IEEE computer society

FINAL CALL FOR PAPERS

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 extended abstracts 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 6 pages in length. Accepted abstracts will be published in the IEEE Xplore Digital Library. Full versions of selected extended abstracts will be published in *BMC Bioinformatics* and *BMC Genomics*. A limited number of student travel awards will be made (conditional upon NSF support).

KEYNOTE SPEAKERS

- ***Christina Leslie*, Memorial Sloan-Kettering Cancer Center**
- ***Andrea Califano*, Columbia University**
- ***John Reif,* Duke University**

KEY DATES

Abstract submission	**Extended to Dec. 17, 2010**
Notification of acceptance	**Jan. 10, 2011**
Camera-ready version and author registration	**Jan. 20, 2011**

http://www.iccabs.org/

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