Markov Chain Monte Carlo for Automated Tracking of Genealogy in Microscopy Videos Kathleen Champion

Abstract

Cell biologists use fluorescence time-lapse microscopy to follow the dynamics of proteins in organelles in time and space. Variation in timing during the cell division process can be studied in multinucleate cells by following individual nuclei through time to generate nuclear pedigrees. To undertake a quantitative analysis of mitosis timing, nuclei should be tracked through time over many frames of a time-lapse data set. This is challenging because the images have a low time resolution as well as a low signal to noise ratio, making both tracking and object identification challenging. While methods have been developed for tracking the movement of particles, there are few which have successfully incorporated mitosis to track dividing nuclei. In this paper, we treat the tracking problem as a high-dimensional statistical inference with noisy data and use Markov chain Monte Carlo to sample the posterior distribution. We present cases in 1D and 2D. We also introduce an algorithm for fitting 3D locations given multiple focal planes.