Note that there is no lecture on Fri 11 April, due to the lecturer's business trip. Also remember to bring a short description of your programming assignment (what model do you intend to simulate/optimise & using which method) with you to the lecture on Wed 9 April, or if you cannot attend then, send the description by e-mail to the lecturer. (Further instructions available on the course's web page.)

1. Establish the validity of the Hastings MCMC design scheme (p. 142 of the lecture notes), i.e. show that with the given choices of acceptance probabilities, the resulting Markov chains are guaranteed to be reversible.

2. Construct a Barker-Hastings sampler for the setting of tutorial problem 5/5, with uniform generation probability $q = 1/n$ for each of the Hamming neighbours of a given state $\sigma \in \{0, 1\}^n$. Compare this to the Gibbs sampler designed earlier.

3. Verify the claim at the bottom of p. 141 of the lecture notes, i.e. that in the case of a reversible chain, the asymptotic variance of an MCMC estimate satisfies:

$$\lim_{n \to \infty} \frac{1}{n}(\sum_{k=1}^{n} f(X_k)) = \sum_{i=2}^{r} \frac{1 + \lambda_i}{1 - \lambda_i}|\langle f, v_i \rangle_\pi|^2,$$

   where $1 = \lambda_1 > \lambda_2 \geq \cdots \geq \lambda_r > -1$ are the eigenvalues of the transition probability matrix P, and u_i and v_i are the left and right eigenvectors associated to eigenvalue λ_i, normalised so that $u_i^T v_i = 1$.

4. [*Computer problem.*] Consider the following simple genetic algorithm: A population consists of two 2-bit strings, and the values of the objective function c are determined as $c(00) = 1$, $c(01) = c(10) = 2$, $c(11) = 4$. At each computation step, a one-point crossover occurs between the two strings with probability 25%, and results in simply replacing the given two strings by the ones obtained by interchanging their first and second bits. Following that, each bit of each string is mutated (flipped) with a 10% probability, independent of the other bits. Selection is performed based on a relative cost fitness measure, i.e. two new strings are selected from the two existing ones (with replacement), so that both existing strings have a probability of being selected proportional to their objective function value. Determine the stationary population distribution in this setting using the Vose-Liepins canonical GA model (lecture notes p. 156). What would the stationary distribution be if no selection between individuals were performed? (*Note:* You will definitely need the help of a computer algebra system such as Maple, Mathematica, or Matlab to work on this problem.)