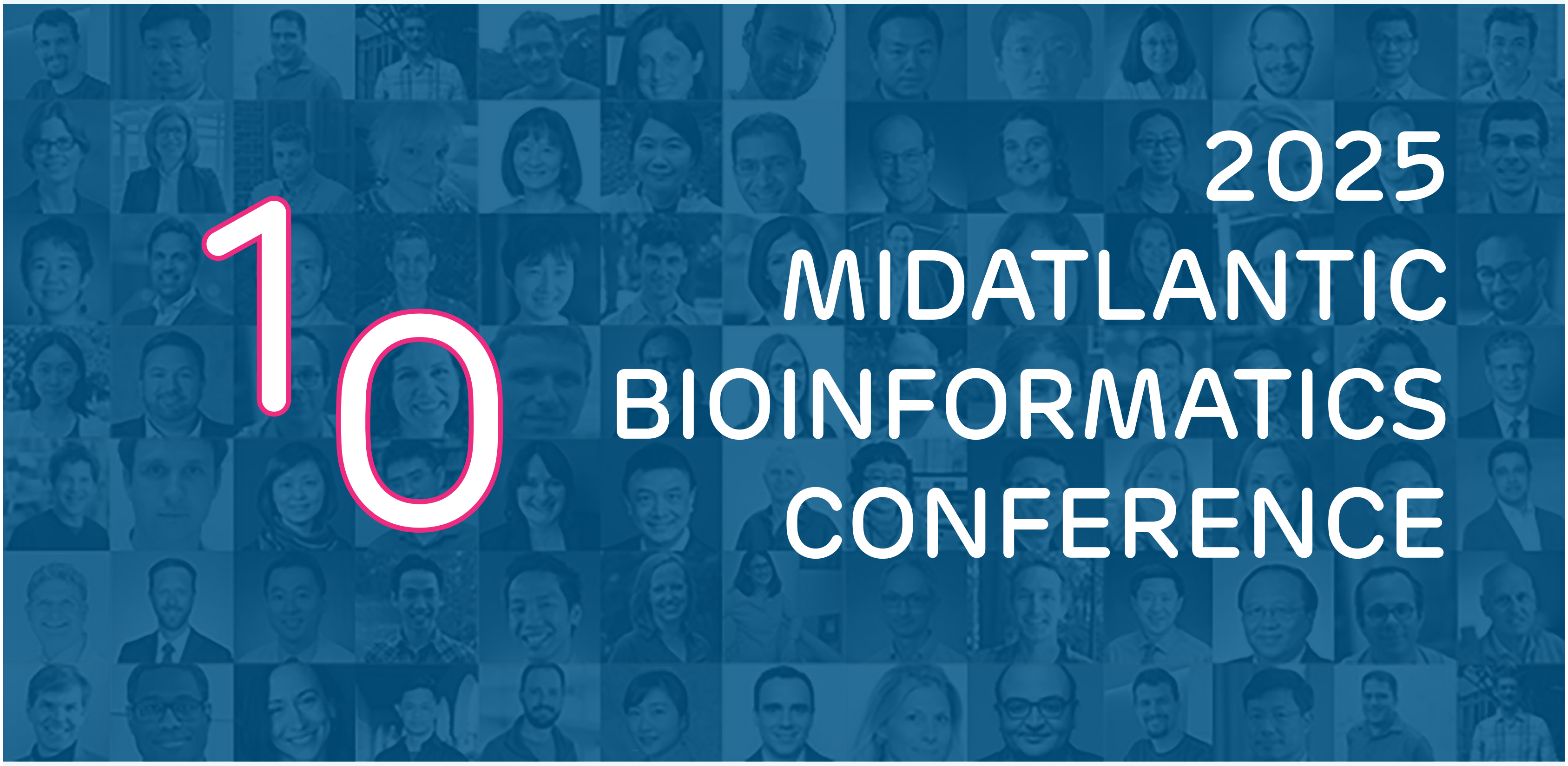


2025 MIDATLANTIC BIOINFORMATICS CONFERENCE

Children's Hospital of Philadelphia
Department of Biomedical & Health Informatics

Penn Institute for Biomedical Informatics

Thank you for attending the 10th Annual MidAtlantic Bioinformatics Conference.

We appreciate your continued support and commitment to advancing bioinformatics.

For Poster Session

Colket Address:
3501 Civic Center Blvd, Philadelphia, PA 19104

Wi-Fi Information:

Penn Employees: AirPennNet-Guest
(No password needed)

Guest: UPHS-GUEST
(Accept Terms & Conditions and submit form)

CHOP employees will be able to access CHOPNET from Colket.

Non-CHOP staff will use CHOP Guest.

For more information, please visit, www.midatlanticbioinformatics.org.

CONFERENCE AGENDA

8:30 AM
Conference Introduction/ Welcome
Yi Xing, PhD/Derek Oldridge, MD, PhD

8:45 AM
Keynote - Molly Przeworski, PhD
Columbia University

9:30 AM
David Van Valen, MD, PhD
CalTech

10:00 AM
Morning Break

10:15 AM
Tamar Sofer, PhD
Harvard University

10:45 AM
Aaron McKenna, PhD
Dartmouth University

11:15 AM
Lightning Talks

11:45 AM
Lunch Poster Session

2:00 PM
Keynote - Faisal Mahmood, PhD
Harvard University

2:45 PM
Ernest Turro, PhD
Icahn School of Medicine, Mt Sinai

3:15 PM
Afternoon Break

3:30 PM
Fei Zhang, PhD
Rutgers University

4:00 PM
Zhi Huang, PhD
University of Pennsylvania

4:30 PM
Closing Remarks/Trainee Award Presentation
Derek Oldridge, MD, PhD

4:45 PM
Adjourn

KEYNOTE SPEAKERS

Molly Przeworski, PhD
Professor
Center for Computational Biology and Bioinformatics
Mathematical Genomics
Columbia University

Dr. Molly Przeworski is currently a Professor of Biological Sciences and of Systems Biology. The focus of her work is in population genetics. Dr. Przeworski earned her BA in mathematics from Princeton University, her PhD in evolutionary biology from the University of Chicago, and completed a postdoc in the statistics department at the University of Oxford. Prior to joining Columbia in 2014, she was a researcher at the Max Planck Institute for Evolutionary Anthropology and on the faculty at Brown and the University of Chicago. She is the recipient of an Alfred P. Sloan fellowship, a Howard Hughes Medical Institute Early Career Scientist award, and the Rosalind Franklin Young Investigator award, and most recently elected a member of the National Academy of Sciences and American Academy of Arts and Sciences. Dr. Przeworski's research has contributed to a better understanding of how natural selection operates in humans and in other species and of how and why recombination and mutation processes evolve in vertebrates.

Faisal Mahmood, PhD
Associate Professor
Harvard Medical School
Brigham and Women's Hospital
Division of Computational Pathology

Dr. Mahmood is an Associate Professor of Pathology at Harvard Medical School and the Division of Computational Pathology at the Brigham and Women's Hospital. He received his PhD in Biomedical Imaging from the Okinawa Institute of Science and Technology, Japan and was a postdoctoral fellow at the department of biomedical engineering at Johns Hopkins University. His research interests include pathology image analysis, morphological feature, and biomarker discovery using data fusion and multimodal analysis.

The Mahmood Lab at the Brigham and Women's Hospital aims to utilize machine learning, data fusion and medical image analysis to develop streamlined workflows for cancer diagnosis, prognosis and biomarker discovery. They are interested in developing automated and objective mechanisms for reducing interobserver and intraobserver variability in cancer diagnosis using artificial intelligence as an assistive tool for pathologists. The lab also focuses on the development of new algorithms and methods to identify clinically relevant morphologic phenotypes and biomarkers associated with response to specific therapeutic agents. His lab develops multimodal fusion algorithms for combining information from multiple imaging modalities, familial and patient histories and multi-omics data to make more precise diagnostic, prognostic and therapeutic determinations.

SPEAKERS

David Van Valen, MD, PhD
Assistant Professor
California Institute of
Technology (CalTech)

Dr. David Van Valen is an Assistant Professor in the Division of Biology and Bioengineering at the California Institute of Tech ology. At Caltech, his research group develops new technologies at the intersection of imaging, genomics, and machine learning to produce quantitative measurements of living systems with single-cell resolution. David is the recipient of numerous awards, including the NIH New Innovator award. The Van Valen Lab seeks to understand how living systems and their respective viruses process information to understand both their internal state and the world around them using he latest advances in imaging, machine learning, and genomics to measure the interactions between viruses and their hosts.

Tamar Sofer, PhD
Associate Professor
Harvard T.H. Chan School
of Public Health

Dr. Tamar Sofer's research focuses on genetic and omics analyses of diverse and complex populations. She did her PhD in Biostatistics at the Harvard T.H. Chan School of Public Health and later became a research scientist at the Genetic Analysis Center at the University of Washington in Seattle. She moved to Brigham and Womens's Hospital and Harvard University, where she continues to develop and implement methodology for genetic and omics analyses of sleep, cognitive, cardiopulmonary, and metabolic phenotypes, with the goal of understanding the genetic basis of such phenotypes, and how environmental exposures modify the pathways from genotypes to phenotypes.

Aaron McKenna, PhD
Assistant Professor
Geisel School of Medicine
Dartmouth College

Dr. McKenna's lab is interested in how cells grow and divide to form complex structures, such as the transformation from the zygote to an adult human or from a transformed cell into a tumor mass. To study these processes, his team develops technologies to trace pattern of cell divisions which recovers the lineage of each cell. This information can be combined with other measures of cell state such as single-cell transcriptomic data to develop a rich picture of how choices are made in development and how this process is dysregulated in diseases such as cancer.

SPEAKERS

Ernest Turro, PhD
Associate Professor
Icahn School of Medicine

Dr. Ernest Turro is a biostatistician with extensive research experience in genetics, genomics, and molecular diagnostics. He has made important contributions towards understanding the genetic causes of rare hereditary disorders, particularly neurodevelopmental, hematological and immune disorders. He has also developed a number of influential statistical methods, including methods for inferring genetic associations with rare diseases and methods for modeling the expression and splicing of genes.

Fei Zhang, PhD
Associate Professor
Rutgers University

Dr. Fei Zhang is an associate professor at Rutgers University-Newark. Her research is focused on understanding how biological molecular building blocks self-assemble into nanoarchitectures with structural complexity and functional diversity, elucidating the molecular interactions and mechanisms of assembly exhibit in nature, and focusing on structural DNA and RNA nanotechnology especially for establishing a diverse set of fundamental design principles for various architectures.

Zhi Huang, PhD
Assistant Professor
University of Pennsylvania
Perelman School of
Medicine

Dr. Huang is a tenure-track assistant professor at the University of Pennsylvania, with multiple appointments and affiliations in the Perelman School of Medicine. His research focusses on AI/ML innovation and its application to medicine, with topics including vision-language foundation model for pathology, human-AI collaboration, neurodegenerative diseases, optimizing LLMs. His research has drawn wide public attention, including from the New York Times, Stanford Medicine, and Stanford Scope, and has resulted in translational innovations. In 2022, Dr. Huang, along with his postdoctoral mentors, co-founded a human-in-the-loop AI platform for digital pathology.

LIGHTNING TALKS

Use this QR code to link to score the presentations. Rank each presentation from 1 – 5 with 1 being the lowest and 5 the highest. After you have ranked all presentations, click **SUBMIT**.

1. **Lindsay Guare, University of Pennsylvania**
   Beyond PRS: Geno2Vec Learns Rich SNP Embeddings to Predict Endometriosis Risk

2. **Haedong Kim, PhD, Children's Hospital of Philadelphia**
   Exome-Wide Copy Number Variation in 142,357 Individuals from Autism Spectrum Families in the Simons SPARK Cohort

3. **Fahimeh Palizban, PhD, Children's Hospital of Philadelphia**
   Investigating pediatric cancer through deep learning-enabled genomics and phenomics

4. **Stephanie Mohammed, PhD, University of Pennsylvania**
   From Phenome to Casuality: A Multilayered Analysis of Age at Natural Menopause and its Health-Related Consequences

5. **Simon Chu, PhD, The Wistar Institute**
   Contribution of de novo retroelements to birth defects and childhood cancers in 3244 trios

6. **Karleena Rybacki,MS, University of Pennsylvania**
   Long-Read Whole-Transcriptome Sequencing Uncovers Gene Fusions and Structural Rearrangements in Fusion Panel-Negative Gliomas

7. **Krystal Kuang, Rutgers University**
   Understanding the role of LINE-1 expression in Hematopoietic Stem Cell development using targeted long-read RNA sequencing

8. **Christopher Sottolano, PhD Children's Hospital of Philadelphia**
   Revealing the hidden landscape of selection: detecting divergent, soft, and background signatures in diverse human genomes

9. **Yuheng Du, MS, University of Michigan**
   Cell-Type-Resolved Placental Epigenomics Identifies Clinically Distinct Subtypes of Preeclampsia

10. **Lannawill Caruth, University of Pennsylvania**
    Training Breast Cancer Genetic Association Models using biobank scale data for effective risk prediction.

POSTER SESSION

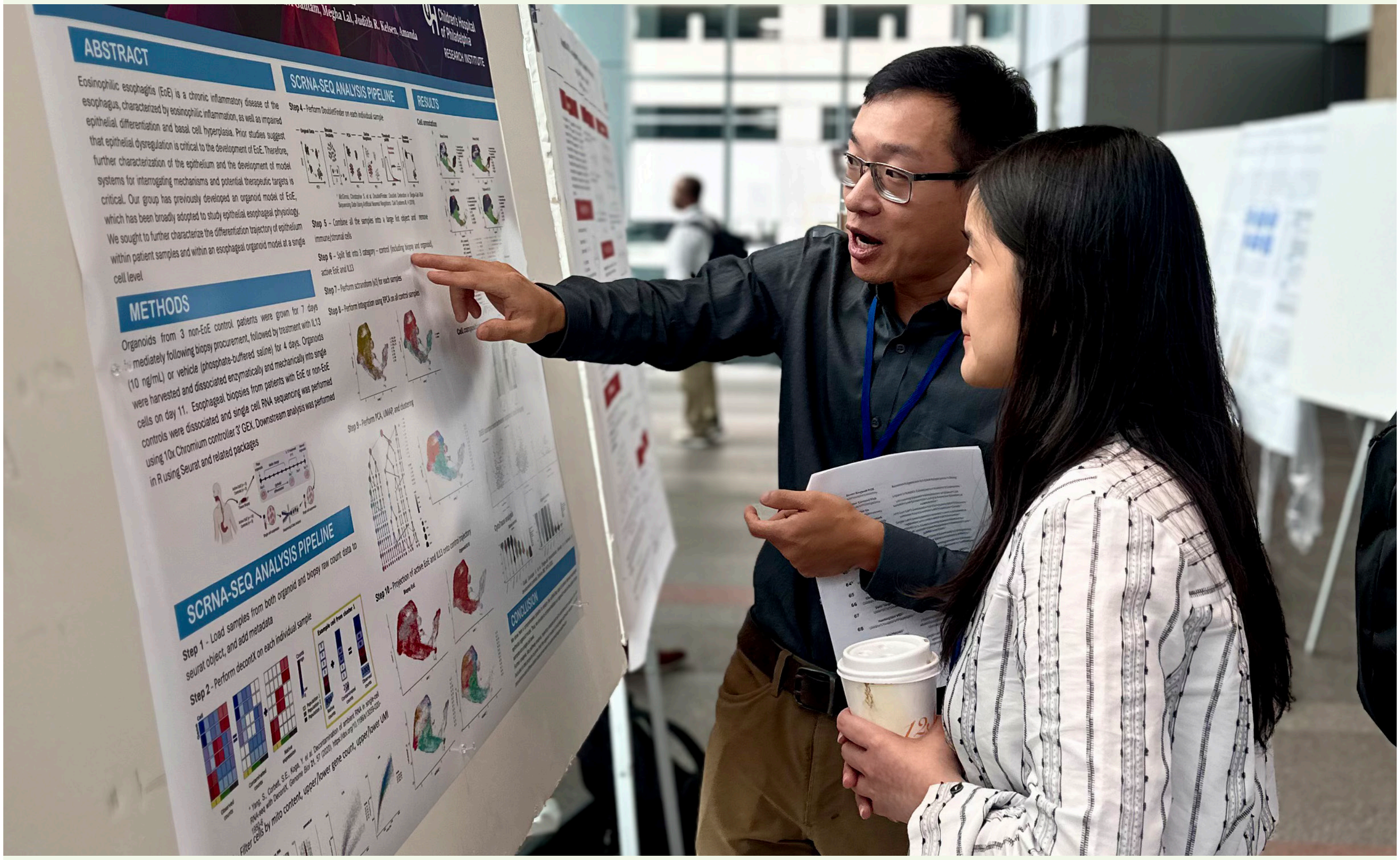
Important Information:

Our poster session will take place from 11:45 AM to 1:45 PM in the Colket Lobby. We know how you value the poster session and want to make sure you get the most out of the time available.

To maximize your time at the poster session, we have prepared a listing of all the posters. Please refer to this list in advance of your visit to choose posters you wish to visit.

Poster boards will be numbered according to the list.

Please scan the QR code to acess listing or click here.



THANK YOU

We would like to extend our thanks to our speakers for sharing their expertise and innovative research. A special thank you to the organizing committee for their hard work and dedication.