



# ICCABS 2016

**2016 IEEE 6th International Conference on  
Computational Advances in Bio and medical Sciences  
(ICCABS)**

**October 13–15, 2016,  
Georgia Institute of Technology,  
Atlanta, GA  
<http://www.iccabs.org>**



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# Message from the General Chairs



Welcome to the Sixth IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2016)! 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 at Georgia Tech, Atlanta.

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

We would like to thank Program Chairs Li-San Wang and Scott Emrich 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 Russell Schwartz, May Wang, and Cathy Wu) and seven invited talks (from Mukul Bansal, Krish Karuturi, Yury Khudyakov, Yuk Yee Leung, Rahul Singh, Jijun Tang and Ellen Tsai). 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 Chairs (Reda Ammar and Mukul Bansal), Local Arrangements Chair (Sharma Valliyil Thankachan), Workshops Chairs (Yury Khudyakov, Ion Mandoiu, Pavel Skums, and Alex Zelikovsky), Proceedings Chairs (Abdullah-Al Mamun and Soumitra Pal), Publicity Chair (Bob Weiner), and Webmaster (Soumitra Pal) for their tireless efforts.

Selected papers from ICCABS 2016 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 Karen Kuca and Rebecca Randazzo for their incessant support.

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

*Srinivas Aluru*, Georgia Institute of Technology

*Sanguthevar Rajasekaran*, University of Connecticut

# Message from the Program Chairs



We would like to welcome you to the 6th IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2016) in Atlanta, Georgia. The conference program covers a wide range of topics in computational biology and medicine and includes 18 extended abstracts selected by the Program Committee from all 36 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 Srinivas Aluru and Sanguthevar Rajasekaran 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 2016 program exciting and stimulating, and enjoy the opportunity to interact with researchers around the world. Welcome!

*Scott Emrich*, University of Notre Dame, Notre Dame, Indiana, USA

*Li-San Wang*, University of Pennsylvania, Philadelphia, Pennsylvania, USA

# Message from CANGS Workshop Chairs



Welcome to the 6<sup>th</sup> Workshop on Computational Advances for Next Generation Sequencing, held on October 13-15, 2016 in Atlanta, GA in conjunction with ICCABS 2016. 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 10 invited talks on a variety of current research topics including de novo transcriptome assembly, comparison of scaffold assemblies, single nucleotide and indel variant calling, pathogen detection in microbiomes, identification of non-coding RNAs, and pairing T-cell receptor sequences using min-cost flows.

We would like to thank ICCABS General Chairs Srinivas Aluru and Sanguthevar Rajasekaran for the opportunity to organize CANGS 2016, 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 CAME Workshop Chairs



Welcome to the 5th Workshop on Computational Advances in Molecular Epidemiology, held on October 13-15, 2016 in Atlanta, GA in conjunction with ICCABS 2016. Molecular epidemiology is essentially an integrative scientific discipline that considers molecular biological processes in specific epidemiological settings. It relates molecular biological events to etiology, distribution and prevention of disease in human populations. Over years, molecular epidemiology has become extensively fused with mathematical and computational science and immensely benefitted from this tight association. The CAME workshop aims to provide a forum for presentation and discussion of the latest computational research in molecular epidemiology. This multidisciplinary workshop will bring together field practitioners of molecular epidemiology, molecular evolutionists, population geneticists, medical researchers, bioinformaticians, statisticians and computer scientists interested in the latest developments in algorithms, mining, visualization, modeling, simulation and other methods of computational, statistical and mathematical analysis of genetic and molecular data in the epidemiological context.

This year's workshop program will span 3 sessions comprising 11 invited talks on a variety of current research topics, including transmission network inference from sequencing data, integration of molecular mapping and social media signals, molecular surveillance of viral diseases genomic data comparison, vaccine derived viruses, and detecting patterns of co-variation in deep-sequenced virus populations.

We would like to thank ICCABS General Chairs Srinivas Aluru and Sanguthevar Rajasekaran for the opportunity to organize CAME 2016, and all speakers for presenting their work at the workshop.

*Yury Khudyakov, CDC/CCID/NCHHSTP*  
*Ion Mandoiu, University of Connecticut*  
*Alex Zelikovsky, Georgia State University*

# Conference Organization

## Steering Committee

*Srinivas Aluru - Iowa State University*  
*Reda A. Ammar - University of Connecticut*  
*Tao Jiang - U.C. Riverside*  
*Vipin Kumar - University of Minnesota*  
*Ming Li - University of Waterloo*  
*S. Rajasekaran (Chair) - University of Connecticut*  
*John Reif - Duke University*  
*Sartaj Sahni - University of Florida*

## General Chairs

*Srinivas Aluru - Georgia Institute of Technology*  
*S. Rajasekaran - University of Connecticut*

## Program Chairs

*Scott Emrich - University of Notre Dame*  
*Li-San Wang - University of Pennsylvania*

## Workshop Chairs

*Yury Khudyakov, CDC*  
*Ion Mandoiu - University of Connecticut*  
*Pavel Skums - Georgia State University*  
*Alex Zelikovsky - Georgia State University*

## Finance Chairs

*Reda A. Ammar - University of Connecticut*  
*Mukul Bansal - University of Connecticut*

## Publicity Chair

*Bob Weiner - University of Connecticut*

## Proceedings Chair

*Abdullah-Al Mamun - University of Connecticut*  
*Soumitra Pal - University of Connecticut*

## Local Arrangements Chair

*Sharma Valliyil Thankachan - Georgia Institute of Technology*

## Webmaster

*Soumitra Pal - University of Connecticut*

## Program Committee Members

*Lipi Rani Acharya*  
*Tatsuya Akutsu*  
*Matteo Comin*  
*Jaime Davila*  
*Jorge Duitama*  
*Richard Edwards*  
*Oliver Eulenstein*  
*Liliana Florea*  
*Katia Guimaraes*  
*Steffen Heber*  
*Sumit Kumar Jha*  
*Mehmet Koyuturk*  
*Danny Krizanc*

*Serghei Mangul*  
*Nadia Pisanti*  
*Maria Poptsova*  
*Joao Setubal*  
*Amarda Shehu*  
*Xinghua Shi*  
*Rahul Singh*  
*Sing-Hoi Sze*  
*Ugo Vaccaro*  
*Jianxin Wang*  
*Yufeng Wu*  
*Fang Xiang Wu*



# ICCABS 2016 Program

Thursday, October 13, 2016

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

9:00am - **Keynote Talk**  
9:45am **Chair:** *Sanguthevar Rajasekaran*

*May Wang* (Georgia Tech and Emory University)  
Title: [Biomedical Big Data Analytics for Personalized, Predictive, and Precision Health](#)

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

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

**Session 1A:** ICCABS 1, 1116 E  
**Chair:** *Nurit Haspel*

- *Chunchun Zhao and Sartaj Sahni.* [Cache and Energy Efficient Algorithms for Nussinov RNA Folding](#)
- *Shenglong Zhu, Danny Chen and Scott Emrich.* [Single Molecule Sequencing-guided Scaffolding and Correction of Draft Assemblies](#)
- *Pedro Henrique de Brito Souza, José Olímpio Ferreira, Adson Ferreira Da Rocha and Talles Marcelo Gonçalves de Andrade Barbosa.* [HRVcam: A Software for Real-Time Feedback of Heart Rate and HRV](#)
- *Wen-Chyi Lin, Ching-Chung Li, Jonathan I. Epstein and Robert W. Veltri.* [Curvelet-based Texture Classification of Critical Gleason Patterns of Prostate Histological Images](#)
- *Guangyu Yang and Liliana Florea.* [JULiP: An efficient model for accurate intron](#)

**Session 1B:** ICCABS 2, 1116 W  
**Chair:** *Krishna Karuturi*

- *Samuele Giroto, Matteo Comin and Cinzia Pizzi.* [Higher Recall in Metagenomic Sequence Classification Exploiting Overlapping Reads](#)
- *Zhe Xiao, Ruohan Huang, Yi Ding, Tian Lan, Rongfeng Dong, Xinjie Zhang, Wei Wang and Zhiguang Qin.* [A Deep Learning-Based Segmentation Method for Brain Tumor in MR Images](#)
- *Ralph Crosby and Tiffani Williams.* [Fast Algorithms for Computing Phylogenetic Divergence Time](#)
- *Ankit Agrawal, Jason Mathias, David Baker and Alok Choudhary.* [Identifying HotSpots in Five Year Survival Electronic Health Records of Older Adults](#)
- *Osamu Maruyama and Yuki Kuwahara.* [RocSampler: Regularizing Overlapping Protein](#)

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

1:30pm - **Invited Talk**  
2:05pm **Chair:** *Ion Mandoiu*

*Krishna Karuturi* (Jackson Lab)

Title: [Multi-factor Differential Co-expression Analysis of High-throughput Gene Expression Data](#)

2:05pm - **Invited Talk**  
2:40pm **Chair:** *Yury Khudyakov*

*Ellen Tsai* (Partners)

Title: [Informatics workflow applied to a large genotyping biobank cohort](#)

2:40pm - **Invited Talk**  
3:15pm **Chair:** *Krishna Karuturi*

*Yury Khudyakov* (CDC)

Title: [GHOST and Molecular Epidemiology](#)

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

3:45pm - **Parallel Sessions**  
5:25pm

**Session 2A:** ICCABS 3, 1116 E

**Chair:** *Ralph Crosby*

- *Yue Guo, Johan Wrammert, Kavita Singh, Ashish Kc, Kira Bradford and Ashok Krishnamurthy.* [Automatic Analysis of Neonatal Video Data to Evaluate Resuscitation Performance](#)
- *Mohammad Ruhul Amin, Steven Skiena and Michael Schatz.* [NanoBLASter: Fast Alignment and Characterization of Oxford](#)

**Session 2B:** ICCABS 4, 1116 W

**Chair:** *Sharma V. Thankachan*

- *Nurit Haspel, Eduardo Gonzalez and Dong Luo.* [Detecting Intermediate Protein Conformations Using Algebraic Topology](#)
- *Jan Jelinek, Petr Škoda and David Hoksza.* [Utilizing knowledge base of amino acids structural neighborhoods to predict protein-protein interaction sites](#)

[Nanopore Single Molecule Sequencing Reads](#)

- *Erik Andersson, Rebecca Hsieh, Howard Szeto, Roshanak Farhoodi, Nurit Haspel and Filip Jagodzinski. [Assessing How Multiple Mutations Affect Protein Stability Using Rigid Cluster Size Distributions](#)*
- *Ernur Saka, Benjamin Harrison, Kirk West, Jeffrey Petruska and Eric Rouchka. [Region-Based Custom Chip Description Formats for Reanalysis of Publicly Available Affymetrix® GeneChip® Data Sets](#)*
- *Pakeeza Akram and Li Liao. [Prediction of missing common genes for disease pairs using network based module separation](#)*

# Friday, October 14, 2016

## 9:00am - Invited Talk

9:35am Chair: *Alex Zelikovsky*

*Mukul Bansal* (University of Connecticut)

Title: [Deciphering microbial evolution using phylogenetic reconciliation](#)

## 9:35am - Invited Talk

10:10am Chair: *Mukul Bansal*

*Rahul Singh* (San Francisco State University)

Title: [Quantifying multidimensional phenotypic dose-responses for drug screening](#)

## 10:10am - Coffee Break 10:40am

## 10:40am - Parallel Sessions 12:20pm

### Session 3A: CAME 1, 1116 E

Chair: *Rahul Singh*

- *Mukul Bansal*. [Phylogenetic Uncertainty and Transmission Network Inference: Lessons from Phylogenetic Reconciliation](#)
- *Pavel Skums, Olga Glebova, Igor Mandric, Zoya Dimitrova, David Stiven Campo Rendon, Leonid Bunimovich, Alex Zelikovsky and Yury Khudyakov*. [Bayesian reconstruction of transmission networks from intra-host viral populations](#)
- *Rahul Singh*. [Computational Analysis of Drug Addiction Epidemiology by Integrating Molecular Mapping and Social Media Signals](#)
- *Atkinson G. Longmire, Seth Sims, Inna Rytsareva, David S. Campo, Pavel Skums,*

### Session 3B: CANGS 1, 1116 W

Chair: *Sing-Hoi Sze*

- *Mohammad Shabbir Hasan, Xiaowei Wu, Layne S Watson, Zhiyi Li and Liqing Zhang*. [UPS-indel: A better approach for variant normalization and finding indel redundancy](#)
- *Sing-Hoi Sze, Jonathan Parrott and Aaron Tarone*. [A Divide-and-Conquer Algorithm for Large-Scale De Novo Transcriptome Assembly through Combining Small Assemblies from Existing Algorithms](#)
- *Ning Yu, Zeng Yu and Yi Pan*. [A Deep Learning Method for lincRNA Identification using Auto-encoder Algorithm](#)
- *Guangyu Yang and Liliana Florea*. [Ultra-sensitive detection of splicing variation](#)

Massimo Mirabito, Silver Wang, Robin Tracy, Thomas Sukalac, Christopher Lynberg and Yury Khudyakov. [GHOST: Global Health Outbreak and Surveillance Technology](#)

[from a single and from multiple RNA-seq samples](#)

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

1:30pm - **Keynote Talk**  
2:15pm **Chair: Srinivas Aluru**

*Russell Schwartz (CMU)*

**Title: Computationally resolving heterogeneity in mixed genomic samples**

2:15pm - **Coffee Break**  
2:30pm

2:30pm - **Parallel Sessions**  
4:10pm

**Session 4A: CAME 2, 1116 E**  
**Chair: June Zhang**

- Walker Gussler, David Stiven Campo Rendon, Pavel Skums, Seth Sims, Atkinson Longmire and Yury Khudyakov. [Application of locality-sensitive hashing to the detection of viral transmissions](#)
- Susana Posada Céspedes. [Detecting patterns of co-variation in deep-sequenced virus populations](#)
- June Zhang, David S. Campo and Yury Khudyakov. [The Role of Stochasticity on the Transmission of Hepatitis C Viral Variants](#)
- Olga Glebova, Pavel Skums, Sergei Knyazev, Alexander Artyomenko and Alex Zelikovsky. [Simulation-based](#)

**Session 4B: CANGS 2, 1116 W**  
**Chair: Liliana Florea**

- Sergey Aganezov and Max Alekseyev. [CAMSA: A Tool For Comparative Analysis And Merging Of Scaffold Assemblies](#)
- Todd Treangen and Mihai Pop. [Promises, pitfalls, and perils of pathogen detection in microbiomes](#)
- Yongchao Liu and Srinivas Aluru. [An Integrated Solution to Call Germline and Somatic Single-Nucleotide and Indel Mutations](#)
- Mohammad Mohebbi, Liang Ding, Russell Malmberg, Cory Momany, Khaled Rasheed and Liming Cai. [Accurate Prediction of Human miRNA](#)

[inference of genetic relatedness between viral populations](#)

[Targets via Graph Modeling of miRNA-Target Duplex](#)

4:10pm -  
4:30pm **Coffee Break**

4:30pm -  
5:45pm **Parallel Sessions**

**Session 5A:** CAME 3, 1116 E

**Chair:** *James Lara*

- *Kun Zhao* [Are Circulating Type 2 Vaccine-Derived Polioviruses \(VDPVs\) Genetically Distinguishable from Immunodeficiency-associated VDPVs?](#)
- *Fredrik Vannberg*. [Linear Algebraic and Boolean Analysis of Genomic Sequence](#)
- *James Lara, Mahder Asefa Teka, David Stiven Campo Rendon, Guo-Liang Xia and Yury Khudyakov* [Identification of recent HCV infection using dinucleotide auto covariance and a radial basis function neural network](#)

**Session 5B:** CANGS 3, 1116 W

**Chair:** *Ion Mandoiu*

- *Ying Sun, Sal Lamarca, Russell Malmberg, Liming Cai, Willie Rogers and Katrien Devos*. [Genome-Wide Identification and Evolutionary Analysis of Long Non-Coding RNAs in Cereals](#)
- *Tyler Daddio and Ion Mandoiu*. [Pairing T-cell receptor sequences using pooling and min-cost flows](#)

**ICCABS 5:**

- *Mohammed Aldhoayan and Leming Zhou*. [An Accurate and Customizable Text Classification Algorithm: Two Applications in Healthcare](#)

6:30pm - **Banquet at Homewood Suites by Hilton Atlanta Midtown**  
10:00pm **Dinner at 7:00pm**

# Saturday, October 15, 2016

9:00am - **Keynote Talk**

9:45am **Chair:** *Sanguthevar Rajasekaran*

*Cathy H. Wu* (University of Delaware)

Title: [Semantic Literature Annotation and Integrative Panomics Analysis for Disease Knowledge Network Discovery](#)

9:45am -  
10:20am

**Coffee Break**

10:20am - **Invited Talk**

10:55am **Chair:** *Ching-Chung Li*

*Yuk Yee Leung* (University of Pennsylvania)

Title: [Bioinformatics for small RNA sequencing](#)

10:55am - **Invited Talk**

11:30am **Chair:** *Yuk Yee Leung*

*Jijun Tang* (University of South Carolina)

Title: [Analysis of gene copy number changes in tumor phylogenetics](#)

11:30am -  
12:00pm

**Parallel Sessions**

**Session 6:** ICCABS POSTER, 1116 E

**Chair:** *Russell Schwartz*

- *Mohammad Shabbir Hasan*
- *Andrew Schumann*
- *Matej Lexa*