

1st IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)

Feb. 3-5, 2011, Holiday Inn – in the Walt Disney Resort, Orlando, Florida

Advances in high-throughput technologies such as DNA sequencing and mass spectrometry are profoundly transforming life sciences, resulting in the collection of unprecedented amounts of biological and medical data. Using this data to advance our knowledge about fundamental biological processes and improve human health requires novel computational models and advanced analysis algorithms. IEEE ICCABS aims to bring together leading academic and industry researchers to discuss the latest advances in computational methods for bio and medical sciences.

SCOPE

Topics of interest include but are not limited to:

- **Biological modeling and simulation**
Molecular and cellular modeling, stochastic and rule-based modeling, modeling languages and systems
- **Biomedical image processing**
Image segmentation and classification, visualization, functional and molecular imaging
- **Biomedical data and literature mining**
Data integration, knowledge discovery from electronic medical records and scientific literature
- **Computational genetic epidemiology**
Linkage and association analysis, gene-gene and gene-environment interaction modeling, genetic risk analysis
- **Computational metabolomics**
Metabolomics databases, metabolite identification, spectral analysis, metabolic network modeling
- **Computational proteomics**
Peptide identification and quantification, post-translational modifications, protein-protein interactions
- **Databases and ontologies**
Biomedical data warehouses, database integration, biomedical ontologies and semantic web services
- **Gene regulation**
Regulatory motifs and modules, post-transcriptional regulation, regulatory networks
- **Genome analysis**
Genome assembly, genome annotation, comparative genomics, metagenomics
- **Health Informatics**
Medical data management and privacy, medical recommender systems, therapy optimization
- **High-performance bio-computing**
Cloud and grid computing, advanced multi-core, GPU, and FPGA biomedical applications
- **Immunoinformatics**
Epitope prediction, vaccine design, immune system simulators
- **Molecular evolution**
Models of evolution, reconstruction of phylogenetic trees and networks, comparative genomics
- **Population genomics**
Haplotype and recombination analysis, structural genomic variation, signatures of natural selection
- **Sequence analysis**
Multiple sequence alignment, motif discovery, sequence search and clustering
- **Structural bioinformatics**
RNA and protein structure prediction and classification, molecular docking, RNA and protein design
- **Systems biology**
Systems approaches to molecular biology, multi-scale modeling, biological networks, synthetic biology
- **Transcriptomics**
Microarray and sequencing-based transcriptome profiling, novel transcript discovery, alternative splicing, non-coding RNA analysis

SUBMISSION INSTRUCTIONS

Authors are invited to electronically submit an abstract in PDF format by following the instructions at <http://www.easychair.org/conferences/?conf=iccabs11>. Submissions should be prepared using IEEE Computer Society's Word/LaTeX templates available at <http://www2.computer.org/portal/web/cscps/formatting> and should not exceed 1 page in length. Accepted abstracts will be published in the IEEE Xplore Digital Library. In addition to being displayed, each accepted poster will also be allocated a short time for an oral presentation. Each poster title should start with the word "Poster:"

POSTER CHAIRS

- **Rachel O'Neill, University of Connecticut**
- **Raj Sunderraman, Georgia State University**

KEY DATES

Abstract submission	Jan. 5, 2011
Notification of acceptance	Jan. 10, 2011
Camera-ready version and author registration	Jan. 20, 2011

<http://www.iccabs.org/>

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