

STATISTICS COLLOQUIUM

MONDAY, MAY 2, 2011

TALK: 4:00 PM — SCIENCE CENTER RM. 705

RECEPTION: 5:15 PM — SCIENCE CENTER, 7TH FLOOR

“Monte Carlo Methods on Random Fields: Brains, Networks, Proteins”

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ABSTRACT

A random field is a collection of several observed values corresponding to positions in space. Probabilistic models for random fields typically have unknown normalizing constants and complicated correlation structures. It can be difficult to both sample from and make inference on these models. Standard methods for sampling (e.g., Metropolis) are often prohibitively slow, and standard methods for inference (e.g., pseudolikelihood) prohibitively inaccurate. Domain-specific Monte Carlo methods can provide an accurate, computationally efficient alternative. This talk introduces Monte Carlo methods for three particular applications of random fields: fMRI brain scans, social networks and protein folding. The first two settings are inferential: we consider the problems of hypothesis testing for smooth Gaussian random fields (fMRI brain scans) and parameter estimation for an exponential random graph model (social networks). Specifically, we propose a thresholding test for hypothesis testing a Monte Carlo and a maximum likelihood method for parameter estimation. The third setting (protein folding) involves sampling an atomic conformation from the Boltzmann distribution, for which we develop a fast configurational bias sampler. In each case we consider both speed and accuracy, finding substantial gains for our methods over conventional alternatives.

(This is joint work with with Prof. Samuel S. C. Kou, Prof. Jun S. Liu and Prof. Joseph K. Blitzstein.)