Stats 270, Homework 3

Due date: February 11

1. A Markov chain on a countable state-space E proceeds from its current state i by randomly drawing another state j with proposal probability q_{ij} and then accepting/rejecting this proposed state with probability

$$a_{ij} = \frac{\pi_j q_{ji}}{\pi_j q_{ji} + \pi_i q_{ij}}, \tag{1}$$

where $\boldsymbol{\pi} = (\pi_1, \pi_2, \dots)$ is a probability mass function on E. This MCMC construction is called Barker's algorithm. Notice that $0 \leq a_{ij} \leq 1$ by definition.

   (a) What are the transition probabilities of this Markov chain, p_{ij}, for $i \neq j$?

   (b) Show that $\boldsymbol{\pi}$ is a stationary distribution of Barker's Markov chain.

2. Consider a toric Ising model with state-space $\Omega = \{\mathbf{x} = (x_1, \dots, x_k) : x_i = \pm 1\}$ and $\pi(\mathbf{x}) = \frac{1}{Z} e^{\beta \sum_{i=1}^k x_i x_{i+1}}$, where x_{k+1} is understood to be equal to x_1. Set $k = 50$ and $\beta = 0.9$. Implement the Metropolis-Hastings sampler discussed in class to approximate $\mathrm{E}[M(\mathbf{x})]$ and $\mathrm{Var}[M(\mathbf{x})]$, where $M(\mathbf{x}) = \sum_{i=1}^k x_i$ is the total magnetization. In each algorithm, start from a random state $\mathbf{x} = (x_1, \dots, x_k)$, obtained by flipping k independent fair coins and assigning values 1 or -1 to each component of $\mathbf{x}$. Run your MCMC chains for N iterations. During the first $L < N$ iterations, do not save sampled states of the system. L is the length of a "burn-in period", needed for the Markov chain to achieve stationarity (hopefully).

3. Consider a two state continuous-time Markov SIS model, where the disease status X_t cycles between the two states: 1=susceptible, 2=infected. Don't worry about continuous-time — everything will be defined in the problem formulation. Let the infection rate be λ_1 and clearance rate be λ_2. Suppose that an individual is susceptible at time 0 ($X_0 = 1$) and infected at time T ($X_T = 2$). We don't know anything else about the disease status of this individual during the interval $[0, T]$. If T is small enough, it is reasonable to assume that the individual was infected only once during this time interval. We would like to obtain the distribution of the time of infection I, conditional on the information we have:

$$\Pr(I \mid X_0 = 1, X_t = 2, N_t = 1) \propto \Pr(0 < t < I : X_t = 1, I < t < T : X_t = 2),$$

where N_t is the number of infections. Since X_t is a continuous-time Markov chain, the last probability (it is actually a density) can be written as

$$\Pr(0 < t < I : X_t = 1, I < t < T : X_t = 2) = \underbrace{\lambda_1 e^{-\lambda_1 I}}_{\text{density of waiting time until infection}} \times \overbrace{e^{-\lambda_2 (T - I)}}^{\text{prob of staying infected}}.$$

Set $\lambda_1 = 0.1$, $\lambda_2 = 0.2$ and $T = 1.0$ and implement a Metropolis-Hastings sampler to draw realizations from the above posterior distribution. For your proposal distribution, use a uniform random walk with reflective boundaries 0 and T. In other words, given a current value of the infection time t_c, generate $u = \text{Unif}_{[t_c-\delta, t_c+\delta]}$ $(2\delta < T)$ and then make a proposal value

$$t_p = \begin{cases} u & \text{if } 0 < u < T, \\ 2T - u & \text{if } u > T, \\ -u & \text{if } u < 0. \end{cases}$$

This is a symmetric proposal. Plot the histogram of the posterior distribution of the infection time. Try a couple of sets of values for λ_1 and λ_2 and examine the effect of these changes on the posterior distribution of the infection time.