

8TH ANNUAL MIDATLANTIC BIOINFORMATICS CONFERENCE

AN IN-PERSON LIVE NETWORKING EVENT

COMPUTATIONAL APPROACHES TO
DIFFERENTIATION IN DISEASES

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: Mona Singh, PhD

Professor, Computer Science

Lewis Sigler Institute for Integrative Genomics
Princeton University

9:30 AM – 10:00 AM

Jian Zhou, PhD

Assistant Professor, Bioinformatics
Department of Biostatistics
University of Texas Southwestern

10:00 AM – 10:15 AM

Morning Break

10:15 AM – 10:45 AM

Mingyao Li, PhD

Professor, Biostatistics

Chair, Graduate Program in Biostatistics

Member, Graduate Group in Genomics and Computational Biology

Dept. of Biostatistics, Epidemiology and Informatics

University of Pennsylvania

10:45 AM – 11:15 AM

Obi Griffith, PhD

Associate Professor

Department of Medicine

Department of Genetics

McDonnell Genome Institute

Washington University St. Louis

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. Yonghyun Nam, University of Pennsylvania2. Carlos Castelan Angel, Columbia University3. Kyle Coleman, University of Pennsylvania4. Krishnamurthy Subramanian, Rutgers University5. Sora Yoon, University of Pennsylvania6. Da Wu, Children's Hospital of Philadelphia7. Annie Abioye, University of Pennsylvania
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: Mark Gerstein, PhD</u> Professor Biomedical Informatics, Molecular Biophysics & Biochemistry, Computer Science, Statistics & Data Science Yale University</p>
2:45 - 3:15 PM	<p>Beth Cimini, PhD Senior Group Leader Cimini Lab Broad Institute Harvard University Massachusetts Institute of Technology</p>
3:15 PM – 3:30 PM	<p>Afternoon Break</p>
3:30 PM - 4:00 PM	<p>Li Shen, PhD Professor Informatics University of Pennsylvania Department of biostatistics, Epidemiology, and Informatics Perelman School of Medicine University of Pennsylvania</p>

4:00 PM - 4:45 PM

Keynote Presentation: David Baker, PhD

Professor
Biochemistry
Director, Institute for Protein Design
University of Washington

4:45 PM - 5:00 PM

Closing Remarks and Presentation of Trainee Awards

Bo Li, PhD
Associate Professor
Computational Immunology
Perelman School of Medicine
University of Pennsylvania
Children's Hospital of Philadelphia

THANK YOU CONFERENCE OPERATIONS

Donna Vito, Outreach Manager

Ariana Downs, MS, Outreach Specialist

Hannah Lazarus, Research Coordinator

THANK YOU POSTER REVIEW COMMITTEE

Sharon Diskin, 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

Iain Matheson, PhD, University of Pennsylvania

Noor Dawany, PhD, Children's Hospital of Philadelphia

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

Ana Cristancho, MD, PhD, Children's Hospital of Philadelphia

Ramakrishnan Rajagopalan, Children's Hospital of Philadelphia

KEYNOTE SPEAKERS



Mona Singh, PhD

Professor
Computer Science
Lewis Sigler Institute for
Integrative Genomics

Mona Singh is a professor of computer science and the Lewis Sigler Institute for Integrative Genomics. She has been on the faculty at Princeton University since 1999. She received her A.B. and S.M degrees from Harvard University, and her Ph.D. from MIT, all three in computer science. She works broadly in computational molecular biology, as well as its interface with machine learning and algorithms. Much of her work is on developing algorithms to decode genomes at the level of proteins and she is especially interested in developing data-driven methods for predicting and characterizing protein sequences, functions, interactions and networks, both in healthy and disease contexts. Among her awards are the Presidential Early Career Award for Scientists and Engineers (PECASE) in 2001, and the Rheinstein Junior Faculty Award from Princeton's School of Engineering and Applied Science in 2003. She was named a Fellow of the ACM in 2019, and of the ISCB in 2018. (Source: Princeton University)



Mark Gerstein, PhD

Albert L Williams Professor of Biomedical Informatics
Professor of Molecular Biophysics & Biochemistry of Computer Science, and of Statistics & Data Science
Yale University

After graduating from Harvard with an A.B. in physics in 1989, Prof. Mark Gerstein earned a doctorate in theoretical chemistry and biophysics from Cambridge University in 1993. He did postdoctoral research in bioinformatics at Stanford University from 1993 to 1996. He came to Yale in 1997 as an assistant professor and in 2003 became co-director of the Yale Computational Biology and Bioinformatics Program. Gerstein has published appreciably in the scientific literature, with an H index of ~185 and >600 publications in total, including a number of them in prominent venues, such as Science, Nature, Cell, and Scientific American. His research is focused on biomedical data science, and he is particularly interested in machine learning, macromolecular simulation, human genome annotation & disease genomics, and genomic privacy. (Source: Yale University)



David Baker, PhD

Henrietta and Aubrey Davis Endowed Professor in Biochemistry
Director, Institute for Protein Design
University of Washington

Dr. Baker's research group is focused on the design of macromolecular structures and functions.

He received his Ph.D. in biochemistry with Randy Schekman at the University of California, Berkeley, and did postdoctoral work in biophysics with David Agard at UCSF. Dr. Baker has published over 550 research papers, been granted over 100 patents, and co-founded 17 companies. Over 70 of his mentees have gone on to independent faculty positions. Dr. Baker is a member of the National Academy of Sciences and the American Academy of Arts and Sciences. He is also a project leader with The Audacious Project.

Dr. Baker has received awards from the National Science Foundation, the Beckman Foundation, and the Packard Foundation. He is the recipient of the Breakthrough Prize in Life Sciences, The Wiley Prize in Biomedical Sciences, Irving Sigal and Hans Neurath awards from the Protein Society, the Overton Prize from the ISCB, the Feynman Prize from the Foresight Institute, the AAAS Newcomb Cleveland Prize, the Sackler Prize in Biophysics, and the Centenary Award from the Biochemical Society. (Source: University of Washington)

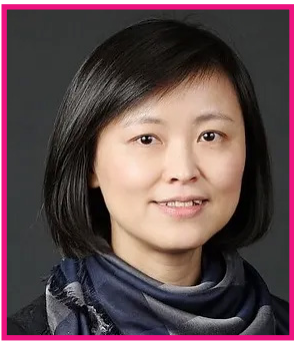
SPEAKERS



Obi Griffith, PhD

Associate Professor
Department of Medicine
Department of Genetics
McDonnell Genome Institute
Washington University St. Louis

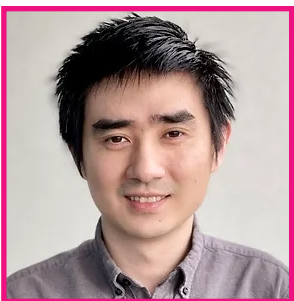
Dr. Griffith is Associate Professor of Medicine (Oncology) and Genetics and Assistant Director of the McDonnell Genome Institute at Washington University. Dr. Griffith's research is focused on the development of personalized medicine strategies for cancer. He develops bioinformatics tools and methods for the analysis of high throughput sequence data and identification of biomarkers for diagnostic, prognostic and drug response prediction. Dr. Griffith is President of the Cancer Genomics Committee, on the Steering Committee for the Global Alliance for Genomic Health, and co-chair of the Variant Interpretation for Cancer Consortium. He has published over 100 studies, received numerous research awards and honors and held several large grants from the NIH including a K22 Transition Career Development Award, U01/U24 for Development of Informatics Technologies for Cancer Research, and others. He has mentored more than 50 bioinformatics trainees and taught hundreds more as an Instructor for Cold Spring Harbor Laboratories and the Canadian Bioinformatics Workshops. (Source: Washington University St. Louis)



Mingyao Lee, PhD

Professor of Biostatistics
Chair, Graduate Program in Biostatistics
Member, Graduate Group in Genomics and Computational Biology

Dr. Mingyao Li joined the Biostatistics faculty in 2006. She is also a faculty member of the Genomics and Computational Biology graduate program. Her main research area is statistical genetics and genomics. The central theme of her current research is to use statistical and machine learning approaches to understand cellular heterogeneity in human disease relevant tissues, to characterize gene expression diversity across cell types, and to study the patterns of cell state transition and crosstalk of various cells using data generated from single-cell transcriptomics studies. In addition to methods development, Dr. Li is also interested in collaborating with researchers seeking to identify complex disease susceptibility genes. Her collaborative research includes cardiometabolic diseases, age-related macular degeneration, Alzheimer's disease, chronic kidney disease, type 1 diabetes, and cancer. Findings from her research will seed cell-specific functional studies, in vivo modeling, and precision therapeutic targeting of human diseases. Dr. Li actively serves in the scientific community. She is an Associate Editor of Statistics in Biosciences, and was a regular member of the Genomics, Computational Biology and Technology study section and a member of the review committee of the Center for Inherited Disease Research of the NIH. (Source; University of Pennsylvania)



Jian Zhou, PhD

Assistant Professor
Bioinformatics
Lupe Murchison Foundation Scholar in Medical Research

Since November 2019, Jian Zhou has been appointed as Assistant Professor in the Lyda Hill Department of Bioinformatics. He is a Lupe Murchison Foundation Scholar in Medical Research and is a Scholar of the Cancer Prevention and Research Institute of Texas (CPRIT). Prior to joining UTSW, he was a Flatiron Research Fellow at the Center of Computational Biology at Flatiron Institute, New York. He received his B.S. in Biological Sciences from Peking University and Ph.D. in Quantitative and Computational Biology from Princeton University.

The Zhou lab works at the intersection of machine learning and genomics. The lab develops computational methods to improve our understanding of genome-based regulation and the genetic basis of human health and diseases. Advancing machine learning and AI methods for science, especially genomics is a long-term goal of the lab. Visit the lab website for more details <https://zhoulab.io>. (Source: UT Southwestern)



Beth Cimini, PhD

Professor
Department of Biostatistics
Columbia University

Beth Cimini leads the Cimini Lab within the Imaging Platform of the Broad Institute. Her team works with biologists to help them create image analysis workflows and makes the open-source image analysis software CellProfiler. In 2020, she was named a CZI Imaging Scientist for her work on making open-source image analysis tools more accessible to the bioimaging community and for her creation of a postdoctoral training program in bioimage analysis.

Cimini's lab started at the Broad in 2021, after 5 years as a postdoc then computational biologist in Anne Carpenter's lab at the Broad Institute. She holds a PhD in biochemistry and molecular biology from the Blackburn Lab at the University of California-San Francisco and a BA in biochemistry and molecular biology from Boston University.

Dr. Cimini's laboratory is best known for our popular open source software CellProfiler and CellProfiler Analyst. (Source: Broad Institute)



Li Shen PhD

Professor
Director of Folding@home
Department of Bioengineering and Biochemistry
University of Pennsylvania

Dr. Li Shen is a Professor of Informatics in the Department of Biostatistics, Epidemiology and Informatics at the Perelman School of Medicine in the University of Pennsylvania. He also holds a secondary appointment in the Department of Radiology. He is a Senior Fellow at the Penn Institute for Biomedical Informatics and the Leonard Davis Institute of Health Economics. He obtained his Ph.D. degree in Computer Science from Dartmouth College.

Dr. Shen's research interests include medical image computing, biomedical informatics, machine learning, network science, imaging genomics, multi-omics and systems biology, Alzheimer's disease, and big data science in biomedicine. He has authored over 300 peer-reviewed articles in these fields. His work has been continuously supported by the NIH and NSF. His current research program is focused on developing and applying informatics, computing and data science methods for discovering actionable knowledge from complex biomedical and health data (e.g., genetics, omics, imaging, biomarker, outcome, EHR, health care), with applications to complex disorders such as Alzheimer's disease.

Dr. Shen has served on a variety of scientific journal editorial boards, grant review committees, and organizing committees of professional meetings in medical image computing and biomedical informatics. He served as the Executive Director of the Medical Image Computing and Computer Assisted Intervention (MICCAI) Society between 2016 and 2019. He is a fellow of the American Institute for Medical and Biological Engineering (AIMBE), a distinguished member of the Association for Computing Machinery (ACM), and a distinguished contributor of the IEEE Computer Society. (Source: University of Pennsylvania)

Please review this list before attending the Poster Session to make the best use of the time during the session. Poster boards will be numbered in Colket Lobby.

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| 1 | Yonghyun Nam, PhD*
University of Pennsylvania | Network diffusion-based risk scoring models for coronary artery diseases in UK biobank individuals: Fusing polygenic impact of intermediate clinical factors on complex disease |
| 2 | Jonathan Perdomo
Children's Hospital of Philadelphia | ContextSV: A novel computational method for calling structural variants and integrating information across sequencing platforms |
| 3 | Melina Malkani
Bullis School | Top 15 Attributes for the Design of Advanced Health Dashboards |
| 4 | Tomer Lapidot, PhD
CHOP/UPenn | Spatial mapping of stress induced RNA binding protein localization changes using pooled gene tagging and optical sequencing |
| 5 | Rahul Shubhra Mandal, PhD
Perelman School of Medicine University of Pennsylvania | Impact of DNA repeat silencing on ATR inhibitor-driven genomic breaks |
| 6 | Stepan Nersisyan, PhD
Thomas Jefferson University | Characterization of all small RNAs in and comparisons across cultured megakaryocytes and platelets of healthy individuals and COVID-19 patients |
| 7 | Saishi Cui, MS
Drexel University | Mcadet: a feature selection method for fine-resolution single-cell RNA-seq data based on multiple correspondence analysis and community detection |
| 8 | Laine Marrah
University of Virginia | High-Performance Computing Predicts Double Minute Chromosomes in Cancer Cell Lines |
| 9 | Manju Anandakrishnan
University of Delaware | KSFinder - A knowledge graph model for link prediction of novel phosphorylated substrates of kinases |
| 10 | Krishnamurthy Subramanian*
Rutgers University | Identifying Chronic Tic Disorder subtypes using clinical diagnostic data |
| 11 | Karleena Rybacki
University of Pennsylvania | Assessing the expression of Long INterspersed Elements (LINEs) via long-read sequencing in diverse human tissues and cell lines |
| 12 | Xuexin Yu, PhD
Children's Hospital of Philadelphia | MitoTracer facilitates the identification of informative mitochondrial mutations and precise lineage reconstruction |
| 13 | Daniel Vo, MS
Perelman School of Medicine, University of Pennsylvania | Genetic and methylomic interrogation of brain cell-type shifts in autism, schizophrenia, and Alzheimer's disease |
| 14 | Rasika Venkatesh
University of Pennsylvania Perelman School of Medicine | Rare variants enhance the ability to identify associated phenotypes in disease networks |
| 15 | Vivek Sriram, MA
University of Pennsylvania | A network-based comparison of sex-stratified disease-variant associations reveals genotype-by-sex effects on cross-phenotype interactions in the UK Biobank |
| 16 | Lauren Mazur
Penn State College of Medicine | Association of surfactant protein genetic variants with risk of hospitalization in COVID-19 positive children |

*Lightning Talk Presenter

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17	Hongyi Zhang, PhD Children's Hospital of Philadelphia	Precise tracing of mitochondrial transfer between cancer and T cells at single cell resolution
18	Sora Yoon, PhD* University of Pennsylvania	Hi-Cociety: network-based approach for comparing chromatin architecture features
19	J. Carlos Castelan Angel* Columbia University, New York Genome Center	Enhancing Hi-C resolution data with computational construction of three-dimensional chromatin ensembles
20	Rohan Alibutud Rutgers University	Exploring the impact of structural variants on the genetic etiology of autism spectrum disorder and language impairments
21	Onyekachi Nwogu, MS The University of Cincinnati and Cincinnati Children's Hospital Medical Center	Antibody structure classification improves prediction of food allergen sensitization from immune repertoire sequencing data
22	Van Truong , MS University of Pennsylvania	Empowering Immunogenetic Analysis with Biofilter 3.0 via Enhanced Annotation and Filtering Capabilities
23	Michelle Gee University of Delaware and Thomas Jefferson University	Closed-loop modeling of central and intrinsic cardiac nervous system circuit dysfunction following myocardial infarction
24	Anni Moore University of Pennsylvania	Underlying pleiotropic connections between Alzheimer's Disease and its comorbidities may contribute to progression.
25	Thomas Roule, PhD Children's Hospital of Philadelphia	Regulation of Neuronal Maturation through EZH1-Driven H3K27me3 Deposition
26	Eunji Ha, PhD University of Pennsylvania	Multimodal profiling of chromatin accessibility and gene expression in single cells enables the identification of cellular signatures underlying the pathogenesis of chronic kidney disease/Single-cell sequencing and analyses
27	Annie Tran, MS Rowan University	Unveiling the Intricacies of HIV-1's gp120 and gp41 Glycoprotein Envelope Gene Evolution through a Novel Near-Neutral Balance Theory Approach
28	Da Wu, PhD* Children's Hospital of Philadelphia	MULTIMODAL MACHINE LEARNING COMBINING CLINICAL TEXTS AND FACIAL IMAGES IMPROVE DIAGNOSIS OF RARE GENETIC DISEASES
29	Kyle Coleman, MS* University of Pennsylvania	Analysis of Multi-modal Spatial Omics with MISO
30	Ene Belleh, MBA, MLS, AHIP-D Children's Hospital of Philadelphia	Data Archiving for Long-Term Research Sustainability
31	Sai Guna Ranjan Gurazada, MS University of Delaware	Exploring the promise of multi-omics and machine learning in modeling CHO cell productivity
32	No Poster	No Poster
33	Mohammad Erfan Mowlaei, MS Temple University	Improving Genotype Imputation Quality Through a Transformer Model

*Lightning Talk Presenter

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| 34 | Maxwell Konnaris
Penn State University | Nucleic Quasi-primers: Identification of the Shortest Unique Oligonucleotide Sequences in a Species |
| 35 | Nicholas Paradis, MS
Rowan University | Does the Evolutionary Nature of a Hemagglutinin and Neuraminidase Gene from Influenza A Virus (H3N2) Follow a Recently Proposed Molecular Evolution Theory: Near-Neutral Balanced Selectionist Theory(NNBST). |
| 36 | Syeda Aiman Nadeem
Rutgers - Camden | IDENTIFYING AND VALIDATING RECURRENT STRUCTURAL VARIANTS AFFECTING TUMOR GENOMES USING GROM AND VN |
| 37 | Nimay Kumar
University of Pennsylvania | ColoQuium: A software package for performing colocalization between QTL and GWAS analyses and visualizing colocalization results |
| 38 | Rachit Kumar
University of Pennsylvania | Bayesian Mixture Model for the Identification of Loci of Interest from GWAS Summary Statistics |
| 39 | Yong Chen, PhD
Rowan University | Inferring Gene Regulatory Networks from Case Versus Control scRNA-seq Datasets |
| 40 | Nikhil Damle
Rutgers University | The contribution of chromatin accessibility to the risk of inflammatory bowel disease in different populations |
| 41 | Hemma Murali
University of Pennsylvania, Children's Hospital of Pennsylvania | Leveraging predicted protein structures to improve the classification of genetic Variants of Uncertain Significance |
| 42 | Jason Liu
Rutgers University | Using PAPER to identify active modules in an aneuploidy dataset |
| 43 | Alexandra Manchel
Thomas Jefferson University | Genome-Scale Metabolic Modeling of Liver Metabolic Reprogramming in Alcoholic Hepatitis |
| 44 | Khushbu Patel, MS
Children's Hospital of Philadelphia | Pediatric Cancer Web Portal: From Data to Discovery, Enhancing Pediatric Cancer Research |
| 45 | Noah Peles
Temple University | Identification of adaptive sites in modern humans utilizing evolutionary probability |
| 46 | Jason Lamanna
Temple University | ProGenAT: Elevating VAE Protein Sequence Generation with Transformer-Driven Adversarial Training |
| 47 | Margaret Cassidy
University of Pennsylvania | RNA Velocity Reveals Altered RNA Processing Kinetics in Prenatal Hypoxic Cortex |
| 48 | Alyssa Pivrotto
Temple University | A comparison of allele age estimators on WGS and WES datasets |
| 49 | Katherine Beigel, MS
Children's Hospital of Philadelphia | Single-cell RNA sequencing of mouse periosteal cells suggests that Mitochondrial Transcription Factor A (TFAM) regulation of oxidative phosphorylation is important for bone balance modulation |
| 50 | Jingye Yang, PhD*
University of Pennsylvania
Children's Hospital of Philadelphia | Large language models for phenotype concept recognition from clinical notes on genetic diseases |
| 51 | James Kelley, MS
Rutgers University | Use of Machine Learning to Improve Accuracy of SV Calls |

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| 52 | Ankita Srivastava, PhD
Thomas Jefferson University | Expanding the pool of Transplantable Livers using Molecular profiling and Histopathological Analysis |
| 53 | Connor Pitman
Rutgers University -- Camden | The blobulator: visualizing hydrophobic domains for protein sequences |
| 54 | Austin Montgomery
Penn State College of Medicine | Utilizing nullomers in cell-free RNA for cancer detection |
| 55 | Katharina Hayer, MS
CHOP, Drexel | A Comprehensive Benchmark of Chromatin Loop Detection Methods |
| 56 | Aditya Lahiri, PhD
Children's Hospital of Philadelphia | A computational pipeline for comprehensive analysis of cancer, drugs, and target databases |
| 57 | Mudassir Lodi
Rutgers University | Investigating Genetic Risk Factors Associated with Autism Spectrum Disorder and Language Impairment Phenotypes |
| 58 | David Zhang
Perelman School of Medicine | Investigating ancestry-specific genetic variation in apolipoprotein L genes associated with electronic health record phenotypes in patient biobanks |
| 59 | Chong Li, MS
Temple University | Cataloging Structural Variants in the Human Genome: Impact on 3D Chromatin Structure and Gene Regulation |
| 60 | Mina Mahboubi, MS
Temple University | Effect of Epistasis on Phylogenetic Tree Shape |
| 61 | Rashid Al-Abri*
Columbia University | ScatTR: Monte Carlo Sampling for Long Tandem Repeat Length Estimation |
| 62 | Philip Gance
Rowan University | Navigating Zika Virus Evolution with the Unprecedented Near-Neutral Balanced Selection Theory: Illuminating Pathways for Effective Vaccines |
| 63 | Ronit Chakraborty
Lake Forest College | Analysis and Predictive Modeling of Anxiety and Depression Prevalence in the US Since the Onset of the COVID-19 Pandemic |
| 64 | Rima Zinjuwadia MS
Northeastern University | The Paradigm Shift in Tumor Immunology through Single Cell Technologies and Artificial Intelligence (AI). |
| 65 | Nigel Michki, PhD
Children's Hospital of Philadelphia | Identification of novel biomarkers using from peripheral blood mononuclear cells in people with Ataxia Telangiectasia |
| 66 | Neha Sindhu, MS
University of Delaware | An integrative proteotranscriptomic approach identifies new substrates and downstream pathways for ADAM9 in colorectal cancer cells |
| 67 | Bin Li
Temple University | Enhancing Fairness in Disease Prediction by Optimizing Multiple Domain Adversarial Networks |
| 68 | Theron Palmer
Johns Hopkins University School of Medicine | Evaluating splicing-derived neoantigen burden pan-cancer using SpliceMutr |
| 69 | Kelsey Zhu, MS
Children's Hospital of Philadelphia | Measure Intolerance to Mutation in Children with a Pediatric Condition |

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| 70 | Rawan Shraim, MS
Drexel University and The Children's Hospital of Philadelphia | IMMUNOTAR - Integrative Prioritization of Surface Proteins from Proteogenomic Data to Identify Novel Immunotherapeutic Targets for Cancer |
| 71 | Erin Theiller, MS
Children's Hospital of Philadelphia | Empowering Global Disease Surveillance: The CURED Tool for Rapid Identification of Unique Clonal Biomarkers |
| 72 | Ahmed Moustafa, PhD
Children's Hospital of Philadelphia, Perelman School of Medicine | Redcarpet: A Tool for Rapid Recombination Detection Amidst Expanding Genomic Databases |
| 73 | Thatchayut Unjitwattana, MS
University of Michigan | Cell origin deconvolution pipeline for scRNA-seq data |
| 74 | Daniel Ringwalt, MSE
Johns Hopkins University | Sparse PCA resolves Drosophila intestinal stem cell genomics in scRNA-seq |
| 75 | Jacob Fanale
Children's Hospital of Philadelphia | CytoMethIC: A Comprehensive R/Bioconductor Package for DNA Methylation-based Human Cancer Classification and Phenotyping |
| 76 | Eden Hornung
Thomas Jefferson University | Plasticity of cardiac vagal motoneurons in response to remote ischemic preconditioning |
| 77 | Hunter Gaudio
Children's Hospital of Philadelphia | Machine Learning Model Predicts the Likelihood of Achieving Return of Spontaneous Circulation During Cardiopulmonary Resuscitation Using the Hemodynamic Response to Vasopressor Administration |
| 78 | Wenkang Zhan
Temple University | E2EGAT: Interpretable graph attention networks for pathological stage prediction of prostate cancer |
| 79 | Mehwish Khan, MS
University Of Illinois Urbana Champaign | Investigating Cisplatin Hypersensitivity in Testicular Germ Cell Tumors and Molecular-Subtype Prediction using Deep Learning |
| 80 | Chen Song, PhD
Temple University | GenoDiffusion: Conditional Denoising Diffusion Model for Genomic Data Augmentation |
| 81 | William Flynn, MPH
Children's Hospital of Philadelphia | A Data Ecosystem for Provisioning Complex Clinical Datasets |
| 82 | Siddharth Bhadra-Lobo, MS
Rutgers University, Camden | SE(3)-Convolutional neural network molecular semantic inpainting on protein structure representations |
| 83 | Maryam Daniali, PhD
Children's Hospital of Philadelphia | Enriching representation learning using 53 million patient notes through human phenotype ontology embedding |
| 84 | Umair Ahsan, MS
Children's Hospital of Philadelphia | Detection of differentially methylated and imprinted regions using Oxford Nanopore sequencing |
| 85 | Thomas Brooks, PhD
University of Pennsylvania | Simulating correlated data for omics |
| 86 | Sen Yang, PhD
UT Southwestern Medical Center
Southern Methodist University | GCL-Omics: A Generalized Supervised Contrastive Learning Framework for Multi-Omics Integration |
| 87 | Laura, Prosser, PT, DPT, PCS
Children's Hospital of Philadelphia | Physical Therapy Database Development at Children's Hospital of Philadelphia: An Administrative Case Report |

*Lightning Talk Presenter

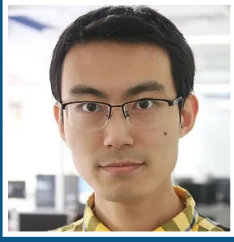


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| 88 | Annie Abioye*
Children's Hospital of Philadelphia | Interactions Between SNX14 and its Homologue SNX13 in Cerebellar Ataxia |
| 89 | Tom Reynolds, MFA, MBA
Children's Hospital of Philadelphia | A clinical data outcomes archive for patients presenting to a fetal center, a focus on efficiency and validity |
| 90 | Taha Mohseni Ahooyi, PhD
Children's Hospital of Philadelphia | MIS: A Multimodal Measure of Human Protein Intolerance to Functional Missense Variations |
| 91 | Jenny Li
University of Pennsylvania | Platform-robust DNA methylome-based cancer classification |
| 92 | Anushriya Subedy, MS
Rutgers University | Learning biology from data: Development of deep learning architectures for the prediction of biomolecular interactions in vivo |
| 93 | Evangeline Williams, MS
Drexel University College of Medicine | Maximally Diverse Haemophilus influenzae isolates Undergo Varied Transcriptional Responses during Biofilm Development |
| 94 | Nayelis Manon
University of Massachusetts Lowell | Rare Variant burden testing on neuroblastoma patients using public cohort as Controls. |
| 95 | David Goldberg
University of Pennsylvania, Children's Hospital of Philadelphia | KnowYourCG: automated discovery of biological and technical links from DNA methylation data |

*Lightning Talk Presenter

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2023 Conference Chairs

Bo Li, PhD
Associate Professor
Computational Immunology
Perelman School of Medicine
University of Pennsylvania
Children's Hospital of Philadelphia



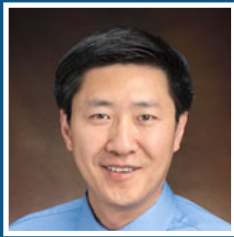
Co-Chair Conference Chairs

Dokyoon Kim, PhD
Associate Professor of Informatics
Institute of Biomedical Informatics,
Associate Director of Informatics, Immune Health,

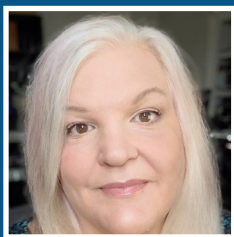
Conference Committee



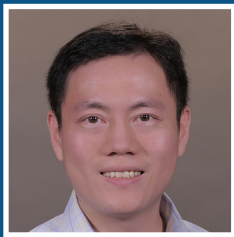
Laura Almasy, PhD
Professor of Genetics
Children's Hospital of Philadelphia
University of Pennsylvania Perelman School of Medicine



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



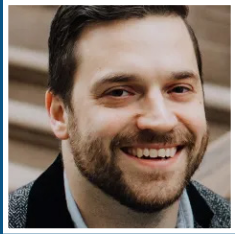
Wanding Zhou, PhD
Assistant Professor of Pathology and Laboratory Medicine
University of Pennsylvania, Children's Hospital of Philadelphia
University of Pennsylvania Perelman School of Medicine
University of Pennsylvania Perelman School of Medicine

THANK YOU TO OUR ORGANIZERS



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



Tristan Hayeck, PhD

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