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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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

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<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>8:50am - 9:00am</td>
<td>Opening Remarks</td>
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</table>
| 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 Sazal, 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

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<td>Time</td>
<td>Session</td>
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<tr>
<td>1:30pm - 2:05pm</td>
<td>Invited Talk</td>
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<tr>
<td>2:05pm - 2:40pm</td>
<td>Invited Talk</td>
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<tr>
<td>2:40pm - 3:15pm</td>
<td>Invited Talk</td>
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<td>3:15pm - 3:45pm</td>
<td>Coffee Break</td>
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<td>3:45pm - 5:50pm</td>
<td>Parallel Sessions</td>
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**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.
- 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

- 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.
<table>
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<tr>
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<tr>
<td>9:00am-9:45am</td>
<td>Keynote Talk &lt;br&gt;Chair: TBD &lt;br&gt;&lt;br&gt;Aidong Zhang - University at Buffalo, The State University of New York &lt;br&gt;Title: Deep Learning and Networks for Integrative Analysis of Multi-Omic Data</td>
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<td>9:45am-10:15am</td>
<td>Coffee Break</td>
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<td>12:20pm-1:30pm</td>
<td>Lunch</td>
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<td>1:30pm-2:15pm</td>
<td>Keynote Talk &lt;br&gt;Chair: TBD &lt;br&gt;&lt;br&gt;Srinivas Aluru - Georgia Institute of Technology &lt;br&gt;Title: TBD</td>
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2:15pm - 2:50pm
Invited Talk
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 - 10:00pm
Banquet
Saturday, October 20, 2018

9:00am - 9:35am Invited Talk
Chair: TBD

Cuncong Zhong - University of Kansas
Title: TBD

9:35am - 10:00am Coffee Break

10:00am - 11:40am Parallel Sessions

**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

- Sze, Kaplan. *Codon-based sequence alignment for mutation analysis by high-throughput sequencing*
- Karuturi. *Reduction to Homozygicity Driven Network Analysis to Identify Sample Specific Tumor Suppressor Genes*
- Xiao, Rajasekaran. *EMS3: An Improved Algorithm for Finding Edit-distance Based Motifs*