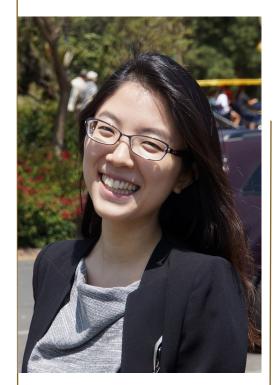
Analytical Chemistry Seminar

Tuesday, February 6, 2024 3:30 p.m. ~ WTHR 320

"Micro-and Nano-Technologies for Data-Driven Systems Biology"



Bio:

Han obtained her B.S. degree in Chemistry from Seoul National University, Korea, graduating summa cum laude as valedictorian. She pursued her Ph.D. in Physical Chemistry at MIT, Cambridge, MA, as a Samsung and KASF fellow, under the guidance of Prof. Moungi G. Bawendi. Her doctoral work focused on developing quantum dot-based intravital imaging platforms. Following her Ph.D., Han conducted postdoctoral research at Harvard University, working with Prof. David Weitz. During this time, she developed droplet-microfluidic platforms for high-throughput genome sequencing. Currently, Han is the Mark A. Pytosh Scholar and Assistant Professor of Chemistry at UIUC. Her research group develops new biophysical and analytical tools for datadriven systems biology and implement them to quantitatively delineate fundamental mechanisms governing the ensemble behaviors of native biological systems. Han is a co-founder and leader of the 'Spatial Omics Initiative' at the Carl R. Woese Institute for Genomic Biology. Her contributions to bioanalytical science have been recognized through Johnson&Johnson WiSTEM2D Award for Science and the NIH Maximizing Investigator Research Award.

Hee-Sun Han

Assistant Professor of Chemistry University of Illinois at Urbana-Champaign Carl R. Woese Institute for Genomic Biology

Abstract::

My research focuses on developing biophysical and analytical tools for data-driven systems biology. We integrate advances in chemistry, engineering, and data science to characterize native biological systems at unprecedented resolution and details and to quantitatively profile the fundamental mechanisms that govern the system's ensemble behavior. We have pioneered 'Single Virus Genomics' by developing microfluidic platforms that enable direct profiling of individual virus genomes, bypassing the need for virus culture. This technology allows large-scale, unbiased profiling of single virus genomes, enabling a quantitative assessment of viral evolution and infection dynamics. In parallel, we are actively developing and applying spatial omics tools to leverage spatial information to identify the key molecular and cellular features that drive system-level phenotypes. Molecular and cellular interactions are mediated by physical contact. Thus, the spatial organization of molecules and cells is strongly linked to their functional organization. In my talk, I will present our technical innovations in achieving single virus sequencing and demonstrate the application of this novel technology in the quantitative assessment of influenza reassortment. Reassortment is a crucial mechanism for zoonosis, facilitating the transmission of viruses from animals to humans. Thus, analysis of reassortment statistics between natural influenza strains provides valuable insights into influenza evolution and emerging human strains. In addition, I will present insights gained from a spatial transcriptomics map of the honey bee brain, demonstrating how spatial information reveals new biological insights into the collective performance of molecules and cells in system-level functions.

