



CALL FOR PAPERS

9th International Conference on Bioinformatics and Computational Biology

March 20–22, 2017 – Honolulu, HI USA
Waikiki Beach Marriott Resort and Spa

BICOB-2017

in conjunction with
CATA-2017

Conference website: <http://sce.uhcl.edu/bicob17>

Paper submission: <https://easychair.org/conferences/?conf=bicob2017>

Most research areas of bioinformatics, computational biology and medical informatics have experienced significant advances in recent years driven by computational techniques in bioinformatics. The 9th International Conference on Bioinformatics and Computational Biology (BICOB) will provide an utmost venue for researchers and practitioners in 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. BICOB-2017 seeks original and high quality papers in the fields of bioinformatics, computational biology, systems biology, medical informatics and the related areas. The conference includes a **Best Paper Award** to be given during the conference banquet. 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: computational intelligence and its application in bioinformatics, bio-data mining and text mining, evolutionary algorithms, nature-inspired computation, machine learning and bio-NLP, biomedical ontology, biomathematics, modeling and simulation, pattern recognition, data visualization, biostatistics. The topics of interest include (and are not limited to):

- **Genome analysis:** Genome assembly, Next-Gen genomics and metagenomics, genome and chromosome annotation, gene finding, alternative splicing, EST analysis and comparative genomics.
- **Sequence analysis:** Multiple sequence alignment, sequence search and clustering, next generation sequencing NGS, 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, transcriptomics - microarray data analysis, proteomics, epigenomics.
- **Healthcare Informatics:** healthcare data acquisition, analysis and mining. Clinical decision support systems, and healthcare information systems.
- **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, Query Languages, Interoperability, Bio-ontology and bio-data Mining.
- **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.

Important Dates

Paper Submission Deadline:	October 31, 2016
Notification of Acceptance:	December 18, 2016
Pre-registration and Camera-ready paper:	January 20, 2017

Submission Procedures:

Papers will be accepted only by electronic submission in PDF format. A full paper, including title, author's name(s) and affiliation, mailing address, and email of the principal author, should be submitted online at the submission website: <https://easychair.org/conferences/?conf=bicob2017> on or before **October 31, 2016**. 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. All BICOB-2017 Proceedings papers will be accessible and available online at www.seachDL.org and also will appear in Google scholar full text.

Journal Publication

Authors of selected high quality papers in BICOB-2017 will be invited to submit extended version of their papers for possible publication in bioinformatics journals including JBCB (*selected papers in previous BICOB conferences were published in JBCB*).

For more information: please contact Program co-Chairs:

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