

Abstract Submitted
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Techniques for Statistically Scrutinizing Stochastic Model Assumptions Using a Single Noisily Measured Trajectory¹ CHRISTOPHER CALDERON, Numerica Corporation — The increased spatial and temporal resolution afforded by recent single-molecule experiments has inspired researchers to consider new techniques for quantifying molecular-level kinetics. Many researchers have contributed methods for improving the quality of estimators characterizing single-molecule kinetics, however techniques for checking the consistency of implicit distributional assumptions behind an assumed stochastic against a single experimental trajectory are under-developed. In this talk, likelihood-based goodness-of-fit testing and other model-based hypotheses tests accounting for the complexities of single-molecule trajectory analysis (heterogeneity, transient kinetic regime shifts, measurement noise, etc.) are discussed. Utility of the testing procedures are demonstrated on (i) single particle tracking (SPT) experiments characterizing mRNA motion in the cytoplasm of yeast cells and (ii) protein kinetics in the primary cilium of mammalian cells. In both cases, the testing procedures facilitated the discovery of new kinetic signatures of molecular motor facilitated transport not accounted for in traditional SPT models.

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