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Mean field theory and Bayesian inference in single molecule biophysics

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Single molecule experiments opens new windows to molecular biology and biophysics, by allowing us to follow individual proteins at work in real time. However, instrumental artifacts and the inherent randomness of Brownian motion and low copy number chemistry often makes for noisy data that can be challenging to interpret.

A very common problem is to analyze noisy time series with abrupt changes, reflecting for example binding events, or conformational changes in a protein complex. I will describe an approach to tackle such problems using physical modeling and a Bayesian version of mean field theory, and show results for two techniques that use diffusive motion as a reporter on the underlying chemical or conformational state: single particle tracking of fluorescent proteins in vivo, and DNA looping experiments using tethered particle motion in vitro.

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