



Analyzing Single-Molecule Protein-Targeting Experiments via Hierarchical Models

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Recent technological advances allow scientists to follow a biological process on a single-molecule basis. These advances also raise many interesting data-analysis problems. In this talk we will focus on recent single-molecule experiments on protein targeting. To maintain proper cellular function, proteins often need to be transported inside or out of a cell. The detailed molecular mechanism behind such a process (often referred to as protein targeting) is not well understood. Single-molecule experiments are designed to unveil the detailed mechanism and reveal the functions of different organelles involved in the process. The experimental data consist of hundreds of stochastic time traces (from the fluorescence recording of the experimental system). We introduce a Bayesian hierarchical model on top of a hidden Markov model (HMM) to analyze these data and use the statistical results to answer the biological questions. We will discuss model selection, the construction of the hierarchical model, their biological meaning as well as our new understanding of the detailed mechanism behind protein transportation.

Keywords: hidden Markov model; model selection; posterior predictive check; step-signal segmentation.