

		Monday, June 2
9:00am-10:00am	ICCABS+CANGS Keynote Talk: Metagenomics and NGS, Giri Narasimhan	
10:00am-10:30am	Coffee break	
10:30am-12:30pm	ICCABS Session 1 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 Najjar	CANGS Session 1 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
	How genome complexity can explain the hardness of aligning reads to genomes, Vinhthuy Phan, Shanshan Gao, Quang Tran and Nam Vo	Hierarchical Genome Assembly, Anas Al-Okaily and Ion Mandoiu
	Characterization of probabilistic signaling networks through signal propagation, Haitham Gabr and Tamer Kahveci	SILP3: Maximum Likelihood Approach to Scaffolding, Igor Mandric, James Lindsay, Ion Mandoiu and Alex Zelikovsky
	Putting Humpty-Dumpty Together: Mining Mechanistic Biochemical Models from Big Data, Sumit Kumar Jha, Susmit Jha, Emily Sassano and Faraz Hussain	Efficient algorithms for error correction and compression of NGS data, Subrata Saha and Sanguthevar Rajasekaran
12:30pm-1:30pm	Lunch	
1:30pm-3:00pm	Special Session on Radiation Oncology Computational Processing and Real Time Planning for Radiation Therapeutics, David Schwartz, M.D., The University of Texas Southwestern Medical Center	CANGS Session 2 Revealing transcription units in Clostridium Thermocellum by High-Density Tiling Arrays and RNAseq data, Andrey Gorin
	Correlating Online Stories with Offline Health Behavior, Mark A. Finlayson, Ph.D., Massachusetts Institute of Technology	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
	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	An SVM-based approach for discovering splicing junctions with RNA-Seq, Chong Chu and Yufeng Wu
3:00-3:30	Coffee break	
3:30pm-5:30pm	Special Session on Radiation Oncology Use of Computational Biology in Assessing Treatment Response and Disease Progression, John Yordy, M.D., Ph.D., The University of Texas Southwestern Medical Center	CANGS Session 3 Reference-free Inference of Tumor Phylogenies from Single-Cell Sequencing Data, Ayshwarya Subramanian and Russell Schwartz
	Imaging and Image Guidance in Lung Cancer Therapeutics, Amit Sawant, Ph.D., The University of Texas Southwestern Medical Center	Allele Specific Gene Expression Analysis from Single Cell RNA-Seq Data, Sahar Al Seesi and Ion Mandoiu
	Medical Image Analysis in Assessing Treatment Response and Disease Progression, Tsuhan Chen, Ph.D. (Presenter: Ruogu Fang), Cornell University	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

	Computer-Based Pattern Recognition to Assist Clinical Decision Making in Oculofacial Plastic Surgery, Benjamin Erickson, University of Miami	
		Tuesday, June 3
9:00am-10:00am		ICCABS Keynote Talk: John Reif
10:00am-10:30am		Coffee break
10:30am-12:30pm	ICCABS Session 2	CANGS + CAME Joint Session
	In search of perfect reads, Soumitra Pal and Srinivas Aluru	A Combinatorial Algorithm to Identify Independent and Recurrent Copy Number Aberrations Across Cancer Types, Hsin-Ta Wu and Ben Raphael
	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	Viral quasispecies assembly from paired-end reads, Armin Töpfer and Niko Beerenwinkel
	Optimization of IMRT Treatment Plan with Kinetic Data Structures, David Allen and Ovidiu Daescu	Accurate viral population assembly from ultra-deep sequencing, Serghei Mangul, Nicholas Wu, Nicholas Mancuso, Alex Zelikovsky, Ren Sun and Eleazar Eskin
	Identification of Protein Interaction Methods from Biomedical Literature, Deepali Jhamb, Anand Krishnan, Meelia Palakal, Yogesh Pandit, Premkumar Duraiswamy and Mathew Palakal	Deterministic Regression Algorithm for Transcriptome Frequency Estimation, Adrian Caciula, Olga Glebova, Alexander Artyomenko, Serghei Mangul, James Lindsay, Ion Mandoiu and Alex Zelikovsky
12:30pm-1:30pm		Lunch
1:30pm-3:00pm	ICCABS Session 3	CAME Session 2
	An Integrated Model of Human Biomedical and Clinical Data Structures, Egidijus Paliulis and Hesham H. Ali	Oak Ridge Bio-surveillance Toolkit (ORBIT): Scalable Machine Learning for Public Health Surveillance, Laura Pullum and Arvind Ramanathan
	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	Prediction of Representative Drug-Resistant Mutants of HIV Reverse Transcriptase, Xiaxia Yu, Robert Harrison and Irene Weber
	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	Reconstruction of Influenza A Virus Variants from PacBio Reads, Alexander Artyomenko, Serghei Mangul, Nicholas Wu, Eleazar Eskin, Ren Sun and Alex Zelikovsky
3:00-3:30		Coffee break
3:30pm-5:00pm	ICCABS Poster Presentations	CAME Session 3
		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
TBD		Banquet
		Wednesday, June 4
9:00am-10:00am		ICCABS Keynote Talk: Alex Zelikovsky
10:00am-10:30am		Coffee break
10:30am-12:30pm	ICCABS Session 4	ICCABS Session 5
	Improving Bisulfite Short-Read Mapping Efficiency with Hairpin-Bisulfite Data, Jacob Porter, Liqing Zhang, Mingan Sun and Hehuang Xi	Constructing Regulatory Gene Set Network to Reveal Novel Insights into Biological Systems, Chayaporn Suphavilai, Liugen Zhu, Xiaogang Wu and Jake Chen
	Comparison of Data Discretization Methods for Cross Platform Transfer of Gene-expression based Tumor Subtyping Classifier, Segun Jung, Yingtao Bi and Ramana Davuluri	A New Multi-level Thresholding Algorithm for Finding Peaks in ChIP-Seq Data, Iman Rezaiean and Luis Rueda
	A Weighted Classification Model for Peptide Identification, Xijun Liang, Zhonghang Xia, Xinnan Niu and Andrew Link	SAIS-OPT: On the Characterization and Optimization of the SA-IS Algorithm for Suffix Array Construction, Nataliya Timoshevskaya and Wu-Chun Feng
	A New Compact Set of Biomarkers for Distinguishing among Ten Breast Cancer Subtypes, Forough Firoozbakht, Iman Rezaiean, Lisa Porter and Luis Rueda	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