## CALL FOR PAPERS

# 10<sup>th</sup> IEEE International Workshop on High Performance Computational Biology HiCOMB 2011

May 16, 2011 - Anchorage, Alaska www.hicomb.org

## **Important Dates:**

Submissions due: December 17, 2010 Notification: January 10, 2011 Camera-ready due: February 10, 2011

#### Location:

Anchorage, Alaska co-located with the 25<sup>th</sup> International Parallel & Distributed Processing Symposium (IPDPS)

#### **Workshop Co-Chairs:**

David A. Bader (Georgia Tech.) Srinivas Aluru (Iowa State U.)

## **Program Chair:**

Ananth Kalyanaraman Washington State University Email: ananth@eecs.wsu.edu

## **Program Committee:**

Gagan Agarwal, Ohio State U. Eric Aubanel, U. New Brunswick Sanjukta Bhowmick, U. Nebraska Umit Catalyurek, Ohio State U. Vipin Chaudhary, SUNY Buffalo Mark Clement, BYU Wuchun Feng, Virginia Tech. Robert Germain, IBM Research Martin Herbordt, BU Heshan Lin, Virginia Tech. Kamesh Madduri, LBNL Harald Meier, TUM Chris Oehmen, PNNL Jacques Rogemont, EPFL Nagiza Samatova, NCSU Bertil Schmidt, NTU Alexandros Stamatakis, TUM Tjerk P. Straatsma, PNNL Michela Taufer, U. Delaware Chau-Wen Tseng, U. Maryland CP Tiffani Williams, TAMU Jaroslaw Zola, Iowa State U. Albert Zomaya, U. Sydney

High-performance computing is fast becoming an integral part of research and application in bioinformatics and computational biology. 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 data-intensive and compute-intensive problems arising from molecular biology and related life sciences areas. We are especially interested in parallel algorithms, memory-efficient algorithms, large scale data mining techniques, algorithms on multicores and GPUs, and design of high-performance software for biological applications. The workshop will feature contributed papers as well as invited talks from reputed researchers in the field.

Topics of interest include but are not limited to:

- \* Bioinformatic databases
- \* Computational genomics and metagenomics
- \* Computational proteomics and metaproteomics
- \* DNA assembly, clustering and mapping
- \* Gene expression and microarrays
- \* Gene identification and annotation
- \* Parallel algorithms for biological analysis
- \* Parallel architectures for biological applications
- \* Molecular evolution and phylogenetic reconstruction algorithms
- \* Protein structure prediction and modeling
- \* String data structures and algorithms
- \* Parallel algorithms in chemical genetics and chemical informatics
- \* High performance algorithms for systems biology

### **Submission Guidelines:**

Papers reporting original research (both theoretical and experimental) in all areas of bioinformatics and computational biology are sought. Surveys of important recent results and directions are also welcome. To submit a paper, upload a postscript or PDF copy of the paper from the workshop webpage <a href="http://www.hicomb.org/">http://www.hicomb.org/</a>. The paper should not exceed 12 single-spaced pages (US Letter or A4 size) in 11pt font or larger. All papers will be reviewed. IEEE CS Press will publish the IPDPS symposium and workshop abstracts as a printed volume. The complete symposium and workshop proceedings will also be published by IEEE CS Press on CD-ROM and will also be available in the IEEE Digital Library.