Featured speakers

Dana Pe'er

Dr. Pe'er is Chair of the Computational and Systems Biology Program and the Scientific Director of the The Alan and Sandra Gerry Metastasis and Tumor Ecosystems Center, Sloan Kettering Institute. Dr. Pe'er's lab develops novel computational techniques to characterize the dynamics of regulatory circuits at the single cell level, in the context of diverse multi-cellular cohorts within complex tissues, including the tumor microenvironment. Recent work has focused upon the characterization of cell types, their organization on developmental trajectories, the regulatory circuits controlling each cell type and at the next level, how diverse cell types within a tissue act together in a coordinated fashion, particularly in the context of tumor immune ecosystems. Pe'er studied at Hebrew University of Jerusalem receiving her bachelor's degree in mathematics and her PhD in computer science, with Dr. Nir Friedman. At Harvard University, she trained as a postdoctoral research fellow in the department of genetics in the lab of Dr. George Church. Dr. Pe'er has received numerous honors including a Burroughs Wellcome Fund Career Award, an NSF CAREER award, a Stand Up To Cancer Innovative Research Grant, an NIH Director's New Innovator Award, an NIH Director's Pioneer Award, the Packard Fellowship in Science and Engineering and the ISCB Overton Prize. Dr. Pe'er currently serves on the editorial board of the journal Cell and the organizing committee of the Human Cell Atlas project, leading the computational analysis for this project.

Peter Kharchenko

Dr. Kharchenko is an Assistant Professor at the Department of Biomedical Informatics at the Harvard Medical School. He received his Ph.D from the Biophysics program at Harvard University, under the mentorship of George Church. He then conducted his postdoctoral training with Peter Park at the Harvard Medical School, focusing on analysis of epigenetic regulation in model organisms and mammalian tissues. Kharchenko lab specializes in developing statistical and computational methods for analysis of high-throughput assays, including transcriptional, epigenetic and genetic analysis at a single-cell level.

Christina Kendziorski

Dr. Kendziorski is a mathematical scientist working at the interface of biology and statistics. Her research is motivated by questions arising in studies of genetics and genomics, specifically as they pertain to complex diseases. Her group has developed statistical methods to address the design and analysis of static and time course microarray experiments, expression quantitative trait loci (eQTL) mapping, network reconstruction, next-generation sequencing experiments, and most recently personalized genomic medicine. She serves on the editorial boards of Genetics, Bayesian Analysis, and the Genomics, Bioinformatics, and Systems Biology Section of Biology Direct, and is a member of the NIH Genomics, Computational Biology, and Technology (GCAT) study section. She also serves as a training faculty on the Computation and Informatics in Biology and Medicine (CIBM) Training Program and the Genomic Sciences Training Program (GSTP). In addition to expertise in statistical methods and software development, Dr. Kendziorski is the head of Statistical Genetics and Genomics at UW-Madison's Institute for Clinical and Translational Research (ICTR), and maintains active collaborations with many biologists and clinicians. These activities ensure that the methods developed in her group accommodate important features in real data, address salient and relevant questions in a meaningful way, and are disseminated in such a way that non-statisticians find accessible. Other than her primary focus on research and training, Dr. Kendziorski has been dedicated to eradicating socio-economic and geographic inequities in education. Towards that end she recently chaired the UW Committee on undergraduate admissions, recruitment, and financial aid (CURAFA).

Emma Lundberg

Dr. Lundberg is Associate Professor in cell biology proteomics at KTH Royal Institute of Technology, Sweden, and Director of the Cell Atlas, part of the Human Protein Atlas program. For this work she was recently top 10 under 40; future leaders in biopharma. Dr. Lundberg is currently spending a sabbatical year as visiting Associate Professor at Stanford and the Chan-Zuckerberg Biohub. In the interface between bioimaging, proteomics and artificial intelligence her research aims to define the spatiotemporal organization of the human proteome at a subcellular level, with the goal to understand how variations and deviations in protein expression patterns can contribute to cellular function and disease. Dr. Lundberg has a keen interest in citizen science, and has engaged over 300,000 gamers to help her research through the first MMO citizen science computer game.