



## Delineating Protein Transportation Processes: Hierarchical Models for Single-Molecule Data

**Prof. Dr. Yang Chen**

*Department of Statistics & Michigan Institute of Data Science,  
University of Michigan, Ann Arbor/USA*

Single-molecule experiments investigate the kinetics of individual molecules and thus can substantially enhance our understandings of various organisms. Analyzing data from single-molecule experiments poses a number of challenges: (a) the inherent stochasticity of molecules is usually buried in random experimental noise; (b) single-molecule behavior can be highly volatile. For both of these reasons, replicated experiments are usually required. In order to combine information from replicated experiments while accounting for the heterogeneities among experimental replicates, we introduce a Bayesian hierarchical model on top of an experiment-level hidden Markov model, where the hidden Markov model has been widely adopted to analyze each experimental replicate individually in previous studies. We apply the proposed model to three data sets obtained from experiments aimed at unveiling mechanisms underlying protein transportation – a biological process vital for the proper functioning of cells. Our statistical results enable us to give a comprehensive picture of the protein transportation mechanism and provide a general framework for rigorous statistical analysis of experimental replicates from single-molecule experiments.