



# 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



Welcome to the 8<sup>th</sup> Workshop on Computational Advances for Next Generation Sequencing, held on October 18-20, 2018 in Las Vegas, NV in conjunction with ICCABS 2018. Massively parallel DNA and RNA sequencing have become widely available, placing the capacity to generate gigabases to terabases of sequence data into the hands of individual investigators. These next-generation technologies have the potential to dramatically accelerate biological and biomedical research by enabling the comprehensive analysis of genomes and transcriptomes to become inexpensive, routine and widespread.

The CANGS workshop aims to accelerate progress in the field by bringing together experts to discuss new directions of research and exchange ideas on the many mathematical and computational challenges presented by analysis of the exploding volume of next-generation sequencing data. This year's workshop program includes 3 sessions comprising 14 invited talks on a variety of current research topics including read clustering in metagenomics, scaffolding and assembly in presence of repeats, inference of viral transmission networks, classification of viral infections, pathogen detection in microbiomes, dynamics of microbial communities, transcriptome analysis, integration of bulk and single-cell sequencing data, motif finding, and identification of tumor suppressor genes.

We would like to thank ICCABS General Chairs Wuchun Feng and Sanguthevar Rajasekaran for the opportunity to organize CANGS 2018, and all speakers for presenting their work at the workshop.

*Ion Mandoiu*, University of Connecticut  
*Pavel Skums*, Georgia State University  
*Alex Zelikovsky*, Georgia State University

# Message from CASCODA Workshop Chairs



Welcome to the 1<sup>th</sup> Workshop on Computational Advances for Single-Cell Omics Data Analysis (CASCODA), held on October 18-20, 2018 in Las Vegas, NV in conjunction with ICCABS 2018. Recent technological advances have enabled high-throughput profiling of genomes, transcriptomes, epigenomes, and proteomes at single cell resolution. These revolutionary single-cell -omics technologies promise to bring unprecedented insights into tissue heterogeneity and unveil subtle regulatory processes that are undetectable by bulk sample analysis. However, fully realizing their potential requires the development of novel computational and statistical analysis methods capable of handling the massive data sizes and significant levels of technical and biological noise.

The goal of the CASCODA workshop is to bring together bioinformaticians, biologists, computer/data scientists, and statisticians to discuss the latest developments in computing infrastructure, mathematical and statistical modeling, algorithms, and visualization methods for single-cell -omics data. This year the workshop program includes 2 sessions comprising 10 invited talks on a variety of current research topics including primary analysis of single-cell RNA-Seq reads, cell cycle analysis of single cell RNA-Seq data, imputation of missing data and integrated pipelines for single-cell RNA-Seq analysis, genotype calling and reconstruction of tumor evolutionary history from single cell DNA sequencing data, inferring tissue of origin and fitness landscapes of heterogeneous populations of cancer cells, and differential analysis of high-dimensional cytometry data. All workshop speakers are invited to submit full length articles to the [special issue devoted to “Computational Advances for Single-Cell Omics Data Analysis” by the \*Genes\* journal.](#)

We would like to thank General Chairs Wuchun Feng and Sanguthevar Rajasekaran for the opportunity to organize CASCODA as part of ICCABS 2018. Last but not least, we would like to thank the speakers for presenting their work at the workshop.

*Ion Mandoiu*, University of Connecticut  
*Pavel Skums*, Georgia State University  
*Alex Zelikovsky*, Georgia State University

# Conference Organization

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*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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# Program Committee Members

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Jorge Duitama - Universidad de los Andes, Colombia  
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Faraz Hach - Simon Fraser University, Canada  
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Sing-Hoi Sze - Texas A&M University  
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Ugo Vaccaro - University of Salerno, Italy  
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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 - **Keynote Talk**  
9:45am **Chair:** *Sanguthevar Rajasekaran*

*George Weinstock - The Jackson Laboratory*  
Title: The human microbiome: a new frontier that might just affect everything

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

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

**Session 1A: ICCABS 1**  
**Chair:** *Patrick Perkins*

- 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:** *Ion Mandoiu*

- 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:** *Cuncong Zhong*

*Bin Xue - University of South Florida*  
[Title: Improving prediction accuracy by Integrating meta-strategy with novel data-analysis techniques](#)

**2:05pm - Invited Talk**  
**2:40pm Chair:** *Giri Narasimhan*

*Keith Dunker - Indiana University-Purdue University Indianapolis*  
[Title: Intrinsically Disordered Proteins, Alternative Splicing, and Post-translational Modification \(IDP-AS-PTM\): A Toolkit for Developmental Biology](#)

**2:40pm - Invited Talk**  
**3:15pm Chair:** *Keith Dunker*

*Xia Ning - The Ohio State University*  
[Title: Computational methods toward better drugs](#)

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

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

**Session 2A: ICCABS 2**  
**Chair:** *Musfiqur Sazal*

- 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:** *Pavel Skums*

- 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:** *Sanguthevar Rajasekaran*

*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:** *Sahar Hooshmand*

- 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:** *Mukul Bansal*

- 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
- Narasimhan. Causality and Dynamics in Microbial Communities
- Sledzieski, Zhang, Mandoiu, Bansal. TreeFix-VP: Phylogenetic Error-Correction for Viral Transmission Network Inference
- Karuturi. Reduction to Homozygosity Driven Network Analysis to Identify Sample Specific Tumor Suppressor Genes

12:20pm -

1:30pm

**Lunch**

1:30pm - **Keynote Talk**

2:15pm **Chair:** *Sharma V. Thankachan*

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

**2:15pm - Invited Talk**  
**2:50pm Chair:** *Giri Narasimhan*

*Bhaskar DasGupta - University of Illinois at Chicago*  
Title: Topological implications of negative curvature for biological networks

**2:50pm - Coffee Break**  
**3:10pm**

**3:10pm - Parallel Sessions**  
**5:15pm**

**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:** *Yufeng Wu*

- 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:** *Keith Dunker*

*Cuncong Zhong - University of Kansas*

[Title: Analyzing metagenomics sequencing data using the simultaneous alignment and assembly approach](#)

9:35am -

**Coffee Break**

10:00am

10:00am -

**Parallel Sessions**

11:40pm

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

**Chair:** *Ovidiu Daescu*

- 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 Koupaei, 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:** *Alex Zelikovsky*

- Basodi, Skums, Burcak Icer, Khudyakov, Zelikovsky, Pan. Classification of HCV Infections through Sequence Image Normalization
- 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
- Xiao, Rajasekaran. EMS3: An Improved Algorithm for Finding Edit-distance Based Motifs