MIT ChemE

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Design of Microanalytical Tools to Understand Single-cell Biology

Amy E. Herr

John D. & Catherine T. MacArthur Professor
University of California, Berkeley

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In this talk, I will focus on two areas where precision microfluidic tools for molecular and cellular measurements are accelerating biological understanding. First, single-cell genomics and transcriptomics tools have radically changed the biological sciences and biomedicine. Further, microfluidic tools have radically expanded the capabilities of these sequencing tools (e.g., sequencing flow cells and droplet systems). Our aim is to bring the power of single-cell understanding to proteomics (targeted & discovery) by leveraging the precision of microfluidic design.

Second, I will describe recent research from my lab that physically links together multiple, independent measurement modalities in a 'single-cell, same-cell' paradigm. Such so-called "joint analyses" are important to directly correlate different – but interrelated – layers of molecular information. These types of joint analyses may play important roles in generative models of cells and cellular systems, owing to low biological and technical noise. Here, I will describe a suite of approaches that allow us to interrogate the nuclear nucleic acid compartment versus cytoplasmic protein compartment. Our long-term vision is to create tools that allow researchers to ex-post query a unique originating cell for protein-level information, as informed by a priori sequencing-based discovery.

Taken together, we strive to introduce tools uniquely equipped to measure both cellular and molecular heterogeneity as a means to more comprehensively understand cellular form and function.

kbriana@mit.edu

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