Call for Papers – BICOB 2015

7th International Conference on Bioinformatics and Computational Biology
in conjunction with CATA-2015

Waikiki Beach Marriott Resort & Spa, **Honolulu, Hawaii USA**
March 9 - 11, 2015

http://www.cs.umb.edu/bicob

The 7th International Conference on Bioinformatics and Computational Biology (BICoB) provides an excellent venue for researchers and practitioners in the fields of bioinformatics to present and publish their research results and techniques. Bioinformatics and computational biology continue to be a vibrant research area with broadening applications and new emerging challenges. In recent years, bioinformatics and computational biology have experience significant advances driven by computational techniques in bioinformatics. The BICoB conference seeks original and high quality papers in the fields of bioinformatics, computational biology, systems biology, medical informatics and the related 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.

IMPORTANT DATES

Paper Submission Deadline: **October 24, 2014.**
Notification of Acceptance: **December 15, 2014.**
Pre-registration and Camera-ready paper:
January 16, 2015.

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, and email of the principal author, should be submitted at the submission website: https://www.easychair.org/conferences/?conf=bicob2015 on or before **October 24, 2014.** 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.

Journal Publication: Authors of selected high quality papers in BICoB-2015 will be invited to submit extended version of their papers for possible publication in bioinformatics journals (*selected high quality papers in BICOB-2013 were published in JBCB special issue for BICOB-2013*).

CONFERENCE COMMITTEE

Conference Chair: Hisham Al-Mubaid: University of Houston, Clear Lake, USA, hisham@uhcl.edu
Program Co-Chairs: Fahad Saeed: Western Michigan University, USA, fahad.saeed@wmich.edu
Nurit Haspel: University of Massachusetts at Boston, USA, nurit.haspel@umb.edu