2014 IEEE 4th International Conference on Computational Advances in Bio and Medical Sciences

(ICCABS 2014)

Miami, Florida, USA
2-4 June 2014

ICCABS 2014 Program

Monday, June 2, 2014

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

9:00am- 10:00am	**ICCABS+CANGS Keynote Talk: Metagenomics and NGS** **Chair:** *Srinivas Aluru*

Giri Narasimhan (Florida International University), keynote talk

10:00am - 10:30am	**Coffee break**

10:30am - 12:30pm	**Parallel Sessions**

Session 1A: ICCABS 1
Chair: *Sanguthevar Rajasekaran*

- *Discriminating between structural and functional mechanisms for duplicate gene loss following whole genome doubling*, David Sankoff, Baoyong Wang, Chunfang Zheng and Carlos Fernando Buen Abad Najar
- *How genome complexity can explain the hardness of aligning reads to genomes*, Vinhthuy Phan, Shanshan Gao, Quang Tran and Nam Vo
- *Characterization of probabilistic signaling networks through signal propagation*, Haitham Gabr and Tamer Kahveci
- *Putting Humpty-Dumpty Together: Mining Mechanistic Biochemical Models from Big Data*, Sumit Kumar Jha, Susmit Jha, Emily Sassano and Faraz Hussain

Session 1B: CANGS 1
Chair: *Alex Zelikovsky*

- *Role Of ADAR In Determining The Substitution Pattern In Sigma Virus (Rhabdoviridae) In Drosophila Melanogaster*, Helen Piontkivska, Sinu Paul, Brian Scharfenberg, Marta Wayne, Luis Matos, William Farmerie and Michael Miyamoto
- *Hierarchical Genome Assembly*, Anas Al-Okaily and Ion Mandoiu
- *SILP3: Maximum Likelihood Approach to Scaffolding*, Igor Mandric, James Lindsay, Ion Mandoiu and Alex Zelikovsky
- *Efficient algorithms for error correction and compression of NGS data*, Subrata Saha and Sanguthevar Rajasekaran

12:30pm - 01:30pm	**Lunch**

1:30pm - 3:00pm	**Parallel Sessions**

Session 2A: Session on Radiation Oncology 1
Chair: *Puneeth Iyengar*

- *Informatics in Radiation Oncology*, David Schwartz, M.D., The University of Texas Southwestern Medical Center
- *Correlating Online Stories with Offline Health Behavior*, Mark A. Finlayson, Ph.D., Massachusetts Institute of Technology
- *A Global View of How Technology Is Guiding Radiation Therapeutics for Cancers*, Puneeth Iyengar, M.D., Ph.D., The University of Texas Southwestern Medical Center

Session 2B: CANGS 2
Chair: *Ion Mandoiu*

- *Revealing transcription units in Clostridium Thermocellum by High-Density Tiling Arrays and RNAseq data*, Andrey Gorin
- *Heuristic Pairwise Alignment of de Bruijn Graphs to Facilitate Simultaneous Transcript Discovery in Related Organisms from RNA-Seq Data*, Shuhua Fu, Aaron M. Tarone and Sing-Hoi Sze
- *An SVM-based approach for discovering splicing junctions with RNA-Seq*, Chong Chu and Yufeng Wu

3:00pm - 3:30pm	**Coffee break**

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

Session 3A: Session on Radiation Oncology 2
Chair: *Puneeth Iyengar*

- *Use of Computational Biology in Assessing Treatment Response and Disease Progression*, John Yordy, M.D., Ph.D., The University of Texas Southwestern Medical Center
- *Imaging and Image Guidance in Lung Cancer Therapeutics*, Amit Sawant, Ph.D., The University of Texas Southwestern Medical Center
- *Medical Image Analysis in Assessing Treatment Response and Disease Progression*, Ruogu Fang, Ph.D., Tsuhan Chen, Ph.D., Cornell University
- *Computer-Based Pattern Recognition to Assist Clinical Decision Making in Oculofacial Plastic Surgery*, Benjamin Erickson, University of Miami

Session 3B: CANGS 3
Chair: *Andrey Gorin*

- *Reference-free Inference of Tumor Phylogenies from Single-Cell Sequencing Data*, Ayshwarya Subramanian and Russell Schwartz
- *Allele Specific Gene Expression Analysis from Single Cell RNA-Seq Data*, Sahar Al Seesi and Ion Mandoiu
- *Bootstrapping-based differential gene expression analysis for RNA-Seq data with and without replicates*, Sahar Al Seesi, Yvette Blanche Temate-Tiagueu, Alex Zelikovsky and Ion Mandoiu

6:30pm - 9:00pm	**Reception in Dr. Iyengar's House**

Tuesday, June 3, 2014

9:00am-10:00am	**ICCABS Keynote Talk** **Chair: *Ion Mandoiu***

Alex Zelikovsky (Georgia State University), keynote talk

10:00am - 10:30am	**Coffee break**

10:30am - 12:30pm	**Parallel Sessions**

Session 4A: ICCABS 2
Chair: *Sanguthevar Rajasekaran*

- *In search of perfect reads*, Soumitra Pal and Srinivas Aluru
- *A Computational Method for Drug Repositioning using Publicly Available Gene Expression Data*, Shabana K M, Abdul Nazeer K A, Meeta Pradhan and Mathew J Palakal
- *Optimization of IMRT Treatment Plan with Kinetic Data Structures*, David Allen and Ovidiu Daescu
- *Identification of Protein Interaction Methods from Biomedical Literature*, Deepali Jhamb, Anand Krishnan, Meelia Palakal, Yogesh Pandit, Premkumar Duraiswamy and Mathew Palakal

Session 4B: CANGS 4 + CAME 1(Joint session)
Chair: *Pavel Skums*

- *A Combinatorial Algorithm to Identify Independent and Recurrent Copy Number Aberrations Across Cancer Types*, Hsin-Ta Wu and Ben Raphael
- *Viral quasispecies assembly from paired-end reads*, Armin Töpfer and Niko Beerenwinkel
- *Accurate viral population assembly from ultra-deep sequencing*, Serghei Mangul, Nicholas Wu, Nicholas Mancuso, Alex Zelikovsky, Ren Sun and Eleazar Eskin
- *Deterministic Regression Algorithm for Transcriptome Frequency Estimation*, Adrian Caciula, Olga Glebova, Alexander Artyomenko, Serghei Mangul, James Lindsay, Ion Mandoiu and Alex Zelikovsky

12:30pm - 01:30pm	**Lunch**

1:30pm - 3:00pm	**Parallel Sessions**

Session 5A: ICCABS 3
Chair: *Egidijus Paliulis*

- *An Integrated Model of Human Biomedical and Clinical Data Structures*, Egidijus Paliulis and Hesham H. Ali
- *A systems biology framework for the downstream analysis of the whole genome sequencing data*, Deepali Jhamb, Meeta Pradhan, Akshay Desai, Premkumar Duraiswamy and Mathew Palakal
- *Parameter Discovery for Stochastic Computational Models in Systems Biology Using Bayesian Model Checking*, Faraz Hussain, Christopher Langmead, Qi Mi, Joyeeta Dutta-Moscato, Yoram Vodavotz and Sumit Kumar Jha

Session 5B: CAME 2
Chair: *James Lara*

- *Oak Ridge Bio-surveillance Toolkit (ORBiT): Scalable Machine Learning for Public Health Surveillance*, Laura Pullum and Arvind Ramanathan
- *Prediction of Representative Drug-Resistant Mutants of HIV Reverse Transcriptase*, Xiaxia Yu, Robert Harrison and Irene Weber
- *Reconstruction of Influenza A Virus Variants from PacBio Reads*, Alexander Artyomenko, Serghei Mangul, Nicholas Wu, Eleazar Eskin, Ren Sun and Alex Zelikovsky

3:00pm - 3:30pm	**Coffee break**

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

Session 6A: ICCABS Poster Presentations
Chair: *Ramana Davuluri*

- *Multi-scale modeling of microvascular reactivity*, Jaimit Parikh, Adam Kapela, Daniel Rodriguez and Nikolaos Tsoukias
- *Context-Sensitive Use of Bioinformatics Tools with Complementary Functionalities for Hypothesis Generation*, Vida Abedi, Mohammed Yeasin and Ramin Zand
- *Efficient Record Linkage Techniques*, Abdullah-Al Mamun, Robert Aseltine and Sanguthevar Rajasekaran
- *Highlights: PlantTFDB – A database of plant transcription factors*, Jingchu Luo, Ge Gao, and Jinpu Jin

Session 6B: CAME 3
Chair: *Serghei Manngul*

- *Modeling Genetic Heterogeneity in Hepatitis C Virus Hyper-variable Region 1 infers Demographic Characteristics of Infected Hosts*, James Lara and Yury Khudyakov
- *New Computational Methods for Assessing the Genetic Relatedness of Close Viral Variants*, David S. Campo, Zoya Dimitrova, Guo-Liang Xia, Pavel Skums, Lilia Ganova-Raeva and Yury Khudyakov
- *Detection of genetic relatedness between viral samples using EM-based clustering of next-generation sequencing data*, Pavel Skums, Alexander Artyomenko, Alex Zelikovsky, David S. Campo, Zoya Dimitrova, Olga Glebova and Yury Khudyakov

6:00pm - 9:00pm	**Banquet**

Wednesday, June 4, 2014

9:00am-10:00am	**ICCABS Keynote Talk** **Chair:** *Sartaj Sahni*

John Reif (Duke University), keynote talk

10:00am - 10:30am	**Coffee break**

10:30am - 12:30pm	**Parallel Sessions**

Session 7A: ICCABS 4
Chair: *Zhonghang Xia*

- *Improving Bisulfite Short-Read Mapping Efficiency with Hairpin-Bisulfite Data*, Jacob Porter, Liqing Zhang, Mingan Sun and Hehuang Xi
- *Comparison of Data Discretization Methods for Cross Platform Transfer of Gene-expression based Tumor Subtyping Classifier*, Segun Jung, Yingtao Bi and Ramana Davuluri
- *A Weighted Classification Model for Peptide Identification*, Xijun Liang, Zhonghang Xia, Xinnan Niu and Andrew Link
- *A New Compact Set of Biomarkers for Distinguishing among Ten Breast Cancer Subtypes*, Forough Firoozbakht, Iman Rezaeian, Lisa Porter and Luis Rueda

Session 7B: ICCABS 5
Chair: *Faraz Hussain*

- *Constructing Regulatory Gene Set Network to Reveal Novel Insights into Biological Systems*, Chayaporn Suphavilai, Liugen Zhu, Xiaogang Wu and Jake Chen
- *A New Multi-level Thresholding Algorithm for Finding Peaks in ChIP-Seq Data*, Iman Rezaiean and Luis Rueda
- *SAIS-OPT: On the Characterization and Optimization of the SA-IS Algorithm for Suffix Array Construction*, Nataliya Timoshevskaya and Wu-Chun Feng
- *EpiSpec: A Formal Specification Language for Parameterized Agent-Based Models against Epidemiological Ground Truth*, Raj Gautam Dutta, Faraz Hussain, Sumit Kumar Jha, Arvind Ramanathan and Laura L Pullum