Kalyanaraman, S. Aluru, and S. Kothari, Iowa State University
- Parallel Out-of-core Algorithm for Genome-Scale Enumeration of Metabolic Systematic Pathways
N. F. Samatova, A. Geist, and G. Ostrouchov, Oak Ridge National Laboratory
A. V. Melechko, University of Tennessee
- Massively Parallel Solutions for Molecular Sequence Analysis
B. Schmidt and H. Schröder, Nanyang Technological University
M. Schimmler, Institut für Datenverarbeitungsanlagen
- Monte Carlo Simulation of HIV-1 Evolution in Response to Selection by Antibodies
J. Silva, North Carolina Supercomputing Center
A. Hughes, University of South Carolina
- Aligning Two Fragmented Sequences
V. Veeramachaneni, P. Berman, W. Miller, Pennsylvania State University
- Quasiperiodic Biosequences and Modulo Incidence Matrices
H. Wan, National Center for Biotechnology Information
E. Song, University of California at San Francisco