



CALL FOR PAPERS

4th International Conference on Bioinformatics and Computational Biology

March 12-14, 2012 - Las Vegas, Nevada USA

<http://scweb.sce.uhcl.edu/bicob12/>

BICoB-2012

in conjunction with

CATA-2012

IMPORTANT DATES

Full paper Submission Deadline:	November 28, 2011
Notification of Acceptance:	December 29, 2011
Pre-registration and Camera-ready paper due:	January 20, 2012

Journal Publication: Authors of selected papers in BICoB-2012 will be invited to submit extended version of their papers for possible publication in the *Journal of Bioinformatics and Computational Biology (JBCB)*.

For paper submission: <https://cmt.research.microsoft.com/BICOB2012/>

The 4th International Conference on Bioinformatics and Computational Biology (BICoB) <http://scweb.sce.uhcl.edu/bicob12/> provides an excellent venue for researchers and practitioners in the fields of bioinformatics and computational biology 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. The conference also includes a **Best Paper Award** given during the conference banquet. We also encourage work in progress and research results in the emerging and evolutionary computational areas. Computational techniques have already enabled unprecedented advances in modern biology and medicine. This continues to be a vibrant research area with broadening of computational techniques and new emerging challenges. Work in the computational methods related to, or with application in, bioinformatics is also encouraged including: data mining, text mining, machine learning, 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 and comparative genomics.
 - **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.
 - **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.
 - **Systems biology:** Systems approaches to molecular biology, multiscale modeling, pathways, gene networks.
 - **Computational Proteomics:** Filtering and indexing sequence databases, Peptide quantification and identification, Genome annotations via mass spectrometry, Identification of post-translational modifications, Structural genomics via mass spectrometry, Protein-protein interactions, Computational approaches to analysis of large scale Mass spectrometry data, Exploration and visualization of proteomic data, Data models and integration for proteomics and genomics, Querying and retrieval of proteomics and genomics data etc
- Other topics:**
- Parallel and high-performance techniques
 - Unifying computational techniques
 - Data and image mining techniques
 - Approximation and randomized algorithms and systems
 - Computational biology on emerging architectures and hardware accelerators

SUBMISSION PROCEDURES:

Papers will be accepted only by electronic submission (PDF only). A full paper, including title, author's name(s) and affiliation, mailing address, telephone, fax and email of the principal author, should be submitted by **November 28, 2011** at the following web site: <https://cmt.research.microsoft.com/BICOB2012/> (site will be activated soon). 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.

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