Perfect Sampling via Cross-monotonicity for Simple Mixtures

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1. Introduction

Given an ergodic Markov chain $\boldsymbol{X}$, the idea of perfect sampling is, in essence, to generate a sample from the exact stationary distribution π in finite steps. Two methods for developing such a perfect sampling algorithm are known, the one based on coupling from the past (CFTP) by Propp and Wilson (1996), and the other via rejection method by Fill (1998). Hobert et al. (1999) considered a simple mixture model $p_1 f_1(\xi) + \cdots + p_k f_k(\xi)$ with weight parameters $p_1, \ldots, p_k$ and with known components $f_1, \ldots, f_k$. They studied a Markov Chain Monte Carlo (MCMC) evaluation for the posterior density $\pi(p)$ of weight parameters which is proportional to

$$f(x \mid p) = \prod_{i=1}^{n} \left[p_1 f_1(x_i) + \cdots + p_k f_k(x_i) \right], \tag{1}$$

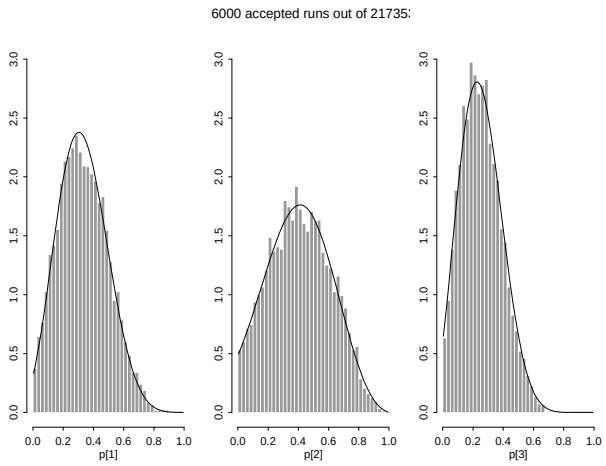
and presented the CFTP implementation when $k = 2$ or $k = 3$. We investigate the Fill's algorithm for the simple mixtures, and develop techniques necessary for its implementation. Particularly we demonstrate the idea of cross-monotonicity in practice.

2. Fill's algorithm using cross-monotonicity

Fill et al. (2000) gave a general framework of Fill's algorithm, and explained various extensions of perfect sampling algorithms via rejection method. A simple MCMC procedure generates a Markov chain X_t at time t, and samples it approximately from the stationary distribution π when the running time t is "long enough." In contrast the Fill's algorithm is a rejection sampling with a fixed running time t. The key ingredients in the algorithm are the coupling of two Markov chains $\boldsymbol{X}$ and $\boldsymbol{Y}$, and the imputation of another chain $\boldsymbol{Y}$ given the chain $\boldsymbol{X}$ of interest. The coupling allows us to detect the independence between X_0 and X_t by simply observing the other chain $\boldsymbol{Y}$. Specifically, if (i) values taken by the chains are partially ordered with the maximum value $\hat{1}$ and the minimum value $\hat{0}$, and (ii) the coupling is cross-monotone so that X_s is comparable and always smaller than Y_s for every $s = 0, \ldots, t$, then we can provide the mechanism for such detection by checking the event "$Y_t = \hat{0}$" for the chain $\boldsymbol{Y}$ started from $Y_0 = \hat{1}$. In an actual implementation, the algorithm runs a time-reversed chain $X_t, X_{t-1}, \ldots, X_0$ started from $X_t = \hat{0}$, and then imputes $Y_0, \ldots, Y_t$ given $X_0, \ldots, X_t$. Thus, it

is important to devise an elaborate and efficient imputation technique. When the chain $\boldsymbol{Y}$ is imputed, we accept the observation X_0 given $Y_t = \hat{0}$, which produces an exact sample from π.

Figure 1. Marginal distributions from Fill's algorithm



To see the performance of Fill's algorithm, we have used the simple mixture with $k = 3$ and the normal components whose parameters are taken from Hobert et al. (1999). Furthermore, we have chosen a relatively small running time $t = 22$ for the algorithm. Figure 1 shows the histograms of respective weights p_1, p_2, and p_3 obtained by simulation, and compares them with the solid lines of the exact marginal densities computed from (1).

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RESUME

Positions: Postdoctoral Fellow, Utah State University from 2000 to present; Research Fellow, Johns Hopkins University from 1999 to 2000; Systems Development Laboratory, Hitachi, Ltd. from 1990 to 1992. Education: Ph.D. in Mathematical Sciences in 1999 from Johns Hopkins University; Master of Science in Operations Research in 1994 from University of Delaware; Master of Science in System Sciences in 1990 from Tokyo Institute of Technology.