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ICCABS 2016 Program

Thursday, October 13, 2016

8:50am - Opening Remarks
9:00am

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](#) N/A

9:45am - Coffee Break
10:15am

10:15am - Parallel Sessions
12:20pm

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

- *Chunchun Zhao and Sartaj Sahni.* [Cache and Energy Efficient Algorithms for Nussinov RNA Folding](#) 1
- *Shenglong Zhu, Danny Chen and Scott Emrich.* [Single Molecule Sequencing-guided Scaffolding and Correction of Draft Assemblies](#) 2
- *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](#) 3
- *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](#) 9

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- *Ralph Crosby and Tiffani Williams.* [Fast Algorithms for Computing Phylogenetic Divergence Time](#) 28
- *Ankit Agrawal, Jason Mathias, David Baker and Alok Choudhary.* [Identifying HotSpots in Five Year Survival Electronic Health Records of Older Adults](#) 29

- *Guangyu Yang and Liliana Florea. [JULiP: An efficient model for accurate intron selection from multiple RNA-seq samples](#)* 15
- *Osamu Maruyama and Yuki Kuwahara. [RocSampler: Regularizing Overlapping Protein Complexes in Protein-Protein Interaction Networks](#)* 35

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](#) N/A

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

Ellen Tsai (Partners)

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

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

Yury Khudyakov (CDC)

Title: [GHOST and Molecular Epidemiology](#) N/A

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](#)* 36
- *Mohammad Ruhul Amin, Steven Skiena and*

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Chair: *Sharma V. Thankachan*

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- *Jan Jelinek, Petr Škoda and David Hoksza. [Utilizing knowledge base of amino acids structural neighborhoods to predict protein-](#)* 59

Michael Schatz. [NanoBLASter: Fast Alignment and Characterization of Oxford Nanopore Single Molecule Sequencing Reads](#) 42

- 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](#) 48

[protein interaction sites](#)

- 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](#) 60
- Pakeeza Akram and Li Liao. [Prediction of missing common genes for disease pairs using network based module separation](#) 61

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](#) N/A

9:35am - Invited Talk

10:10am Chair: *Mukul Bansal*

Rahul Singh (San Francisco State University)

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

10:10am - Coffee Break

10:40am

10:40am - Parallel Sessions

Session 3A: CAME 1, 1116 E

Chair: *Rahul Singh*

- *Mukul Bansal*. [Phylogenetic Uncertainty and Transmission Network Inference: Lessons from Phylogenetic Reconciliation](#) 66
- *Pavel Skums, Olga Glebova, Igor Mandric, Zoya Dimitrova, David Steven Campo Rendon, Leonid Bunimovich, Alex Zelikovsky and Yury Khudyakov*. [Bayesian reconstruction of transmission networks from intra-host viral populations](#) N/A
- *Rahul Singh*. [Computational Analysis of Drug Addiction Epidemiology by Integrating Molecular Mapping and Social Media Signals](#) 67
- *Atkinson G. Longmire, Seth Sims, Inna Rytsareva, David S. Campo, Pavel Skums,*

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- *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](#) 73
- *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](#) 74
- *Ning Yu, Zeng Yu and Yi Pan*. [A Deep Learning Method for lincRNA Identification using Auto-encoder Algorithm](#) 75
- *Guangyu Yang and Liliana Florea*. [Ultra-sensitive detection of splicing variation](#) N/A

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

[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](#) 77

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](#) N/A
- Susana Posada Céspedes. [Detecting patterns of co-variation in deep-sequenced virus populations](#) 68
- June Zhang, David S. Campo and Yury Khudyakov. [The Role of Stochasticity on the Transmission of Hepatitis C Viral Variants](#) N/A
- Olga Glebova, Pavel Skums, Sergei Knyazev, Alexander Artyomenko and Alex Zelikovsky. [Simulation-based](#) N/A

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Chair: Liliana Florea

- Sergey Aganezov and Max Alekseyev. [CAMSA: A Tool For Comparative Analysis And Merging Of Scaffold Assemblies](#) 76
- Todd Treangen and Mihai Pop. [Promises, pitfalls, and perils of pathogen detection in microbiomes](#) ^{***P IC}
- Yongchao Liu and Srinivas Aluru. [An Integrated Solution to Call Germline and Somatic Single-Nucleotide and Indel Mutations](#) ^{***P IC}
- Mohammad Mohebbi, Liang Ding, Russell Malmberg, Cory Momany, Khaled Rasheed and Liming Cai. [Accurate Prediction of Human miRNA](#) 72

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

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

4:10pm - Coffee Break
4:30pm

4:30pm - Parallel Sessions
5:45pm

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?](#) 69
- *Fredrik Vannberg*. [Linear Algebraic and Boolean Analysis of Genomic Sequence](#) N/A
- *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](#) N/A

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](#) 71
- *Tyler Daddio and Ion Mandoiu*. [Pairing T-cell receptor sequences using pooling and min-cost flows](#) 70

ICCABS 5:

- *Mohammed Aldhoayan and Leming Zhou*. [An Accurate and Customizable Text Classification Algorithm: Two Applications in Healthcare](#) 54

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

