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

April 22, 2003

Nice Acropolis Convention Center, Nice, France

in conjunction with 17th International Parallel and Distributed Processing Symposium

Message from Workshop Chairs

Welcome to the Second 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 14 members. Each submission was thoroughly reviewed by three to five program committee members. Manuscripts submitted by program committee members were 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 11 countries. Based on the reviews, twelve 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.

David A. Bader and Srinivas Aluru

Workshop Organizers

WORKSHOP CO-CHAIRS:

David A. Bader, University of New Mexico

Srinivas Aluru, Iowa State University

PROGRAM COMMITTEE:

Suchendra Bhandarkar, University of Georgia

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Joel Saltz, Ohio State University

Quinn Snell, Brigham Young University

Stefan Unger, Sun Microsystems

Geert Wenes, National Center for Genome Resources

Albert Y. Zomaya, University of Western Australia

List of Accepted Papers

HICOMB-01 Sequence Alignment on the Cray MTA-2
S. H. Bokhari and J. R. Sauer; University of Engineering & Technology, Pakistan, and Eagle Research & Development, USA

HICOMB-02 Using Hybrid Alignment for Iterative Sequence Database Searches
Y. Li, M. Lauria, and R. Bundschuh; Ohio State University, USA

HICOMB-03 A Fast Algorithm for the Exhaustive Analysis of 12-Nucleotide-Long DNA Sequences: Applications to Human Genomics
V. Arnau and I. Marín; University of Valencia, Spain

HICOMB-04 Realtime Primer Design for DNA chips
H. Simmler, H. Singpiel, and R. Männer; Acconovis GmbH, and University of Mannheim, Germany

HICOMB-05 Accurate method for fast design of diagnostic oligonucleotide probe sets for DNA microarrays
A. Krause, M. Kräutner, and H. Meier; Technical University of Munich, Germany

HICOMB-06 Gene Clustering using Self-Organizing Maps and Particle Swarm Optimization
X. Xiao, E. Dow, R. Eberhart, Z. Ben Miled, and R. J. Oppelt; Indiana University Purdue University Indianapolis, and Eli Lilly Corporate Center, USA

HICOMB-07 Protein Structure Prediction by Applying an Evolutionary Algorithm
R. O. Day, G. B. Lamont, and R. Pachter; Air Force Institute of Technology, and Wright-Patterson AFB, USA

HICOMB-08 PROSIDIS: a Special Purpose Processor for PROtein SImilarity DIScovery
A. Marongiu, P. Palazzari, and V. Rosato; IPITEC and ENEA, Rome, Italy

HICOMB-09 Parallelisation of IBD computation for determining genetic disease map
N. J. Rizk; Notre Dame University, Lebanon

HICOMB-10 Parallel Detection of Regulatory Elements with gMP
B. Schmidt, L. Feng, A. Laud, and Y. Santoso; Nanyang Technological University and Helixense Pte Ltd, Singapore

HICOMB-11 Solving the Protein Threading Problem in Parallel
N. Yanev and R. Andonov; University of Sofia, Bulgaria, and IRISA, France

HICOMB-12 Phylogenetic Tree Inference on PC Architectures with AxML/PAxML
A. P. Stamatakis and T. Ludwig; Technical University of Munich, and Ruprecht-Karls-University, Germany