**Description**

**Q1)** A non-homogeneous Poisson process is similar to an ordinary Poisson process, except that the average rate of arrivals is allowed to vary with time. Many applications that generate random points in time are modeled more faithfully with such non-homogeneous processes. In our case, we have a Single Server Queuing system, where customers arrive according to a non-homogeneous Poisson process with intensity function lambda(t), t>=0. Server handles customer if free else joins queue. When server completes serving a customer, it begins handling longest waiting customer( First come first served) or remains free if queue is empty. The amount of time to service a customer follows a particular probability distribution. Fixed time T after which no new arrivals occur. But server continues to handle all customers in queue. The quantities of interest to us here is

* The average time customer spends in queue
* The average time past T that last customer departs.

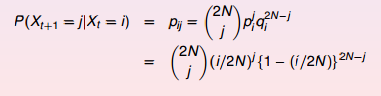
**Q2)** Consider an N × N input-queued switch - time is slotted, so that at most one packet can arrive (depart) per time slot - packets arrive at each input with probability p, independently across inputs/time - the destination of a packet is equally likely to be one of the outputs and independent across all packets

**Q3)** The Wright Fisher model is explained as follows. Assume a simple haploid model; it consists of a population of 2N genes (or alternatively – N diploid organisms) of random reproduction, with each haploid possessing either allele A1 or allele A2. Initially, we may disregard mutation as well as selective forces. At each time-step, a gene (allele) reproduces some number of offspring (which are the exact copies of itself) and dies immediately after that; thus has a life-span of only one generation. The process, modeled thus, describes how the genes get transmitted from one generation to the next

Process of birth and death in the population remains hidden. The only observable is the frequency of alleles changing from generation to generation. The allele frequency of the next generation is governed only by a genetic drift. The Genetic drift is defined as a force that reduces heterozygosity by the random loss of alleles. We should just focus on the frequency of allele A1 in the population of 2N haploids. Think of this process as changing from one generation to the next in terms of a Markov Chain, where the state X of the chain corresponds to the number of haploids (genes) of type A1.

In any generation X takes one of the values 0, 1, . . . , 2N, which constitutes a state space. Denote the value taken by X in generation t as Xt . The model assumes that genes for the generation t + 1 are derived by sampling with replacement from the genes of generation t. Thus, the make-up of the next generation is determined by 2N independent Bernoulli trials so that Xt is a binomial random variable. Let the initial generation consist of i genes of type A1 and 2N − i genes of type A2. Then we define a probability of success (resulting in allele A1) pi and a probability of failure qi (resulting in allele A2) for each Bernoulli trial as pi = i/2N, qi = 1 – i/2N. The process generates a Markov Chain {Xn}, where Xn is the number of A1 genes in the nth generation, among a constant population size of 2N individuals. Basically, Xt+1 is a binomial random variable with index 2N and parameter (probability of success) Xt/2N.

the transition probabilities from Xt = i to Xt+1 = j for this Markov Chain are computed according to the binomial distribution as



A matrix for which all the column vectors are probability vectors is called transition or stochastic matrix. A Markov chain is a process that consists of a finite number of states and some known probabilities pij, where pij is the probability of moving from state j to state i. Of particular interest is a probability vector **p** such that **Ap**=**p**, that is, an eigenvector of **A** associated to the eigenvalue 1. Such vector is called a steady state vector. The **Perron–Frobenius theorem**, asserts that a [real square matrix](https://en.wikipedia.org/wiki/Real_square_matrix) with positive entries has a unique largest real [eigenvalue](https://en.wikipedia.org/wiki/Eigenvalue) and that the corresponding [eigenvector](https://en.wikipedia.org/wiki/Eigenvector) can be chosen to have strictly positive components, and also asserts a similar statement for certain classes of nonnegative matrices. A Markov chain is ergodic if there is a number N such that any state can be reached from any other state in at most N steps (in other words, the number of steps taken are bounded by a finite positive integer N). In case of a fully connected transition matrix, where all transitions have a non-zero probability, this condition is fulfilled with N=1. A Markov chain with more than one state and just one out-going transition per state is either not irreducible or not aperiodic, hence cannot be ergodic