

# ICCABS 2020

**10th International Conference on Computational  
Advances in Bio and medical Sciences (ICCABS)**

**December 10-12, 2020,  
Virtual Conference (Due to COVID'19)**  
<http://www.iccabs.org>



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# Message from the General Chairs



Welcome to the 10<sup>th</sup> International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2020)! 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. 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 virtually.

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 ensuring the success of this conference.

We would like to thank the Program Chair Sumit Kumar Jha 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 Leslie Loew, Amarda Shehu, and May Wang). 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 (Ahmed Soliman, Haarith Vohra, and Yijue Wang), 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 2020 will appear as a special issue in the Journal of Computational Biology. We are grateful to Sorin Istrail for his efforts in this regard. Last but not least, we would like to thank UConn for the constant administrative support rendered to ICCABS.

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

*Sanguthevar Rajasekaran*, Univ. of Connecticut

*Sartaj Sahni*, University of Florida

# Message from the Program Chair



We would like to welcome you to the 10th International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2020). The conference program covers a wide range of topics in computational biology and medicine and includes 6 regular papers. In addition, there are a total of 30 presentations from two workshops (CANGS and CASCODA).

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 Sartaj Sahni 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 2020 program exciting and stimulating, and enjoy the opportunity to interact with researchers around the world. Welcome!

*Sumit Kumar Jha*, Computer Science Department, University of Texas at San Antonio

# Message from CANGS Workshop Chairs



Welcome to the 10<sup>th</sup> Workshop on Computational Advances for Next Generation Sequencing (CANGS), held in virtual format on December 10-12, 2020 in conjunction with the 10<sup>th</sup> International Conference on Computational Advances in Bio and medical Sciences (ICCABS). 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 the workshop program includes four sessions comprising 15 invited talks on a variety of current research topics ranging from metagenomics and RNA-Seq data analysis to genome rearrangements and cancer genomics. An entire session is devoted to SARS-CoV-2 sequencing data analysis.

We would like to thank ICCABS General Chairs Sanguthevar Rajasekaran and Sartaj Sahni for the opportunity to organize CANGS 2020. We hope you will find the workshop talks and discussions during Gather Town breaks stimulating.

Enjoy!

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

# Message from CASCODA Workshop Chairs



Welcome to the 3<sup>rd</sup> Workshop on Computational Advances for Single-Cell Omics Data Analysis (CASCODA), held in virtual format on December 10-12, 2020 in conjunction with the 10<sup>th</sup> International Conference on Computational Advances in Bio and medical Sciences (ICCABS). 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 four sessions comprising 15 invited talks on a variety of current research topics ranging from methods for single cell RNA-Seq data analysis to machine learning methods for regulatory network inference and cell classification and single cell -omics data integration.

We would like to thank ICCABS General Chairs Sanguthevar Rajasekaran and Sartaj Sahni for the opportunity to organize CASCODA 2020. We hope you will find the workshop talks and discussions during Gather Town breaks stimulating.

Enjoy!

*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

*Sanguthevar Rajasekaran - University of Connecticut*  
*Sartaj Sahni - University of Florida*

## Program Chair

*Sumit Kumar Jha - University of Texas, San Antonio*

## 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

*Ahmed Soliman - University of Connecticut*  
*Haarith Vohra - University of Connecticut*  
*Yijue Wang - University of Connecticut*

## Publication Chair

*Zigeng Wang - University of Connecticut*

## Publicity Chairs

*Orlando Echevarria - University of Connecticut*  
*Bob Weiner - University of Connecticut*

## Webmaster

*Zigeng Wang - University of Connecticut*

# Program Committee Members

Max Alekseyev - George Washington University  
Jaime Davila - Mayo Clinic  
Jorge Duitama - Universidad de los Andes, Colombia  
Richard Edwards - University of New South Wales, Australia  
Oliver Eulenstein - Iowa State University  
Danny Krizanc - Wesleyan University  
M. Oğuzhan Külekci - Istanbul Technical University, Turkey  
Manuel Lafond - Université de Montréal, Canada  
Yuk Yee (Fanny) Leung - University of Pennsylvania  
Maria Poptsova - Moscow State University, Russia  
Subrata Saha - IBM Thomas J. Watson Research Center  
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  
Jianxin Wang - Central South University, China  
Fang Xiang Wu - University of Saskatchewan, Canada  
Shibu Yooseph - University of Central Florida  
Shaojie Zhang - University of Central Florida  
Wei Zhang - University of Central Florida  
Cuncong Zhong - University of Kansas

# ICCABS 2020 Program

**Thursday, Dec. 10, 2020 (EST)**

Videoconferencing access link for main conference: <http://snp.engr.uconn.edu/b/ICCABS-2020>

Access link for workshop: <http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>

Access link for breaks: <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>

Note: All links require the access code that was emailed to all registrants; contact [zigeng.wang@uconn.edu](mailto:zigeng.wang@uconn.edu) (for main conference), [ion@engr.uconn.edu](mailto:ion@engr.uconn.edu) (for workshops) if you have not received it.

**8:50am - 9:00am**    **Opening Remarks**    **Link:** <http://snp.engr.uconn.edu/b/ICCABS-2020>

**9:00am - 10:00am**    **Keynote Talk**    **Link:** <http://snp.engr.uconn.edu/b/ICCABS-2020>  
**Chair:** Sanguthevar Rajasekaran

*Leslie M. Loew - University of Connecticut Health Center*  
[Title: The Virtual Cell Project](#)

**10:00am - 10:30am**    **Break**    **Link:** <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>

**10:30am - 11:30pm**    **Keynote Talk**    **Link:** <http://snp.engr.uconn.edu/b/ICCABS-2020>  
**Chair:** Ion Mandoiu

*May Dongmei Wang - Georgia Institute of Technology and Emory University*  
[Title: Translating AI for Biomedicine and Healthcare: Challenges and Opportunities](#)

**11:30am - 12:30pm**    **Break**    **Link:** <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>

**12:30pm -  
2:30pm**      **Parallel Sessions**

**Session 1A: ICCABS 1**

**Chair:** Yijue Wang

**Link:**

<http://snp.engr.uconn.edu/b/ICCABS-2020>

- Francesco Andrace, Cinzia Pizzi and Matteo Comin. MetaProb 2: Improving Unsupervised Metagenomic Binning with Efficient Reads Assembly using Minimizers
- Joana Godinho, Alexandra M. Carvalho and Susana Vinga. Latent variable modelling and variational inference for scRNA-seq differential expression analysis
- Chitaranjan Mahapatra. Computational Study of Action Potential Generation in Uterine Smooth Muscle cell
- Jacob Porter. DNA Read Feature Importance using Machine Learning for Read Alignment Categories

**Session 1B: CANGS 1**

**Chair:** Alex Zelikovsky

**Link:**

<http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>

- Jaqueline Brito, Varuni Sarwal, Serghei Mangul and David Koslicki, Tampa: interpretable analysis and visualization of metagenomics-based taxon abundance profiles
- Alex Zelikovsky and Filipp Rondel, EM based estimating of enzyme participation in metabolic pathways for microbial communities
- Nathan LaPierre, Mohammed Alser, Eleazar Eskin, David Koslicki and Serghei Mangul, Metalign: efficient alignment-based metagenomic profiling via containment min hash
- Liqing Zhang, MetaMLP: A fast word embedding based classifier to profile target gene databases in metagenomic samples

**2:30pm -  
3:00pm**      **Break**

**Link:** <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>

**3:00pm -  
5:30pm**      **Parallel Sessions**

**Session 2A: ICCABS 2**

**Chair:** Haarith Vohra

**Link:**

<http://snp.engr.uconn.edu/b/ICCABS-2020>

- Abdur Rahman Mohd Abul Basher, Ryan J. McLaughlin and Steven J. Hallam. Metabolic pathway prediction using non-negative matrix factorization with improved precision
- Subrata Saha, Ahmed Soliman and

**Session 2B: CANGS 2**

**Chair:** Pavel Skums

**Link:**

<http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>

- Daniel Novikov, Alex Zelikovsky and Sergey Knyazev, Dijkstra Phylogeny for SARS-CoV-2
- Murray Patterson and Zahra Tayebi, Fast phylogeny approximation of Covid-19 with community detection
- Arjun Bhattacharya, Alina Hamilton, Melissa

Sanguthevar Rajasekaran. A novel pathway network analytics method based on graph theory

Troester and Michael Love, DeCompress: tissue compartment deconvolution for targeted RNA panels using compressed sensing

- Jessica Parks and Steffen Heber, Towards the Genome-wide Identification of Translated Splice Variants in *Arabidopsis thaliana*
- Kun Zhao, PASS: Polio Assessment by Sequence Screening

# Friday, Dec. 11, 2020 (EST)

9:00am -  
10:30pm

**CANGS Workshop**

**Link:** <http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>

**Session 3: CANGS 3**

**Chair:** Ion Mandoiu

- Andrii Melnyk, Sergey Knyazev and Alex Zelikovsky, Clustering of SARS-CoV-2 genomic sequences
- Sergey Knyazev and Alex Zelikovsky, eMST for SARS-CoV-2 genomes
- Viachaslau Tsyvina, Ezekiel Adeniyi, Alex Zelikovsky and Pavel Skums, Inference of intra-host SARS-CoV-2 heterogeneity from noisy NGS data

10:30am -  
11:00am

**Break**

**Link:** <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>

11:00am -  
12:30pm

**CANGS Workshop**

**Link:** <http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>

**Session 4: CANGS 4**

**Chair:** Alex Zelikovsky

- Qiaoji Xu, Lingling Jin, Chunfang Zheng, Jim Leebens-Mack and David Sankoff, Ancestral flowering plant chromosomes and gene orders based on generalized adjacencies and chromosomal gene co-occurrences
- R. Krishna Murthy Karuturi, Multiple Hypothesis Correction for Heterogeneous Discrete Distributions: A Review
- Russell Schwartz, Multiomic data integration to resolve clonal copy number evolution in the presence of chromosome instability

12:30pm -  
1:30pm

**Break**

**Link:** <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>

1:30pm -  
3:30pm

**CASCODA Workshop**

**Link:** <http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>

**Session 5: CASCODA 1**

**Chair:** Pavel Skums

- Mark Robinson, Flexible differential analyses of abundance and state for single

cell RNA-seq datasets

- Oliver Stegle, Latent variable models for multi-omics spatio-temporal data integration
- Rebecca Santorella, Ritambhara Singh, Pinar Demetci, Bjorn Sandstede and William Noble, Gromov-Wasserstein optimal transport to align single-cell multi-omics data
- Angela Oliveira Pisco, Tabula Hub: building single cell transcriptomics atlases across species

**3:30pm -  
4:00pm**

**Break**

**Link:** <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>

**4:00pm -  
6:00pm**

**CASCODA Workshop**

**Link:** <http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>

**Session 6: CASCODA 2**

**Chair:** Ion Mandoiu

- Welles Robinson, Fiorella Schischlik, Michael Gertz, Alejandro Schäffer and Eytan Ruppin, Identifying the Landscape of intratumoral Microbes via a Single Cell Transcriptomic Analysis
- Smita Krishnaswamy, Deep representations for uncovering heterogeneity and dynamics in single cell data
- Qianqian Song and Wei Zhang, Statistical modeling and leveraging of single cell data
- Paola Bonizzoni, Simone Ciccolella, Gianluca Della Vedova and Murray Patterson, On a generalization of the mutational loss model in inferring cancer progression from SC sequencing data

# Saturday, Dec. 12, 2020 (EST)

9:00am - **Keynote Talk** **Link:** <http://snp.engr.uconn.edu/b/ICCABS-2020>  
10:00am **Chair:** Pavel Skums

*Amarda Shehu - George Mason University*

[Title: Great Disruptions and Expectations: A Perspective in Protein Modeling Research](#)

10:00am - **CASCODA Workshop** **Link:** <http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>  
11:30am

**Session 7: CASCODA 3**

**Chair:** Alex Zelikovsky

- James Cai and Daniel Osorio, Machine Learning Analysis of Single-cell Gene Regulatory Networks Reveals Potential Mechanisms of Action of Antimalarials Against SARS-CoV-2
- Tianyu Wang and Sheida Nabavi, Single-Cell Classification Using Graph Convolutional Networks
- Matthew Bernstein, Zhongjie Ma, Michael Gleicher and Colin Dewey, CellO: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology

11:30am - **Break** **Link:** <https://gather.town/app/irnseZ4RJIQyr7o0/ICCABS-2020>  
12:00pm

12:00pm - **CASCODA Workshop** **Link:** <http://snp.engr.uconn.edu/b/CANGS-CASCODA-2020>  
2:00pm

**Session 8: CASCODA 4**

**Chair:** Pavel Skums

- Florian Schmidt, Bobby Ranjan, Xiao Xuan Lin, Vaidehi Krishnan, Ignasius Joanito Irwan, Mohammad Amin Honardoost, Zahid Nawaz, Prasanna Nori Venkatesh, Joanna Tan, Nirmala Arul Rayan, Ong Sin Tiong and Shyam Prabhakar, Robust clustering and interpretation of scRNA-seq data using reference component analysis
- Thanh Nguyen, Zongliang Yue and Jake Y Chen, Addressing new challenges for scRNA-seq downstream analysis
- Marmar Moussa and Ion Mandoiu, Cell Cycle Effect Analysis in Single Cell RNA-Seq Data
- Ewa Szczurek, CACTUS: integrating clonal architecture with genomic clustering and transcriptome profiling of single tumor cells