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

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Omni Interlocken Resort, Denver, CO

in conjunction with 19th International Parallel and Distributed Processing Symposium

Message from the Workshop Chairs

Welcome to the Fourth International Workshop on High Performance Computational Biology (HiCOMB). The explosion of biological data and the compute-intensive nature of many biological applications, has caused computing to become an increasingly crucial resource for furthering biological knowledge, which, in turn, has led to the fast emergence of Computational Biology and Bioinformatics as important disciplines for academic research and industrial application. Moreover, it has become recognized that many biological applications require high-performance computing to handle the large run-time and memory requirements arising from the inherent complexity of biological problems, the large number and size of biological data sets, and the need to handle noisy, error-prone data. The goal of this workshop is to provide a forum for discussion of the latest research in developing high-performance computing solutions to problems arising from molecular biology.

The technical program was put together by Program Chair Nancy M. Amato and a distinguished program committee consisting of 21 members. The program includes 10 contributed papers and an invited keynote presentation by Vijay Pande from Stanford University describing the advances in biophysics and biomedicine that have been enabled by his Folding@Home grid computing project. This year we had a significant increase in the number of submissions, receiving 32 submissions from 11 countries. Each submission was thoroughly reviewed by at least three program committee members. Based on the reviews, ten 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.

Nancy M. Amato, 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:

Nancy M. Amato, Texas A&M University

PROGRAM COMMITTEE:

Frank Dehne, Griffith University
Ken Dill, University of California at San Francisco
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Siang Wun Song, University of Sao Paulo
Michael Thorpe, Arizona State University
Jerry Tsai, Texas A&M University
Tiffani Williams, Radcliffe Institute of Advanced Study

List of Accepted Papers

Folding@Home: Advances in biophysics and biomedicine from world-wide grid computing (Invited Keynote)
Vijay Pande, Stanford University

ESTmapper: Efficiently Aligning DNA Sequences to Genomes
Xue Wu, Woei-Jyh (Adam) Lee and Chau-Wen Tseng

RC-BLAST: Towards an Open Source Hardware Implementation
Krishna Muriki, Keith Underwood and Ron Sass

Comparison of Different Versions of Current BLAST Software on Nucleotide Sequences
I. Elizabeth Cha and Eric Rouchka

A Case Study on Pattern-based Systems for High Performance
Weiguo Liu and Bertil Schmidt

BioFilter: An architecture for parallel deployment and dynamic chaining of standalone bioinformatics tools
Thomas Brettin and Avinash Kewalramani

An Efficient Program for Phylogenetic Inference Using Simulated Annealing
Alexandros Stamatakis

High-Performance Direct Pairwise Comparison of Large Genomic Sequences
Chris Mueller, Mehmet Dalkilic and Andrew Lumsdaine

Statistical Methods for the Discovery of Co-operative Transcription Factors: the Co-bind code revised
Giovanni Lavorgna, Alessandro Marongiu, Simone Melchionna, Paolo Palazzari, Vittorio Rosato, and Paolo Verrecchia

FROST: Revisited and Distributed
Vincent Poirriez, Antoine Marin, Rumen Andonov and Jean-Francois Gibrat

Predictor@Home: A ”Protein Structure Prediction Supercomputer” Based on Public-Resource Computing
Michela Taufer, Chahm An, Andre Kerstens, and Charles L. Brooks III