**IV. Parameter Estimation:**

1. Markov Chain parameter estimation for the SEIS Model

Consider three discrete states: susceptible (state 0), exposed (state 1), and infected (state 2) states. If (Xi, i=0,1,2 ) represent the number of individuals at any state from the underlying diseases at any time t, then clearly, is a stochastic process with states 0, 1, and 2.

Thus, the Markov dependency (1) can be illustrated as following:

P(Xn = in | Xn-1 = in-1, ..., X1 = i1, X0 = i0) = P(Xn = in | Xn-1 = in-1)

Then the transition probability (Pij) for i,j = 0,1,2 is denoted in this matrix:

1. With an infected neighbor:

(Pij) =

1. With no infected neighbor:

(Pij) =

1. Estimating Transition Prob above:

The transition events are independent of one another (as defined by the Markov principle); the likelihood of the transition probability, Pij , follows a binomial model:

where Nij  is the number of observed transition that starts from state *i* to *j*

With the assumption of constant transition probabilities over the period, the transition probability matrix is estimated as a multinomial distribution given as:

V. Justification of the choice of scale-free network:

Random graph is a tool widely adopted by many epidemiologists to illustrate the transmission of a disease in a certain community. Such compartment models with local connectivity emphasizes the general prediction of a nonzero epidemic threshold . The pandemic growth remains stable and persistent when the value of surpasses the threshold value. However, it appears that when , the infection dies out exponentially fast. The empirical data on COVID19 proves that the disease is highly contagious and within just a infinitesimal number of infected cases, the epidemic can be re-occured with the similar extent of spread.