

International Conference on Intelligent Biology and Medicine Program (July 16-19, 2023)

Sunday, July 16th

11:00 AM-6:00 PM	Registration			
CONCURRENT WORKSHOPS				
Room: St. Petersburg I		Room: St. Petersburg II, III		Room: Williams/Demens
Technology Session		Workshop on Applications of AI in Translational Research		Flash Talks
Chair: Zhongming Zhao		Chairs: Zhe He, Rui Yin		Chairs: Kaixiong Ye, Chengqi Wang
2:00 PM-2:30 PM	Unveiling the complexity of breast cancer through advanced analysis of FFPE tissue: single cell, spatial, and in situ mapping of the tumor microenvironment	2:00 PM-2:20 PM	Adaptive graph model deciphers spatial cellular communications	Shared genetic basis informs the roles of polyunsaturated fatty acids in brain disorders
	Dr. Ryan Mote (10x Genomics)		Dr. Qianqian Song (Wake Forest University)	Huifang Xu, Yitang Sun, Michael Francis, Claire Cheng, Nitya Modulla, <u>Kaixiong Ye</u>
				Common Genetic Variants are Associated with Plasma and Skin Carotenoid Metabolism in Ethnically Diverse US Populations
				<u>Yixing Han</u> , Savannah Mwesigwa, Melissa N. Laska, Stephanie B. Jilcott Pitts, Nancy E. Moran, Neil A. Hanchard
2:30 PM-3:00 PM	StereoCell: A bioinformatics tool enables accurate single-cell segmentation for spatial transcriptomics dataset	2:20 PM-2:40 PM	Leveraging the power of genomics to facilitate the diagnosis of undiagnosed diseases with machine learning models	Cross-analysis between P. falciparum Var expression with host immunothrombosis markers to better define pediatric cerebral malaria phenotypes.
	Dr. Shan Yang (Complete Genomics)		Dr. Rui Yin (University of Florida)	Iset Vera, <u>Thomas Keller</u> , Anne Kessler, Visopo Harawa, Wilson L. Mandala, Stephen J. Rogerson, Terrie E. Taylor, Karl B. Seydel, and Kami Kim

				<p>Unveiling Gene Interactions in Alzheimer's Disease by Integrating Genetic and Epigenetic Data with a Network-Based Approach</p> <p><u>Keith Sanders</u>, Astrid M Manuel, Andi Liu, Boyan Leng, Xiangning Chen, Zhongming Zhao</p>
3:00 PM-3:30 PM	<p>A scRNA-seq cell type identifying method based on human curated cell marker database and empirical knowledge</p> <p>Dr. Yaping Feng (Admera Health)</p>	2:40 PM-3:00 PM	<p>Better Acute Kidney Injury Prediction and Risk Factor Analysis with Personalized Transfer Learning</p> <p>Dr. Mei Liu (University of Florida)</p>	<p>MalariaSED: a deep learning framework to decipher the regulatory contributions of noncoding variants in malaria parasites</p> <p><u>Chengqi Wang</u>, Yibo Dong, Jenna Oberstaller, Chang Li, Min Zhang, Justin Gibbons, Camilla Valente Pires, Lei Zhu, Rays H.Y. Jiang, Kami Kim, Jun Miao, Thomas D. Otto, Liwang Cui, John H. Adams, Xiaoming Liu</p> <p>Enhancing DNA Sequence Matching and Ranking through Deep Learning-Based Alignment-Free Model</p> <p><u>Sumarga K. Sah Tyagi</u>, Minh Pham, Yicheng Tu</p>
3:30 PM-3:45 PM	<i>Break</i>	3:00 PM-3:20 PM	<p>Harnessing Explainable, Equitable, and Actionable AI to Improve Health</p> <p>Dr. Zhe He (Florida State University)</p>	<p>3D genome reveals intratumor heterogeneity in Glioblastoma</p> <p><u>Qixuan Wang</u>, Juan Wang, Qiushi Jin, Mark W. Youngblood, Lena Ann Stasiak, Ye Hou, Yu Luan, Radhika Mathur, Joseph F. Costello, Feng Yue</p> <p>Integrated Spatial Multi-omics Analysis Based on MALDI Data</p>

				<u>Xin Ma</u> , Cameron Shedlock, Harrison Clarke, Roberto Ribas, Terrymar Medina, Tara R. Hawkinson, Shannon Keohane, Craig W. Vander Kooi, Matthew S. Gentry, Li Chen, Ramon Sun
		3:20 PM-3:45 PM	<i>Break</i>	
3:45 PM-4:15 PM	Generating real-world evidence using OneFlorida+ clinical research consortium Dr. Yi Guo (University of Florida)	3:45 PM-4:05 PM	Constructing a Large-Scale Biomedical Knowledge Graph and Its Applications in Drug Discovery (via Zoom) Dr. Jinfeng Zhang (Florida State University)	Multimodal machine learning combining image and textual data to predict rare genetic disorders (recorded video) <u>Da Wu</u> , Jingye Yang, Kai Wang A multimodal neuroimaging-based risk score for Alzheimer’s disease by combining clinical and large N>37000 population data <u>Elaheh Zendehtrouh</u> , Mohammad SE. Sendi, Vince D. Calhoun
4:15 PM - 4:45 PM	Unraveling the Challenges of Genomic Sequencing and Computational Analysis: Introducing the Genomics Sequencing Core and Computational Core Drs Min Zhang & Bi Zhao (University of South Florida)	4:05 PM-4:25 PM	Translational Pharmacoinformatics research Dr. Lai Wei (Ohio State University)	Developing an Accurate and Interpretable Risk-Based Model for Lung Cancer Screening <u>Piyawan Conahan</u> , Lary Robinson, Haley Tolbert, Margaret M Byrne, Lee Green, Yi Luo In silico Improvement of Highly Protective Antimalarial Antibodies Mateo Reveiz, Andrew Schaub, Young Do Kwon, Prabhanshu Tripathi, Azza Idris, Amarendra Pegu, Lais Da Silva Pereira, Patience

				Kiyuka, Myungjin Lee, Tracy Liu, Chen-Hsiang Shen, Baoshan Zhang, Yongping Yang, Peter D. Kwong, <u>Reda Rawi</u>
		4:25 PM-4:45 PM	<p>Using Explainable Machine Learning Models to Predict CAR T-Cell Therapy Response with Longitudinal Patient Report Outcomes</p> <p>Dr. Yi Luo (Moffitt Cancer Center)</p>	<p>Comprehensive Investigation of Active Learning Strategies for Anti-Cancer Drug Response Prediction</p> <p><u>Priyanka Vasanthakumari</u>, Yitan Zhu, Thomas Brettin, Alexander Partin, Maulik Shukla, and Rick L. Stevens</p> <p>Bioinformatics and machine learning based identification of potential oxidative stress and glucose metabolism diagnostic Biomarkers in Alzheimer disease</p> <p><u>Sidra Aslam</u>, Fatima Noor, Thomas G. Beach, Geidy E. Serrano</p>

Monday, July 17th

8:00 AM- 6:30 PM	Registration		
CONCURRENT WORKSHOPS/TUTORIALS			
Room: St. Petersburg I	Room: St. Petersburg II, III	Room: Williams/Demens	
Tutorial on Collection and Analyses of Long-Read Transcriptome and Epitranscriptome Data Organizer: Kin Fai Au (University of Michigan) 9:30 AM-12:00 PM Requirement: bring your laptop	Workshop on Microbiome Data Analysis Chair: Qunfeng Dong	Artificial Intelligence on Big Data: Promise for Early-stage Trainees Chairs: Yufang Jin, Chi Zhang, Yongsheng Bai	
	9:30 AM-9:50 AM	Artificial intelligence-based identification of microbes in cancer Dr. Noam Auslander (The Wistar Institute)	Trainee presentations (10 min) 9:00 AM – 11:10 AM Feasibility of a 3D Convolutional Neural Network for the Diagnosis of Alzheimer’s Disease using Brain PET Scans (Troy Zhang) Comparisons of Coronavirus Spike Proteins and the Mutation Effects on Virus-Host Interaction (Crystal Teng) Identification of Key Biomarkers Associated with Ductal Breast Cancer in Spatial Transcriptomics Data (Ellie Xi) Assessing the Clinical Significance Identification Capability of DNA Language Models: A Study of Enformer's Performance on Disease-Causing Variants in Human Cis-Regulatory Elements (Rain Hou) Characterization of oncogenes and tumor suppressor genes with onco-microRNAs and tumor suppressor microRNAs (Claire Shen) FLUXestimator: a webserver for predicting metabolic flux and
	9:50 AM-10:10 AM	Metagenomic read classification using deep learning models (via Zoom) Dr. Ying Zhang (University of Rhode Island)	
	10:10 AM-10:30 AM	De Novo Identification of Contaminants in Low Microbial Biomass Microbiomes Dr. Yunxi Liu (Rice University)	
	10:30 AM-10:50 AM	Multiscale adaptive differential abundance analysis in microbial compositional data Dr. Shulei Wang (University of Illinois Urbana-Champaign)	
	10:50 AM-11:00 AM	Break	
	11:00 AM-11:20 AM	A novel microbial causal mediation analytic pipeline for investigating microbiome’s mediating role in disease and health disparity (via Zoom)	

		Dr. Huilin Li (New York University)	variations using transcriptomics data (Alex Lu)
	11:20 AM-11:40 AM	Incorporating metabolic activity, taxonomy and community structure to improve microbiome-based predictive models for host phenotype prediction Dr. Mahsa Monshizadeh (Indiana University)	Identifying relationships between cellular topology and gene expression in spatial transcriptomics of breast cancer tissues (Isabella Wu) Pan-cancer analysis of metabolic shifts via flux estimation analysis (Kevin Hu) Temporal Phenotyping for Transitional Disease Progress: an application to cardiovascular diseases and neurological diseases (Andy Wang) The artificial intelligence analysis of single-cell transcriptomes highlights the high heterogeneity in bladder cancer (Xilin Wei) Tissue Domains Identification using Spatial Transcriptomics Data (Emily Wei) Adaptive Deep Inference with Collaborative Architecture for IoT (Alejandro Villanueva) Analysis of thermal images for Nearby Animal Behavior using Deep learning architectures for enhancing vehicle safety (Eleni Avlonitis)
	11:40 AM-12:00 PM	Exploring the Male Urethral Microbiome: A Community Ecology Approach Based on the Neutral Theory Dr. Xiang Gao (Loyola University Chicago)	Panel Discussion 11:10 AM – 12:00 PM

12:00 PM - 1:30 PM	Lunch Break		
1:30 PM – 1:40 PM	Opening Remarks (St. Petersburg II, III)		
CONCURRENT SESSIONS/WORKSHOP			
	Room: St. Petersburg I	Room: St. Petersburg II, III	Room: Williams/Demens
	Workshop on Prompt Bioinformatics – Application of ChatGPT and Large Language Models Chair: Gangqing Hu	Genomics, Transcriptomics, Proteomics and Epigenomics I Chairs: Qin Ma, Xiaojing Wang	Medical Informatics, Public Health Informatics and Pharmacoinformatics I Chairs: Mei Liu, Satish Mahadevan Srinivasan
1:40 PM - 2:00 PM	Prompt Bioinformatics with Chatbots Dr. Gangqing Hu (West Virginia University)	Eminent Scholar Nancy Zhang (University of Pennsylvania) Title: Signal recovery in single cell data integration	The association between nonalcoholic fatty liver disease (NAFLD) status and physical exam or biochemical parameters <u>Weiru Han</u> , Tianrui Zhu, Zhengli Tang, Robert Morris, Kun Bu, Fang Wang, Lin Fan, Weijian Wang, Yiming Hao, Yiqin Wang and Feng Cheng
2:00 PM - 2:20 PM	PROMPT BIOINFO. CASE STUDY: Intra-tumor Evolutionary Inference Dr. Sayaka Miura (Temple University)	Mitigating Heterogeneity Effects in Microbiome-based Quantitative Phenotype Prediction: A Comprehensive Workflow for Integrating Multiple Studies with Batch Normalization <u>Yilin Gao</u> and <u>Fengzhu Sun</u>	Behavioral and demographic profiles of HIV contact networks in Florida <u>Yiyang Liu</u> , Christina Parisi, Rebecca Frisk-Hoffman, Marco Salemi, Diego Viteri, Mattia Prospero and Simone Marini
2:20 PM - 2:40 PM	Leveraging Stand-alone RNA-Seq Data for Novel lncRNA Identification and Annotation: A Prompt Bioinformatics Case Study	Comprehensive Cross Cancer Analyses Reveal Mutational Signature Cancer Specificity <u>Rui Xin</u> , Limin Jiang, Hui Yu, Jijun Tang and Yan Guo	Association between ABCG1/TCF7L2 and type 2 diabetes mellitus: An intervention trial based case-control study Yinxia Su, <u>Xiangtao Liu</u> , Conghui Hui, and Hua Yao

	Dr. Chan Zhou (University of Massachusetts)		
2:40 PM - 3:00 PM	Exploring ChatGPT's Ability to Generate Novel Algorithms in Bioinformatics Dr. Li Liu (Arizona State University)	A Weighted Two-stage Sequence Alignment Framework to Identify DNA Motifs from ChIP-exo Data Yang Li, Yizhong Wang, Cankun Wang, Anne Fennell, Anjun Ma, Jing Jiang, Zhaoqian Liu, <u>Qin Ma</u> and Bingqiang Liu	Smoothing spline analysis of variance models: A new tool for the analysis of accelerometer data <u>Rui Xie</u> , Lulu Chen, Joon-Hyuk Park, Jeffrey Stout and Ladda Thiamwong
3:00 PM - 3:15 PM	<i>Coffee/Tea Break</i>		
3:15 PM - 3:35 PM	Enhanced Gene Interaction Analysis and Pathway Reconstruction through Iterative Prompt Refinement by ChatGPT <u>Yibo Chen</u> , Mihail Popescu, Dong Xu	A mouse-specific model to detect genes under selection in tumors Hai Chen, <u>Jingmin Shu</u> and Li Liu	Exploring Drug-drug Interaction Information from PubMed using Association Rules <u>Kun Bu</u> , Weiru Han, Robert Morris and Feng Cheng
3:35 PM - 3:55 PM	Ensemble BERT for Medication Event Classification on Electronic Health Records (EHRs) <u>Shouvon Sarker</u> , Xishuang Dong and Lijun Qian	A machine learning pipeline to detect open chromatin regions from cfDNA sequencing data Yuxin Liu, Yuqian Liu, Xiaoyan Zhu, Jiayi Ren, Xin Lai, Xuanping Zhang and Jiayin Wang	Pan-cancer mutational signature surveys correlated cancer racial disparities with geospatial environmental exposures, and viral infections <u>Judy Bai</u> , Katherine Ma, Shangyang Xia, Richard Geng, Limin Jiang, Hui Yu, Xi Gong, Shuguang Leng and Yan Guo
3:55 PM - 4:15 PM	Enhancing Phenotype Recognition in Clinical Notes Using Large Language Models: PhenoBCBERT and PhenoGPT Jingye Yang, <u>Cong Liu</u> , Wendy Deng, Da Wu, Chunhua Weng, Yunyun Zhou and Kai Wang	Detection of viral infection in cell lines using ViralCellDetector <u>Rama Shankar</u> , Shreya Paithankar, Suchir Gupta and Bin Chen	Characterizing Diseases using Genetic and Clinical Variables: A Data Analytics Approach Madhuri Gollapalli, Harsh Anand and <u>Satish Mahadevan Srinivasan</u>

<p>4:15 PM - 4:35 PM</p>	<p>Flash Talk: PROMPT BIOINFO. CASE STUDY: Shotgun Metagenomic Data Analysis</p> <p><u>Zhu Xing</u>, Qiyun Zhu</p> <hr/> <p>Flash Talk: Cancer Comprehend Annotation – a pipeline for cancer phenotype and clinical extraction</p> <p><u>Thanh Duong</u>, Phillip Szepietowski, Thanh Thieu</p>	<p>A comprehensive benchmark of transcriptomic biomarkers for immune checkpoint blockades (recorded video)</p> <p><u>Hongen Kang</u>, Xiuli Zhu, Ying Cui, Zhuang Xiong, Wenting Zong, Yiming Bao and Peilin Jia</p>	<p>The Association between Warfarin usage and International normalized ratio increase: Systematic analysis of FDA Adverse Event Reporting System (FAERS)</p> <p><u>Robert Morris</u>, Matthew Bruckner, Milagros Salcedo, Nicole Zapata Aponte, Alfredo Suarez Garcia, Megan Todd, Weiru Han, Kun Bu, Feng Cheng and Rachel Webb</p>
<p>4:35 PM - 4:50 PM</p>	<p><i>Coffee/Tea Break</i></p>		
<p>4:50 PM - 5:30 PM</p>	<p>Keynote Lecture (Room: St. Petersburg II, III)</p> <p>Yidong Chen, Ph.D. (University of Texas Health Science Center at San Antonio)</p> <p>Title: Learning cellular responses to genetic and chemical perturbations of cancer</p>		
<p>5:30 PM - 5:40 PM</p>	<p><i>Break</i></p>		
<p>5:40 PM - 6:40 PM</p>	<p>Poster Session (Room: St. Petersburg II, III) Poster size: 3' (width) x 4' (height), portrait form</p>		
<p>7:00 PM – 9:00 PM</p>	<p>Reception (Ford Garage at 200 1st Avenue S)</p>		

Tuesday, July 18th

8:00 AM-5:30 PM	Registration		
8:30 AM - 9:10 AM	Keynote Lecture (St. Petersburg II, III) Bradley Malin, Ph.D. (Vanderbilt University) Title: Building Ethically Viable Biomedical Data Science Environments		
9:10 AM - 9:20 AM	<i>Break for parallel sessions</i>		
CONCURRENT SESSIONS			
	Room: St. Petersburg I	Room: St. Petersburg II, III	Room: Williams/Demens
	Special Session on Dynamics of Transcriptional Regulation Towards Single Cell, Single Molecular, and Spatial Omics Session Chair: Kaifu Chen	Computational Methods for Aging and Brain Research Chairs: Shaolei Teng, Guogen Shan	Genomics, Transcriptomics, Proteomics and Epigenomics II Chairs: Renzhi Cao, Jing Wang
9:30 AM - 9:50 AM	Uncovering Disease-Associated Novel lncRNAs: A Computational Perspective Dr. Chan Zhou (University of Massachusetts)	Eminent Scholar Peilin Jia (Beijing Institute of Genomics, China) Title: Deep learning approaches for accurate drug response imputation (via Zoom)	AlphaCluster: Coevolutionary driven residue-residue interaction models enable quantifiable clustering analysis of de novo variants to enhance predictions of pathogenicity Joseph Obiajulu, Ranger Kuang, Lesi He, Guojie Zhong, Jacob Hagen, Chang Shu, Wendy Chung and <u>Yufeng Shen</u>
9:50 AM - 10:10 AM	Data-driven and AI-empowered systems biology Dr. Chi Zhang (Indiana University)	Clustering Alzheimer's Disease Subtypes via Similarity Learning and Graph Diffusion <u>Tianyi Wei</u> , Shu Yang, Davoud Ataee Tarzanagh, Jingxuan Bao, Jia Xu, Patryk Orzechowski,	Mutation Density Analyses on Long Noncoding RNA Reveal Comparable Patterns to Protein-Coding RNA and Prognostic Value

		Joost B. Wagenaar, Qi Long and Li Shen	<u>Chaoyi Troy Zhang</u> , Hui Yu, Yongsheng Bai and Yan Guo
10:10 AM - 10:30 AM	Deep learning reveals cellular state transition Dr. Guangyu Wang (Houston Methodist Research Institute)	Machine Learning Analysis for Studying Aging-Associated Hearing Loss Safa Shubbar	Systematic assessment of small RNA profiling in human extracellular vesicles <u>Jing Wang</u> , Hua-chang Chen, Quanhu Sheng, Renee Dawson, Robert J. Coffey, James G. Patton, Alissa M. Weaver, Yu Shyr, Qi Liu
10:30 AM - 10:50 AM	MEBOCOST: Metabolite-mediated Cell Communication Modeling by Single Cell Transcriptome Dr. Kaifu Chen (Harvard Medical School)	Vagus nerve stimulation and blood pressure modulate neuronal activity in the periventricular cerebellum Maria Alejandra Gonzalez-Gonzalez	Flash Talk: Genomic disparities between cancers in adolescent and young adults and in older adults Xiaojing Wang, Anne-Marie Langevin, Peter Houghton, <u>Siyuan Zheng</u>
			Flash Talk: TSSr: an R package for comprehensive analyses of TSS sequencing data Zhaolian Lu, Keenan Berry, Zhenbin Hu, Yu Zhan, Tae-Hyuk Ahn, <u>Zhenguo Lin</u>
10:50 AM - 11:05 AM	<i>Coffee/Tea Break</i>		
11:05 AM - 11:25 AM	Enhancing Cell-Type Identification in Single-Cell RNA-seq Data with Interpretable Deep Learning Dr. Liang Chen (University of Southern California)	A Machine Learning Based Multiple Imputation Method for the Health and Aging Brain Study-Health Disparities (via Zoom) <u>Fan Zhang</u> , Melissa Petersen, Leigh Johnson, James Hall, Raymond Palmer and Sid O'Bryant	The genetic regulation of the biogenesis of human isomiRs <u>Guanglong Jiang</u> , Jill L. Reiter, Chuanpeng Dong, Yue Wang, Fang Fang, Zhaoyang Jiang and Yunlong Liu

11:25 AM - 11:45 AM	The Whole is More Than the Parts: Decoding Synergistic Networks of Multiple Non-coding Variants Linked to Cancer Risk Dr. Xueqiu Lin (Stanford University)	Structure-learning-based causal comorbidities mining from UK biobank: an exploratory study for Alzheimer's disease <u>Yiheng Pan</u> , Pingjian Ding, Zhenxiang Gao and Rong Xu	SynthQA - Hierarchical Machine Learning-based Protein Quality Assessment Mikhail Korovnik, Sheng Wang, Junyong Zhu, Kyle Hippe, Jie Hou, Dong Si, Kiyomi Kishaba and <u>Renzhi Cao</u>
11:45 AM - 12:05 PM	Flash Talk: Building the Human Ensemble Cell Atlas and Learning the Underlying Unified Coordinate System Xuegong Zhang	Flash Talk: Decentralization of Brain age Estimation with Structural Magnetic Resonance Imaging Data <u>Sunitha Basodi</u> , Rajikha Raja, Bhaskar Ray, Harshvardhan Gazula, Jingyu Liu, Eric Verner and Vince D. Calhoun	Characterizing protein structural features of alternative splicing and isoforms using AlphaFold 2 <u>Yuntao Yang</u> , Yuhan Xie, Zhao Li, Chiamaka Diala, Meer Ali, Rongbin Li, Yi Xu, Sayed-Rzgar Hosseini, Erfei Bi, Hongyu Zhao and Wenjin Zheng
	Flash Talk: Deep Transfer Learning of Cancer Drug Responses by Integrating Bulk and Single-cell RNA-seq data Junyi Chen, Xiaoying Wang, <u>Anjun Ma</u> , Qi-En Wang, Bingqiang Liu, Lang Li, Dong Xu, Qin Ma	Flash Talk: An integrative study to identify the link between dysregulated intercellular signaling and genetic variants in Alzheimer's disease <u>Andi Liu</u> , Xiaoyang Li, Brisa S Fernandes, Yulin Dai, Zhongming Zhao	
12:05 PM - 1:40 PM	Lunch Break		
1:40 PM - 2:20 PM	Keynote Lecture (St. Petersburg II, III) Brooke Fridley, Ph.D. (Moffitt Cancer Center) Title: Decoding Kidney Cancer: Analytical Strategies for Unveiling the Tumor Immune Microenvironment using Spatial Transcriptomics		
2:20 PM - 2:30 PM	Break for parallel sessions		
CONCURRENT SESSIONS			
	Room: St. Petersburg I	Room: St. Petersburg II, III	Room: Williams/Demens
	Single Cell Omics Data Modeling and Analysis	Machine Learning/Deep Learning in Biomedical Research I	Medical Informatics, Public Health

	Chairs: Qianqian Song, Guangyu Wang	Chairs: Jinchuan Xing, Qian Liu	Informatics and Pharmacoinformatics II Chairs: Yi Guo, Lijun Cheng
2:30 PM - 2:50 PM	Improving cellular phylogenies through integrated use of mutation order and optimality principles <u>Sayaka Miura</u> , Tenzin Dolker, Maxwell Sanderford and Sudhir Kumar	Eminent Scholar Lorin Crawford (Microsoft Research and Brown University) Title: Interpretable Probabilistic Models to Identify Multi-scale Enrichment in Complex Traits	Predicting COVID-19 Severity of Emergency Room Patients using Chest X-ray Images <u>Jonathan Stubblefield</u> and <u>Xiuzhen Huang</u>
2:50 PM - 3:10 PM	Gradient boosting reveals spatially diverse cholesterol gene signatures in colon cancer Xiuxiu Yang, Justin Couetil, Debolina Chatterjee, Valerie Ardon, Jie Zhang, Kun Huang and Travis Johnson	Revealing the impact of genomic alterations on cancer cell signaling with an interpretable deep learning model <u>Shuangxia Ren</u> , Jonathan Young, Xinghua Lu and Lujia Chen	Quantifying the Growth of Glioblastoma Tumors Using Multimodal MRI Brain Images <u>Anisha Das</u> , Shengxian Ding, Rongjie Liu and Chao Huang
3:10 PM - 3:30 PM	scDemultiplex: An iterative beta-binomial model-based method for accurate demultiplexing with hashtag oligos Li-Ching Huang, Lindsey Stolze, Alexander Gelbard, Yu Shyr, Qi Liu and <u>Quanhu Sheng</u>	DeepCORE: An interpretable multi-view deep neural network model to detect co-operative regulatory elements <u>Pramod Bharadwaj Chandrashekar</u> , Hai Chen, Matthew Lee, Navid Ahmadinejad and Li Liu	Comparing the risk of deep vein thrombosis of two combined oral contraceptives: norethindrone/ethinyl estradiol and drospirenone/ethinyl estradiol Jennifer Stalas, <u>Robert Morris</u> , Kun Bu, Kevin von Bargen, Rebekah Largmann, Kathryn Sanford, Jacob Vandeventer, Weiru Han and Feng Cheng
3:30 PM - 3:50 PM	Decoding ecosystem heterogeneity and transcriptional regulation	A novel interpretable k-hop graph attention network model of integrative omics data	An In-silico Study of Antisense Oligonucleotide Antibiotics (via Zoom)

	<p>characteristics of multi-subtype renal cell carcinoma (recorded video)</p> <p><u>Kailong Xu</u>, Jie Liu, Heng Yang, Lixin Ma, Gang Dou and Yang Wang</p>	<p>analysis to infer target-specific core signaling pathways</p> <p><u>Ruoying Yuan</u>, Jiarui Feng, Heming Zhang, Yixin Chen, Philip Payne and Fuhai Li</p>	<p>Erica Chen and <u>Eric Ho</u></p>
3:50 PM - 4:00 PM	<i>Coffee/Tea Break</i>		
4:00 PM - 4:20 PM	<p>Improving cell type identification at single-cell level</p> <p><u>Mostafa Malmir</u>, Jinyan Li, Anita Omo-Okhuasuy, Umar Jamil, Yidong Chen and Yufang Jin</p>	<p>Proformer-based Ensemble Learning for Gene Expression Prediction</p> <p>Lucy Nwosu, Xiangfang Li, Seungchan Kim, Lijun Qian and <u>Xishuang Dong</u></p>	<p>Reducing the Data for Radiation Cancer Therapy Quality Assurance</p> <p>Maryam Albuainin, Richard Shaw and <u>Shuang Luan</u></p>
4:20 PM – 4:40 PM	<p>Osteogenic Differentiation Potential of Mesenchymal Stem Cells using Single Cell Multiomic Analysis</p> <p>Duojiao Chen, <u>Xiaona Chu</u>, Hongyu Gao, Patrick McGuire, Xuhong Yu, Xiaoling Xuei, Yichen Liu, Sheng Liu, Jill Reiter, Jun Wan, Yunlong Liu and Yue Wang</p>	<p>DeepDecon accurately estimates cancer cell fractions in bulk RNA-seq data</p> <p><u>Jiawei Huang</u>, Yuxuan Du, Andres Stucky, Jiang F. Zhong and Fengzhu Sun</p>	<p>Exploring How Healthcare Organizations Use Twitter: A Discourse Analysis</p> <p><u>Aditya Singhal</u> and Vijay Mago</p>
4:40 PM – 5:00 PM	<p>Do Single-cell Hi-C Data Follow A Power Law Distribution?</p> <p>Bin Zhao, Patrick Shen and <u>Lu Liu</u></p>	<p>Accurate prediction of functional effect of single missense variants with deep learning</p> <p><u>Houssemeddine Derbel</u>, Zhongming Zhao and Qian Liu</p>	<p>The Association Between Bradycardia and the Use of Remdesivir</p> <p>Gibret Umeukeje, Robert Morris, Weiru Han, Kun Bu, Jin Wei, Ruisheng Liu and <u>Feng Cheng</u></p>
5:00 PM - 5:30 PM	<i>Award presentation</i> (Williams/Demens)		
6:00 PM – 9:00 PM	Banquet (St. Petersburg II, III)		

Wednesday, July 19th

8:00 AM-12:00 PM	Registration		
8:30 AM - 9:10 AM	Keynote Lecture (St. Petersburg II, III) Jeffrey Townsend, Ph.D. (Yale University) Title: Dismantling the Coarse Paradigm of Cancer 'Drivers' and 'Passengers'		
9:10 AM - 9:20 AM	<i>Break for parallel sessions</i>		
CONCURRENT SESSIONS/TUTORIAL			
	Room: St. Petersburg I	Room: St. Petersburg II, III	Room: Williams/Demens
	Special Topics on Genomics and Translational Bioinformatics Chairs: Ece Uzun, Shulan Tian AMIA GenTBI Working Group 9:30 AM – 11:10 PM	Cancer Informatics and Network Biology Chairs: Noam Auslander, Xinna Zhang	Machine Learning/Deep Learning in Biomedical Research II Chairs: Xiao Fan, Yijie Wang
9:30 AM - 9:50 AM	Chromatin-mediated transcriptional dysregulation in T-cell Prolymphocytic Leukemia Dr. Huihuang Yan (Mayo Clinic)	Eminent Scholar Tae Hyun Hwang (Mayo Clinic) Title: Harnessing single cell and spatial genomics with machine learning and AI to develop biomarker and therapeutic strategies for immuno and cellular therapy in cancer	Metastatic cancer expression generator (MetGen): A generative contrastive learning framework for metastatic cancer generation <u>Zhentao Liu</u> , Yu-Chiao Chiu, Yidong Chen and Yufei Huang
9:50 AM - 10:10 AM	Decoding Genomic Variations with Variant Graph Craft: A User-Friendly Tool for VCF Analysis Dr. Alper Uzun (Brown University)	CoMatch: a transfer learning model connecting in vivo finding to outcome prediction to distinguish prognostic/predictive biomarkers in breast cancer <u>Abhishek Majumdar</u> , Aida Yazdanparast, Huanmei Wu, Lang Li and Lijun Cheng	Neural relational inference optimization to analyze enzyme allosteric interactions in regular enzymes (recorded video) <u>Shuang Wang</u> , Yan Wang, Yi He, Xuhong Zhang,

			Weiwei Han and Juexin Wang
10:10 AM - 10:30 AM	Genomics and Artificial Intelligence in Clinical Care Dr. Nephi Walton (Intermountain Healthcare)	Identifying Significantly Perturbed Subnetworks in Cancer Using Multiple Protein-Protein Interaction Networks <u>Le Yang</u> , Runpu Chen, Thomas Melendy, Steve Goodison and Yijun Sun	CCLHunter: an efficient toolkit for cancer cell line authentication (recorded video) <u>Congfan Bu</u> , Xinchang Zheng, Jialin Mai, Zhi Nie, Jingyao Zeng, Qiheng Qian, Tianyi Xu, Yanling Sun, Yiming Bao and Jingfa Xiao
10:30 AM - 10:50 AM	Unified somatic calling and machine learning-based classification enhance the discovery of clonal hematopoiesis of indeterminate potential Dr. Shulan Tian (Mayo Clinic)	Integrating and interpreting multi-omics data via novel k-hop graph neural network models to uncover core disease signaling pathways in medulloblastoma <u>Zitian Tang</u> , Jiarui Feng, Yixin Chen, Philip Payne and Fuhai Li	Seizure prediction based on deep learning driven by nonlinear dynamics Wei Xiaoyan, Zhen Zhang and Yi Zhou
10:50 AM - 11:00 AM	Unveiling the Hidden Web of Protein-Protein Interactions in Cancer and Subtypes Dr. Ece Uzun (Brown University) 10:50 AM – 11:10 AM	<i>Coffee/Tea Break</i>	
11:00 AM - 11:20 AM		scGEM: unveiling the nested tree-structured gene co-expressing modules in single-cell transcriptome data <u>Han Zhang</u> , Xinghua Lu, Binfeng Lu and Lujia Chen	A Transformer-Based Deep Learning Approach for Fairly Predicting Post-Liver Transplant Risk Factors <u>Can Li</u> , Xiaoqian Jiang and Kai Zhang
11:20 AM - 11:40 AM	Unlocking the Power of Single-Cell Gene Expression Analysis with SCGEATOOL: A Hands-On Tutorial for Non-Programmers and Machine Learning Experts Organizer: James Cai (Texas A&M University)	Repurposing drugs for Group3 and Group4 medulloblastoma subtypes by inhibiting novel common core signaling targets <u>Fuhai Li</u> , William Buchser, Clifford Luke, Di Huang, Maxene Ilgan and Joshua Rubin	DRLCOMPLEX: Reconstruction of Protein Quaternary Structures Using Deep Reinforcement Learning Elham Soltanikazemi, <u>Raj Roy</u> , Farhan Quadir, Nabin Giri, Alex Morehead and Jianlin Cheng
11:40 AM - 12:00 PM	11:20 AM – 12:30 AM	Prediction of prognosis, immunotherapy and	Pan-cancer drug response prediction

	(Note: free Matlab license available for software installation)	<p>chemotherapy with an immune-related risk score model in endometrial cancer (recorded video)</p> <p>Wei Wei, Zhenting Huang, Bo Ye, Xiaoling Mu, Jing Qiao, <u>Peng Zhao</u>, Yuehang Jiang, Jingxian Wu and Xiaohui Zhan</p>	<p>through tumor decomposition by cancer cell lines</p> <p><u>Yu-Ching Hsu</u>, Yu-Chiao Chiu, Tzu-Pin Lu, Tzu-Hung Hsiao and Yidong Chen</p>
12:00 PM – 12:20 PM		<p>Flash Talk: A massive proteogenomic screen identifies thousands of novel peptides from the human “dark” proteome</p> <p>Xiaolong Cao, Siqi Sun, <u>Jinchuan Xing</u></p>	<p>Flash Talk: HiC4D: Forecasting spatiotemporal Hi-C data with residual ConvLSTM</p> <p>Tong Liu, <u>Zheng Wang</u></p>
		<p>Flash Talk: Mutated processes predict immune checkpoint inhibitor therapy benefit in metastatic melanoma</p> <p><u>Andrew Patterson</u>, Noam Auslander</p>	<p>Flash Talk: Integrating Hydrogen Bonding Information into Graph Neural Networks for Protein Structure Classification</p> <p><u>Yi-Shan Lan</u>, Tsung-Yi Ho</p>
12:20 PM - 12:30 PM	Closing Remarks (St. Petersburg II, III)		