



# CALL FOR PAPERS

## 5<sup>th</sup> International Conference on Bioinformatics and Computational Biology

March 4-6, 2013 - Honolulu, Hawaii USA

<http://bicob.ece.iastate.edu/>

**BICoB-2013**

in conjunction with  
CATA-2013

Significant advances in modern biology and medicine have been enabled by computational techniques in bioinformatics. Bioinformatics and computational biology continue to be a vibrant research area with broadening applications and new emerging challenges. The 5th International Conference on Bioinformatics and Computational Biology (BICoB) <http://bicob.ece.iastate.edu/> will provide an excellent venue for researchers and practitioners in the fields of bioinformatics to present and publish their research results and techniques. The BICoB conference seeks original and high quality papers in the fields of bioinformatics, computational biology, system biology, medical informatics and the related disciplines. We also encourage work in progress and research results in the emerging and evolutionary computational areas. Work in the computational methods related to, or with application in, bioinformatics is also encouraged including: data mining, text mining, machine learning, biomathematics, modeling and simulation, pattern recognition, data visualization, biostatistics, etc. The topics of interest include (and are not limited to):

- **Genome analysis:** Genome assembly, genome and chromosome annotation, gene finding, alternative splicing, EST analysis, comparative genomics, and metagenomics.
- **Sequence analysis:** Multiple sequence alignment, sequence search and clustering, function prediction, motif discovery, functional site recognition in protein, RNA and DNA sequences.
- **Phylogenetics:** Phylogeny estimation, models of evolution, comparative biological methods, population genetics.
- **Systems biology:** Systems approaches to molecular biology, multiscale modeling, pathways, gene networks.
- **Structural Bioinformatics:** Structure matching, prediction, analysis and comparison; methods and tools for docking; protein design
- **Analysis of high-throughput biological data:** Microarrays (nucleic acid, protein, array CGH, genome tiling, and other arrays), EST, SAGE, MPSS, proteomics, mass spectrometry.
- **Genetics and population analysis:** Linkage analysis, association analysis, population simulation, haplotyping, marker discovery, genotype calling.

Moreover, BICoB welcomes submissions in all areas of computing with impact on life sciences including algorithms, databases, languages, systems, and high performance computing. For example: Parallel and high-performance techniques. Computational biology on emerging architectures and hardware accelerators

### CONFERENCE ORGANIZATION

#### Conference Co-Chairs:

**Hisham Al-Mubaid:** [hisham@uhcl.edu](mailto:hisham@uhcl.edu)  
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**Jia Zeng**  
Baylor College of Medicine, Houston, TX, USA

### SUBMISSION PROCEDURES:

Papers will be accepted only by electronic submission in PDF format only. A full paper, including title, author's name(s) and affiliation, mailing address, tel., fax and email of the principal author, should be submitted at the submission website:

<https://cmt.research.microsoft.com/BICOB2013/> on or before

**October 28, 2012.** The submitted manuscript should closely reflect the final paper as it will appear in the Proceedings. Maximum paper length for the proceedings is six pages, with up to two additional pages accepted with page charges (6+2). ISCA double-column format will be used.

### IMPORTANT DATES

Full paper Submission Deadline:	October 28, 2012
Notification of Acceptance:	December 15, 2012
Pre-registration and Camera-ready paper:	January 20, 2013

**Journal Publication:** Authors of selected high quality papers in BICoB-2013 will be invited to submit extended version of their papers for possible publication in bioinformatics journals (e.g., JBCB, IJCA,...etc).