Analytical Chemistry Seminar

Tuesday, November 28, 2023 3:30 p.m. ~ WTHR 320

"Fluorescent Barcoding: Illuminating the Future of Spatial Mapping with MERFISH"



Caitlin Dunlap is a second-year graduate student. She graduated from Butler University in 2022 with a B.S. in chemistry. Her undergraduate research, advised by Dr. Olujide Akinbo, involved evaluating a singlequadrupole inductively coupled plasma mass spectrometer (ICP-MS) for absolute quantitation of proteins. In the fall of 2022, she joined Dr. Garth Simpson's lab where she focuses on developing and applying novel nonlinear optical instruments for studying interfaces and chiral crystals.

Caitlin Dunlap

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Abstract:

Fluorescence in situ hybridization (FISH) is a widely adopted versatile probe technology for RNA and DNA imaging. In FISH, fluorescently labeled nucleic acid probes selectively bind to predetermined target sequences within cellular RNA, enabling precise localization and visualization of genetic material. Recent advancements in transcriptomic imaging technologies have enabled single-cell analysis, facilitating in situ identification and spatial mapping of cells and tissues. However, traditional single-molecule imaging tools, in particular single-molecule FISH (smFISH) have limited multiplexing capacity, hindering the simultaneous observation of multiple RNA species within a single cell. To address these limitations, multiplexed error-robust fluorescence in situ hybridization (MERFISH) has emerged as a transformative solution. MERFISH employs a distinctive combinatorial FISH labeling approach, assigning each RNA species a unique combination of fluorophores that read out as a barcode (a series of 0s and 1s). The novelty and enhanced multiplexing capacity of MERFISH stems from its advanced encoding scheme facilitating the detection and correction of errors during the imaging process. These improvements to the FISH technology enable MERFISH to simultaneously image thousands of RNA species, enabling a comprehensive and spatially resolved analysis of the transcriptome. By overcoming the limitations of previous techniques, MERFISH provides valuable insights into gene expression and regulatory processes at the single-cell level, revealing its significance in advancing the understanding of cellular dynamics.

