

1. Assume that two random variables A and B with finite state spaces S_A and S_B and a joint distribution $\Pr(A = a, B = b)$ are given. Further assume that for each $a \in S_A$ there is a Markov chain on S_B with transition law $P_{b \rightarrow b'}^{(a)}$ with equilibrium distribution $\Pr(B = b|A = a)$, and for all $b \in S_B$ there is a Markov chain on S_A with transition law $P_{a \rightarrow a'}^{(b)}$ with equilibrium distribution $\Pr(A = a|B = b)$. Define a Markov chain transition law as follows: Given the current state (a, b) , toss a fair coin, and if it shows “head” go to (a, b') with probability $P_{b \rightarrow b'}^{(a)}$. If it shows “tail”, go to (a', b) with probability $P_{b \rightarrow b'}^{(a)}$. Show that the resulting Markov chain has equilibrium distribution $\Pr(A = a, B = b)$.
2. Explore with simulated datasets how one can increase the efficiency of MCMC Methods like LAMARC and IM/IMa by using MCMCMC and fine-tuning the heating parameters.
3. Two populations emerged from a recent split of an ancestral population. The new population may have grown or shrunken. There may still be a little amount of gene-flow between the populations.
 - (a) Explore for different sizes of datasets how accurate you can estimate the model parameters θ for the ancestral and the two descendant populations, time of populations split, migration rates and population growth rates.
 - (b) How can we deal with recombination within loci? Does recombination within loci increase or decrease the accuracy of parameter estimations?