



CALL FOR PAPERS

6th International Conference on Bioinformatics and Computational Biology March 24-26, 2014 - Las Vegas, Nevada USA

BICoB-2014

in conjunction with
CATA-2014

Sponsored by the International Society for Computers and Their Applications (ISCA)

Conference website: <http://www.cs.umb.edu/bicob>

In recent years, computational biology and medical informatics have seen significant advances driven by computational techniques in bioinformatics. Bioinformatics and computational biology continue to be a vibrant research area with broadening applications and new emerging challenges. The 6th International Conference on Bioinformatics and Computational Biology (BICoB) 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, systems biology, medical informatics and the related areas. 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: bio-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 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.
- **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 COMMITTEE

Conference Co-Chairs:

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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://www.easychair.org/conferences/?conf=bicob2014> on or before **October 31, 2013**. 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. Accepted papers will be indexed in Scopus, EI, and INSPEC, and submitted to DBLP for indexing.

IMPORTANT DATES

Paper Submission Deadline: October 31, 2013
Notification of Acceptance: December 29, 2013
Pre-registration and Camera-ready paper: January 20, 2014

Journal Publication: Authors of selected high quality papers in BICoB-2014 will be invited to submit extended version of their papers for possible publication in bioinformatics journals (*selected high quality papers in BICoB-2013 are currently under review for publication in JBCB special issue for BICoB-2013*).