

9TH ANNUAL MIDATLANTIC BIOINFORMATICS CONFERENCE

AN IN-PERSON LIVE NETWORKING EVENT

October 4, 2024

HOSTED BY



AGENDA

8:30 AM

Welcome

Yi Xing, PhD

Executive Director, Department of Biomedical and Health Informatics
Children's Hospital of Philadelphia

Marylyn Ritchie, PhD

Director of the Institute for Biomedical Informatics (IBI)
University of Pennsylvania Perelman School of Medicine

8:45 AM - 9:30 AM

Keynote Presentation #1: Eytan Ruppin, MD,PhD

Chief, Cancer Data Science Laboratory

Head, Computer Precision Oncology Section

National Institutes of Health - National Cancer Institute

9:30 AM – 10:00 AM

Qian Cong, PhD

Assistant Professor

Southwestern Medical Foundation Scholar

University of Texas Southwestern Medical Center

10:00 AM – 10:15 AM

Morning Break

10:15 AM – 10:45 AM

Jiyang Yu, PhD

Associate Member, St. Jude Faculty

Interim Chair, Department of Computational Biology

St. Jude Children's Research Hospital

10:45 AM – 11:15 AM

Glennis Logsdon, PhD

Assistant Professor

Genetics

Core Member, Epigenetics Institute

University of Pennsylvania

Perelman School of Medicine

AGENDA CONT'D

11:15 – 11:45 AM	<p><i>Poster Lightning Round (3-minute Flash Presentations)</i></p> <ol style="list-style-type: none">1. <i>Shovan Bhowmik - University of Delaware</i>2. <i>Ian Chen - Children's Hospital of Philadelphia</i>3. <i>Pavel Kuksa, PhD - University of Pennsylvania</i>4. <i>Athylia Paremski - Children's Hospital of Philadelphia</i>5. <i>Colette Trouillot, MS - Drexel University</i>6. <i>Jonathan Perdomo - Children's Hospital of Philadelphia</i>7. <i>Yuhao Tan - University of Pennsylvania</i>8. <i>Akshatha Nayak - Penn State University</i>9. <i>Jing Hu, PhD - Children's Hospital of Philadelphia</i>10. <i>Michael Troka - University of Pennsylvania</i>11. <i>Christopher Sottolano - Children's Hospital of Philadelphia</i>
11:45 AM – 2:00 PM	<p><i>Break for Lunch Poster Networking Session Colket Translational Research Building</i></p>
2:00 – 2:45 PM	<p><u>Keynote Presentation #2: Feng Yu, PhD</u> Director, Institute for AI in Medicine Duane and Susan Burnham Professor of Molecular Medicine, Professor, Biochemistry and Molecular Genetics & Pathology Northwestern University</p>
2:45 - 3:15 PM	<p>Ashley Kiemen, PhD Assistant Professor, Pathology Johns Hopkins Institute for NanoBio Technology</p>
3:15 PM – 3:30 PM	<p>Afternoon Break</p>
3:30 PM - 4:00 PM	<p>Zhonghua Liu, PhD Assistant Professor Biostatistics Mailman School of Public Health Columbia University Data Science Institute</p>

4:00 PM - 4:30 PM

Saad Nadeem, PhD

Assistant Attending Computer Scientist
Memorial Sloan Kettering Cancer Center
Department of Medical Physics & Pathology
Stony Brook University

4:30 PM - 4:45 PM

Closing Remarks and Presentation of Trainee Awards

Mingyao Li, PhD

Professor of Biostatistics
Chair, Graduate Program in Biostatistics
Member Graduate Group, Genomics & Computational Biology
Dept. of Biostatistics, Epidemiology and Informtics
University of Pennsylvania

THANK YOU CONFERENCE OPERATIONS

Donna Vito, Outreach Manager

Ariana Downs, MS, Outreach Specialist

Hannah Lazarus, Research Coordinator

THANK YOU POSTER REVIEW COMMITTEE

Michael Xie, PhD, Children's Hospital of Philadelphia

Joseph Daniel Romano, PhD, Mphil, MA, University of Pennsylvania

Mark Porter, Children's Hospital of Philadelphia

Michael Xie, PhD, Children's Hospital of Philadelphia

Chloe Paris, PhD, University of Pennsylvania

Noor Dawany, PhD, Children's Hospital of Philadelphia

Asif Chinwalla, MS, MBA, Children's Hospital of Philadelphia

Alison Merikangas, PhD, Children's Hospital of Philadelphia

Conference Organizing Committee members also participate in poster reviews.

KEYNOTE SPEAKERS



Eytan Ruppin, MD, PhD

Chief, Cancer Data Science Laboratory
Head, Computational Precision Oncology Section
National Institutes for Health National Cancer Institute
Center for Cancer Research

Eytan Ruppin received his MD and PhD (Computer Science) from Tel-Aviv University where he has served as a professor of Computer Science & Medicine since 1995, conducting computational multi-disciplinary research spanning a wide variety of topics, including neuroscience, evolutionary computation, natural language processing, machine learning and systems biology. He joined the University of Maryland in July 2014 as a Computer Science professor and director of its center for bioinformatics and computational biology (CBCB), before joining the NCI in January 2018, where he founded and is Chief of its Cancer Data Science department. He is a member of the editorial board of EMBO Reports and Molecular Systems Biology, a fellow of the International Society for Computational Biology (ISCB), and is the recipient of the NCI Director award and the Delano Award for Computational Biosciences. Dr. Ruppin is also a co-founder of startup companies involved in precision medicine and cancer drug discovery. (Source: NIH National Cancer Institute)



Feng Yue, PhD

Director, Institute for Artificial Intelligence in Medicine
Center for Advanced Molecular Analysis
Duane and Susan Burnham Professor of Molecular Medicine
Professor of Biochemistry and Molecular Genetics and Pathology
Northwestern University Feinberg School of Medicine

Dr. Yue is the founding director of the Center for Cancer Genomics at the Robert H. Lurie Comprehensive Cancer Center of Northwestern University, director of the Center for Advanced Molecular Analysis at Northwestern Institute for Augmented Intelligence in Medicine, the Duane and Susan Burnham Professor of Molecular Medicine, Professor of Biochemistry and Molecular Genetics, and Professor of Pathology. He serves in the editorial board of Genome Research and is an associate Editor for Science Advances.

Dr. Yue's main research interest is epigenetic regulation and 3D genome organization in human cancer. His group has been using modern genomic technologies, machine learning, and CRISPR genome editing to identify biomarkers and investigate the impact of genetic variants. Dr. Yue has been an active member and leader of several large NIH-funded consortia, including the ENCODE, Roadmap/Epigenomics, and 4D Nucleome projects. He led the integrative analysis effort for the mouse ENCODE consortium. He serves as co-chair for the Integrative Analysis Workgroup in the 4D Nucleome Project and currently co-chairs the Steering Committee of the NIH Impact of Genomic Variation on Function Consortium (IGVF).

(Source: Northwestern University)

SPEAKERS



Qian Cong, PhD

Assistant Professor, Eugene McDermott Center for Human Growth and Development
Southwestern Medical Foundation Scholar in Biomedical Research
UT Southwestern Medical Center

Qian Cong is an assistant professor in the McDermott Center for Human Growth and Development at UT Southwestern. Dr. Cong's research focused on evolutionary genomics as a graduate student in the Grishin lab and worked on computational structure biology as a postdoctoral fellow in the Baker lab. Leveraging on expertise in genomics, evolution and protein structure modeling, Dr. Cong works on predicting protein-protein interaction (PPI) and modeling protein complex structures on a proteome-wide scale based on coevolution signal between proteins. The Cong Lab has been applying the methods they developed and the knowledge gained about genome and protein evolution to systems of biomedical importance. Going forward, through collaborations with other labs and establishing an experimental component in my lab, Dr. Cong wants to develop a research program to combine evolutionary perspectives, large-scale data, Deep Learning methods, and experimental validations to make biological discoveries about the functional mechanisms of human proteins and pathogenetic factors of infectious bacteria and viruses. (Source: UT Southwestern)



Jiyang Yu, PhD

Associate Member, St. Jude Faculty
Interim Chair, Department of Computational Biology
St Jude Children's Research Hospital

Dr. Yu's research is focused on developing data-driven systems biology algorithms to integrate bulk, single-cell, and spatial omics data to decipher these (re)wiring events and hidden drivers underpinning biological processes in health and disease. Ultimately, we aim to translate the hidden driver discoveries into therapeutic targets, biomarkers, and combination therapies for cancer and other disorders. He earned his undergraduate degree in Computer Science from Zhejiang University, China in 2006. He trained in Dr. Andrea Califano's laboratory at Columbia University 2008–2012 and earned his PhD degree in Biomedical Informatics. His studies were focused on integrating functional genomics with systems biology to discover drivers and therapeutic targets of human malignancies. After his PhD training, Dr. Yu joined Pfizer Oncology as a senior scientist to work on cancer precision medicine. In November 2016, Dr. Yu joined St. Jude as faculty in the Department of Computational Biology where he continues to pursue his passion for perfecting translational systems biology approaches to developing cancer treatment. (Source: St. Jude Children's Research Hospital)



Glennis Logsdon, PhD

Assistant Professor of Genetics
Core Member, Epigenetics Institute
University of Pennsylvania
Perelman School of Medicine

Dr. Logsdon is an Assistant Professor in the Department of Genetics and a Core Member of the Epigenetics Institute at the University of Pennsylvania Perelman School of Medicine. She performed her postdoctoral training at the University of Washington School of Medicine with Dr. Evan Eichler, where she studied the sequence, structure, and evolution of human centromeres using long-read sequencing and computational approaches. She is involved in several national consortia, including the Telomere-to-Telomere (T2T) consortium, Human Pangenome Reference Consortium (HPRC), and Human Genome Structural Variation Consortium (HGSVC). She also works with non-profit, patient-led organizations, such as Project 8p, to better understand complex structural variation in the human genome. Dr. Logsdon's laboratory uses a combination of long-read sequencing, innovative computational methods, and synthetic biology approaches to investigate the variation, evolution, and function of human centromeres, which are among the most dynamic and rapidly evolving regions in the human genome. (Source: University of Pennsylvania)



Ashley Keimen, PhD

Assistant Professor
Pathology
Johns Hopkins
Institute for NanoBiotechnology

Dr. Kiemen, PhD is an assistant professor in the computational division of the Johns Hopkins Department of Pathology. Her main research interest is understanding microanatomical invasion patterns of pancreatic cancer by using a unique 3D reconstruction technology of serial histological sections. She integrates deep learning tissue labelling techniques with MRI images, DNA sequencing, immunohistochemistry, spatial transcriptomics, and immunofluorescence to characterize pancreatic cancer tissues. She also helped to map the microanatomy of a diabetic pancreas, skin, heart, fallopian tubes, liver, and lungs.

She earned her BS in chemical engineering from the University of Michigan in 2016, her MS in philosophy from the London School of Economics and Political Science in 2017, and her PhD in chemical & biomolecular engineering from Johns Hopkins University in 2021.

(Source: Johns Institute for NanoBiotechnology)



Zhonghua Liu, PhD

Assistant Professor of Biostatistics
Mailman School of Public Health
Columbia University Data Science Institute

Dr. Zhonghua Liu obtained his doctorate in Biostatistics from Harvard University advised by Professor Xihong Lin. His current research interests include causal inference, semiparametric efficiency theory, machine (deep) learning theory and applications, statistical genetics/genomics, causal mediation analysis, Mendelian randomization. (Source: Columbia University Data Science Institute)



Saad Nadeem PhD

Assistant Attending Computer Scientist
Departments of Medical Physics and Pathology & Laboratory Medicine.
Memorial Sloan Kettering Cancer Center
Assistant Professor
Department of Applied Mathematics and Statistics, Stony Brook University
Biomedical Imaging Program, Weill Cornell Graduate School of Medical Sciences

Dr. Saad Nadeem is an Assistant Attending Computer Scientist in the Service for Predictive Informatics at Memorial Sloan Kettering Cancer Center with dual appointments in the Departments of Medical Physics and Pathology & Laboratory Medicine. He serves as an Advisory Board Member for the largest open-source industrial-academia MONAI (Medical Open Network for Artificial Intelligence) Consortium. He is also an Assistant Professor in the Department of Applied Mathematics and Statistics at Stony Brook University and in the Biomedical Imaging Program at Weill Cornell Graduate School of Medical Sciences. His research focuses on multimodal and multiscale integrative biomedical data analysis, spanning radiology, surgery, pathology, and molecular data, to improve patient outcomes. His lab is specifically focused on building user-friendly tools that seamlessly fit into the clinical workflows and facilitate accurate and timely diagnosis/prognosis/decision-making while aiding in novel biomarker discovery.

Poster Listing

- | | | |
|----|---|---|
| 2 | Judith Rodriguez MSc
Penn State University | Leveraging FracMinHash Containment for Genomic dN/dS Estimations |
| 3 | Aditya Lahiri PhD
Children's Hospital of Philadelphia | Standardization of Tumor Names in NIH-Clinical Trials Registry using Embedding Analysis |
| 4 | William Welsh PhD
Rutgers University
Robert Wood Johnson Medical School | Machine Learning Models to Accelerate the Discovery of Therapeutics for Digestive Cancers that Target the Orexin 1 Receptor |
| 5 | Saad Althabiti
University of Delaware | Prediction of Behavioral Determinants of Health Using Domain-Specific BERT Embeddings and BiLSTM: A Study on the MIMIC-III Dataset |
| 6 | Hannah Verdonk
Temple University | MSS: Codon models with Multiple classes of Synonymous Substitutions |
| 7 | William Welsh PhD
Rutgers University-Robert Wood Johnson Medical School | Machine Learning Accelerated Discovery of Novel Sigma-1 Receptor Antagonists as Therapy for Painful Diabetic Neuropathy |
| 8 | Ene Belleh MBA, MLIS
Children's Hospital of Philadelphia
(Jenna Luecke presenting) | Unveiling Insights: A Novel Framework for Scientific Data Discovery and Cataloging |
| 9 | Stephanie Hao MS
Boston University | PANDORA: An Advanced Computational Framework for Systems Immunology Utilizing Machine Learning |
| 10 | Omar Alharbi MS
University of Delaware | Leveraging BERT and BiLSTM-CRF for Enhanced Extraction of Adverse Drug Events in Clinical Notes |
| 11 | Lyla Atta
Johns Hopkins University | Gene count normalization in single-cell imaging-based spatially resolved transcriptomics |
| 12 | Hanying Yan MS
University of Pennsylvania | Benchmarking cell segmentation algorithms for neuron detection in Xenium spatial transcriptomics data |
| 13 | Amelia Schroeder MS
Children's Hospital of Philadelphia | Scaling up spatial transcriptomics for large-sized tissues: uncovering cellular-level tissue architecture beyond conventional platforms |
| 14 | Hossein Fazelinia PhD
Children's Hospital of Philadelphia | Urinary Peptide Profiling via MS-Based Proteomics to Identify High-Risk Neurogenic Bladder in Spina Bifida |
| 15 | Aditya Birla PhD
Rutgers University | Prediction of binding affinities for protein-peptide systems using SE(3) equivariant neural networks |

16	Shovan Bhowmik University of Delaware	A Generalizable Relation Extraction System for Mining Protein Post-Translational Modification from Literature
17	Ian Chen Children's Hospital of Philadelphia	African and European Cybrids Differ in Transcriptomes and Resistance to Oxidative Stress
18	Elijah Gunther PhD University of Pennsylvania	Gromov-Wasserstein for Protein Structure Alignment
19	Eden Teferedegn PhD Children's Hospital of Philadelphia	miRNAs in Multiple Sulfatase Deficiency as a Signature of Neurodegeneration
20	Pavel Kuksa PhD University of Pennsylvania	BTS is scalable Bayesian framework for prioritizing GWAS variants across >1,000s omics datasets
21	Jonathan Perdomo Children's Hospital of Philadelphia	Long-read based detection of large copy number variants with potential functional significance using the ContextSV structural variant caller
22	Hami Lee PhD Temple University	Understanding epigenetic biomarkers of Attention deficit hyperactivity disorder and co-occurring anxiety phenotypes: an epigenome-wide association studies
23	Sriya Potluri University of Pennsylvania	ImmunoPheno: A Data-Driven Bioinformatics Platform for the Design and Analysis of Immunophenotyping Experiments
24	Alexis Garofalo University of Pennsylvania	Comprehensive Analysis of Rare Genetic Variants in Hepatocellular Carcinoma Across Diverse Population Groups
25	Yuhao Tan University of Pennsylvania	Quantitative insights into antigen presentation: integrating immunopeptidomics and deep learning
26	Mingyao Pan MS University of Pennsylvania	TCR-HLA Interactive Network for HLA Typing prediction and Transplantation Matching
27	Weijun Zeng Rutgers University	Identification and Prioritization of Candidate Genes Influencing Aneuploidy During Meiosis Using PGT-A Data
28	David Zhang University of Pennsylvania	Leveraging genetic similarity to investigate genetic variations associated with electronic health record phenotypes in diverse patient biobanks

29	Manju Anandakrishnan University of Delaware	KSFinder 2.0 - A knowledge graph and deep learning model for predicting kinases of phosphorylated substrates at site level
30	Jason Liu Rutgers University	Systematic Assessment of Active Module Identification Algorithms
31	Nasreen Bano PhD School of Veterinary Medicine University of Pennsylvania	Unraveling YY1's mechanism in determining B-cell lineage commitment
32*	Milton Pividori PhD University of Colorado Anschutz Medical Campus	Integrating genetic studies with gene co-expression patterns highlights shared and distinct transcriptional mechanisms associated with asthma, COPD and asthma-COPD overlap (ACO) syndrome*
33	Athylia Paremski Children's Hospital of Philadelphia	Enabling Technology for the Study of Neuromotor Impairment: Naturalistic, MEG-Compatible 'Reach-to-Target' Imaging Paradigm
34	Robert Hu University of Pennsylvania	Characterizing cell morphology and subcellular protein localization using optimal transport
35	James Kelley MS Rutgers University	Crowdsourcing With NJ High School Students for Validation of Novel Structural Variants in the IGH Locus of Myeloma Samples
36	Quan Nguyen University of Pennsylvania	Task-specific fine-tuning of Large Language Models facilitates clinical interpretation of somatic variants for precision oncology
37	Anil Wadhvani MD, PhD University of Pennsylvania	DNA Methylation Distinguishes Primary Age-Related Tauopathy from Alzheimer's Disease.
38	Kushagra Goel Children's Hospital of Philadelphia	Characterization of Natural Killer Cell Subpopulations in the Blood of Congenital Heart Disease Patients Using Single-Cell RNA Sequencing
39	Karleena Rybacki University of Pennsylvania	FusionRank: A Machine Learning Framework for Annotating and Prioritizing Oncogenic Gene Fusions/Machine learning methods applied to single- and multi-level 'omics data
40	Milad Markhali University of Delaware	Enhanced Neural Cell Segmentation for Multiplexed Spatial Proteomics in Peripheral Somatosensory Ganglia
41	Shihong Max Gao PhD Janelia Research Campus Howard Hughes Medical Institute	Integrative Bioinformatics Support 4D Physiology Area in Janelia

42	Catherine Lalman MS Thomas Jefferson University	Mapping transcriptomic patterns that may underlie the fibrotic response to lens injury
43	Pamela Chansky Children's National Hospital; George Washington University	A Generative AI Approach to Predict Patient Response to Virus-Specific T-Cell Therapy
44	Neha Sindhu MS University of Delaware	An integrative proteotranscriptomic approach identifies new substrates and downstream pathways for ADAM9 in colorectal cancer cells
45	Sabrina Chunn Rowan University	Novel Probabilistic Model for Differential Gene Expression Analysis in RNA-seq Data Using DOTNB
46	Dana Mitchell PhD Children's Hospital of Philadelphia	Using genome-scale metabolic modeling to prioritize genetic variants in patients with rare mitochondrial disorders
47	Thomas Westbrook University of Pennsylvania	Plasma protein-based and polygenic risk scores serve complementary roles in predicting inflammatory bowel disease
48	Evangeline Williams MS Drexel University College of Medicine	Designing a Molecular Diagnostic for Chronic Otitis Media Using Bacterial Gene Expression Profiles
49	Akshatha Nayak Penn State College of Medicine	Quadrupia: Derivation of G-quadruplexes for organismal genomes across the tree of life
50*	Ioannis Mouratidis MS Penn State College of Medicine	kmerDB: A database encompassing the set of genomic and proteomic sequence information for each species
51	Nikol Chantzi Penn State College of Medicine	The repertoire of short tandem repeats across the tree of life
52	Chong Li MS Temple University	TRUHiC: Integrating transformer and U-2 Net models to enhance Hi-C data for 3D chromatin structure identification
53	Chuming Chen PhD University of Delaware	Combining Text-Mining and Knowledge Graph Approach to Inform Glycan Profile Optimization in Biopharmaceutical Manufacturing
54	Jing Hu PhD Children's Hospital of Philadelphia	Deep Learning Enables Recognition of Autoreactive Antibodies and Autoimmune Disease Signatures
55	Sathyanarayanan Vaidhyanathan Rutgers University	rRFtargetDB: a database of Ago1-mediated targets of ribosomal RNA fragments.

- 56** **Daniel Ringwalt MSE**
Johns Hopkins University Bayesian Regression for DNA Replication Timing
- 57** **Thaise Carneiro PhD**
University of Pennsylvania Impact of NRXN1 Deletions on Isoform Expression
- 58** **Kim Ha**
University of Pennsylvania Uncovering Genetic Mechanisms of Blood Cell Variation and Stroke Risk Using Advanced Statistical Approaches
- 59** **Aaryan Mahesh Sarnaik**
Pennsylvania State University An Exact SAT Formulation for Computing DCJ Distance between Two Genomes with Duplicate Genes
- 60** **Po-Lun Kung**
University of Pennsylvania Single cell transcriptomics reveals novel cytoskeletal regulators of in vitro blood cell formation
- 61** **Madison Dautle MS**
Rowan University scTIGER2.0: A Deep Learning-based Method for Inferring Cell-specific Gene Regulatory Networks from scRNA-seq Data
- 62** **Taha Mohseni Ahooyi PhD**
Children's Hospital of Philadelphia Improved Prediction of Gene Essentiality by Integrating Graph Embeddings and Gene Intolerance Metrics
- 63** **Michael Troka**
University of Pennsylvania School of Dental Medicine TrokaChatML: A machine learning model for disease-driving cell-cell communication discovery in scRNAseq data
- 64*** **Khoa Huynh**
Virginia Commonwealth University Advancing Multimodal Spatial Biology: TACIT's Unveiling of Immune Microenvironments in Health and Disease
- 65** **Qianxuan (Sean) She MS**
University of Pennsylvania High transmission of Staphylococcus aureus in the neonatal intensive care unit predicts invasive infection
- 66** **Christopher Sottolano PhD**
Children's Hospital of Philadelphia Integrative Statistical Framework for Detecting Divergent Selection and Linking to Disease
- 67** **Dana Tango MPH**
University of Delaware Tales from the Crypts: HPV Gene Activity Bioinformatically Discovered at Healthy Tonsil/Translational Bioinformatics
- 68** **Haedong Kim PhD**
Children's Hospital of Philadelphia Exome-Wide Copy Number Variation in 106,744 Individuals from Autism Spectrum Families in the Simons SPARK Cohort
- 69** **Ada Metaxas**
Princeton University Predicting Thickening of the Carotid Artery in Young Adults Using DNA Methylation Measured in Childhood: The Future of Families and Child Wellbeing Cardiovascular Study
- 70** **Yusen Zhou PhD**
Children's Hospital of Philadelphia Single-cell analysis of patient-derived esophageal epithelial organoid model reveals cell state heterogeneity and a conserved differentiation hierarchy

71	Hanying Jiang University of Wisconsin-Madison	Enhancing High-Dimensional Mediation Analysis with an Adaptive-LASSO Approach: Causal Pathways Selection in Complex Biological systems.
72	Connor Pitman Rutgers University	Coevolution analysis incorporating contiguous hydrophobicity via the blobulator
73	Mudassir Lodi Rutgers University	Identifying Risk Genes Associated with Neural Progenitor Cell (NPC) Hyperproliferation in Macrocephalic ASD Patients
74*	Katarzyna Tyc PhD Virginia Commonwealth University	TACIT: A Novel Algorithm for Precise Cell Type Identification in Spatial Omics
75	Ilya Tyagin University of Delaware	Dyport: Dynamic Importance-based Biomedical Hypothesis Generation Benchmarking Technique
76	Shunzhou Jiang MS University of Pennsylvania	Reconstructing refined spatial tissue architecture in single-cell RNA-seq with REPAIR
77	Yiyun Rao Penn State	Understanding Genetic Variation and Evolutionary Landscape in Kinase P-loop
78*	Katherine Beigel MS Children's Hospital of Philadelphia	Human intestinal smooth muscle stretching rapidly induces proinflammatory phenotypes potentially altering signaling to adjacent cells
79	Dana Tango MPH University of Delaware	Medical Comorbidities in Depression and Bioinformatic Applications: Creation of a Knowledge Map/Translational Bioinformatics and Visualization and Visual Analytics of Biological and Health Data
80	Xinyi Zhao MS Columbia University (Cong Liu presenting)	Empowering Patients with AI: Integrating AI into Patient-Centric Healthcare Apps
81	Beoung Hun Lee University of Pennsylvania	Long-read sequencing on diverse populations identifies an association of a haplotype with two CAA interruptions in the CAG trinucleotide repeats of the ATXN2 gene
82	Erin Reichenberger PhD Children's Hospital of Philadelphia (Katherine Beigel presenting)	SWANS - A comparative single-entity workflow analysis pipeline
83	Colette Trouillot MS Drexel University	Combined bulk RNA-sequencing and single-cell RNA-sequencing data reveals the role of FOXD3 in melanoma cell plasticity and phenotypic states

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|------------|--|--|
| 84 | Jamie Catalano PhD
Children's Hospital of Philadelphia | Genetic Insights into Cerebral Palsy: A Comprehensive GWAS and Functional Enrichment Study |
| 85 | Ben Stear MS
Children's Hospital of Philadelphia | A GraphRAG pipeline for quantitative data retrieval using a large-scale biomedical knowledge graph |
| 86 | Simon Cole
Penn Neurodegeneration
Genomics Center | CHARMER: An end-to-end pipeline for detecting high-confidence chromatin regulatory interactions across multiple cell types/tissues |
| 87* | My Nguyen
Virginia Commonwealth University | Improving prediction of 3D chromatin structures (Topologically Associating Domains) |
| 88 | Tianhao Luo
University of Pennsylvania | Rectifying Batch Effect in Histology Images for Imputing Super-pixel Gene Expressions in Spatial Transcriptomics |
| 89 | Pamela Mishra MS
Children's Hospital of Philadelphia | Correlation of bulk RNA-Seq and CHIP-Seq in neuroblastoma reveals signature types. |
| 90 | Glenn Mersky MS
Thomas Jefferson University | A classifier to identify melanoma cell states in mouse cell lines to better model human disease |

*Poster accepted, but not being presented.

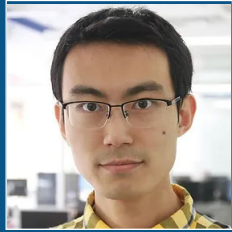
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2023 Conference Chair

Mingyao Li, PhD

Associate Professor of Informatics
Institute of Biomedical Informatics,
Associate Director of Informatics, Immune Health,



2024 Conference Co-Chair

Bo Li, PhD

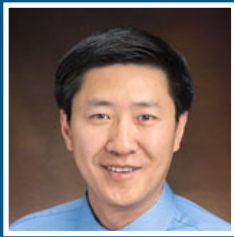
Associate Professor Computational
Immunology Perelman School of
Medicine University of Pennsylvania
Children's Hospital of Philadelphia

Conference Committee



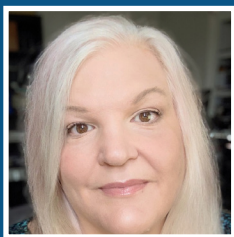
Laura Almasy, PhD

Professor of Genetics
Children's Hospital of Philadelphia
University of Pennsylvania Perelman School of Medicine



Kai Tan, PhD

Professor of Pediatrics
University of Pennsylvania Perelman School of Medicine
Director, Center for Single Cell Biology
Children's Hospital of Philadelphia



Deanne Taylor, PhD

Director, Bioinformatics
DBHi Children's Hospital of Philadelphia
Research Assistant Professor
University of Pennsylvania Perelman School of Medicine



Kai Wang, PhD

Associate Professor of Pathology and Laboratory Medicine
Children's Hospital of Philadelphia
University of Pennsylvania Perelman School of Medicine



Yi Xing, PhD

Executive Director
DBHi Children's Hospital of Philadelphia
Professor, Pathology and Laboratory Medicine
University of Pennsylvania Perelman School of Medicine



Wanding Zhou, PhD

Assistant Professor of Pathology and Laboratory Medicine
University of Pennsylvania, Children's Hospital of Philadelphia
University of Pennsylvania Perelman School of Medicine
University of Pennsylvania Perelman School of Medicine

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Derek Oldridge, MD, PhD

Assistant Professor of Pathology and Laboratory Medicine
Perelman School of Medicine
University of Pennsylvania
Assistant Director
Immunogenetics Laboratory
Children's Hospital of Philadelphia



Priya Sivaramakrishnan, MSc, PhD

Assistant Professor
Perelman School of Medicine
University of Pennsylvania
Children's Hospital of Philadelphia



Rebecca Ganetsky, MD

Assistant Professor of Pediatrics
Perelman School of Medicine
University of Pennsylvania
Division of Human Genetics
Children's Hospital of Philadelphia



Xinghua Mindy Shi, PhD

Associate Professor
Department of Computer & Information Sciences
College of Science and Technology
Temple University