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Understanding the richness of single cell phenotype through measurement and modeling

A combination of several subtle changes in protein concentration or modification can create remarkable phenotypic differences among cells. In this talk, I will explore both top down and bottom up approaches that couple single cell measurement with mathematical modeling to uncover the diversity of cell behaviors. I will focus on the host-pathogen interactions that cause tuberculosis. *Mycobacterium tuberculosis* infects billions of people worldwide and kills more than 1.5 million per year. The variable course of disease and treatment response suggests that functionally heterogeneous populations of mycobacteria respond differently to stress. We use an integrated approach that includes live cell microscopy, mechanistic modeling, phase-diagram analysis, and pharmacodynamic modeling to develop a quantitative understanding of the mechanisms that lead to mycobacterial drug tolerance and virulence.