



ICIBM 2019

INTERNATIONAL CONFERENCE ON INTELLIGENT BIOLOGY AND MEDICINE

JUNE 9 - 11, 2019



COLUMBUS, OHIO

CO-HOSTED BY:

**THE INTERNATIONAL ASSOCIATION FOR INTELLIGENT BIOLOGY AND MEDICINE (IAIBM)
& THE DEPARTMENT OF BIOMEDICAL INFORMATICS, THE OHIO STATE UNIVERSITY**

Welcome to ICIBM 2019!

On behalf of all our conference committees and organizers, we welcome you to the 2019 International Conference on Intelligent Biology and Medicine (ICIBM 2019). ICIBM is the official conference of The International Association for Intelligent Biology and Medicine (IAIBM, <http://iaibm.org/>), a non-profit organization whose mission is to promote the intelligent biology and medical science, through member discussion, network communication, collaborations, and education. This year, ICIBM 2019 is co-hosted by the Department of Biomedical Informatics at The Ohio State University.

The fields of bioinformatics, systems biology, and intelligent computing are continuing to evolve at a rapid pace and continue to have a strong impact in scientific research and medical innovations. With this in mind, we are pleased to provide a forum that fosters inter-disciplinary research and discussions, educational opportunities, and collaborative efforts among these ever growing and progressing fields. We are proud to have built on successes of previous years' conferences to provide an exciting program that provides a balanced mix spanning trainees and world-renown scientists, oral and poster presentations, workshops, tutorials, and plenty of built-in breaks for invaluable discussions.

This year, we have an exciting line-up for our keynote speakers, including world-renowned experts Drs. Jeremy Edwards, Peter Karp, Elaine Mardis, and T.M. Murali. Throughout the conference, we will also feature eminent scholar speakers, Drs. Bruce Aronow, Alla Karnovsky, Jeff Parvin, and Haixu Tang, and will be hosting four tutorials and workshops on the first day of the conference. In addition, talks will be given from faculty members, postdoctoral fellows, PhD students and trainee level awardees selected from a substantial number of outstanding manuscripts and abstracts that span a diverse array of research subjects. These researchers, chosen through a rigorous review process, will showcase the innovative technologies and approaches that are the hallmark of our featured interdisciplinary fields and their related applications.

Overall, we anticipate this year's program will be incredibly valuable to research, education, and innovation, and we hope you are as excited as we are to experience ICIBM 2019's program. We'd like to extend our thanks to our sponsors for making this event possible, including the National Science Foundation, BGI Americas, UHealth, and Karger.

Last but not least, our sincerest thanks to members of all our ICIBM 2019 committees, and to our volunteers for their valuable efforts. Their dedication to making ICIBM 2019 a success is invaluable, and demonstrates the strength and commitment of our community.

On behalf of all of us, we hope that our hard work has provided a conference that is thought provoking, fosters collaboration and innovation, and is enjoyable for all of our attendees. Thank you for attending ICIBM 2019. We look forward to your participation in all our conference has to offer!

Sincerely,

Lang Li, PhD
ICIBM General Chair
Professor and Chair,
Department of
Biomedical Informatics
The Ohio State University

Ewy Mathé, PhD
ICIBM Program Co-Chair
Assistant Professor,
Department of
Biomedical Informatics
The Ohio State University

Chi Zhang, PhD
ICIBM Program Co-Chair
Assistant Professor of
Medical & Molecular
Genetics, School of
Medicine, Indiana University

International Conference on Intelligent Biology and Medicine Program-at-a-glance June 9-11, 2019

Sunday, June 9th

9:00	Registration Opens and Continental Breakfast		
10:15-11:00	Keynote Lecture (Room: Ballroom) Elaine Mardis, PhD Co-executive Director of the Institute for Genomic Medicine at Nationwide Children's Hospital Nationwide Foundation Endowed Chair of Genomic Medicine Professor of Pediatrics at The Ohio State University College of Medicine Title: <i>A System for Pediatric Precision Cancer Medicine</i>		
11:00-11:20	Boxed Lunches Pickup for next session		
CONCURRENT WORKSHOPS/TUTORIALS			
Room	Ballroom	Pfahl 202	Pfahl 302
11:20-1:30	Dr. Wenjin Zheng, UTH Dr. Yidong Chen, UTH Dr. Yufei Huang, UTSA Data Driven Cancer Research: Data Science Research and Applications		Dr. Yan Guo, UNM Machine Learning Demystified
1:30-1:45	Break		
1:45-3:45	Dr. Wenjin Zheng, UTH Dr. Yidong Chen, UTH Dr. Yufei Huang, UTSA Data Driven Cancer Research: Tutorial on Deep Learning for Cancer Genomics	Dr. Peter Karp SRI International Tutorial for the BioCyc Microbial Genomes Web Portal	Dr. Jianrong Wang, MSU Epigenetics data analysis
3:45-4:00	Break		
4:00-6:00	Poster Session (Room: Ballroom) <i>Hors d'oeuvres Served</i>		

Monday, June 10th

7:30-8:30	Registration Open and Continental Breakfast		
8:30-8:40	Opening Remarks		
8:40-9:30	Keynote Lecture (Room: Ballroom) Peter Karp, PhD Director, Bioinformatics Research Group Artificial Intelligence Center SRI International Title: <i>BioCyc Tools for Metabolic Modeling and Omics Data Analysis</i>		
9:30-9:40	Break		
9:40-10:00	Eminent Scholar Talk (Room: Ballroom) Jeffrey Parvin, MD, PhD Professor, Department of Biomedical Informatics Associate Dean of Graduate Studies Co-Director, Biomedical Sciences Graduate Program The Ohio State University Title: <i>The impact of sequence variants on protein function</i>		
10:00-10:10	Break for parallel sessions		
CONCURRENT SESSIONS			
Room	Ballroom NGS & Tools Session Chair: 1	Pfahl 202 General Genomics Session Chair: 2	Pfahl 302 Bioinformatics Session Chair: 3
10:10-10:30	An ancestral informative marker panel design for individual ancestry estimation of Hispanic population using whole exome sequencing data Li-Ju Wang, Catherine Zhang, Sophia Su, Hung-I Chen, Yu-Chiao Chiu, Zhao Lai, Hakim Bouamar, Francisco Cigarroa, Lu-Zhe Sun and Yidong Chen	Association Analysis of Common and Rare SNVs using Adaptive Fisher Method to Detect Dense and Sparse Signals Xiaoyu Cai, Lo-Bin Chang and Chi Song	The Comparisons of Prognostic Power and Expression Level of Tumor Infiltrating Leukocytes in Hepatitis B- and Hepatitis C-related Hepatocellular Carcinomas Yi-Wen Hsiao, Lu-Ting Chiu, Ching-Hsuan Chen, Wei-Liang Shih and Tzu-Pin Lu
10:30-10:50	normGAM: An R package to remove systematic biases in genome architecture mapping data Tong Liu and Zheng Wang	An integrative, genomic, transcriptomic and network-assisted study to identify genes associated with human cleft lip with or without cleft palate Fangfang Yan, Yulin Dai, Junichi Iwata, Zhongming Zhao and Peilin Jia	SigUNet: signal peptide recognition based on semantic segmentation Jhe-Ming Wu, Yu-Chen Liu and Tien-Hao Chang

10:50-11:10	Sparse Convolutional Denoising Autoencoders for Genotype Imputation Junjie Chen and Xinghua Shi	Association between ALS and retroviruses: Evidence from bioinformatics analysis Jon Klein, Zhifu Sun and Nathan Staff	Integrated metabolomics and transcriptomics study of traditional herb Astragalus membranaceus Bge. var. mongolicus (Bge.) Hsiao reveals global metabolic profile and novel phytochemical ingredients Xueting Wu, Xuetong Li, Wei Wang, Yuanhong Shan, Cuiting Wang, Mulan Zhu, Qiong La, Yang Zhong, Ye Xu, Peng Nan and Xuan Li
11:10-11:20	<i>Coffee/Tea Break</i>		
11:20-11:40	High dimensional model representation of log likelihood ratio: Binary classification with SNP data Ali Foroughi Pour, Maciej Pietrzak, Lara E. Sucheston-Campbell, Ezgi Karaesmen, Lori A. Dalton and Grzegorz A. Rempala	ManiNetCluster: A novel manifold learning approach to reveal the functional links between gene networks Nam Nguyen, Ian Blaby and Daifeng Wang	BayesMetab: Treatment of Missing Values in Metabolomic Studies using a Bayesian Modeling Approach Jasmit Shah, Guy Brock and Jeremy Gaskins
11:40-12:00	Decoding regulatory structures and features from epigenomics profiles: a Roadmap-ENCODE Variational Auto-Encoder (RE-VAE) model Ruifeng Hu, Guangsheng Pei, Peilin Jia and Zhongming Zhao	Human protein-RNA interaction network is highly stable across vertebrates Aarthi Ramakrishnan and Sarath Chandra Janga	Dense module searching for gene networks associated with multiple sclerosis Astrid Manuel, Yulin Dai, Leorah Freeman, Peilin Jia and Zhongming Zhao
12:00-12:20	A unified STR profiling system across multiple species with whole genome sequencing data Liu Yilin, Xu Jiao and Li Shuaicheng	Differential co-expression analysis reveals early stage gene dis-coordination in Alzheimer's disease Yurika Upadhyaya, Linhui Xie, Paul Salama, Sha Cao, Kwagnsik Nho, Andrew Saykin and Jingwen Yan	Expression correlation attenuates within and between key signaling pathways in CKD progression Hui Yu, Danqian Chen, Olufunmilola Oyebamiji, Yan Guo and Ying-Yong Zhao
12:20-1:30	<i>Lunch Break-Boxed Lunches</i>		

1:30-1:50	Eminent Scholar Talk (Room: Ballroom)		
	<p>Alla Karnovsky, PhD Research Associate Professor of Computational Medicine & Bioinformatics Assistant Director, Masters Program University of Michigan</p> <p>Title: <i>Identifying biologically relevant modules in metabolomics and lipidomics data with Differential Network-based Enrichment Analysis (DNEA)</i></p>		
1:50-2:00	Short Break		
2:00-2:50	Keynote Lecture (Room: Ballroom)		
	<p>T.M. Murali, PhD Professor, Department of Computer Science Co-director, ICTAS Center for Systems Biology of Engineered Tissues Virginia Tech</p> <p>Title: <i>Pathways on Demand: Automated Reconstruction of Human Signaling Networks</i></p>		
2:50-3:00	Break for parallel sessions		
CONCURRENT SESSIONS			
Room	Ballroom NGS & Tools Session Chair: 4	Pfahl 202 Bioinformatics Session Chairs: 5	Pfahl 302 Cancer Genomics Session Chairs: 6
3:00-3:20	<p>Investigating Skewness to Understand Gene Expression Heterogeneity in Large Patient Cohorts Benjamin Church, Henry Williams and Jessica Mar</p>	<p>M3S: A comprehensive model selection for multi-modal single-cell RNA sequencing data Yu Zhang, Changlin Wan, Pengcheng Wang, Wennan Chang, Yan Huo, Jian Chen, Qin Ma, Sha Cao and Chi Zhang</p>	<p>Comparative evaluation of network features for the prediction of breast cancer metastasis Nahim Adnan, Zhijie Liu, Tim Huang and Jianhua Ruan</p>
3:20-3:40	<p>Clonal reconstruction from time course genomic sequencing data Wazim Mohammed Ismail and Haixu Tang</p>	<p>Multi-objective optimized fuzzy clustering for detecting cell clusters from single cell expression profiles Saurav Mallik and Zhongming Zhao</p>	<p>Highly robust model of transcription regulator activity predicts breast cancer overall survival Chuanpeng Dong, Jiannan Liu, Steven X. Chen, Tianhan Dong, Guanglong Jiang, Yue Wang, Huanmei Wu, Jill L. Reiter and Yunlong Liu</p>
3:40-4:00	<p>CNV detection from circulating tumor DNA in late stage non-small cell lung cancer patients Hao Peng, Qiangsheng Dai, Zisong Zhou, Xiaochen Zhao, Dadong Zhang, Kejun Nan, Zhu-An Ou, Fugen Li, Hua Dong, Lei Tian, Yu Yao</p>	<p>Network-based single-cell RNA-seq data imputation enhances cell type identification Maryam Zand and Jianhua Ruan</p>	<p>Pseudogene-gene functional networks are prognostic of patient survival in breast cancer Sasha Smerekanych, Travis Johnson, Kun Huang and Yan Zhang</p>

4:00-4:10	<i>Coffee/Tea Break</i>		
4:10-4:30	A Protocol to Evaluate RNA Sequencing Normalization Methods Zachary Abrams, Travis Johnson, Kun Huang, Philip Payne and Kevin Coombes	The landscape of alternative splicing in HIV-1 infected CD4 T-cells Seyoun Byun, Seonggyun Han, Yue Zheng, Vicente Planelles and Younghee Lee	Deep Learning-based Cancer Survival Prognosis from RNA-seq Data: Approaches and Evaluations Zhi Huang, Travis Johnson, Zhi Han, Bryan Helm, Sha Cao, Chi Zhang, Paul Salama, Maher Rizkalla, Christina Yu, Jun Cheng, Shunian Xiang, Xiaohui Zhan, Jie Zhang and Kun Huang
4:30-4:50	Fully Moderated T-statistic in Linear Modeling of Mixed Effects for Differential Expression Analysis Lianbo Yu, Jianying Zhang, Guy Brock and Soledad Fernandez	Biological Representation of Chemicals Using Latent Target Interaction Profile Mohamed Ayed, Hansaim Lim and Lei Xie	Transcription factor expression as a predictor of colon cancer prognosis: A machine learning practice Jiannan Liu, Chuanpeng Dong, Guanglong Jiang, Xiaoyu Lu, Yunlong Liu and Huanmei Wu
4:50-5:10	SMaSH: Sample Matching using SNPs in Humans Maximillian Westphal, David Frankhouser, Carmine Sonzone, Peter G. Shields, Pearly Yan and Ralf Bundschuh	Long non-coding RNA expression levels modulate cell-type specific splicing patterns by altering their interaction landscape with RNA-binding proteins Felipe Wendt Porto, Swapna Vidhur Daulatabad and Sarath Chandra Janga	A pan-cancer study of class-3 semaphorins as therapeutic targets in cancer Xiaoli Zhang, Brett Klamer, Jin Li, Soledad Fernandez and Lang Li
5:10-5:30	BISR-RNAseq: An efficient and scalable RNAseq analysis workflow with interactive report generation Venkat Sundar Gadepalli, Hatice Gulcin Ozer, Ayse Selen Yilmaz, Maciej Pietrzak and Amy Webb	Super Clustering Approach for Fully Automated Single Particle Picking in Cryo-EM Adil Al-Azzawi, Anes Ouadou and Jianlin Cheng	Predicting Re-admission to Hospital for Diabetes Treatment: A Machine Learning based Solution Satish Mahadevan Srinivasan, Yok-Fong Paat, Philmore Halls, Ruth Kalule and Thomas E. Harvey.
5:30	Cocktail Hour (Conference Center Lobby)		
6:30	Shuttle Bus Transportation provided to Park of Roses		
7:00	BANQUET (Park of Roses- 3901 N High St, Columbus, OH 43214)		

Tuesday, June 11th

7:30-8:40	Registration Open and Continental Breakfast		
8:40-9:30	Keynote Lecture (Room: Ballroom) Jeremy Edwards, PhD Professor, Department of Chemistry & Chemical Biology The University of New Mexico Title: <i>Technologies for Human Genome and Transcriptome Sequencing</i>		
9:30-9:40	Break		
9:40-10:00	Eminent Scholar Talk (Room: Ballroom) Bruce Aronow, PhD Professor, UC Department of Pediatrics Co-director, Computational Medicine Center Cincinnati Children's Hospital Medical Center Title: <i>ToppCell: A Workbench for the Analysis, Modeling and Prediction of the Molecular Basis of Development and Function of Cells and Tissues based on Single Cell Atlas Datasets</i>		
10:00-10:10	Break for parallel sessions		
CONCURRENT SESSIONS			
Room:	Ballroom Cancer Genomics Session Chair: 7	Pfahl 202 Scientific Databases Session Chair: 8	Pfahl 302 Computational Drug Discovery Session Chair: 9
10:10-10:30	Identify rewired pathways between primary breast cancer and liver metastatic cancer using transcriptome data Limei Wang, Jin Li, Enze Liu, Garrett Kinnebrew, Yang Huo, Zhi Zeng, Wanli Jiang, Lijun Cheng, Hongchao Lv, Weixing Feng and Lang Li	MIRIA: a webserver for statistical, visual and meta-analysis of RNA editing data in mammals Xikang Feng, Zishuai Wang, Hechen Li and Shuaicheng Li	A deep learning-based method for drug-target interaction prediction based on long short-term memory neural network Yanbin Wang, Zhuhong You, Shan Yang, Haicheng Yi, Zhanheng Chen and Kai Zheng
10:30-10:50	Kinetic modeling of DUSP regulation in Herceptin-resistant HER2-positive breast cancer Petronela Buiga, Ari Elson, Lydia Tabernero and Jean-Marc Schwartz	dbMTS: a comprehensive database of putative human microRNA target site SNVs and their functional predictions Chang Li, Michael Swartz, Bing Yu and Xiaoming Liu	Mining and visualizing high-order directional drug interaction effects using the FAERS database Xiaohui Yao, Tiffany Tsang, Sara Quinney, Pengyue Zhang, Xia Ning, Lang Li and Li Shen

10:50-11:10	Gene co-expression networks restructured by gene fusion in rhabdomyosarcoma cancers Bryan Helm, Xiaohui Zhan, Zhi Han, Dong Ni, Jie Zhang and Kun Huang	A harmonized neurodegenerative transcriptome database to nominate mouse models for functional follow-up and validation of Alzheimer's gene networks Rami Al-Ouran, Ying-Wooi Wan and Zhandong Liu	SCNrank: Spectral Clustering for Network-based target Ranking to reveal potential drug targets and its application in pancreatic ductal adenocarcinoma Enze Liu, Xiaoqi Liu, Zhuangzhuang Zhang, Xiaolin Cheng, Murray Korc and Lijun Cheng
11:10-11:20	<i>Coffee/Tea Break</i>		
11:20-11:40	Convolutional neural network models for cancer type prediction based on gene expression Milad Mostavi, Yu-Chiao Chiu, Yufei Huang and Yidong Chen	Forming Big Datasets through Latent Class Concatenation of Imperfectly Matched Databases Features Christopher Bartlett, Brett Klamer, Steven Buyske, Stephen Petrill and William Ray	Network as a biomarker: A novel network-based sparse Bayesian machine for pathway-driven drug response prediction Lei Frank Huang, Hongting Liu, Yi Zheng and Richard Lu
11:40-12:00	Integrative Network Analysis Identifies Potential Targets and Drugs for Ovarian Cancer Tianyu Zhang, Liwei Zhang and Fuhai Li	Challenges in proteogenomics: a comparison of analysis methods with the case study of the DREAM Proteogenomics Sub-Challenge Tara Eicher, Andrew Patt, Esko Kautto, Raghu Machiraju, Ewy Mathe and Yan Zhang	Computational Drug Repositioning for Precision Cancer Medicine Based on Cancer Cells Screening Abhishek Majumdar, Shaofeng Wu and Yaoqin Lu
12:00-12:10	A Novel Graph Regularized Non-negative Matrix Factorization based on Error Weight Matrix for High Dimensional Biomedical Data Clustering Meijun Zhou, Xianjun Shen, Limin Yu, Xingpeng Jiang, Jincal Yang and Yujian Yang	PATH: An interactive web platform for analysis of time-course high-dimensional genomic data Yuping Zhang, Yang Chen and Zhengqing Ouyang	Development of a RNA-Seq based Prognostic Signature for Colon Cancer Bjarne Bartlett, Yong Zhu, Mark Menor, Vedbar Khadka, Jicai Zhang, Jie Zheng, Bin Jiang and Youping Deng
12:10-12:20	Skyhawk: An Artificial Neural Network-based discriminator for reviewing clinically significant genomic variants Ruibang Luo, Tak-Wah Lam and Michael Schatz	LCLE: a web portal for comprehensive gene distance analysis for correlation networks in liver cancer Xiuquan Wang, Xiaoqian Zhu, Keli Xu, Junqing Wang and Yunyun Zhou	Machine Learning Distilled Metabolite Biomarkers for Early Stage Renal Injury Yan Guo, Dianqian Chen, Hui Yu and Ying-Yong Zhao

12:20-1:35	Lunch Break - Boxed Lunches				
1:35-1:55	Eminent Scholar Talk (Room: Ballroom)				
	<p>Haixu Tang, PhD Professor of Informatics and Computing Director, Data Science Academic Programs Adjunct Professor of Biology Indiana University</p> <p>Title: <i>Prediction, Searching and Clustering of Tandem Mass Spectra of Peptides</i></p>				
1:55-2:10	Award presentation (Room: Ballroom)				
2:10-2:20	Coffee/Tea Break				
CONCURRENT SESSIONS					
Ballroom		Pfahl 202		Pfahl 302	
International PI Talk		General Bioinformatics		Cancer and Medical Genomics	
Session Chair: 10		Session Chair: 11		Session Chair: 12	
2:20-2:40	<p>Development of predictive models to distinguish metals from non-metal toxicants, and individual metal from one another Zongtao Yu, Yong Zhu, Junmei Ai, Jicai Zhang, Bin Jiang, Youping Deng and Bjarne Bartlett</p>	2:20-2:30	<p>On the analysis of the human immunome via an information theoretical approach Maciej Pietrzak, Gerard Lozanski, Michael Grever, Jeffrey Jones, Leslie Andritsos, James Blachly, Kerry Rogers and Michal Seweryn.</p>	2:20-2:30	<p>Rapid Evolution of Expression Levels in Hepatocellular Carcinoma Fan Zhang and Kuo Michael D. Kuo</p>
		2:30-2:40	<p>Elimination of DNase nucleotide-specific bias to enhance recognition of DNA-binding proteins Weixing Feng, Chongchong Luo, Duoqiao Chen, Weixin Xie, Ruida Cong, Chengkui Zhao, Bo He and Yunlong Liu</p>	2:30-2:40	<p>Identifying Interaction Clusters for MiRNA and MRNA Pairs in TCGA Network Xinqing Dai, Lizhong Ding, Hui Jiang, Samuel Handelman and Yongsheng Bai</p>
2:40-3:00	<p>DNA methylation markers for pan-cancer prediction by deep learning Biao Liu, Yulu Liu, Mengyao Li, Shuang Yang, Shuai Cheng Li and Xingxin Pan</p>	2:40-2:50	<p>RNASEqR: an R package for automated two-group RNA-Seq analysis workflow Kuan-Hao Chao, Yi-Wen Hsiao, Yi-Fang Lee, Chien-Yueh Lee, Liang-Chuan Lai, Mong-Hsun Tsai, Tzu-Pin Lu and Eric Y. Chuang</p>	2:40-2:50	<p>Generating Simulated CGH and Sequencing Data to Assess Genomic Segmentation Algorithms Mark Zucker and Kevin Coombes</p>

		2:50-3:00	The Minimum Weight Clique Partition Problem and its Application to Structural Variant Calling Matthew Hayes and Derrick Mullins	2:50-3:00	Mapping genes and pathways to age-associated psychological changes in humans using latent semantic analysis Pankaj Dholaniya, Vikram Naik and Baby Kumari
3:00-3:20	Molecular evolution of circadian clock genes in spotted gar (<i>Lepisosteus oculatus</i>) Yi Sun, Chao liu, Xiaolong Liu, Xudong Pan, Moli Huang, Jian Huang, Changhong Liu, Jiguang Zhang, John H. Postlethwait and Han Wang	3:00-3:10	GPU Empowered Pipelines for Calculating High-Dimensional Kinship Matrices and Facilitating 1D and 2D GWAS Wenchao Zhang, Xinbin Dai, Shizhong Xu and Patrick Zhao	3:00-3:10	Cross - species Conserved Proteins Complex Identification and Exploration of Species Functional Evolution Xianjun Shen, Meijun Zhou, Limin Yu, Li Yi, Cuihong Wan, Xingpeng Jiang and Tingting He
3:20-3:40	DeepShape: Estimating Isoform-Level Ribosome Abundance and Distribution with Ribo-seq data Hongfei Cui, Hailin Hu, Jianyang Zeng and Ting Chen				
3:40	Adjourn				

MANY THANKS TO OUR SPONSORS!



National Science Foundation
WHERE DISCOVERIES BEGIN

