# 7th IEEE International Workshop on High Performance Computational Biology
# HiCOMB 2008

## April 14, 2008
## Hyatt Regency Resort, Miami Florida, USA

in conjunction with 22nd International Parallel and Distributed Processing Symposium

## Message from the Workshop Chairs

Welcome to the Seventh 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 Chair Bertil Schmidt and thirteen members of a distinguished program committee. This year we had a significant increase in the number of submissions, receiving 28 submissions. After an initial screening 25 submissions were thoroughly reviewed by at least three experts in the field. 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 forth-coming years and look forward to your continuing support in this endeavour.

Bertil Schmidt, Srinivas Aluru, and David A. Bader

# Workshop Organizers

Workshop Co-Chairs:

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

Program Chair:

    Bertil Schmidt (NICTA VRL, University of Melbourne)

Program Committee:

    Alexandros Stamatakis (EPFL, Switzerland)
    Michela Taufer (University of Delaware)
    Albert Zomaya (University of Sydney)
    Jaroslaw Zola (Iowa State University)
    Ananth Kalyanaraman (Washington State University)
    Dominique Lavenier (IRISA, France)
    Weiguo Liu (NTU, Singapore)
    Heiko Schroder (RMIT, Australia)
    Feng Lin (NTU, Singapore)
    Vipin Chaudhary (SUNY Buffalo)
    Jeremy Buhler (Washington University)
    Martin Middendorf (University of Leipzig, Germany)
    Bharadwaj Veeravalli (NUS, Singapore)

# List of Accepted Papers

Ordered Index Seed Algorithm for Intensive DNA Sequence Comparison
D. Lavenier

Parallel, Scalable, Memory-Efficient Backtracking for Combinatorial Modeling of Large-Scale Biological Systems
B.-H. Park, M. Schmidt, K. Thomas, T. Karpinets, N.F. Samatova

Parallelized preprocessing algorithms for high-density oligonucleotide array data
M. Schmidberger, U. Mansmann

On the Effectiveness of Rebuilding RNA Secondary Structures from Sequence Chunks
M. Taufer, T. Solorio, A. Licon, D. Mireles, M.-Y. Leung

A Parallel Architecture for Regulatory Motif Algorithm Assessment
D. Quest, K. Dempsey, D. Bastola, H. Ali

Design and Development of a FPGA-based Cascade Markov Model for Recognition of Steroid Hormone Response Elements
M. Stepanova, F. Lin, V. Lin

Supporting High Performance Bioinformatics Flat-File Data Processing
X. Zhang, G. Agrawal

Sample-Align-D: A High Performance Multiple Sequence Alignment System using Phylogenetic Sampling and Domain Decomposition
F. Saeed, A. Khokhar

Adaptive Locality-Effective Kernel Methods for Phosphorylation Site Prediction
P. Yoo, Y.S. Ho, B.B. Zhou, A. Zomaya

Impacts of Multicores on Large-scale Molecular Dynamics Simulations
S. Alam, J. Vetter, P. Agarwal, H. Ong, S. Hampton