2015 IEEE 5th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2015)

Miami, Florida, USA 15 – 17 October 2015



IEEE Catalog Number: ISBN:

CFP15CAB-POD 978-1-4673-9664-6

ICCABS 2015 Program

Thursday, October 15, 2015

8:50am -9:00am Opening Remarks

9:00am- Keynote Talk

10:00am Chair: Sanguthevar Rajasekaran

Srinivas Aluru (Georgia Institute of Technology)

Title: Approximate Sequence Matching: Algorithms and Applications

10:00am -10:30am Coffee break

10:30am -12:30pm Parallel Sessions

Session 1A: ICCABS 1
Chair: Max Alexeyev

- Trevor Cickovski, Eli Peake, Vanessa Aguiar-Pulido and Giri Narasimhan. ATria: A Novel Centrality Algorithm Applied to Biological Networks 1
- Amirhossein Jabalameli and Aman Behal.
 A Constrained Linear Approach to Identify a
 Multi-timescale Adaptive Threshold
 Neuronal Model 2
- Ekaterina Nenastyeva, Yurij Ionov, Ion Mandoiu and Alex Zelikovsky. <u>Identification</u> of Cancer-Specific Motifs in Mimotope Profiles of Serum Antibody Repertoire 8
- Cintia Palu, Leandra Linhares-Lacerda,
 Marcelo Ribeiro-Alves and Wilson Savino.
 Genetic Modulation During Thymocyte
 Development: an Integrative Approach
 Based on Microarray Meta-analysis

Session 1B: ICCABS 2 Chair: Rahul Singh

- Chunchun Zhao and Sartaj Sahni. Cache and Energy Efficient Alignment of Very Long Sequences
- Da Zhang, Hao Wang, Kaixi Hou, Jing Zhang
 and Wu-Chun Feng. pDindel: Accelerating
 InDel Detection on Modern Multi-Core SIMD
 CPU Architecture
- Shailesh Appukuttan, Rohan Sathe and Rohit
 Manchanda. Modular Approach to Modeling
 Homotypic and Heterotypic Gap Junctions
- Zhichao Lian, Xiang Li, Yi Pan, Xuan Guo, Le Chen, Guantao Chen, Zhihui Wei, Tianming Liu and Jing Zhang. <u>Dynamic Bayesian Brain</u> 85 <u>Network Partition and Connectivity Change</u> <u>Point Detection</u>

12:30pm -02:00pm Lunch

2:00pm - Invited Talk

2:50pm Chair: Alex Zelikovsky

Giri Narisimhan (Florida International University)
Title: Microbiome Analysis: Past, Present and Future

2:50pm -3:30pm Coffee break

3:30pm -5:30pm

Parallel Sessions

Session 2A: ICCABS 3 **Chair:** *James Lara*

- Inna Rytsareva, David S Campo, Yueli
 Zheng, Seth Sims, Cansu Tetik, Jain Chirag,
 Sriram Chockalingam, Sharma Thankachan,
 Amanda Sue, Srinivas Aluru and Yury
 Khudyakov. Efficient Detection of Viral
 Transmission with Threshold-based
 Methods 15
- Pavel Skums, Olga Glebova, David Campo, Nana Li, Zoya Dimitrova, Seth Sims, Leonid Bunimovich, Alex Zelikovsky and Yury Khudyakov. Algorithms for Prediction of Viral Transmissions Using Analysis of Intra-Host Viral Populations 21
- Alexander Artyomenko, Nicholas Wu, Serghei Mangul, Eleazar Eskin, Ren Sun and Alex Zelikovsky. <u>2SNV: Quasispecies</u> <u>Reconstruction from PacBio Reads</u> 22
- James Lara, Livia Rossi, Gilberto Vaughan and Yury Khudyakov. Predicting the Crossimmunoreactivity of Hepatitis C Virus Hypervariable Region 1 Peptides using Polynomial Neural Networks 23

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- Faraz Hussain, Zubir Husein, Neslisah Torosdagli, Narsingh Deo, Sumanta Pattanaik, Chung-Che Jeff Chang and Sumit Kumar Jha. <u>SANJAY</u>: 91 <u>Automatically Synthesizing Visualizations of</u> <u>Flow Cytometry Data Using Decision Procedures</u>
- Bogdan Armaselu, Harish Arunachalam, Ovidiu Daescu, John-Paul Bach, Kevin Cederberg, Dinesh Rakheja, Anita Sengupta, Stephen Shapek and Patrick Leavey. Whole Slide Images Stitching for Osteosarcoma Detection

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 Sanguthevar Rajasekaran. <u>Efficient Techniques</u> for k-mer Counting

Friday, October 16, 2015

9:00am- Invited Talk 9:50am Chair: *Ion Mandoiu*

Sheida Nabavi (University of Connecticut)

Title: Machine Learning for Identifying Candidate Biomarkers of Resistant to Anti-Cancer

Drugs

9:50am -10:30am

Coffee break

10:30am -12:30pm

Parallel Sessions

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- Sharma V. Thankachan, Sriram
 Chockalingam, Yongchao Liu, Ambujam
 Krishnan and Srinivas Aluru. A Greedy
 Alignment-free Distance Estimator for
 Phylogenetic Inference
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- Michael Coulombe, Kristian Stevens and Dan Gusfield. Construction, Enumeration, and Optimization of Perfect Phylogenies on Multi-state Data. 25
- Nikita Alexeev and Max Alekseyev.
 Estimation of the True Evolutionary
 Distance under the Fragile Breakage
 Model 31
- Lauren Assour and Scott Emrich. Global <u>Maximum-Parsimony Based Ancestral</u> <u>Reconstruction with Non-Universal</u> Genes 32

Session 3B: CANGS 1 Chair: Sing-Hoi Sze

- Sing-Hoi Sze, Meaghan Pimsler, Jeffery
 Tomberlin, Corbin Jones and Aaron
 Tarone. A Scalable and Memory-Efficient
 Algorithm for De Novo Transcriptome
 Assembly of Non-Model Organisms
- David Seifert, Monica Dragan and Niko
 Beerenwinkel. MinPEPCo: Inferring Viral N/A
 Haplotypes by Paired-end Sequencing using Minimal Path Covers
- Siu Ming Yiu. Metagenomics Binning and N/A Annotation: Issues and Challenges
- Erin-Elizabeth Durham, Chinua Umoja and Robert Harrison. A Novel Approach to Determine Protein Docking Locations Using Fuzzy Shape Recognition

12:30pm -2:00pm Lunch

2:00pm - Keynote Talk

3:00pm Chair: Sanguthevar Rajasekaran

S. Cenk Sahinlap (Simon Fraser University)

Title: Algorithms for Data Driven Cancer Research

3:00pm -3:30pm Coffee break

3:30pm -5:30pm Parallel Sessions

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- Oyetunji Enoch Ogundijo, Dan He and Laxmi Parida. Performance Evaluation of Different Encoding Strategies for Quantitative Genetic Trait Prediction 39
- Hamid Ismail, Ahoi Jones, Jung Kim, Robert Newman and Dukka KC.
 Phosphorylation Site Prediction using Random Forest 45
- Ning Yu, Xuan Guo, Alexander Zelikovsk and Yi Pan. GaussianCpG: A Gaussian Model for Detection of Human CpG Island 51

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- Sergey Aganezov and Max Alekseyev. <u>Scaffold</u> N/A <u>Assembly Based on the Analysis of Gene Orders</u> <u>and Genomic Repeats</u>
- Tak-Wah Lam. A Simple and Economical Method 98 for Improving Whole-genome Alignment
- Steffen Heber. <u>Using PacBio Long-read Sequencing</u> N/A to Investigate Genes with Complex Splicing <u>Behavior</u>
- Ning Yu, Xuan Guo, Alexander Zelikovsky
 John Malone. Gene Dose, Compensation, and N/A
 and Yi Pan. GaussianCpG: A Gaussian
 Phenotype

6:00pm -9:00pm Banquet

Saturday, October 17, 2015

09:00am- ICCABS Invited Talk 09:50am Chair: *Alex Zelikovsky*

Ion Mandoiu (University of Connecticut)

Title: Computational Methods for Genomics-guided Immunotherapy

10:00am -10:30am Coffee break

10:30am -12:30pm Parallel Sessions

> Session 7A: ICCABS 7 Chair: Ion Mandoiu

- Qiwen Hu, Catharina Merchante, Anna Stepanova, Jose Alonso and Steffen Heber. Mining Transcript Features Related to Translation in Arabidopsis Using LASSO and Random Forest 52
- Eric C.H. Chen, Annie Morin, Jean-Hugues
 Chauchat and David Sankoff. Statistical
 Analysis of Fractionation Resistance by
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- Yinjiao Ma, Lingling Zhang, Christian Geneus and Haijun Gong. Weighted Gene 59 Coexpression Network Analysis of Prostate Cancer
- Yina Cifuentes, Sergio Latorre, Mario
 Velasquez and Andrés Pinzón. Poster: Draft
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Chair: Alex Zelikovsky

- Yuanyuan Feng, Vandana P. Janeja, Yelena Yesha, Naphtali Rishe, Michael A. Grasso and Amanda Niskar. Poster: Classifying Primary Outcomes in Rheumatoid Arthritis: Knowledge Discovery from Clinical Trial Metadata
- Igor Mandric, Yvette Temate Tiagueu, Adriano Senatore, Paul Katz and Alex Zelikovsky.
 Poster: DORFA: Database-guided ORFeome Assembly from RNA-Seq Data
- Michael Robinson and Naphtali Rishe. Poster: 101
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- Maryam Hassanzadeh, Akbar Farhoodinejad and Shahrokh Yousefzadeh-Chabok. <u>Poster: A</u> 103 <u>Prediction Model of Traumatic Patients'</u> <u>Outcome by Data Mining Technique</u>