Project #5 – Markov chains and discrete events
EE 511: Spring 2017

Due: 09 March at 18:00 in EE511 project locker (near EEB B24). Late penalty: 15% per day.

1. Suppose that jobs arrive at a single-server queue system according to a nonhomogeneous Poisson process. The arrival rate is initially 4 jobs per hour and increases steadily (linearly) until it hits 19 jobs per hour after 5 hours. The rate then decreases steadily until it returns to 4 jobs per hour after another 5 hours. The rate repeats indefinitely in this fashion: $\lambda(t + 10) = \lambda(t)$. Suppose that the service-time distribution is exponential with rate 25 jobs per hour. Suppose also that whenever the server completes a job and finds no jobs waiting it goes on break for a time that is uniformly distributed on (0, 0.3). The server goes on another break if upon returning from break there are still no jobs waiting. Estimate the expected amount of time that the server is on break in the first 100 hours of operation.

2. In class we considered the 2x2 HOL-blocking switch performance under the heavy-load assumption, *i.e.* there was always a packet at each input. A more realistic model includes modeling the buffer for each input. Assume the probability that a packet arrives at input port i in a time slot is $p_i = p$ (a constant) for each input. Assume also that the probability that a packet arriving at input i should be switched to output j is r_{ij}. Define the system state to be the number of packets in the buffer at each input in the middle of time slot k and the desired output port of the packet at the HOL of each input, *i.e.* decide the desired output when the packet moves to the HOL-slot. Assume that packets arrive to the input buffers at the end of a time slot. If there is a packet in the buffer at the beginning of a time slot the switch attempts. If the delivery attempt succeeds the switch removes the packet from the input queue at the end of the time slot. If the delivery attempt fails then the packet stays at the head of the line and the switch will attempt delivery in the next time slot.

    a. Assume $r_{ij} = 0.5$. Plot the distribution and compute the mean of the number of packets in the buffer at input 1 and input 2 as a function of the arrival probability p. Plot the distribution and compute the mean of the number of packets processed by the switch per time slot.   Estimate a 95% confidence interval for the overall efficiency of the switch.

    b. Repeat (a) assuming asymmetrically targeted packets: $r_1 = 0.75$ and $r_2 = 0.25$.

3. The Wright-Fisher model uses a Markov chain to simulate stochastic genotypic drift during successive generations. The Wright-Fisher model applies to populations under the following assumptions:

    a. the population size N remains constant between generations
    b. no selective difference between alleles
    c. non-overlapping generations.

    Consider a gene with 2 alleles (A1 and A2) in a population with N diploid individuals. The population contains $2N$ copies of the gene since each diploid individual has 2 copies of the gene. Let the state vector $x(t)$ represent the allele distribution at time t. Then at time t:

$$x_0(t) = P\left[0 \text{ copies A1}, 2N \text{ copies A2}\right]$$
$$x_1(t) = P\left[1 \text{ copies A1}, 2N - 1 \text{ copies A2}\right]$$

$$x_2(t) \; = \; P \left[2 \text{ copies A1}, 2N - 2 \text{ copies A2} \right]$$
$$\dots$$
$$x_{2N}(t) \; = \; P \left[2N \text{ copies A1}, 0 \text{ copies A2} \right]$$

The Wright-Fisher model produces successive generations with a 2-step process. The model first creates *N* pairs of parents selected randomly and with replacement from the population. Then each pair produces a single offspring with its genotype inherited by selecting one gene from each parent. All parents die after mating. The allele distribution *x(t)* is a Markov chain that advances by random sampling with replacement from the pool of parent genes. The density of alleles evolves according to a binomial probability density with

$$P[x(t+1) = j | x(t) = i] = \text{Bin}\left(j, 2N, \frac{i}{2N}\right).$$

Thus the Markov chain transition matrix has elements

$$P_{i,j} = \binom{2N}{j} \left(\frac{i}{2N}\right)^j \left(1 - \frac{i}{2N}\right)^{2N-j}.$$

Consider a population of $N = 100$ diploid heterozygous individuals, *i.e.* all 100 individuals have (A1,A2) genotype. Simulate the population's genetic drift using a Markov chain simulation. Repeat the experiment 100 times. Comment on the steady-state population's genetic composition.

Repeat the process above using different initial allele distributions. Comment on the steady-state population's genetic composition. How does the composition of the initial population affect the steady-state outcome? Why does this scenario seem to defy the assertions of the Perron-Frobenius theorem and the Markov chain ergodic theorem?