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

Atlanta, Georgia, USA
13 – 15 October 2016
Thursday, October 13, 2016

8:50am - 9:00am  Opening Remarks

9:00am - 9:45am  Keynote Talk
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 - 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  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

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

- Samuele Girotto, Matteo Comin and Cinzia Pizzi. Higher Recall in Metagenomic Sequence Classification Exploiting Overlapping Reads  21

- 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  22


- Ankit Agrawal, Jason Mathias, David Baker and Alok Choudhary. Identifying HotSpots in Five Year Survival Electronic Health Records of Older Adults  29
<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>12:20pm -</td>
<td>Lunch</td>
</tr>
</tbody>
</table>
| 1:30pm -     | Invited Talk  
   **Chair:** Ion Mandoiu |
| 2:05pm -     | Invited Talk  
   **Chair:** Yury Khudyakov |
| 2:40pm -     | Invited Talk  
   **Chair:** Krishna Karuturi |
| 3:15pm -     | Coffee Break                               |
| 3:45pm -     | Parallel Sessions                          |

**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

**Session 2B:** ICCABS 4, 1116 W  
**Chair:** Sharma V. Thankachan

- Nurit Haspel, Eduardo Gonzalez and Dong Luo.  
  **Detecting Intermediate Protein Conformations Using Algebraic Topology**  
  [58]

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

- 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

- 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**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Chair</th>
<th>Speaker(s)</th>
<th>Title</th>
<th>N/A</th>
</tr>
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<tbody>
<tr>
<td>9:00am</td>
<td>Invited</td>
<td>Alex Zelikovsky</td>
<td>Mukul Bansal (University of Connecticut)</td>
<td><strong>Deciphering microbial evolution using phylogenetic reconciliation</strong></td>
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<tr>
<td>9:35am</td>
<td>Invited</td>
<td>Mukul Bansal</td>
<td>Rahul Singh (San Francisco State University)</td>
<td><strong>Quantifying multidimensional phenotypic dose-responses for drug screening</strong></td>
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<td>10:10am</td>
<td>Coffee</td>
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<td>10:40am</td>
<td>Parallel</td>
<td>Rahul Singh</td>
<td><strong>Phylogenetic Uncertainty and Transmission Network Inference:</strong> Mukul Bansal</td>
<td><strong>Lessons from Phylogenetic Reconciliation</strong></td>
<td>66</td>
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<td><strong>Bayesian reconstruction of transmission networks from intra-host viral populations:</strong> Pavel Skums, Olga Glebova, Igor Mandric, Zoya Dimitrova, David S. Campo Rendon, Leonid Bunimovich, Alex Zelikovsky and Yury Khudyakov</td>
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<td><strong>Computational Analysis of Drug Addiction Epidemiology by Integrating Molecular Mapping and Social Media Signals:</strong> Rahul Singh</td>
<td><strong>A Divide-and-Conquer Algorithm for Large-Scale De Novo Transcriptome Assembly through Combining Small Assemblies from Existing Algorithms</strong></td>
<td>74</td>
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<td><strong>UPS-indel: A better approach for variant normalization and finding indel redundancy:</strong> Mohammad Shabbir Hasan, Xiaowei Wu, Layne S Watson, Zhiyi Li and Liqing Zhang</td>
<td><strong>N/A</strong></td>
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<td><strong>A Deep Learning Method for lincRNA Identification using Auto-encoder Algorithm:</strong> Ning Yu, Zeng Yu and Yi Pan</td>
<td><strong>Ultra-sensitive detection of splicing variation</strong></td>
<td>75</td>
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<td><strong>Ultra-sensitive detection of splicing variation:</strong> Guangyu Yang and Liliana Florea</td>
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Massimo Mirabito, Silver Wang, Robin Tracy, Thomas Sukalac, Christopher Lynberg and Yury Khudyakov. **GHOST: Global Health Outbreak and Surveillance Technology**

### Schedule

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>12:20pm - 1:30pm</td>
<td>Lunch</td>
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<td>1:30pm - 2:15pm</td>
<td>Keynote Talk</td>
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<td>2:15pm - 2:30pm</td>
<td>Coffee Break</td>
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<tr>
<td>2:30pm - 4:10pm</td>
<td>Parallel Sessions</td>
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#### 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

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

- 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

ICCABS 5:

- Mohammed Aldhoayan and Leming Zhou. An Accurate and Customizable Text Classification Algorithm: Two Applications in Healthcare

6:30pm - 10:00pm  Banquet at Homewood Suites by Hilton Atlanta Midtown  
Dinner at 7:00pm
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<tr>
<td>9:00am - 9:45am</td>
<td>Keynote Talk</td>
<td>Sanguthevar Rajasekaran</td>
<td><em>Cathy H. Wu (University of Delaware)</em>&lt;br&gt;Title: <strong>Semantic Literature Annotation and Integrative Panomics Analysis for Disease Knowledge Network Discovery</strong> N/A</td>
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<tr>
<td>9:45am - 10:20am</td>
<td>Coffee Break</td>
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<tr>
<td>10:20am - 10:55am</td>
<td>Invited Talk</td>
<td>Ching-Chung Li</td>
<td><em>Yuk Yee Leung (University of Pennsylvania)</em>&lt;br&gt;Title: <strong>Bioinformatics for small RNA sequencing</strong> N/A</td>
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<td>10:55am - 11:30am</td>
<td>Invited Talk</td>
<td>Yuk Yee Leung</td>
<td><em>Jijun Tang (University of South Carolina)</em>&lt;br&gt;Title: <strong>Analysis of gene copy number changes in tumor phylogenetics</strong> N/A</td>
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<tr>
<td>11:30am - 12:00pm</td>
<td>Parallel Sessions</td>
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**Session 6:** ICCABS POSTER, 1116 E<br>**Chair:** Russell Schwartz
- Mohammad Shabbir Hasan
- Andrew Schumann
- Matej Lexa

**01 ŌÔÔÔ** Diagnosing and Treating Code-Duplication Problems in Bioinformatics Libraries<br>*M. Hasan, S. Tithi, E. Tilevich, L. Zhang*

Additional Paper: Semi-automatic Mining of Correlated Data from a Complex Database: Correlation Network Visualization<br>*Matej Lexa, Radovan Lapar*