



# ICCABS 2018

**2018 IEEE 8th International Conference on  
Computational Advances in Bio and medical Sciences  
(ICCABS)**

**October 18-20, 2018,  
Stan Fulton Building, University of Nevada,  
Las Vegas, Nevada**

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



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# **Message from the General Chairs**

# **Message from the Program Chairs**

## Message from CANGS Workshop Chairs



# Message from CASCODA Workshop Chairs



# Conference Organization

## Steering Committee

*Srinivas Aluru - Georgia Institute of Technology*  
*Reda A. Ammar - University of Connecticut*  
*Tao Jiang - University of California, Riverside*  
*Vipin Kumar - University of Minnesota*  
*Ming Li - University of Waterloo*  
*Sanguthevar Rajasekaran - University of Connecticut (Chair)*  
*John Reif - Duke University*  
*Sartaj Sahni - University of Florida*

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*Wuchun Feng - Virginia Polytechnic Institute and State University*  
*Sanguthevar Rajasekaran - University of Connecticut*

## Program Chairs

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*Yoo-Ah Kim - National Institutes of Health*

## Workshop Chairs

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*Pavel Skums - Georgia State University*  
*Alex Zelikovsky - Georgia State University*

## Finance Chair

*Reda A. Ammar - University of Connecticut*

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*Martin Schiller - University of Nevada, Las Vegas*  
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*Orlando Echevarria - University of Connecticut*  
*Bob Weiner - University of Connecticut*

## Publication Chair

*Zigeng Wang - University of Connecticut*

## Webmaster

*Zigeng Wang - University of Connecticut*

# Program Committee Members

Lipi Rani Acharya - Dow AgroSciences  
Tatsuya Akutsu - Kyoto University, Japan  
Max Alekseyev - George Washington University  
Jaime Davila - Mayo Clinic  
Jorge Duitama - Universidad de los Andes, Colombia  
Richard Edwards - University of New South Wales, Australia  
Scott Emrich - University of Notre Dame  
Oliver Eulenstein - Iowa State University  
Liliana Florea - Johns Hopkins University  
Osamu Gotoh - Computational Biology Research Center (CBRC) and AIST  
Faraz Hach - Simon Fraser University, Canada  
Sumit Kumar Jha - University of Central Florida  
Danny Krizanc - Wesleyan University  
M. Oğuzhan Külekci - Istanbul Technical University, Turkey  
Manuel Lafond - Université de Montréal, Canada  
Ion Mandoiu - University of Connecticut  
Serghei Mangul - University of California, Los Angeles  
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Amarda Shehu - George Mason University  
Pavel Skums - Georgia State University  
Yanni Sun - Michigan State University  
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Sharma V. Thankachan - University of Central Florida  
Ugo Vaccaro - University of Salerno, Italy  
Balaji Venkatachalam - Google  
Li-San Wang - University of Pennsylvania  
Jianxin Wang - Central South University, China  
Fang Xiang Wu - University of Saskatchewan, Canada  
Alex Zelikovsky - Georgia State University  
Jin Zhang - Washington University School of Medicine in St. Louis  
Shaojie Zhang - University of Central Florida  
Wei Zhang - University of Central Florida  
Cuncong Zhong - University of Kansas



# ICCABS 2018 Program

Thursday, October 18, 2018

8:50am - 9:00am **Opening Remarks**

9:00am - 9:45am **Keynote Talk**  
**Chair:** *TBD*

*George Weinstock - The Jackson Laboratory*  
Title: TBD

9:45am - 10:15am **Coffee Break**

10:15am - 12:20pm **Parallel Sessions**

**Session 1A: ICCABS 1**  
**Chair:** *TBD*

- Jianhong Zhou, Christopher J. Oldfield, Fei Huang, Wenying Yan, Bairong Shen and A. Keith Dunker. [Identification of intrinsic disorder in complexes from Protein Data Bank](#)
- Sahar Hooshmand, Paniz Abedin, Daniel Gibney, Srinivas Aluru and Sharma Thankachan. [Highlight: Faster Computation of Genome Mappability with one Mismatch](#)
- Musfiqur Szal, Daniel Ruiz-Perez, Trevor Cickovski and Giri Narasimhan. [Inferring Relationships in Microbiomes from Signed Bayesian Networks](#)
- Simone Ciccolella, Mauricio Soto, Murray Patterson, Gianluca Della Vedova, Iman Hajirasouliha and Paola Bonizzoni. [gpps: An ILP-based approach for inferring cancer progression with mutation losses from single cell data](#)

**Session 1B: CASCODA 1**  
**Chair:** *TBD*

- Guryev. From library to count table: protocol-specific steps and their order when processing single-cell RNA-Seq data
- Gogolewski, Gambin. PCA-like Methods for the Integration of Single Cell RNA-seq Data with Metabolic Networks.
- Li, Li. scImpute: an accurate and robust imputation method for single-cell RNA-seq data
- Moussa, Mandoiu. SC1: A web-based single cell RNA-seq analysis pipeline
- Weber, Robinson. Methods, Tools, and Resources for Differential Discovery in High-Dimensional Cytometry Data

12:20pm - 1:30pm **Lunch**

**1:30pm - Invited Talk**  
**2:05pm Chair: TBD**

*Bin Xue - University of South Florida*  
Title: TBD

**2:05pm - Invited Talk**  
**2:40pm Chair: TBD**

*Keith Dunker - Indiana University-Purdue University Indianapolis*  
Title: TBD

**2:40pm - Invited Talk**  
**3:15pm Chair: TBD**

*Xia Ning - The Ohio State University*  
Title: TBD

**3:15pm - Coffee Break**  
**3:45pm**

**3:45pm - Parallel Sessions**  
**5:50pm**

**Session 2A: ICCABS 2**  
**Chair: TBD**

- Maryam Zand, Zhen Gao, Jinmao Wei, Garry Sunter and Jianhua Ruan. [An integrative approach to transcriptional co-regulatory network construction and characterization in Arabidopsis](#)
- Sudipta Pathak, Xingyu Cai and Sanguthevar Rajasekaran. [Ensemble Deep TimeNet : An Ensemble Learning Approach with Deep Neural Networks for Time Series](#)
- Dina Abdelhafiz, Sheida Nabavi, Reda Ammar, Clifford Yang and Jinbo Bi. [Convolutional Neural Network for Automated Mass Segmentation in Mammography](#)
- Daniel Ruiz-Perez, Haibin Guan, Purnima Madhivanan, Kalai Mathee and Giri Narasimhan. [So you think you can PLS-DA?](#)

**Session 2B: CASCODA 2**  
**Chair: TBD**

- Oldham, Wu. Accurate and Efficient Genotype Calling from Single Cell DNA Sequence Data
- Mandric, Zelikovsky, Skums. Reconstruction of tumor evolutionary history with and without mutation losses from single cell sequencing data
- Tsyvina, Zelikovsky, Skums. Inferring fitness landscapes for heterogeneous cancer populations
- Guryev. Identifying cell types from genome sequencing data - new approach for finding origin for carcinomas of unknown primary
- Moussa. Computational cell cycle analysis of single cell RNA-Seq data

# Friday, October 19, 2018

9:00am - **Keynote Talk**

9:45am **Chair:** *TBD*

*Aidong Zhang - University at Buffalo, The State University of New York*  
[Title: Deep Learning and Networks for Integrative Analysis of Multi-Omic Data](#)

9:45am - **Coffee Break**  
10:15am

10:15am - **Parallel Sessions**  
12:20pm

## **Session 3A: ICCABS 3**

**Chair:** *TBD*

- Kelly Daescu. [endo-siRBase: A multi-species developmental endo-siRNA repository and searchable database](#)
- Nasrin Akhter, Gopinath Chennupati, Hristo Djidjev and Amarda Shehu. [ML-Select: Improved Decoy Selection via Machine Learning and Ranking](#)
- Arfeen Khalid and Sumit Kumar Jha. [Parameter Estimation of Stochastic Biochemical Models using Multiple Hypothesis Testing](#)
- Patrick Perkins and Steffen Heber. [Identification of Ribosome Pause Sites Using riboStreamR, a Z-Score Based Peak Detection Algorithm 2](#)

## **Session 3B: CANGS 1**

**Chair:** *TBD*

- Balvert, Schoenhuth, Dutilh. Metagenomic Read Clustering Based on Overlap Graphs
- Li, Leung, Wong, Zhang, Chun, Xin, Luo, Ting, Lam. Megapath: low-similarity pathogen detection from metagenomic NGS data
- Basodi, Skums, Burcak Icer, Khudyakov, Zelikovsky, Pan. Classification of HCV Infections through Sequence Image Normalization
- Narasimhan. Causality and Dynamics in Microbial Communities
- Sledzieski, Zhang, Mandoiu, Bansal. TreeFix-VP: Phylogenetic Error-Correction for Viral Transmission Network Inference

12:20pm - **Lunch**  
1:30pm

1:30pm - **Keynote Talk**

2:15pm **Chair:** *TBD*

*Srinivas Aluru - Georgia Institute of Technology*  
[Title: TBD](#)

**2:15pm - Invited Talk**

**2:50pm Chair: TBD**

*Bhaskar DasGupta - University of Illinois at Chicago*

Title: Topological implications of negative curvature for biological networks

**2:50pm -**

**3:10pm**

**Coffee Break**

**3:10pm -**

**5:15pm**

**Parallel Sessions**

**Session 4A: SPECIAL SESSION:**

*Applications of Computation Biology to Personalized Medicine*

**Chair: Martin Schiller**

- Martin R. Schiller. [A scalable graph-document model for personalized medicine](#)
- Jingchun Chen. [Identification of CHST9 as A Candidate Gene for Schizophrenia from Whole Genome Sequencing](#)
- Fatma Nasoz. [Machine Learning Applications in Genomics](#)
- Surbhi Sharma. [Identifying false positive affinity mass spectrometry result with a multiplexed dataset](#)

**Session 4B: CANGS 2**

**Chair: TBD**

- Lei, Lyu, Gertz, Schaffer, Schwartz. Tumor Copy Number Data Deconvolution Integrating Bulk and Single-cell Sequencing Data
- Corrada Bravo, Gunady, Mount. Segment-based transcriptome analysis using Yanagi
- Sehra, Farhana, Heber. Identifying Signatures of Missing Transcripts
- Mandric, Zelikovsky. Solving scaffolding problem with repeats
- AlQahtani, Mandoiu. Statistical Mitogenome Assembly with Repeats

**6:30pm - Banquet**

**10:00pm**

# Saturday, October 20, 2018

9:00am - **Invited Talk**

9:35am **Chair:** *TBD*

*Cuncong Zhong - University of Kansas*

Title: TBD

9:35am - **Coffee Break**

10:00am

10:00am - **Parallel Sessions**  
11:40pm

## **Session 5A: ICCABS 4**

**Chair:** *TBD*

- Chunchun Zhao and Sartaj Sahni. [Linear Space String Correction Algorithm Using The Damerau-Levenshtein Distance](#)
- Saloni Agarwal, Rami Hallac, Chao Li, Rashika Mishra, Ovidiu Daescu and Alex Kane. [Image Based Detection of Craniofacial Abnormalities using Feature Extraction by Classical Convolutional Neural Network](#)
- Mahnaz Koupaee, Yuanyang Zhang, Tie Bo Wu, Mitchell Cohen and Linda Petzold. [Identification of Disease States for Trauma Patients using Commonly Available Hospital Data \(Poster\)](#)
- Chitaranjan Mahapatra and Rohit Manchanda. [Computational Study of Hodgkin-Huxley Type Calcium-Dependent Potassium Current in Urinary Bladder Over Activity \(Poster\)](#)

## **Session 5B: CANGS 3**

**Chair:** *TBD*

- Tang, Hasan, Zhang, Zhu, Wu. *vi-HMM: A novel HMM-based method for sequence variant identification in short read data*
- Sze, Kaplan. *Codon-based sequence alignment for mutation analysis by high-throughput sequencing*
- Karuturi. *Reduction to Homozygosity Driven Network Analysis to Identify Sample Specific Tumor Suppressor Genes*
- Xiao, Rajasekaran. *EMS3: An Improved Algorithm for Finding Edit-distance Based Motifs*