

Abstract Submitted  
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**A theoretical analysis of inferring molecular interactions from single particle trajectories**<sup>1</sup> ZIYA KALAY, Kyoto University — Single molecule/particle tracking has become a valuable tool in microscopy that allows for recording trajectories of probes such as individual biological molecules with high temporal and spatial resolution. With the trajectory of a particle, mesoscale transport properties such as diffusion coefficients and first-passage times can be calculated. With the trajectories of two particles that interact, we can investigate the kinetics of reactions by analyzing the statistics of overlap between trajectories. This approach is useful for single molecule biophysics in exploring the kinetics of reversible binding among molecules in biological membranes and on the DNA. Nevertheless, extracting information from noisy trajectories, where the noise stems from a combination of thermal fluctuations and uncertainty introduced by measuring apparatus, is a challenging task. In this work, we consider an exactly solvable model of diffusion and reversible binding in a 1-D structure, such as the DNA, and present a mathematical analysis of how much information about the binding kinetics can be reliably extracted from experimental data. With insight gained from this low-dimensional model, we discuss the analysis of trajectory pairs in two-dimensional systems such as biological membranes.

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