

1. Proof that any distribution p that fulfills the reversibility condition for an irreducible aperiodic Markov chain X on a finite state space must be a stationary distribution of X .
2. (for bioinformaticians) Write an efficient program that reads a tree in Newick format and simulates the evolution of DNA sequences along the tree according to the Jukes-Cantor model.
3. Analyze one or two of the datasets in `turtle:/home/dirk/Teach/WS1112/CompPopGen/DataSets`. (The alignment programs `mafft`, `muscle` and `probcons` are installed on turtle.)
4. Simulate datasets for a population that consists of four sub-populations, with gene flow between the populations.
 - (a) How accurately can you estimate the rates and favored directions of migration between each pair of sub-populations and how does this depend on the number of loci and other properties of the dataset?
 - (b) Assume that each of the sub-populations has a substructure. How does this influence the results, especially if the sampling was limited to some of the sub-subpopulations. What if the sub-substructure is ignored or unknown?