COLUMBIA | HERBERT AND FLORENCE IRVING INSTITUTE FOR CANCER DYNAMICS

IICD Symposium
Next-Generation Cancer Research
AI and Computation

Monday, March 16, 2026 | 1 PM - 6:30 PM
Location: Faculty House, Presidential Ballroom
(Morningside Campus)

Register to Attend

https://bit.ly/IICDSymposium_AI_Cancer

Elham Azizi, Columbia University
Generative AI Models of Cellular Dynamics in the Tumor Microenvironment

Andrew Blumberg, Columbia University
Evaluating Frontier AI Models for Mathematical Research

Bianca Dumitrascu, Columbia University
Interpretable Representation Learning for Single Cell Transcriptomics

Itai Yanai, NYU School of Medicine
How Do Cells Learn? A Mechanism for Adaptive Genome Regulation in Cancer

Keynote Speaker: Dana Pe'er, Sloan Kettering Institute
Through the Wasserstein Wormhole: Developing Biologically Meaningful Latents

Keynote Address

Dana Pe'er, Chair of Computational and Systems Biology and Scientific Director of the Single-Cell Analytics Innovation Lab, Sloan Kettering Institute, Memorial Sloan Kettering Cancer Center, and a Howard Hughes Medical Institute Investigator.

Through the Wasserstein Wormhole: Developing Biologically Meaningful Latents

Dana Pe'er is Chair of Computational and Systems Biology and Scientific Director of the Single-cell Analytics Innovation Lab at the Sloan Kettering Institute, Memorial Sloan Kettering Cancer Center, and a Howard Hughes Medical Institute Investigator. The Pe'er lab has pioneered foundational machine learning approaches to derive cell states, trajectories and cell–cell interactions from single-cell genomics and spatial profiling data, which it uses to investigate the roles of cellular plasticity in tumor initiation, progression and therapeutic resistance. Dr. Pe'er's work has been recognized with the Burroughs Wellcome Fund Career Award, NSF CAREER award, NIH Director's New Innovator and Pioneer awards, Packard Fellowship in Science and Engineering, Ernst W. Bertner Memorial Award, ISCB Overton Prize and ISCB Innovator Award, and fellowship in the AACR Academy.

Elham Azizi is the Herbert and Florence Irving Associate Professor of Cancer Data Research (in the Herbert and Florence Irving Institute for Cancer Dynamics and in the Herbert Irving Comprehensive Cancer Center) and Associate Professor of Biomedical Engineering, Columbia University

Generative AI Models of Cellular Dynamics in the Tumor Microenvironment

Tumors evolve as dynamic ecosystems shaped by cellular plasticity, clonal evolution, and spatially structured immune interactions. In this talk, I will present generative AI frameworks for modeling cellular dynamics in the tumor microenvironment using single-cell and spatial multi-omic data. I will describe Bayesian and deep generative models that infer temporal cell–cell interactions, reconstruct continuous cell-state trajectories, and identify altered transcriptional regulatory programs in cancer. I will discuss attention-based generative approaches for inferring intercellular communication programs and how they evolve across tissue, and models that link chromosomal instability and clonal structure to phenotypic heterogeneity. These models have provided novel insights into mechanisms driving response or resistance to immunotherapies in various cancer types. Building on these foundations, we are developing mechanism-aware generative models to simulate therapy-induced state transitions. Altogether, our machine learning toolkit has the potential to advance precision cancer therapies through decoding the principles of TME dynamics.

Elham Azizi is the Herbert and Florence Irving Associate Professor of Cancer Data Research (in the Irving Institute for Cancer Dynamics) and Associate Professor of Biomedical Engineering at Columbia University. She is also affiliated with the Department of Computer Science, Data Science Institute, and the Herbert Irving Comprehensive Cancer Center. Elham holds a BSc in Electrical Engineering from Sharif University of Technology, an MSc in Electrical Engineering and a PhD in Bioinformatics from Boston University. She was a postdoctoral fellow in the Dana Pe'er Lab at Columbia University and Memorial Sloan Kettering Cancer Center. Her multidisciplinary research utilizes novel machine learning techniques and single-cell genomic and imaging technologies to study the dynamics and circuitry of interacting cells in the tumor microenvironment. She is a recipient of the Vilcek Prize for Creative Promise in Biomedical Science, Takeda/NYAS Early-Career Innovator in Science Award, Allen Distinguished Investigator Award, Chan Zuckerberg Initiative SDL Award, NSF CAREER Award, Tri-Institutional Breakout Prize for Junior Investigators, NIH NCI Pathway to Independence Award, American Cancer Society Postdoctoral Fellowship, and IBM Best Paper Award at the New England Statistics Symposium.

Andrew Blumberg, Herbert and Florence Irving Professor of Cancer Data Research (in the Herbert and Florence Irving Institute of Cancer Dynamics and in the Herbert Irving Comprehensive Cancer Center) and Professor of Mathematics and Computer Science, Columbia University

Evaluating Frontier AI Models for Mathematical Research

I will describe our experiences with the First Proof project, which sought to test frontier large language models on real mathematical problems not in the literature but for which solutions were known. I will try to explain the implications for scientific discovery more broadly.

Andrew Blumberg received his PhD from the University of Chicago under the direction of Peter May and Michael Mandell. Andrew was a postdoc at Stanford, a member at IAS, and then a professor for nearly a decade at UT-Austin before coming to Columbia. He works in algebraic topology, computer security, and geometric data analysis with a focus on genomic data.

Bianca Dumitrascu, Herbert & Florence Irving Assistant Professor of Cancer Data Research (in the Herbert and Florence Irving Institute for Cancer Dynamics and in the Herbert Irving Comprehensive Cancer Center) and Assistant Professor of Statistics, Columbia University

Interpretable Representation Learning for Single Cell Transcriptomics

Single-cell RNA-seq enables the study of cell states across diverse biological conditions, such as aging, drug treatments, and tissue injury. However, disentangling shared and condition-specific transcriptomic patterns remains a significant computational challenge, particularly in settings with missing data or complex experimental designs. In this talk, I will introduce new deep generative frameworks designed to disentangle these transcriptomic signals, allowing for robust integration, cross-condition prediction, and biologically interpretable insights. Using real and simulated scRNA-seq datasets, we demonstrate that disentanglement can uncover shared wound healing patterns and distinct changes in cell behavior, including age-dependent immune responses and drug-modulated extracellular matrix remodeling. Finally, I will discuss open problems towards a pipeline for synthetic self-organizing systems.

Bianca Dumitrascu is an assistant professor in the Department of Statistics at Columbia University. Bianca is a member of the Herbert & Florence Irving Cancer Dynamics Institute and holds affiliate appointments in the Department of Computer Science and the Institute of Data Science. Her research focuses on interpretable machine learning methodology with applications to self-organizing systems. She focuses on the genomics and spatial dynamics of wound healing, regeneration, and development, with particular interest in how these processes recapitulate and diverge from the regulatory programs observed in cancer. Previously, Bianca received her B.S. degree in Mathematics from MIT and her Masters and her PhD in Computational Biology from Princeton University. Before joining Columbia University in 2023, she was a Fellow at Cambridge University, a member of the Institute for Advanced Study, and done postdoctoral work at Duke University.

Itai Yanai, Professor, Institute for Systems Genetics, New York University Grossman School of Medicine

How do Cells Learn? A Mechanism for Adaptive Genome Regulation in Cancer

The ability of cancer cells to consistently escape therapy highlights their remarkable adaptive potential. A longstanding debate in the cancer field concerns whether resistance originates primarily from mutational processes or through cellular plasticity. Emerging evidence suggests that adaptive cellular states arise through phenotypic plasticity induced by environmental stress. In this talk I will present a model for a mechanism that drives cellular adaptation in cancer drug resistance. I will highlight key properties of the AP-1 family of transcription factors, including stress-induced feedback, regulatory combinatorics, and cellular memory, and argue that together this system constitutes a molecular framework for establishing drug-resistant cellular states. Finally, I will discuss the potentially broad relevance of this adaptation mechanism across cellular systems.

Itai Yanai is a Professor at the New York University Grossman School of Medicine. After postdoctoral fellowships at Harvard University and the Weizmann Institute of Science, Yanai set up his independent lab at the Technion – Israel Institute of Technology, which became a pioneer of the single-cell RNA-Seq approach and its application to the study of evolution and development. The Yanai lab moved to NYU in 2016 and since then has been using computational and experimental approaches to make contributions to understanding cellular plasticity in the fields of tumor progression, cancer drug resistance, host-pathogen interactions and bacterial genome regulation. Together with Martin Lercher, Yanai has co-founded the Night Science Institute which champions a cultural shift in science by training researchers to embrace the creative Night Science process as an essential complement to rigorous hypothesis testing.