

SCHEDULE

International Conference on Intelligent Biology and Medicine ICIBM 2026 | August 2–5, 2026

*Jacobs School of Medicine and Biomedical Sciences, University at Buffalo
955 Main Street, Buffalo, NY 14203-1121*

Sunday, August 2nd, 2026

8:00 AM – 5:00 PM	Registration		
9:00 AM – 9:30 AM	Opening Remarks (Room 2220A&B)		
	Concurrent Sessions/Workshops		
	Room 2220A&B	Room 2213A	Room 2213B
	Spatial Single-Cell and Multi-Omics Chair: Yuehua Cui	AI and Computational Modeling for Biomedical Discovery and Precision Health Chairs: Yijie Wang, Xun Wu	Genomic Modeling and Biomolecular Structure Chair: Shenglin Mei
9:30 AM – 9:50 AM	Atlas-based analysis of high-resolution spatial transcriptomics H. Robert Frost Dartmouth College	Structured and scalable AI for high-dimensional biological data: beyond lasso under correlation Yijie Wang Indiana University Bloomington	Architecting for Discovery: Scaling AI-Ready Multimodal Data Infrastructure for Precision Oncology Stephan Schürer University of Miami
9:50 AM – 10:10 AM	Tools for comparative spatial transcriptomics Saurabh Sinha, Georgia Institute of Technology	Explainable AI models for decoding proteins and microbiome Yuzhen Ye Indiana University Bloomington	TFBindFormer: A cross-attention transformer for transcription factor–DNA binding prediction Ping Liu University of Missouri
10:10 AM – 10:30 AM	Categorization of 34 computational methods to detect spatially variable genes from spatially resolved transcriptomics data Guanao Yan Michigan State University	Reinforcement post-training aligns flow-matching perturbation models with DEG recovery Xuhong Zhang Indiana University Bloomington	Comprehensive benchmarking of long-read fusion-detection methods leads to improved fusion discovery Pre-recording Fei Zhang Hong Kong Polytechnic University
10:30 AM – 10:50 AM <i>Coffee Break</i>			

10:50 AM – 11:10 AM	CySCI: Regularized multitasking graphical attention for integrative single-cell analysis Xinlei Wang University of Texas, Arlington	Advancing dietary assessment with computer vision Jianpeng He Indiana University Bloomington	KoGNER: A novel framework for knowledge graph distillation on biomedical named entity recognition Heming Zhang Washington University	
11:10 AM – 11:30 AM	Identification of high-risk cells in single-cell spatially resolved transcriptomics data using transfer learning and spatial smoothing Debolina Chatterjee University of Mississippi	Detecting precise adverse drug events from real-world data Pengyue Zhang Indiana University School of Medicine	Multiple versus pairwise sequence alignments for protein phylogenetics using foundation models Rohan Alibutud Temple University	
11:30 AM – 11:50 AM	Decoding pediatric scleroderma across scales using spatial omics and histology Wei Chen University of Pittsburgh	Unbiased in vitro and in vivo CRISPR screens identify novel regulatory genes in macrophage efferocytosis Xun Wu Columbia University	ChromDiffusion: Refining chromatin structure characterization through diffusion models Tomoya Kanno Temple University	
11:50 AM – 12:10 PM	Decipher non-coding SNPs by high-resolution reconstruction of single-cell spatial genome architectures in 3D space Jianrong Wang Michigan State University	Aging Synergizes with Hypercholesterolemia to Drive Smooth Muscle Cell Transdifferentiation Mingqiao Li Tulane University	A structural antibody benchmark of AlphaFold3 reveals hallucinated epitopes and a bias for orderness Arnav Solanki UTHealth Houston	
12:10 AM – 12:30 PM	Multimodal AI for tumor microenvironment characterization and therapeutic prediction Qianqian Song University of Florida	Model-guided reconstruction of single-cell secretion dynamics during live CAR-T/tumor-cell interactions Yujing Song New York University		
12:30 PM – 2:00 PM	Lunch Break (Room 1220)			
CONCURRENT SESSIONS/WORKSHOPS				
Room 2220A&B		Room 2213A	Room 2213B	Room 1220
Eminent Scholar <i>Dr. Han Liang</i> Computational and AI models to decode disease mechanisms based on chromatin and multi-omics integration Chair: Jianrong Wang		AI and Multi-Modal Integration for Disease Characterization Chair: Shibiao Wan	AI and Statistical Methods for Genomics and Multi-Omics Chairs: Wanding Zhou, Gang Peng	From Data to Models to Agents: Using LLMs to Accelerate Clinical Development and Personalize Patient Care Chairs: Huanmei Wu, Yuzhou Chen

2:00 PM – 2:20 PM	<i>Eminent Scholar: Comprehensive Characterization of N6-methyladenosine RNA modification in Cancer</i> <i>Han Liang</i> <i>MD Anderson Cancer Center</i>	Agentic-AI for hypothesis generation for aging and drug repurposing Kyoung Jae Won Cedars-Sinai Medical Center	Advancing the Interpretation of Human Genetic Variation Using Generative AI Xinghua (Mindy) Shi Temple University	Dual-stream cross-modal alignment for clinical trial outcome prediction Yuzhou Chen University of California, Riverside
2:20 PM – 2:40 PM	Combining natural genetic variations with single molecule footprinting to learn about the rules of chromatin regulation Xin He University of Chicago	An optimal-transport based multi-modal integration for categorizing T-cell acute lymphoblastic leukemia Shibiao Wan University of Nebraska Medical Center	Development of Epigenetic Clocks from Oxford Nanopore Methylation Data in Human Caudate Tissue Gang Peng Indiana University	SepsisGuard-ICU: an evidence-grounded multi-agent system for safe and explainable sepsis decision support in the ICU Lei Liu Fudan University
2:40 PM – 3:00 PM	Robust causal inference from imperfect CRISPR interventions in Perturb-seq: Heterogeneous Perturbation Strength and Off-target Bias Sunduz Keles University of Wisconsin-Madison	ShinyFeatures: a Shiny App for prioritizing features for machine learning models Timothy Shaw H Lee Moffitt Cancer Center	The Cancer Proteome Atlas: From Functional Proteomics to Next-Generation Analytics Jun Li University of North Carolina at Chapel Hill	Developing social work language models for SYNC-Smart AI assistant Phillip McCarllion Temple University
3:00 PM – 3:20 PM	Learning single-cell multiomic trajectories using neural ODEs Christina Leslie Memorial Sloan Kettering Cancer Center	TENET+: A tool for reconstructing gene networks by integrating single cell expression and chromatin accessibility data Junil Kim Soongsil University	Unified Statistical Inference Beyond Gene Expression in Single-Cell RNA Sequencing Guoshuai Cai University of Florida	BehaviorGround: a fair benchmark for cognitive decline detection under subjective-complaint contamination Sambit Mukherjee University of South Carolina
3:20 PM – 3:40 PM <i>Coffee Break</i>				
3:40 PM – 4:00 PM	From ontology fingerprints to BRAINCELL-AID: literature-driven gene function and brain cell annotation Wenjin Zheng	Advancing prenatal congenital heart disease screening through artificial intelligence Jieqiong Wang	Can We Trust Protein Search in the Era of Large Language Models? Yang Lu University of Wisconsin	Leveraging synthetic text and image data to improve the robustness and generalizability of biomedical AI models Kai Wang

	UTHealth Houston	University of Nebraska Medical Center		Children's Hospital of Philadelphia
4:400 PM – 4:20 PM	Interpreting deep learning models in genomics via concept attribution Shaun Mahony Pennsylvania State University	Machine learning-based small-RNA liquid biopsy enables accurate classification of benign, malignant, and metastatic breast diseases Xuhang Liu Roswell Park Cancer Center	Transposable Element–Driven Viral Mimicry Constrains Multistep Pancreatic Cancer Progression Siyu Sun University of Rochester	From EHR phenotyping to proactive maternal care: Trustworthy AI for early risk detection and personalized decision support Huanmei Wu Temple University
4:20 PM – 4:40 PM	Spatially-informed reference-free deconvolution for spatial transcriptomics with SpatialCD Yuehua Cui Michigan State University	Interpretable spatial programs from multi-sample tumor spatial transcriptomics Yi Zhang Duke University	Single-molecule RNA modification mapping by AI analysis of nanopore sequencing Yunxia Wang Boston Children's Hospital	AI in biomedical research-- hypothesis generation, drug target and activity prediction Jie Zhang Indiana University
4:40 PM – 5:00 PM	spatiAlytica: Spatially intelligent multimodal agentic system for decoding tumor ecosystems Yufei Huang University of Pittsburgh	Computational techniques for cell-level inference of gene effects on human traits Jinzhuang Dou The University of Alabama at Birmingham	Recurrent Methylation Pattern Encoding for Interpretable Analysis of Sparse DNA Methylomes Wanding Zhou Children's Hospital of Philadelphia	Prompt-tuned open-source large language model for structured extraction of social determinants of health from clinical notes Yan Zhuang, Indiana University
5:00 PM – 5:20 PM	Single-molecule RNA fate modeling by deep learning Dean Li Boston Children's Hospital	A rigorous leak-free microbiome pipeline revealing batch effects as the dominant challenge in a multi-cohort immunotherapy response prediction Amey Garg Santa Clara High School 5:00 PM – 5:10 PM		Identifying subgroups in patient with low back pain for personalized treatment using machine learning Leming Zhou University of Pittsburg

Monday, August 3rd, 2026

8:00 AM – 5:00 PM	Registration
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8:20 AM – 9:00 AM	Keynote Lecture: The Human Pangenome Project Ting Wang, PhD (Room 2220A&B)			
CONCURRENT SESSIONS/WORKSHOPS				
Room 2220A		Room 2213A	Room 2213B	Room 2220B
Eminent Scholar Dr. Yun Li Precision Medicine and Cancer Systems Chair: Rachael Hageman Blair		Computational Multi-Omics Approaches to Dissect Regulatory Variation and Disease Mechanisms Chair: Lei Li	Bridging Methodological Innovation and Real-World Applications in Genetic Studies Chair: Zikun Yang	AI and Multi-omics for Modeling Aging and Disease Chair: Sheng Li
9:00 AM – 9:20 AM	Eminent Scholar: Multi-omics Understanding of Complex Human Diseases Dr. Yun Li	Prediction of rapid fibrosis progression in metabolic dysfunction–associated steatotic liver disease with interpretable machine learning models Tahmina Sultana Priya Virginia Tech	fastGxE: Powering genome-wide detection of genotype-environment interactions in biobank studies Xiang Zhou Yale University	Transcriptional heterogeneity predicts and shapes clonal selection in aging hematopoiesis Sheng Li University of Southern California
9:20 AM – 9:40 AM	Gain and loss of DNA methylation during tumor evolution Deyana Tabatabaei Temple University	Atlas of cell type-specific post-transcriptional genetic impacts in immune-related diseases Lei Li Shenzhen Bay Laboratory	Distributional genetic effects reveal context-dependent molecular regulation in human brain aging and Alzheimer’s disease Tianying Wang Colorado State University	Liquid biopsy biomarkers for cancer detection and disease monitoring Bodour Salhia University of Southern California
9:40 AM – 10:00 AM	Deep learning for early hepatocellular carcinoma risk prediction in patients with chronic liver diseases and diabetes: insights from retrospective cohort analysis Jinlian Wang UT Austin	Multi-omics integration predicts 17 disease incidences in the UK biobank Quan Sun University of Pennsylvania	Powerful statistical frameworks for genome-wide survival association analysis Shiyang Ma Shanghai Jiao Tong University	A transcriptomics-native foundation model for universal cell representation and virtual cell synthesis Jichun Xie Duke University

10:00 AM – 10:20 AM	An immune cell signature for sepsis with multiple organ dysfunction syndrome Rama Shankar Michigan State University	Accurate estimation and correction of open chromatin biases in CUT&Tag data Sheng'en Shawn Hu University of Virginia School of Medicine	Interplay of Polygenic and Monogenic Kidney Disease Atlas Khan Columbia University	RNA stability as a key link between genetic variation and disease: insights from multi-omics and deep learning Xinshu Grace Xiao University of California
10:20 AM – 10:40 AM <i>Coffee Break</i>				
10:40 AM – 11:00 AM	GenePriori: a leakage-aware multi-agent framework for bias-robust gene prioritization with translational oncology relevance Yuxuan Jiang Southwest Medical University	A novel admixed population fine-mapping method: mitigating false discovery rate through local genetic ancestry modeling Kai Yuan Indiana University School of Medicine	Integrating genomic and proteomic data improves complex trait prediction in diverse populations. Haoyu Zhang National Cancer Institute	Precisely integrate single-cell data to decipher aging signatures in the monkey brain under calorie restriction Chao Zhang Boston University
11:00 AM – 11:20 AM	Identification of intrinsic pancreatic cancer expression subtypes from patient-derived xenograft samples Orry Huang University of Texas Health Science Center, San Antonio	Associated cell types and influential genes identified through integration of genome-wide association studies and single-cell transcriptomics for circulating fatty acid traits Elijah Sterling University of Georgia	Multi-ancestry modeling leveraging genetic diversity reveals heterogeneous architecture in primary open-angle glaucoma Jessica Cooke Bailey East Carolina University	Integrative AI-driven multi-omics identifies NR2F1 as a key driver of lineage plasticity and metastatic progression in prostate cancer Ping Mu Yale University
11:20 AM – 11:40 AM	Oncoordinate captures microenvironmental state dynamics and identifies aggressive niches in tumors Vignesh Venkat Rutgers Cancer Institute & Icahn School of Medicine at Mount Sinai	Single-cell multiomics reveals malignant plasticity and immune suppression in high-risk pediatric cancers Wenbao Yu, Temple University	Signatures of recent positive selection refine novel Primary open-angle glaucoma risk loci Timothy Ciesielski Case Western Reserve University	Quantifiable blood TCR repertoire components associated with immune aging Bo Li University of Pennsylvania
11:40 AM – 12:00 PM	A density-based spatial functional modularity framework for characterizing tumor functional niches in HER2-positive breast cancer Fan Jhen Liu National Taiwan University		Tractor-PGS uses local ancestry to improve prediction accuracy in admixed populations Yi-Sian Lin Baylor College of Medicine	Cell-free DNA fragmentomics and methylation as AI-enabled multi-omics biomarkers across cancer and neuroinflammatory disease Yaping Liu Northwestern University

12:00 PM – 1:00 PM		Lunch Break (Room 1220)		
CONCURRENT SESSIONS/WORKSHOPS				
Room 2220A		Room 2213A	Room 2213B	Room 2220B
Invited Speaker Dr. Min Xu Genome Browser Tutorial Chair: Daofeng Li		Biological and Biomedical Ontology Workshop in the AI Era Chairs: Oliver He, Alexander Diehl	Cancer Genomics Chairs: Siyuan Zheng, Xiaojing Wang	Deep Learning and CRISPR Screening Chair: Xueqiu Lin
1:00 PM – 1:20 PM	From Pixels to Biological Reasoning: Semantic, Hierarchical, and Graph-Structured Learning for Interpretable Biomedical AI Min Xu Mohamed bin Zayed University of Artificial Intelligence & CMU	Representing dental care-related fear and anxiety Bill Duncan University of Florida	An embedding-based framework for statistical testing of LLM-inferred gene-set functions Yu-Chiao Chiu University of Pittsburgh Creative applications of AI in biomedical research Yan Guo University of Miami	Decoding Non-Coding Regulatory Mutations in Cancer Using FFPE-CUTAC and Interpretable Deep Learning Xueqiu (Chu) Lin Fred Hutchinson Cancer Center
	1:20 PM – 1:40 PM		Browser tutorial session introduction Daofeng Li Washington University 1:20PM-1:30PM	Pain in both general and specific ontological representation Alexander Diehl University at Buffalo
1:40 PM – 2:00 PM	UCSC Genome Browser: Introduction + 5min QA <u>Zoom</u> Robert Kuhn, UCSC Genomics Institute 1:30PM-2:00PM	Recent developments in social ontology Bill Hogan Medical College of Wisconsin	Phenylalanine reprograms TLS architecture and plasma cell fate in MASH-HCC Chunru Lin The University of Texas MD Anderson Cancer Center	Structured Modeling of Allelic-specific Gene Expression <u>Zoom</u> William H. Majoros Duke University
2:00 PM – 2:20 PM	UCSC Brain Explorer + 5min QA <u>Zoom</u> Mary Goldman UCSC Genomics Institute		Introducing the Injury Ontology Barry Smith University at Buffalo	HOXA9 maintains cancer-specific 3D genome organization in AML

	2:00PM-2:30PM		Qili Shi UT Health San Antonio	
2:20 PM – 2:40 PM	WashU Epigenome Browser: Introduction Daofeng Li Washington University 2:30PM-2:40PM	The 2026 Cell Line Ontology Updating and CellCards Web Display Jie Zheng University of Michigan Medical School	From unresolved variants to actionable biomarkers: defining when long-read sequencing is required Xiaotu Ma, St. Jude Children's Research Hospital	How to Align Unpaired Single-Cell Omics: Benchmarks, Practical Guidelines, and Impacts on Gene Regulatory Modeling Zhana Duren Indiana University School of Medicine
2:40 PM – 3:00 PM	Develop visualization portal (example: BICAN & IGVF) Wenjin Zhang Washington University 2:40PM-2:45PM	A decade of progress in automated quality assurance of biomedical ontologies Zoom Licong Cui University of Texas Health Science Center at Houston	AI-empowered virtual immunopeptidomics of neoantigen immunogenicity Yuhao Tan The Children's Hospital of Philadelphia / University of Pennsylvania	Perturbation of allele specific chromatin variants in human colon organoids links gene regulation to non-coding variants associated with digestive disease Siming Zhao Dartmouth College
3:00 PM – 3:20 PM	HPRC Epigenome Browser Tianjie Liu Washington University 2:45PM-2:50PM	Automating Intervention Discovery from Scientific Literature: A Progressive Ontology Prompting and Dual-LLM Framework Jinjun Xiong University at Buffalo	Genomic alterations across racial/ethnic groups and cancer outcome disparities Xiaoqing Wang UT Health San Antonio Genome-scale discovery of RNA-centered regulation in cancer drug response and immunotherapy Da Yang University of Pittsburgh	Improving Disease Risk Prediction with Functional Genomics Annotations Using LLMs Wanwen Zeng Stanford University
3:20 PM – 3:40 PM	5min QA for WashU Epigenome Browser 2:50PM-2:55PM	From Biomedical Ontologies to Knowledge Discovery: Ontology-Driven Applications in Ignite 2.0 and Vignet Junguk Hur University of North Dakota		Interpret human genetic variants via single-cell multimodal omics and AI/ML models Yang Li Washington University in St. Louis
	5min Break 2:55PM-3:00PM			
	Hands-on for WashU Epigenome Browser Chad Seng, Washington University 3:00PM-3:40PM <u>Bring laptop</u>			
3:40 PM – 4:00 PM <i>Coffee Break</i>				

Clinical Imaging, Multimodal AI, and Healthcare Deployment Chair: Shaolei Teng		Technology Session Chair: Yongfu Wang	Special panel: AI in Research and Scientific Writing Chair: Wei Zhang	Flash Talks Chair: Tong Wang
4:00 PM – 4:20 PM	Matching speech models to ADRD subtypes: A mechanistic benchmark Xiaoyu Zhang SUNY at Buffalo	Empowering genomic discovery: Accelerating regulatory biology through multi-omic solutions <u>Yun Zhao</u> , Zonghui Peng Admera Health (30 minutes) 4:00 PM – 4:30 PM	TBD Zhandong Liu	CO-PICO/PECO: Condition-based occupational PICO/PECO and its applications for LLM extraction and ontological modeling of structured occupational safety and health Hasin Rehana, University of North Dakota 4:00 PM – 4:10 PM
				CIRCA identifies cell- and niche-level interactions with amyloid-β plaques using causal representation learning Tyler Lovelace UTHealth Houston 4:10 PM – 4:20 PM
4:20 PM – 4:40 PM	A framework for dynamically training and adapting deep reinforcement learning models to different, low-compute, and continuously changing radiology deployment environments Pre-recording Vishwa S. Parekh Rice University	Unlocking Archived Pathology Specimens: Robust Single-Cell Transcriptomics from FFPE Tissue <u>Jing Zhou</u> Singleron Biotechnologies (20 minutes) 4:30 PM – 4:50 PM	From Prompt to Publication: Applying AI Agents to Bioinformatics Research Wei Zhang University of Central Florida	Machine learning augmented mechanistic modeling for identifying predictive tumor biomarkers Alexander Silalahi MD Anderson Cancer Center 4:20 PM – 4:30 PM
				Multimodal protein function inference via vision-language models and structural similarity representations, Renzhi Cao Pacific Lutheran University 4:30 PM – 4:40 PM
4:40 PM – 5:00 PM	Multimodal deep learning for Alzheimer's disease prediction with Improved training	Protein interactomics by proximity networks of single cells Zoom <u>Michael Förster</u>	Agentic Loop Engineering for Bioinformatics Research: Data Gathering, Algorithm Development, and Paper Writing	scDCBC: Model-based scRNA-seq deep clustering with batch correction Xiaohe Chen, Florida State University 4:40 PM – 4:50 PM

	stability and flexibility Jianan Liu Southeast University	Pixelgen (30 minutes) 4:50 PM – 5:20 PM	Tejas Sandip Mahajan University of Central Florida	A systematic investigation of molecular encoding methods for drug property predictions across neural network and transformer encoder-based model Shan-Ju Yeh, National Tsing Hua University 5:00 PM – 5:10 PM
5:00 PM – 5:20 PM	RA-CMF: Region-adaptive conditional MeanFlow for CT image reconstruction Md Shifatul Ahsan Apurba University of Alabama at Birmingham	Use of Stereo-seq to dissect cell type spatial differences in human brain organoids and mouse eyeball Zoom <u>Elaine Lim</u> MGI US LLC (20 minutes) 5:20 PM – 5:40 PM	Panel Discussion 5:00 PM – 6:00 PM Dr. Lu Zhang Indiana University Indianapolis Dr. Jianhua Ruan University of Texas at San Antonio Dr. Yan Guo University of Miami Dr. Zhandong Liu Baylor College of Medicine	Beyond PCA: Multiple correspondence analysis for robust cell-type annotation and trajectory inference Tsai-Jung Lu, National Taiwan University UT San Antonio 5:10 PM – 5:20 PM
5:20 PM – 5:40 PM	WoundWise: A mobile deep learning solution for accurate pressure ulcer staging Daniel Change University of Nevada, Las Vegas	Built for What's Next: How 10x's Flex Apex, Xenium, and Atera Platforms Are Powering the AI Era of Biology <u>Aleksandar Janjic</u> 10x Genomics (20 minutes) 5:40 PM – 6:00 PM		
5:40 PM – 6:00 PM	ICA-based analysis of progressive multi-scale structural-functional fusion for Alzheimer's disease Yanteng Zhang TReNDS Center			
6:00 PM – 7:30 PM	Poster Session (Atrium)			

Tuesday, August 4th, 2026

8:00 AM – 5:00 PM	Registration
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8:20 AM – 9:00 AM	Keynote Lecture: Mapping the Multiscale Human Gary Bader, PhD (Room 2220A&B)			
CONCURRENT SESSIONS/WORKSHOPS				
Room 2220A		Room 2213A	Room 2213B	Room 2220B
<i>Invited Speaker</i> <i>Dr. Zemin Zhang</i> AI-Driven Multi-Omics for Disease Mechanisms and Therapeutic Discovery Chairs: Hongying Sun, Kaifu Chen		From Metagenomes to Mechanisms: Functional Microbiome Discovery Chairs: Qiyun Zhu, Xiaofang Jiang	AI and Data Science in Health Informatics Chairs: Yu Huang, Yan Zhuang	Integrative omics to understand and predict disease progression Chairs: Jingwen Yan, Sha Cao
9:00 AM – 9:20 AM	<i>Invited Speaker:</i> Decoding the tumor microenvironment by pan-cancer single cell analysis Zemin Zhang Peking University	Spatiotemporal microbiome dynamics: from early disease prediction to single-cell functional analysis and sorting Shi Huang University of Hong Kong	Agentic AI for complex clinical informatics workflows Xing He Indiana University School of Medicine	Continuous Modeling of Disease Progression in Alzheimer's Disease and Related Dementias Lu Zhang Indiana University Indianapolis
9:20 AM – 9:40 AM	Longitudinal epigenome-wide associations and pre-chemotherapy prediction of post-chemotherapy inflammation in patients with breast cancer undergoing chemotherapy Hongying Sun University of Rochester	Decoding the gut microbiome’s functional dark matter via comparative genomics Xiaofang Jiang National Institutes of Health (NIH)	Multi-modal AI using neuroimaging genomics to study Alzheimer’s and dementia Da Ma Wake Forest University	Stability-aware integrative clustering for characterizing disease progression from multi-modal data Rachael Hageman Blair New York University at Buffalo
9:40 AM – 10:00 AM	Quantum computing for single-cell biology: networks, dynamics, and generative models James J. Cai Texas A&M University	Microbiome-Informed Therapeutic Peptide Discovery Shanlin Ke Ohio State University	Immune digital twin and vascular disease Juilee Thakar University of Rochester	Continuous staging of amyloid progression in Alzheimer’s disease with enhanced sensitivity to early changes Jingwen Yan Indiana University
10:00 AM – 10:20 AM	Cross-Trait PRS and data-driven subtyping to uncover obesity heterogeneity and enable precision risk prediction Shulan Tian	Microbiome-based early screening of intestinal tumors driven by intelligent sensing and privacy protection Xiaoquan Su	Unlocking clinical development innovation with artificial intelligence and real-world evidence Chuan Gao	AD-LLaVA-3D: Forecasting Alzheimer's Disease Progression with a Unified Multimodal

	Mayo Clinic	Qingdao University	Johnson & Johnson Innovative Medicine	Video-Language Framework Sha Cao Oregon Health & Science University
10:20 AM – 10:40 AM <i>Coffee Break</i>				
10:40 AM – 11:00 AM	Agentic AI for atlas analysis of cell-cell communications Kaifu Chen Harvard Medical School	Multi-dimensional virome profiling from bulk metagenomes reveals non-redundant signatures of gut dysbiosis Zheng Sun Harvard University	Agentic AI for automated RNA structural motif analysis and biomedical discovery Jie Hou Michigan State University	Staging and Pseudotime Inference of Alzheimer's Disease Progression Using Multimodal Imaging Data Zixuan Wen University of Pennsylvania
11:00 AM – 11:20 AM	Cellular and molecular dynamics of smooth muscle cells during aortic disease development Yanming Li Maine Health Institute for Research	Predicting metabolite response to dietary intervention using deep learning Tong Wang Purdue University	LLM-Agent-Based clinical trial cohort building: an experimental evaluation using MIMIC-IV Hao Liu Montclair State University	From 2D Snapshots to 3D Molecular Landscapes: Reconstructing Volumetric Spatial Transcriptomics with AI Wei Zhang University of Central Florida
11:20 AM – 11:40 AM	Computational biology in early drug discovery: turning complex data into biological insights Yu Sun Biogen	Calculating differential genome coverages among metagenomic sources Yuhan Weng University of California San Diego	A scalable multi-omics representation framework for disease modeling across proteomic, single-cell, and spatial transcriptomic data Daisy Shen Moffitt Cancer Center	How Much Biological Knowledge Is Encoded in LLM-Derived Gene Embeddings? Jun Li Notre Dame University
11:40 AM – 12:00 PM	Machine learning-based prediction of gene expression using RNA motifs and structural properties Mingyi Zhu Yale School of Medicine	Enabling AI-driven discovery in complex biological systems with scikit-bio Qiyun Zhu Arizona State University	Cross-Hospital privacy-preserving distributed AI Tsung-Ting Kuo Yale University	Toward integrative modeling of drug response in acute myeloid leukemia Olga Nikolova Oregon Health & Science University
12:00 PM – 1:00 PM	Lunch Break (Room 1220)			
1:00 PM – 1:40 PM	Keynote Lecture: A Research Agenda for Clinical Informatics in the Post-AI, Post-EHR Vendor World James Cimino, MD (Room 2220A&B)			

CONCURRENT SESSIONS/WORKSHOPS				
Room 2220A		Room 2213A	Room 2213B	Room 2220B
<i>Eminent Scholar</i> <i>Dr. Chongzhi Zang</i> Multi-Omics, Microbiome, and Metabolomics Chair: Hao Liu		Single-Cell, Spatial, and Regulatory Networks Chair: Lu Li	Flash Talk Chair: Yufang Jin	Future Scientist Session Chair: Chi Zhang, Jingwen Yan, Arhan Patel
1:40 PM – 2:00 PM	<i>Eminent Scholar: Chromatin and Gene Regulation through Transcriptional Condensates</i> <i>Dr. Chongzhi Zang</i>	Single-cell analysis of intracellular transport and expression of cell surface proteins Rekha Mudappathi Arizona State University	Nanoparticle-Induced Thermogenic Adipocytes Improve Endothelial Tube Formation and Network Parker Olkowski UT San Antonio	Derek Ai Park Tudor High School Christopher Barker Pacific Lutheran University
			Electroencephalography (EEG) for Remote Vehicle Control Applications Seth Johnston UT at San Antonio	
2:00 PM – 2:20 PM	Multi-modality foundation model to link pathology with omics Guangyu Wang Houston Methodist, Weill Cornell Medicine School	Knowledge grounded multi-agent orchestration for interpretable functional summarization of single-cell transcriptomics Jinlian Wang UTHealth Houston	Hardware-Oriented Programming for an Autonomous Robot Angela Zhang Basis San Antonio Shavano Campus	Joshua Bie Havard Westlake School Alyssa Chen Carrollwood Day High School
			Bridging Computer Vision and Food Policy: A YOLOv11 Produce Freshness Detector Aligned with California AB 660 Date Label Vocabulary Aston Liu The Kinkaid School, Houston	
2:20 PM – 2:40 PM	Analyzing soil microbial diversity in organically managed fields amended with	miR-CellMap: a graph-transformer framework for single-cell	DUET-Knockoffs: FDR-Controlled Cross-Platform Feature Selection	Bianca Ehling The Ohio State University

	dredged material in northwest ohio Shikshya Gautam Bowling Green State University	microRNA-gene regulatory analysis Jane Ohia University of Nebraska-Lincoln	from Paired 16S and Shotgun Microbiome Count Data Shiyuan Wang UT at San Antonio	 Katelyn Hur Red River High School
			An AI-Powered Single-Cell and Spatial Omics Ecosystem for Neurodegenerative Disease Weidong Wu Ohio State University	 Jason Li Westwood High School
2:40 PM – 3:00 PM	DUET-Knockoffs: fdr-controlled cross-platform feature selection from paired 16S and shotgun microbiome count data Yiqiao Zhu The University of Texas at San Antonio & University of Michigan	Cell segmentation using spatial transcriptomic data from the multi-objective optimization perspective Aleksandar Necakov, Brock University	BindFuse: A Multimodal Graph Learning Framework for Protein-Ligand Binding Affinity Prediction Bilal Ahmad University at Buffalo	 Isabella Jiayi Li Westlake High School
			Integrative Mendelian Randomization and Protein-Protein Interaction Network Analysis Links Multi-Organ Aging to Complex Diseases Chunxuan Ma Cleveland Clinic	 Addison Liu Park Tudor School
3:00 PM – 3:20 PM <i>Coffee Break</i>				
3:20 PM – 3:40 PM	Multiomic integration reveals regulatory function of GWAS variants within transposable elements in brain aging Sreejato Chatterjee, University of Rochester	MolGene-E: inverse molecular design to modulate single cell transcriptomics Rahul Ohlan The City University of New York	STITCH: A Platform-Agnostic Pipeline for Barcoding-Based Spatial Transcriptomics Leo Liu Mayo Clinic	 Sunny Lowel Brock University
			Strategies for Robust, Accurate, and Generalizable Benchmarking of Drug Discovery Platforms Melissa Van Norden University at Buffalo	 Alex Mao Winston Churchill High School
				 Emma K. Molnar Waterford School
				 Christina Teng Thomas S. Wootton High School
				 Alexander Wu Arizona State University

3:40 PM – 4:00 PM	metaSRNA: a unified framework for reprocessing bacterial data from microrna sequencing protocols and drafting bacterial small RNA catalogs Mengyuan Zhou University of Nebraska Lincoln	Dysregulated intercellular communication and signaling pathways across brain regions in Alzheimer’s disease Hani Alostaz UTHealth Houston	Scalable and Reproducible Software for Microbiome Data Analysis Andres Benavides Arevalo Universidad Industrial de Santander MetaAge: A Highly Accurate Ensemble Machine Learning Model for Biological Age Estimation Liguo Wang Mayo Clinic	
4:00 PM – 4:20 PM	SPLISUM: spectral prediction and library searching for untargeted metabolomics Chhavi Thakur Indiana University, Bloomington	EVTS: a topology-aware metric for evaluating RNA velocity embeddings in single-cell transcriptomics Xiuquan Wang Tougaloo College	Building a Psychoplastogenic Signature: A Comparative Evaluation of Compound-Based and Target-Based Approaches in the CANDO Platform Justin Shinkle University at Buffalo Benchmarking Variation Detection Methods with Linear Reference Genomes and Pangenomes in Grapevines Brooke Atamanyk Brock University	Austin Xu Williamsville East High School Shaoyu Xu Shanghai World Foreign Language Academy Adrian Z. Yang Lawrence E. Elkins High School Henry Yang Sage Hill School
4:20 PM – 4:40 PM	Celltamine: a bioinformatic pipeline for rapid detection of pathogenic microorganisms Ahmad Salman Sirajee Rutgers University, New Brunswick	STEP: Spatial Transcriptomics Embedding Procedure for Multi-scale Biological Heterogeneities Revelation in Multiple Samples Xiaojiang Xu Tulane University		Alina Yu Germantown Friends School
Flash Talks Chair: Jun Wan		Flash Talks Chair: Zhaohui Xu, Xiaojiang Xu	Flash Talks Chair: Shengyu Li	

4:40 PM – 4:50 PM	Cross-species gene set and cell type annotation through large language models and agentic AI with literature-grounded validation Wenbo Chen UTHealth Houston	SomAtt: a foundation model for the tumor genome Avinash D Sahu University of New Mexico	Improved drug discovery through accurate prediction of adverse drug reactions within the CANDO platform Vida Bodaghi-Namileh University at Buffalo	Daniel Zhang Canyon Crest Academy -----
4:50 PM – 5:00 PM	Drug-drug interaction prediction using proteomic scale signatures within the CANDO platform Lucille Tomin University at Buffalo	AI-based Characterization of Alzheimer’s Disease Phenotypes from population scale single cell data Chenfeng He University of Wisconsin- Madison	Prevalence and Genetic Determinants of Chronic Diseases in a University Student Population: A Cross-Sectional Analysis with International Comparisons Afagh Bapirzadeh Islamic Azad University Pre-recording	Simon Zhang Lexington High School -----
5:00 PM – 5:10 PM		FACET: criterion- anchored semantic phenotype matching with a guarded LLM for DSM- 5-TR face validity of psychiatric mouse models An Le SUNY Upstate Medical University	AI in Fast Detection of Diseases Zarrin Minuchehr National Research Institute of Genetic Engineering and Biotechnology, Tehran- Karaj Highway Pre-recording	Eva Zhao Middlesex school ----- Katherine Zhou Choate Rosemary Hall -----
5:10 PM – 5:20 PM	Single-Cell viral detection from unmapped scRNA-seq reads Mohammadamin Mahmanzar University of Hawaii at Manoa			Shashvat Hariharan Linganore High School

Wednesday, August 5th, 2026

8:00 AM – 5:00 PM	Registration
8:30 AM – 9:10 AM	Keynote Lecture: Digital Tissue Twins: Shaping the Future of Precision Medicine Mingyao Li, PhD (Room 2220A&B)
9:10 AM –	Award Ceremony (Room 2220A&B)

9:50 AM			
CONCURRENT SESSIONS/WORKSHOPS			
Room 2220A&B		Room 2213A	Room 2213B
Computational Drug Discovery and Therapeutic Modeling Chair: Zackary Falls		Multi-omics, AI, and the Future of Precision Health Chair: Yuanyuan Fu	Emerging BioHealth and Environmental Frontiers Chair: Jane Ohia
9:50 AM – 10:10 AM	KGPredict-Com: a knowledge graph model for drug combination prediction Zhenxiang Gao Case Western Reserve University	From Genetic Susceptibility to Modifiable Biology: Multi-Omic and Dietary Integration Toward Precision Alzheimer’s Disease Prevention Yuxi Liu Harvard T.H. Chan School of Public Health	Weakly-supervised topology-preserving 3D mitochondria segmentation Elliott Seo Stony Brook University,
10:10 AM – 10:30 AM	Sparsity, structure, and interpretability in biologically informed neural networks for drug response prediction Jason Chia Purdue University & Argonne National Laboratory	Evaluation of statistical differential analysis methods for identification of senescent cells using single-cell transcriptomics Dongmei Li University of Rochester	Learning-Augmented Resource Allocation for Healthcare Scheduling Fei Li George Mason University
10:30 AM – 10:50 AM	A DALEX-based explainable ai framework for lymphography prediction Zoom Tapas Si University of Engineering & Management, Jaipur	TRACED: A Graph-Based Algorithm to Infer Single-cell Time-lagged Gene Regulation Yang Yu Boston Children’s Hospital	Hyperspectral deep learning for compositional classification of municipal solid waste: an environmental health informatics application Jason Li Westwood High School
10:50 AM – 11:10 AM <i>Coffee Break</i>			
11:10 AM – 11:30 AM	TransGen: de novo enzyme design via catalytic-conditioned sequence generation Zoom Hongming Cai South China University of Technology	Risk-stratified hepato-pancreato-biliary cancer screening with self-evolving trustworthy AI Zoom He Ren The Affiliated Hospital of Qingdao University	XLCenter: crosslink-induced truncation site identification reveals sequence and structural specificities of RNA binding protein motifs Yuping Zhang University of Connecticut
11:30 AM – 11:50 AM	DrugPTM-Bench: a large-scale dataset for predictive modeling of drug-induced cell type-specific protein post-translational modifications	Genetic heterogeneity underlying breast cancer subtypes: genetic epidemiologic investigations to disentangle disease complexity	Machine learning-derived subtypes of autism reveal distinct genetic contributions from common and rare variants Zoom

	Zoom Amitesh Badkul City University of New York	Xiang Shu Memorial Sloan Kettering Cancer Center	Chang Shu University of Southern California
11:50 AM – 12:10 PM	From generalist to specialist: evolution of PS2 α-integrins and implications for drug targeting Shixi Sun Arizona State University	Leveraging gene-environment interactions to understand colorectal cancer risk Mulong Du Nanjing Medical University	
12:10 PM – 12:30 PM	A reproducible hybrid QSPR- machine learning framework integrating graph-theoretic and cheminformatics descriptors for anticancer drug property prediction Zoom H Muhammad Fraz COMSATS University Islamabad & Riphah International University	Beyond exposure: computational calibration and ancestry-aware genetics of skin carotenoid spectroscopy for precision nutrition Yixing Han National Institutes of Health (NIH)	
12:30 PM – 12:40 PM	Closing Remarks (Room 2220A&B)		