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COMPUTATIONAL POPULATION GENETICS — EXERCISE SHEET 4

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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 $P^{(a)}_{b \to b'}$ 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 $P^{(b)}_{a \to a'}$ 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 $P^{(a)}_{b \to b'}$. If it shows "tail", got to (a', b) with probability $P^{(a)}_{b \to b'}$. 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. There may still be a little amount of gene-flow between the populations.
   (a) Explore for different sizes of datasets how accurate ABC and IMa 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?