

**The International Conference on Intelligent Biology and Medicine  
(ICIBM 2024) Program (October 10-12, 2024, Houston, Texas)**

**Thursday, October 10<sup>th</sup>, 2024**

7:30 AM-8:30 AM		<i>Light Refreshment with Coffee/Drink (Prefunction Space)</i>			
7:30 AM-6:30 PM		<b>Registration</b>			
<b>CONCURRENT WORKSHOPS/TUTORIALS</b>					
Room: <b>Auditorium</b>		Room: <b>280</b>		Room: <b>106</b>	
<b>Integrating Medical Imaging and Genomic Data</b>		<b>Generative AI and ChatGPT in Bioinformatics and Biomedical Informatics</b>		<b>Computational Genomics for Precision Medicine</b>	
Chair: Xiaoqian Jiang		Chairs: Gangqing Hu, Yu-Chiao Chiu		Chair: Travis Johnson	
8:30 AM - 8:45 AM	<b>Opening remarks: welcome and introduction to the workshop</b>  Xiaoqian Jiang, University of Texas Health Science Center at Houston	8:30 AM - 8:50 AM	<b>Applications of ChatGPT for biomedical knowledge mining and data analysis</b>  Dong Xu, University of Missouri-Columbia	8:30 AM - 8:50 AM	<b>Molecular subtyping of cancers through integrative clustering analysis of multi-omics data</b>  Qianxing Mo, Moffit Cancer Center
8:45 AM - 9:15 AM	<b>Integrating genomic data from NIAGADS for Alzheimer's disease research</b>  Li-San Wang, University of Pennsylvania	8:50 AM - 9:10 AM	<b>reguloGPT: Harnessing GPT for end-to-end knowledge graph construction of molecular regulatory pathways</b>  Yufei Huang, University of Pittsburg	8:50 AM - 9:10 AM	<b>Application of deep transfer learning methods for drug discovery: from method development to target validation</b>  Travis Johnson, Indiana University School of Medicine
9:15 AM - 9:45 AM	<b>Translational pharmaco-informatics research</b>	9:10 AM - 9:30 AM	<b>Large language models in molecular pathology for improving rare disease diagnosis</b>	9:10 AM - 9:30 AM	<b>Utilizing genetic information for drug repositioning</b>

	Lang Li, Ohio State University		Kai Wang, University of Pennsylvania		Guoshuai Cai, University of Florida
9:45 AM - 10:10 AM	<b>Unstructured learning for clinical decision-making using imaging data</b>  Luca Giancardo, UTHealth Houston	9:30 AM – 9:50 AM	<b>Integrating retrieval augmentation with GPT-4 to infer drug-gene relationships in cancer</b>  Yu-Chiao Chiu, University of Pittsburg	9:30 AM – 9:50 AM	<b>Single-cell specific high-resolution reconstruction of 3D genomes reveals higher order genetic basis of complex diseases</b>  Jianrong Wang, Michigan State University
		9:50 AM – 10:10 AM	<b>LLMs in decoding cell state from ST and scRNA-seq data</b>  Guangyu Wang, Houston Methodist	9:50 AM – 10:10 AM	<b>Structure-Aware Compound-Protein Affinity Prediction via Graph Neural Network with Group Lasso Regularization</b>  Zanyu Shi, Indiana University
10:10 AM -10:30 AM		<i>Coffee/Tea Break</i>			
10:30 AM -11:00 AM	<b>Health informatics and multimodal real-world data infrastructure</b>  Jiang Bian, University of Florida	10:30 AM – 10:50 AM	<b>ChatGPT applications in decoding bioinformatics and medical images</b>  Gangqing Hu, West Virginia University	10:30 AM – 10:50 AM	<b>Kernel neural networks for high-dimensional genetic data analysis</b>  Qing Lu, University of Florida
11:00 AM -11:20 AM	<b>Insights into the effects of gut microbiota dysbiosis on neurodegenerative disease and cognitive function</b>	10:50 AM – 11:10 AM	<b>Identify Alzheimer’s disease subtypes and markers from multi-omic data of human brain and blood with a subspace merging</b>	10:50 AM – 11:10 AM	<b>Deconvolution of polygenic risk score in single cells unravels cellular and molecular heterogeneity of</b>

	Yiying Zhang, Mass General Research Institute		<b>algorithm</b> Ziyan Song, Indiana University School of Medicine		<b>complex human diseases</b> Sai Zhang, University of Florida
11:20 AM -11:40 PM	<b>Advanced machine learning techniques for analyzing medical imaging data</b> Guangming Zhang, UTHealth Houston				
11:40 AM -12:00 PM	<b>Disentangling accelerated cognitive decline from the normal aging process and unraveling its genetic components: a neuroimaging-based deep learning approach</b> Zhongming Zhao, UTHealth	11:10 AM – 11:30 AM	<b>Expanding the horizons of genomics and biomedical Analysis: GPT-4’s role in automated cell type annotation and beyond</b> Zhicheng Ji, Duke University	11:10 AM – 11:30 AM	<b>GSNCASCR: An R Package to Identify Differentially Co-Expressed Gene Sets with single-cell RNA-seq data</b> Shouguo Gao, National Institutes of Health
				11:30 AM – 11:50 AM	<b>mosGraphFlow: a novel integrative graph AI model mining disease targets from multi-omic data</b> Fuhai Li, Washington University School of Medicine
12:00 PM-1:30 PM		<b>Lunch (Event/Exhibition Hall)</b>			
1:30-1:40 PM		<b>Opening Remarks (Qianqian Song)</b>			
1:40-2:20 PM		<b>Keynote Lecture (Room: Auditorium)</b> <b>Xiaoqian Jiang, PhD</b> <b>University of Texas Health Science Center at Houston</b>			
<b>CONCURRENT WORKSHOPS/TUTORIALS</b>					
Room: <b>Auditorium</b>		Room: <b>280</b>		Room: <b>106</b>	

<b>Advanced Topics in Learning Health System</b>		<b>Computational and AI Models for Multi-Omic Data Analysis</b>		<b>Computational Biomedicine</b>	
Chairs: Sunyang Fu, Ming Huang, Hongfang Liu		Chairs: Fuhai Li, Lang Li		Chair: Sudin Bhattacharya	
2:20 PM - 2:40 PM	<b>The HOUSES Platform: Groundbreaking Social Determinants of Health Platform Accelerating Health Equity, the Goal of Learning Health System</b>	2:20 PM - 2:40 PM	<b>Target and target combination prediction using genome editing</b>	2:20 PM - 2:40 PM	<b>Computational Mutagenesis of GPx7 and GPx8: Structural and Stability Insights into Rare Genetic and Somatic Missense Mutations and Their Implications for Cancer Development</b>
	Young J. Juhn, Mayo Clinic		Lang Li, Ohio State University		Shaolei Teng, Howard University
2:40 PM - 3:00 PM	<b>Construction molecular signatures for cancer classification</b>	2:40 PM - 3:00 PM	<b>Predicting microbial community functions with metabolic network models</b>	2:40 PM - 3:00 PM	<b>Advancing Pancreatic Cancer Prediction with a Next Visit Token Prediction Head on top of Med-BERT</b>
	Boris Reva, Mount Sinai		Jason Papin, University of Virginia		Jianping He, UTHealth Houston
3:00 PM - 3:20 PM	<b>Benchmarking large language models for the diagnosis of rare Mendelian diseases</b>	3:00 PM - 3:20 PM	<b>Explainable multi-branch deep learning model of direct RNA sequencing data for epitranscriptomics</b>	3:00 PM - 3:20 PM	<b>Intronic polyadenylation patterns reveal diverse gene functions in Pan-cancer transcriptomes</b>
	Zhandong Liu, Baylor College of Medicine		Sabine Dietmann, Washington University in St Louis		Wei Zhang, University of Central Florida
3:20 PM-3:40 PM		<i>Coffee/Tea Break</i>			
3:40 PM - 4:00 PM	<b>Tailored healthcare: precision medicine and age-friendly</b>	3:40 PM - 4:00 PM	<b>Single-cell epigenomic analysis of mammalian brains</b>	<b>Technology Session</b>	
				Chairs: Yun Zhao, Andi Liu	

	<b>health systems for older adults</b>  Min Ji Kwak, McGovern Medical School		<b>and neurological disorders</b>  Yang Li, Washington University in St Louis	3:40PM - 4:00PM	<b>An Admera Health Alliance</b>  Gillian Ching-Jung Lin, Admera Health
4:00 PM - 4:20 PM	<b>Tailored healthcare: precision medicine and age-friendly health systems for older adults part2</b>  Nahid J. Rianon, McGovern Medical School	4:00 PM - 4:20 PM	<b>The applications of deep learning techniques in molecular structure prediction</b>  Jie Hou, St Louis University	4:00PM - 4:20PM	<b>Exploring transcriptomic diversity: leveraging single-cell and bulk mRNA sequencing for advanced biological insights</b>  Brittany Porier, Novogene
4:20 PM - 4:40 PM	<b>Discovering signature disease trajectories from Electronic Health Records for early diagnosis</b>  Liwei Wang, McWilliams School of Biomedical Informatics	4:20 PM - 4:40 PM	<b>Leveraging deep learning and large language models for precision oncology</b>  Yu-Chiao Chiu, University of Pittsburgh	4:20PM - 4:40PM	<b>Vazyme Biotech: a leading provider of advanced bioscience tools and NGS solutions</b>  Kenny Nguyen, Vazyme
4:40 PM - 5:00 PM	<b>Learning health systems: applications in behavioral health</b>  Jair Soares, McGovern Medical School, UThealth Houston	4:40 PM - 5:00 PM	<b>Inverse reinforcement learning for predicting and understanding cancer evolution</b>  Nicholas Lee-Ping, Chia, Argonne National Laboratory	4:40PM - 5:00PM	<b>Great design, great data: from data mining to integration – unleash the power of the UK biobank data on your proteomics research</b>  Amrita Kar, Olink
5:00 PM - 5:20 PM	<b>LIVES-living evidence synthesis system for rare disease</b>  Jinlian Wang,	5:00 PM - 5:20 PM	<b>Graph AI models for integrative and interpretable multi-omic data analysis</b>  Fuhai Li, Washington	5:00PM - 5:20PM	<b>Parse Biosciences' Evercode: scalable, accessible single cell</b>  Paige Gear, Parse Biosciences

	McWilliams School of Biomedical Informatics, UTHealth, Houston		University in St Louis	5:20PM - 5:40PM	<b>Title: Automated cell-type annotation using Cell Ranger</b>  Stephen R. Williams, 10x Genomics
5:45-7:00 PM		<b>Poster Session (Event/Exhibition Hall)</b>			
6:00-8:00 PM		<b>Reception (Event/Exhibition Hall)</b>			

**Friday, October 11<sup>th</sup>, 2024**

7:30 AM-8:30 AM		<i>Light Refreshment with Coffee/Drink (Prefunction Space)</i>			
8:30 AM-6:30 PM		<b>Registration</b>			
8:30 AM-9:10AM		<b>Keynote Speaker</b> (Room: Auditorium) <b>Jessica Li, PhD</b> University of California, Los Angeles			
<b>CONCURRENT WORKSHOPS/TUTORIALS</b>					
Room: <b>Auditorium</b>		Room: <b>280</b>		Room: <b>106</b>	
<b>AI in the Drug Development Life Cycle</b>  Chairs: Assaf Gottlieb, AC Tan		<b>AI methods for Single Cell Data Analysis I</b>  Chairs: Qin Ma, Dong Xu		<b>Multi-omics and Multi-modal Data Integration in Biomedicine</b>  Chair: Rama Shankar, Lana Garmire	
9:10AM - 9:30AM	<b>Single-cell spatial multi-omics analysis reveals cell-cell communication within tumor and brain microenvironments for novel drug discovery</b>  Stephen Wong, Methodist Houston	9:10AM - 9:30AM	<b>Overview: deep learning shapes single-cell data analysis</b>  Qin Ma, The Ohio State University	9:10AM - 9:30AM	<b>A quantitative proteome map of the human body</b>  Meng Wang, University of Michigan
9:30AM - 9:50AM	<b>Computational and mathematical modeling on immunotherapy/radiation</b>	9:30AM - 9:50AM	<b>Potential applications of emerging AI techniques in single-cell data analysis</b>	9:30AM - 9:50AM	<b>Human pancreatic cancer single cell atlas reveals association of CXCL10+ fibroblasts</b>

	Heiko Enderling, MD Anderson Cancer Center		Dong Xu, University of Missouri		<b>and basal subtype tumor cell</b> Nina Steele, Henry Ford Hospital
9:50AM - 10:10AM	<b>New predictive models for precision oncology and are developing new AI- guided clinical trials</b>  Aritro Nath, City of Hope National Medical Center	9:50AM - 10:10AM	<b>Implement structure information into protein language model and its application for protein engineering</b>  Qing Shao, University of Kentucky	9:50AM - 10:10AM	<b>Mult tissue multiomics systems biology of complex diseases</b>  Xia Yang, Brain Research Institute, UCLA
10:10AM -10:30AM		<i>Coffee/Tea Break</i>			
10:30AM -10:50AM	<b>From cell lines to tumors transferring drug response prediction models through molecular pathways</b>  Assaf Gottlieb, UTHealth Houston	10:30AM -10:50AM	<b>An extensive computational infrastructure leverages pathology workflow by integrating imaging and omics data</b>  Guangyu Wang, Houston Methodist	10:30AM -10:50AM	<b>Epigenetic alterations associated with probable rem sleep behavior disorder in Parkinson's disease: insights from plasma DNA methylation and epigenetic inflammatory biomarkers</b>  Cynthia Kusters, UCLA
10:50AM- 11:10AM	<b>Statistical/machine learning of drug side effects</b>  Dung-Tsa Chen, Moffitt Cancer Center	10:50AM -11:10AM	<b>A bottom-up strategy to explore sizable structural motifs as building blocks of cell organization using TrimNN</b>  Juexin Wang, Indiana University Indianapolis	10:50AM -11:10AM	<b>A novel machine learning method for longitudinal outcome- guided disease subtyping using high- dimensional omics data</b>  Annie J. Lee, Columbia University
11:10AM -11:30AM	<b>From biomarkers to adverse events</b>	11:10AM -11:30AM	<b>Graph neural diffusion in scRNA-seq data analysis</b>	11:10AM -11:30AM	<b>Artificial Intelligence in cancer research: enhancing deconvolution and imputation methods</b>

	AC Tan, University of Utah		Chao Zhang, Boston University		Yan Guo, University of Miami
11:30AM -11:50AM	<b>ChatGPT and pharmacogenomic</b>  Mullai Murugan, Baylor College of Medicine	11:30AM -11:50AM	<b>Unveiling cell-type-specific senescent cells and signature genes via graph contrastive learning in diseased lungs</b>  Anjun Ma, The Ohio State University	11:30AM -11:50AM	<b>Modeling chemically-induced perturbation of spatiotemporal gene expression in the mammalian liver from single-cell data</b>  Sudin Bhattacharya, Michigan State University
11:50AM -12:10PM	<b>AI/LLMs in precision oncology reporting</b>  Subhayjoti De, Rutgers University			11:50AM -12:10PM	<b>Mapping cellular progression of liver diseases reveals the pro-tumorigenic role of <math>\gamma\delta</math>2 T cells</b>  Rama Shankar, Michigan State University
12:10-1:30 PM		<b>Lunch (Event/Exhibition Hall)</b>			
1:30 PM-2:10 PM		<b>Keynote Speaker (Room: Auditorium)</b> <b>Gaudenz Danuser, PhD</b> <b>UT Southwestern Medical Center</b>			
<b>CONCURRENT SESSIONS/WORKSHOPS</b>					
Room: Auditorium		Room: <b>280</b>		Room: <b>106</b>	
<b>Special Topics on Genomics and Translational Bioinformatics</b>  Chair: Mary Davis, Alper Uzun		<b>AI Methods for Single Cell Data Analysis II</b>  Chairs: Qin Ma, Dong Xu		<b>Computational Methods for Single Cell/Spatial Multi-Omics Data</b>  Chairs: Zhana Duren, Jun Wan	
2:10PM - 2:30PM	<b>Eminent Scholar Presentation</b>  Nicholas Tatonetti, Cedars-Sinai Medical Center	2:10PM - 2:30PM	<b>Graph signal processing in spatial omics</b>  Yuzhou Chang, Ohio State University	2:10PM - 2:30PM	<b>Niche trajectory analysis of spatial transcriptomic data</b>  Guo-Cheng Yuan, Icahn School of Medicine at Mount Sinai

2:30PM - 2:50PM	<b>Genomic alterations in patients with Richter transformation and aggressive chronic lymphocytic leukemia</b>  Huihuang Yan, Mayo Clinic	2:30PM - 2:50PM	<b>MarsGT: Multi-omics analysis for rare population inference using single-cell graph transformer</b>  Xiaoying Wang, The Ohio State University	2:30PM - 2:50PM	<b>Robust integration of single-cell protein measurement by ADTnorm</b>  Ye Zheng, MD Anderson Cancer Center
2:50PM - 3:10PM	<b>Regulators of lung aging and fibrosis, and outcome prediction of lung disease using interpretable AI models</b>  Panayiotis (Takis) Benos, University of Florida	2:50PM - 3:10PM	<b>Enhancing adaptation of single cell large language models in single cell analyses through parameter-efficient fine-tuning</b>  Fei He, University of Missouri	2:50PM - 3:10PM	<b>Disease associated gene regulatory networks from single cell multiome data</b>  Zhana Duren, Clemson University
3:10 PM -3:30 PM		<b>Coffee/tea Break</b>			
3:30PM - 3:50PM	<b>Distinct germline mutational landscape of cancer susceptibility genes in cholangiocarcinoma patients with and without primary sclerosing cholangitis</b>  Shulan Tian, Mayo Clinic	3:30PM - 3:50PM	<b>Machine learning development environment for single-cell sequencing data analyses</b>  Lei Jiang, University of Missouri	3:30PM - 3:50PM	<b>Deep generative AI for affordable and comprehensive single-cell omics</b>  Jun Ding, McGill University
3:50PM - 4:10PM	<b>Integrating protein networks and spatial gene expression to identify potential drug Targets in ovarian cancer</b>	3:50PM - 4:10PM	<b>Characterizing and identifying neoantigen-reactive T cells by using deep learning methods</b>  Li Su, University of	3:50PM - 4:10PM	<b>AirQTL: efficient single-cell eQTL mapping enables causal gene regulatory network inference</b>  Lingfei Wang, University of

	Alper Uzun, Brown University		Missouri		Massachusetts Chan Medical School
4:10PM - 4:30PM	<b>Exploring phenotypic and genomic variability of multiple sclerosis</b>  Mary Davis, Brigham Young University	4:10PM - 4:30PM	<b>Data integration for single cells with cell type imbalance</b>  Yuchen Liu, Boston University	4:10PM - 4:30PM	<b>Biologically inspired deep learning for interpreting cell-type functional genomics in brain diseases</b>  Pramod Chandrashekar, University of Wisconsin-Madison
4:30PM - 5:00PM	<b>Panel Discussion</b>	4:30PM - 4:50PM	<b>Predicting candidate biomarkers for COVID-19 associated leukemia in children</b>  Judy Bai, Greenhills School		

**Saturday, October 12<sup>th</sup>, 2024**

7:30 AM -8:30 AM	<i>Light Refreshment with Coffee/Drink (Prefunction Space)</i>	
8:30 AM-6:30 PM	<b>Registration</b>	
8:30 AM -9:10 AM	<b>Keynote Speaker</b> (Room: Auditorium) <b>Paul Thompson, PhD</b> University of Southern California	
<b>CONCURRENT SESSIONS</b>		
Room: <b>Auditorium</b>	Room: <b>280</b>	Room: <b>106</b>
<b>Advances in Translational Omics</b>	<b>Clinical Genomics and Drug Discovery</b>	<b>Progress in Functional Genomics and Epigenomics</b>

Chair: Yusi Fu		Chair: Bin Chen		Chair: Hongbo Liu	
9:10AM - 9:30AM	<b>Eminent Scholar Presentation</b>  James Zou, Stanford University	9:10AM - 9:30AM	<b>Eminent Scholar Presentation</b>  Kin Fai Au, University of Michigan	9:10AM - 9:30AM	<b>Dynamics of extreme long polycomb loops in cancer</b>  Xiaotian Zhang, UTHealth at Houston
9:30AM - 9:50AM	<b>Time flies, how? Unlocking the Secrets of Aging</b>  Hongjie Li, Baylor College of Medicine	9:30AM - 9:50AM	<b>Transcriptomics-based drug discovery</b>  Bin Chen, Michigan State University	9:30AM - 9:50AM	<b>A splicing isoform atlas of melanoma brain metastases revealed by long-read single cell sequencing</b>  Ruli Gao, Northwestern University
9:50AM - 10:10AM	<b>Elucidation of therapeutic vulnerabilities in TNBC using multi-omics profiling</b>  Reid Powell, Texas A&M University	9:50AM - 10:10AM	<b>Charting the functional landscape of human genetic variation</b>  Xinghua/Mindy Shi, Temple University	9:50AM - 10:10AM	<b>Insufficient RNA editing elicits innate immune response in type 1 diabetes</b>  Qin Li, University of Pennsylvania
10:10AM -10:30AM		<i>Coffee/Tea Break</i>			
10:30AM -10:50AM	<b>Statistical identification of cell type-specific spatially variable genes in spatial transcriptomics</b>  Lulu Shang, MD Anderson Cancer Center	10:30AM -10:50AM	<b>Graph data models: building AI-ready research data commons for clinicogenomics</b>  Jing Su, Indiana University School of Medicine	10:30AM - 10:50AM	<b>Genetic variation determines 24-hour rhythmic gene expression and physiology</b>  Ying Chen, Baylor College of Medicine
10:50AM -11:10AM	<b>Machine learning for omics-based biomedical research</b>	10:50AM -11:10AM	<b>Characterizing the genetic basis and phenotypic impacts of circulating polyunsaturated fatty acids</b>	10:50AM - 11:10AM	<b>Epigenetic age and DNA methylation profiles linked to Inflammation, Immunometabolism, and fatigue in head</b>

	Shibiao Wan, University of Nebraska Medical Center		Kaixiong Ye, University of Georgia		<b>and neck cancer patients</b> Gang Peng, Indiana University
11:10AM -11:30AM	<b>Single-cell genomic copy number evolution in esophageal adenocarcinoma</b>  Jun Xia, Creighton University	11:10AM -11:30AM	<b>Enhancing Autism Status Prediction: A Deep Learning Model Using Whole-Exome Sequencing Data</b>  Ece Uzun, Brown University	11:10AM - 11:30AM	<b>Deciphering cellular epigenome heterogeneity and evolution in cancer within an aged ecosystem</b>  Sheng Li, University of Southern California
11:30AM -11:50AM	<b>Advancing systems biology approaches to study metabolic variations in diseases</b>  Chi Zhang, Indiana University   Oregon Health & Science University	11:30AM -11:50AM	<b>Identifying sex-specific sub-phenotypes in Alzheimer's disease progression using EHR</b>  Rui Yin, University of Florida	11:30AM - 11:50AM	<b>Genomic profiling of the histone variant h2a.z during embryonic development</b>  Fanju Meng, University of North Texas
		11:50AM -12:10AM	<b>Leveraging AI to unveil spatial heterogeneity of drug sensitivity</b>  Qianqian Song, University of Florida	11:50AM - 12:10AM	<b>A new organizer of epigenomic landscape</b>  Zhijun Huang, Van Andel Institute
12:10 PM-1:30 PM		<b>Lunch (Event/Exhibition Hall)</b>			
<b>CONCURRENT SESSIONS</b>					
Room: Auditorium		Room: 208		Room: 106	
<b>Innovations in Biomedical Informatics</b> Chairs: Jing Su		<b>Computational Biology and Biomarker Discovery</b> Chairs: Chi Zhang		<b>Early Stage Scholar Session</b> Chairs: Yufang Jin, Yongsheng Bai	

1:30PM - 1:50PM	<b>Eminent Scholar Presentation</b>  Jasmine Zhou, University of California, Los Angeles	1:30PM - 1:50PM	<b>Single-cell Multiome Characterizing Intercellular Communication and Intracellular Regulation of Epithelium and Mesenchymal during Secondary Palate Development in Mice</b>  Yulin Dai, UTHealth Houston	1:30PM - 1:40PM	<b>Real-Time Fall Detection for Elderly Care Using YOLO Approach</b>  Henry Wang, University of Texas at San Antonio
				1:40PM - 1:50PM	<b>Cell-Type Identification with Single Cell RNA-Sequencing Data for Mammary Gland in Aging</b>  Huey Huang, The University of Texas at San Antonio
1:50PM- 2:10PM	<b>SIN-Seg: A Joint Spatial-Spectral Information Fusion Model for Medical Image Segmentation</b>  Siyuan Dai, University of Pittsburgh	1:50PM- 2:10PM	<b>Robust tRNA Signatures for Liquid Biopsy Diagnostics in NSCLC Through Multicenter Small RNA-Seq Analysis</b>  Zhuokun Feng, University of Hawaii at Manoa	1:50PM- 2:00PM	<b>Vision-based Mini-Manufacturing with Multiple Robots</b>  Karla Sanchez, Alamo College
				2:00PM- 2:10PM	<b>Utilizing Large Language Models (LLMs) for Enhanced Cell Type Annotation: A User-Centric Approach</b>  Anwita Molaka, Greehey Children's Cancer Research Institute
2:10PM- 2:30PM	<b>Multimodal Brain Growth Patterns Using Deep Canonical Correlation Analysis With Auto-Encoder</b>	2:10PM- 2:30PM	<b>BioRSP: A novel tool for identifying spatial patterns and biomarkers in biological data</b>	2:10PM- 2:20PM	<b>Biomed-ML: a comprehensive knowledge portal for machine learning and artificial intelligent applications in biomedical research</b>

	Ram Sapkota, Center Georgia State University		Zeyu Yao, University of Alabama at Birmingham		<b>generated by BioBERT</b>  Vivien Li, The Ohio State University
				2:20PM - 2:30PM	<b>Integrating Binding Interaction and QSAR Modeling for Enhanced BACE1 Inhibitor Discovery through Machine Learning</b>  David Shen, Harriton High School, Bryn Mawr
2:30PM- 2:50PM	<b>PhenoSS: Phenotype semantic similarity- based approach for rare disease prediction and patient clustering</b>  Shihan Chen, University of Pennsylvania	2:30PM- 2:50PM	<b>Cancer heterogeneity explored through immune cell deconvolution of the tumor microenvironment</b>  Limin Jiang, University of Miami	2:30PM- 2:40PM	<b>Characterization of Survival Interaction Landscape for Lung Squamous Cell Carcinoma (SqCC) Risk Genes</b>  Kyle Yang, Qing Luo, Carmel High School
				2:40PM- 2:50PM	<b>Functional Screening of Germline Variants in Undiagnosed Rare Disease Patients Identifies Potential Mechanisms</b>  Erica Zhao, Carmel High School
2:50PM- 3:10PM	<b>A Data-Driven Sliding- window Pairwise Comparative Approach for the Estimation of Transmission Fitness of SARS-CoV-2 Variants and</b>	2:50PM- 3:10PM	<b>Prediction of functional effects of high-order protein variants from low- order variants</b>	2:50PM- 3:00PM	<b>Integrating Multimodal Data for Personalized Nutritional Recommendations in Chronic Disease Management</b>

	<p><b>Construction of the Evolution Fitness Landscape</b></p> <p>Hong Qin, University of Tennessee at Chattanooga</p>		<p>Houssemeddine Derbel, University of Nevada</p>		<p>Kellen Gong, Indiana University School of Medicine</p>
				3:00PM-3:10PM	<p><b>Application of EM algorithms in developing spatial dependent regression analysis for spatial transcriptomics data</b></p> <p>Allen Qian, Indiana University School of Medicine</p>
3:10 PM - 3:30 PM		<i>Coffee/Tea Break</i>			
3:30PM-3:50PM	<p><b>Graph Transformer with Disease Subgraph Positional Encoding for Improved Comorbidity Prediction</b></p> <p>Xihan Qin, University of Delaware</p>	3:30PM-3:50PM	<p><b>mosGraphGPT: a foundation model for multi-omic signaling graphs using generative AI</b></p> <p>Heming Zhang, Washington University School of Medicine</p>	3:30PM-3:40PM	<p><b>Chat-to-code: Conversational DataFrame Analysis Powered by Pandas.AI</b></p> <p>Jasmine Zhang, Carmel High School</p>
				3:40PM-3:50PM	<p><b>Integrating ChatGPT-4 and Bioinformatics to Identify SRC as a Key</b></p> <p>Ayla Zhang, Thomas Jefferson High School for Science and Technology</p>
3:50PM-4:10PM	<p><b>Cancer Cell Characterization with Neighborhood-Enhanced Cellular Embedding Using Deep Learning on H&amp;E-Stained Images</b></p>	3:50PM-4:10PM	<p><b>Computational identification of neuroprogenitor cell biomarkers based on pattern change over time</b></p>	3:50PM-4:00PM	<p><b>AutoSGI: automated feature selection for clinical subgroup identification</b></p> <p>Mythreya Dharani, Englander Institute for Precision Medicine</p>

	Yidong Chen, University of Texas Health San Antonio		Toni C. Tacorda, Jan and Dan Duncan Neurological Research Institute	4:00PM- 4:10PM	<b>Transformer-based Fall Detection Method: A UMA Fall Study</b>  Joanna Zeng Ye, University of Pennsylvania
4:10PM- 4:30PM	<b>Personalized dynamic functional network connectivity state as a predictor of Alzheimer's disease</b>  Elaheh Zendehtrouh, Georgia Institute of Technology	4:10PM- 4:30PM	<b>Deep5mC: Predicting 5-methylcytosine (5mC) Methylation Status by a Deep Learning Transformer Approach</b>  Evan Kinnear, University of Nevada	4:10PM- 4:20PM	<b>Possible interconnection of anemia and proteinuria</b>  Afagh Bapirzadeh, Islamic Azad University
		4:30PM- 4:50PM	<b>EquiRank: improved protein-protein interface quality estimation using protein-language- model-informed equivariant graph neural networks</b>  Md Hossain Shuvo, Prairie View A&M University	4:20PM- 4:50PM	<b>Panel discussion</b>
1:30PM-3:10PM, 3:30PM-4:50 PM	<b>Flash Talks (Event/Exhibition Hall)</b> Chair: Qian Liu <b>1. EpiGePT: a pretrained transformer model for epigenomics</b> , Qiao Liu, Stanford University <b>2. Development of a polygenic score for recovery time after concussion: a concussion assessment, research, and education (CARE) consortium study</b> , Zhiqi Zhang, Indiana University <b>3. LIQA2: efficient isoform detection and quantification from long read sequencing</b> , Anagha Gouru, University of Pennsylvania <b>4. ssREAD: a single-cell and spatial RNA-seq database for Alzheimer's disease</b> , Cankun Wang, The Ohio State University <b>5. Enhancing single-cell RNA-seq feature selection using quantum annealing-empowered quadratic unconstrained binary optimization</b>				

	<p>(QUBO), Selim Romero, Texas A&amp;M University</p> <p>6. <b>Comparing nanopore to MethylationEPIC array and EM-Seq in DNA methylation detection</b>, Steven Brooks, Indiana University</p> <p>7. <b>Single cell digital twins for precision medicine target identification and drug repurposing in Alzheimer’s disease progression</b>, Yunxiao Ren, Lerner Research Institute</p> <p>8. <b>Discovering condition-specific cell populations via integrative clustering of single-cell data</b>, Rekha Mudappathi, Arizona State University</p> <p>9. <b>Metaproteomic analysis to assess the impact of storage media on human gut microbiome in fecal samples</b>, Van-An Duong, UTHealth Houston</p> <p>10. <b>Exploring the Efficiency of Deep Graph Neural Networks for RNA Secondary Structure Prediction</b>, Jie Hou, Saint Louis University</p> <p>11. <b>GKGL-PE: a GNN-based Knowledge Graph Learning framework for Pathway Embedding</b>, Li Sa, Oakland University</p> <p>12. <b>Quantitative analysis of the risk of cervical lesions due to single-infection and co-infection of high-risk HPV genotypes</b>, Rangjiao Liu, Sanway Clinical Laboratory</p> <p>13. <b>TCPGdb: A comprehensive CRISPR screen resources of T cell perturbation genomics for identification of critical T cell regulators</b>, Chuanpeng Dong, Yale University</p> <p>14. <b>scDitu: a cluster-free method for discovering gene-level differential transcript usage in sparse single cell long read sequencing data</b>, Ziqi Rong, University of Pittsburgh</p> <p>15. <b>Harmony-based data integration for distributed single-cell multi-omics data</b>, Ruizhi Yuan, University of Pittsburgh</p> <p>16. <b>Transformer-based Fall Detection Method: A UMAFall Study</b>, Joanna Ye, Winston Churchill High School</p> <p>17. <b>Investigating the role of viral transcriptional regulators in human diseases: An integrative genome wide approach</b>, Citu Citu, UTHealth Houston</p>
5:00PM-5:45PM	<b>Award Presentation</b> (Auditorium)
5:45PM-6:00PM	<b>Closing Remarks</b> (Auditorium, Ece Uzun)