2013 IEEE 3rd International Conference on Computational Advances in Bio and Medical Sciences

(ICCABS 2013)

New Orleans, Louisiana, USA
12-14 June 2013

ICCABS 2013 Program

Wednesday, June 12, 2013

| 8:30am-8:40am | **Opening Remarks** |

| 8:40am-10:20am | **Parallel Sessions** |

Session 1A: ICCABS 1
Chair: *Knut Reinert*

- Shibdas Bandyopadhyay, Sartaj Sahni and Sanguthevar Rajasekaran. *PMS6MC: A Multicore Algorithm for Motif Discovery*
- Junjie Li, Sanjay Ranka and Sartaj Sahni. *Multicore and GPU Algorithms for Nussinov RNA Folding*
- Nam Vo, Quang Tran, Nobal Niraula and Vinhthuy Phan. *A Randomized Algorithm for Aligning DNA Sequences to Reference Genomes*
- Robert Gysel, Kristian Stevens and Dan Gusfield. *Triangulation Heuristics for Maximum Character Compatibility*

Session 1B: CANGS 1
Chair: *Ion Mandoiu*

- Chong Chu, Jin Zhang and Yufeng Wu. *An SVM-based Approach for Genotyping Deletions and Insertions with Population Sequence Reads*
- Meznah Almutairy, Jordan Fish, and C. Titus Brown. *Space-efficient read indexing and retrieval based on compressed de Bruijn graph structures*
- Farhad Hormozdiari and Eleazar Eskin. *Memory Efficient Assembly of Human Genome*
- Sanguthevar Rajasekaran. *Efficient Algorithms for Sequence Assembly*

| 10:20am-10:50am | **Coffee Break** |

| 10:50am-11:50am | **Plenary Session**
Chair: *Sanguthevar Rajasekaran* |

Dan Gusfield (University of California Davis) keynote talk

| 11:50am-1:40pm | **Lunch** |

1:40pm-3:00pm	**Parallel Sessions**

Session 2A: ICCABS 2
Chair: *Jaroslaw Zola*

- Guoxing Fu, Amit Sabnis and Robert Harrison. *A Deterministic-Stochastic Crossover Algorithm for Simulation of Complex Biochemical Systems*
- Inna Rytsareva and Ananth Kalyanaraman. *Scalable heuristics for clustering biological graphs*
- Karthik Tangirala and Doina Caragea. *Extraction of Gene Regulatory Networks from Biological Literature*

Session 2B: CANGS 2
Chair: *Alex Zelikovsky*

- Karen Merchante, Qiwen Hu, Anna N. Stepanova, Jose M. Alonso and Steffen Heber: *Deep sequencing of ribosomal footprints for studying genome-wide mRNA translation in plants*
- Layla Oesper and Benjamin Raphael: *Reconstructing the Organization of Cancer Genomes*
- Serghei Mangul, Sahar Al Seesi, Adrian Caciula, Dumitru Brinza, Ion Mandoiu and Alex Zelikovsky: *Transcriptome Assembly and Quantification from Ion Torrent RNA-Seq Data*

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

3:30pm-5:10pm	**Parallel Sessions**

Session 3A: ICCABS 3
Chair: *Sing-Hoi Sze*

- Rittika Shamsuddin, Milka Doktorova, Sheila Jaswal, Audrey Lee-St.John and Kathryn McMenimen. *Computational Prediction of Hinge Axes in Proteins*
- Mohammad Shamsur Rahman and Alioune Ngom. FAC-PIN: *Fast Agglomerative Clustering Method for Functional Modules and Protein Complex Identification in PINs*
- Jason Kinser, Stephen Lockett, Thomas Turbyville, Karlyne Reilly and John Beutler. *Comparing Analysis Engines for Generated Micro-patterned, Actin Images*

Session 3B: CANGS 3
Chair: *Pavel Skums*

- Sing-Hoi Sze and Aaron Tarone: *A memory-efficient algorithm to obtain splicing graphs and de novo expression estimates from de Bruijn graphs of RNA-Seq data*
- Adrian Caciula, Alex Zelikovsky, Serghei Mangul, James Lindsay and Ion Mandoiu: *Monte-Carlo Regression Algorithm for Isoform Frequency Estimation from RNA-Seq Data*
- Ei-Wen Yang and Tao Jiang. *Differential gene expression analysis from RNA-Seq read counts*
- James Lindsay, Craig Nelson, and Ion Mandoiu: *Towards Whole Transcriptome Deconvolution Using Single-cell Data*

Thursday, June 13, 2013

8:40am-9:40am	**Plenary Session** **Chair:** *Knut Reinert*	**BigLS**

	Oliver Kohlbacher (Universität Tübingen), keynote talk	**Session 4:** BigLS 1 **Chair:** *Ananth Kalyanaraman* ● Kamesh Madduri. *Parallel analysis of large graph-structured data in genomics and proteomics* ● Benjamin Langmead. *Practical software for big genomics data* ● Fabio Vandin. *Identifying significant mutations in large cohorts of cancer genomes*

9:40am-10:10am	**Coffee Break**	10:00am - 10:30am **BigLS Coffee Break**

10:10am - 11:50am	**Parallel Sessions**

Session 5A: ICCABS 4
Chair: *Folker Meyer*

● Emily Flynn, Filip Jagodzinski, Sharon Pamela Santana and Ileana Streinu. *Rigidity and Flexibility of Protein–Nucleic Acid Complexes*
● Kevin Molloy, Jennifer Van, Daniel Barbara and Amarda Shehu. *Higher-order Representations of Protein Structure Space*
● Ionel Rata, Kyle Wessells and Yaohang Li. *An Improved Statistics-based Backbone Torsion Potential Energy for Protein Loop Structure Modeling*
● Ashraf Yaseen and Yaohang Li. *Template-based Prediction of Protein 8-state Secondary Structures*

Session 5B: CANGS 4/CAME1
Chair: *Yuri Khudyakov*

● Armin Töpfer, Francesca Di Giallonardo, Karin J. Metzner, Huldrych F. Günthard and Niko Beerenwinkel: *QuasiRecomb: Probing of viral diversity by global haplotype prediction*
● Alexander Artyomenko, Nicholas Mancuso, Pavel Skums, Ion Măndoiu and Alex Zelikovsky: *kGEM: An Expectation Maximization Error Correction Algorithm for Next Generation Sequencing of Amplicon-based Data*
● Nicholas Mancuso, Pavel Skums, Bassam Tork, Ion Mandoiu, and Alex Zelikovsky. *Estimation of Viral Population Structure from Amplicon-Based Reads*
● Pavel Skums, Olga Glebova, Alex Zelikovsky, Ion Mandoiu and Yury Khudyakov: *Optimizing pooling strategies for the massive next-generation sequencing of viral samples*

Session 5C: BigLS 2, Keynotes
Chair: *Jaroslaw Zola*

● Srini Parthasarathy. *Recent advances in stochastic flow clustering*
● Srinivas Aluru. *Large-scale Metagenomic Clustering via Quasi Clique Enumeration and Read Assignment Ambiguity Resolution*

11:50am-1:30pm	**Lunch**

1:30pm-3:00pm	**Plenary Session** **Chair:** *Knut Reinert*

Yuri Khudyakov, (CDC, Atlanta), invited talk
Ion Moraru, (U Connecticut), invited talk

Session 6: BigLS 3
Chair: *Ananth Kalyanaraman*

● Folker Meyer. *Surviving the NGS data deluge - A scalable architecture for next generation metagenomics*
● Vladimir Filkov. *Big data from plant genomics: elucidating regulatory networks in poplar trees*
● Ilkay Altintas. *Workflow-driven programming paradigms for distributed analysis of biological big data*

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

3:30pm - 4:30pm	**Plenary session** **Chair:** *Vladimir Filkov*

Session 7: BigLS 4

Satoru Miyano (Tokyo university), keynote talk

● BigLS Panel: Big Data in Life Sciences - fad, fiction or fact?
  Moderators: A. Kalyanaraman, J. Zola

4:30pm-6:35pm	Parallel Sessions

Session 8A: ICCABS Posters
Chair: *Sanguthevar Rajasekaran*

● Sanghoon Lee, Saeid Belkasim,: *Poster : User-Centered Query Expansion Model for Health Disparities Research.*
● George Mathew, Zoran Obradovic. *Poster: Auto-reduction of Features for Containing Communication Costs in a Distributed Privacy-Preserving Clinical Decision Support System.*
● Pinheiro, Fabiola, Kuo, Mu-Hsing, Thomo, Alex, Barnett, Jeff. *Extracting association rules from liver cancer data using the FP-growth algorithm.*
● Raed I. Seetan, Anne M. Denton, Omar Al-Azzam, Ajay Kumar, M. Javed Iqbal and Shahryar F. Kianian. *Poster: Clustering-based Approach for Constructing Reliable Radiation Hybrid Framework Maps.*
● Rafael Toledo F. de Souza, José Luiz Rybarczyk Filho, Ney Lemke, Emerson L. de Santa-Helena, Suzana V. Schönwald, Günther J. L. Gerhardt. *Poster: Quantification of correlations between sleep spindles in EEG for patients with sleep apnea.*
● Claudia Vilo, Daniel Kunz, Xiang Gao and Qunfeng Dong. *POSTER: "Pseudomonas fluorescens Strain NCIMB 11764, a unique bacterium with cyanide adaptation features"*

Session 8B: CAME 2
Chair: *Alex Zelikovsky*

● David S. Campo, Zoya Dimitrova, Pavel Skums and Yury Khudyakov: *Mutational robustness of hepatitis C virus intra-host variants*
● Pavel Skums, Leonid Bunimovich, David S. Campo Rendon, Yury Khudyakov. *Computational analysis and modeling of intra-host adaptation of hepatitis C virus: the role of immune cross-reactivity of HCV intra-host variants*
● James Lara, F. Xavier López-Labrador, Fernando Gonzales Candelas and Yury Khudyakov. *HCV genetic association to rate of liver fibrosis progression.*
● Robert Harrison, Xiaxia Yu, and Irene Weber. *Using Triangulation to Include Target Structure Improves Drug Resistance Prediction Accuracy*
Gabriel Ilie, Alex Zelikovsky, and Ion Mandoiu. *Reference Assisted Nucleic Acid Sequence Reconstruction from Mass Spectrometry Data*

7:00pm - 9:00pm	Banquet

Friday, June 14, 2013

8:40am-9:20am	Plenary Session Chair: *Vladimir Filkov*

Mehmet Koyuturk (Case Western Reserve University), invited talk

9:20am-9:50am	Coffee Break

9:50am-11:30am	**Regular Session**

Session 9: ICCABS 5
Chair: *Vladimir Filkov*

- Wei Zhang, Erliang Zeng, Josh Livermore, Dan Liu, Stuart Jones and Scott Emrich. *Predicting Bacterial Functional Traits from Whole Genome Sequences Using Random Forest.*
- Xiaxia Yu, Robert Harrison and Irene Weber. HIV drug resistance prediction using multiple regression
- Irena Lanc and Scott Emrich. *An Unsupervised Learning Approach to Assembly Validation*
- Elena Randou, Daniel Veltri and Amarda Shehu. *Systematic Analysis of Global Features and Model Building for Recognition of Antimicrobial Peptides*