

The University of Chicago

Department of Statistics

Seminar

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“Bayesian Analysis of Single Molecule Experiments”

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ABSTRACT

Recent technological advances allow scientists for the first time to follow a biochemical process on a single molecule basis, which, unlike traditional macroscopic experiments, raises many challenging data-analysis problems and calls for a sophisticated statistical modeling and inference effort. This paper provides the first likelihood-based analysis of the single-molecule fluorescence lifetime experiment, in which the conformational dynamics of a single DNA hairpin molecule is of interest. The conformational change is modeled as a continuous-time two-state Markov chain, which is not directly observable and has to be inferred from changes in photon emissions from a dye attached to the DNA hairpin molecule. In addition to the hidden Markov structure, the presence of molecular Brownian diffusion further complicates the matter. We show that closed form likelihood function can be obtained and a Metropolis-Hastings algorithm can be applied to compute the posterior distribution of the parameters of interest. The data augmentation technique is utilized to handle both the Brownian diffusion and the issue of model discrimination. Our results increase the estimating resolution by several folds. The success of this analysis indicates there is an urgent need to bring modern statistical techniques to the analysis of data produced by modern technologies.

This work is joint with Sunney Xie and Jun Liu.
