



# 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



Welcome to the Eighth IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2018)! Computational techniques are revolutionizing the way in which research is conducted in science and engineering. Unsurpassed advances have been made in myriads of application domains. This is particularly true in the areas of biology, medicine, and drug discovery. Even though a number of conferences exist today in the general area of bioinformatics, they focus on computational biology to a large extent. ICCABS has the goal of bringing together scientists in all the three areas and hence serving as a platform for bridging the research efforts in these areas. The response from these communities to the ICCABS call for papers has been indeed gratifying. We are honored to serve these international communities by bringing together researchers, scientists, and students from academia, laboratories, and industry to this premier meeting held in Las Vegas.

We are thankful to the steering committee members (Srinivas Aluru, Reda A. Ammar, Tao Jiang, Vipin Kumar, Ming Li, John Reif and Sartaj Sahni) who have been instrumental in getting this conference approved by IEEE.

We would like to thank Program Chairs Ananth Kalyanaraman and Yoo-Ah Kim for assembling an outstanding technical program. The program committee members have done a wonderful job of reviewing all the submitted papers thoroughly within a short period of time. We are thankful to them as well as all the authors who have expressed their faith in ICCABS by submitting the fruits of their hard work. ICCABS features three keynote speeches (from Srinivas Aluru, George Weinstock, and Aidong Zhang) and five invited speakers (Bhaskar Dasgupta, Keith Dunker, Xia Ning, Bin Xue, and Cuncong Zhong). We are grateful to these well-established and highly successful researchers for taking time out of their busy schedules to make ICCABS a great success.

Thanks are also due to: Financial Chair (Reda Ammar), Local Arrangements Chairs (Martin Schiller and Sharma Valliyil Thankachan), Workshop Chairs (Ion Mandoiu, Pavel Skums, and Alex Zelikovsky), Proceedings Chair (Zigeng Wang), Publicity Chairs (Orlando Echevarria and Bob Weiner), and Webmaster (Zigeng Wang) for their tireless efforts.

Selected papers from ICCABS 2018 will appear as special issues in BMC Genomics and BMC Bioinformatics. We are grateful to the editors of these journals and Omar El Bakry for their efforts in this regard. Last but not least, we would like to thank UConn and the Booth Engineering Center for Advanced Technology (BECAT) for the constant administrative support rendered to ICCABS. In particular, we offer our special thanks to Joy Billion and Karen Kuca for their incessant support.

We hope you'll continue to support ICCABS in future! Have a wonderful time in the conference!

*Wuchun Feng*, VirginiaTech

*Sanguthevar Rajasekaran*, Univ. of Connecticut

# Message from the Program Chairs



We would like to welcome you to the 8th IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2018) in Las Vegas, Nevada. The conference program covers a wide range of topics in computational biology and medicine and includes 14 regular papers and 2 posters selected by the Program Committee from all 34 submissions.

We would like to express our gratitude to the Program Committee and reviewers for their careful review and evaluation of the submissions. Special thanks to the conference General Chairs Sanguthevar Rajasekaran and Wuchun Feng for their leadership, and the Chairs of the Workshop, Finance, Publicity, Proceedings, Local Arrangements, and the conference Webmaster for their hard work in making the conference a rich experience. Last but not least we would like to thank all the authors for presenting their latest research in this conference.

We hope that you will find the ICCABS 2018 program exciting and stimulating, and enjoy the opportunity to interact with researchers around the world. Welcome!

*Ananth Kalyanaraman*, Washington State University, Pullman, Washington, USA

*Yoo-Ah Kim*, National Institutes of Health, USA

# 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

## 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*

## General Chairs

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

## Program Chairs

*Ananth Kalyanaraman - Washington State University*  
*Yoo-Ah Kim - National Institutes of Health*

## Workshop Chairs

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

## Finance Chair

*Reda A. Ammar - University of Connecticut*

## Local Arrangements Chairs

*Martin Schiller - University of Nevada, Las Vegas*  
*Sharma V. Thankachan - University of Central Florida*

## Publicity Chairs

*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  
Sing-Hoi Sze - Texas A&M University  
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 - **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 - **Lunch**  
1:30pm

1:30pm - **Keynote Talk**

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

*Srinivas Aluru - Georgia Institute of Technology*  
[Title: Long read mapping at scale: Algorithms and applications](#)

**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 -**  
**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:** *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 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:** *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