

Monte Carlo Simulation: Applications

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Abstract

The Monte Carlo simulation technique is one of the common computational tools used to imitate and follow up complex real life systems and their development with time. Variables of a disease problem were defined and the mathematical model for this problem was constructed. The numerical solution of this model was compared with the computational simulation of Markov Renewal Process of the type " Birth and Death ". We obvious from the results we obtained the efficiency of the Monte Carlo simulation technique and through out extended time periods episodes.

1- Introduction

Modeling stochastic system is an art. As such one learns by doing. But the process of learning is long and has a number of steps preliminary to doing. One must learn some basic concepts of stochastic processes and their properties, this step and its output have come to be called "theoretical" and seem to be viewed with a jaundiced eye as though they were unnecessary, irrelevant and an impediment to doing, [3]. In recent years the use of Markov renewal equations as a non-linear model for birth-and-death dynamics has expanded dramatically

Section (2) shows the differential equations of a disease model where the underlying process is a birth-and-death process [5], [10]. As these equations become more detailed, analytical results become very difficult to obtain, for this reason, a technique for conducting experiments on a model of system known as simulation has become an increasingly attractive way for the study of this model. Typically, the goal of the simulation is the estimation of quantitative of the dynamical system under study [8]. To solve the disease problem we developed a method to generate

sample path of the birth-and-death process as our objective.

The main results of this paper are presented in section 4. Section 3 discuss the numerical solution of the disease model, while section 4 simulates the underlying stochastic process for the disease model (so-called birth-and-death process) of a class of Markov renewal equations known as the Chapman Kolmogorov equations. The differential equations of a disease problem have been solved numerically by using the Runge-Kutta-Fehlberg method and the results are compared to those obtained by simulating birth-and-death process through generating sample paths of the process [1], [10].

2- Differential Equations of Disease Model

In the population dynamic problem the state variable represent numbers of three populations which intercept by affecting each other's growth and decay. In our problem we describe the spread of infection disease (epidemic) where recover results in immunity, we use three state variables:

Susc - number of susceptible individuals.

Sick - number of sick disease carries.

Cured- number of cured (and now immune) individuals.

The total population will be a defined variable:

$$\text{Popul} = \text{Susc} + \text{Sick} + \text{Cured}$$

We shall use the approximate differential equation model [5]:

$$\left. \begin{aligned} \frac{dY_1}{dT} &= -P_1 * Y_1 * Y_2 \\ \frac{dY_2}{dT} &= -P_1 * Y_1 * Y_2 - P_2 * Y_2 \\ \frac{dY_3}{dT} &= -P_2 * Y_2 \end{aligned} \right\} \quad (1)$$

Where:

Y_1 = number of individuals susceptible to disease during time T .

Y_2 = number of infectious carriers, and Y_3 are the individuals recovered and immune.

P_1 and P_2 are rate constants for susceptibility and recovery.

3- Numerical Approximation of a Disease Model

Equations (1) discussed in section 2 can be solved numerically by using the deterministic Monte Carlo method. One application of this method is the numerical differentiation. The Runge-Kutta methods are commonly utilized for approximation of the differential equations (1).

These methods were developed to solve a single equation involving a single independent and a single dependent variable [1].

Figure 1 plots the results of solving equations (1) with 3 equations (i.e. $n = 3$, and time $t = 0, 0.5, 1.0, \dots, 50$, with rate constants for susceptibility and recovery $P_1 = 0.001$ and $P_2 = 0.072$ and under the initial conditions $Y_1 = 620$, $Y_2 = 10$ and $Y_3 = 70$ is calculated by using the libraries of Maple so-called RKF45 which use fourth and fifth order Runge-Kutta method [1], [5].

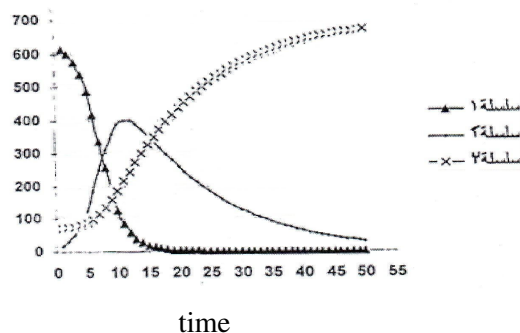


Fig.1:Deterministic results of epidemic problem.

Notice that curve 1 represent the individuals susceptible to disease, curve 2 represent infectious carriers while curve 3 represent the individuals recovered and immune.

4- Simulating the Underlying process of a Disease Model

We started by assuming the disease problem could be modeled as a birth and death process. We will discuss here only the non-regressive model (i.e. the disease could not return to a state it had already visited), thus if we try to simulate this process on a computer, one would have to create values of two random

variable at each iteration, the first is state visited, the second is the sojourn time in each state visited. For example we can generate n random numbers $x_1, x_2, \dots, x_n$ from the uniform distribution in the interval $[0, 1]$ by using the random numbers generator so-called random which is available in the modern computational algebraic system Maple as follows :

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for i to n do
  x = stats[random,uniform [0,1]]
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From the definition of the semi Markov kernel [2], one would have to generate the state of a Markov chain using the one step transition probability of a jump from state i to state J , then knowing that this jump was made one would generate a value of the continuous valued random variables $T_{n+1} - T_n$ from the distribution given by the conditional probability that $T_{n+1} - T_n < t$ knowing the current and next state. The transition function which describes the stochastic evolution of the spread of the disease in this case satisfies a system of differential equations know as the Chapman Kolmogorov equations given by [4], [10]. This system of differential equations is difficult to work with analytically, and is not easy to use for computational purpose. For this reason we have to search for approximation methods to find the numerical approximation for this system (for details see [1]). In order to solve these equations we rewrite them into the following finite system of n first order differential equations as follows:

$$Y_0' = -A Y_0 + B Y_1 \quad (2)$$

$$\left. \begin{aligned} Y_1' &= -(A+B)Y_1 + A Y_0 + B Y_2 \\ Y_2' &= -(A+B)Y_2 + A Y_1 + B Y_3 \\ &\vdots \\ Y_n' &= -(A+B)Y_n + A Y_{n-1} + B Y_{n+1} \end{aligned} \right\} \quad (3)$$

with initial conditions

$$Y_0 = 1, Y_j = 0 \text{ for } j \geq 1 \quad (4)$$

A, B are constant.

In this section we discuss the numerical simulation of birth and death equations (2) and (3) by providing a Markov Chain Monte Carlo (MCMC) method for generating the underlying process of of these equations. MCMC draws samples by running a Markov chain that is constructed so that its limiting distribution is the joint distribution of interest [6]. For this purpose we use the

Poisson Process Monte Carlo (PPMC) algorithm [9]. A typical outcome of these sampling procedures determines a realization of the disease, thus by sampling from exponential and binomial distributions we construct typical sample paths of the disease. Now it is possible to assign to this set of paths a probability measure so that the transition probability is determined as a simulation approximation of the solution of (2) and (3) [7]. Figure 2 plots the sample path of the epidemic behavior [5].

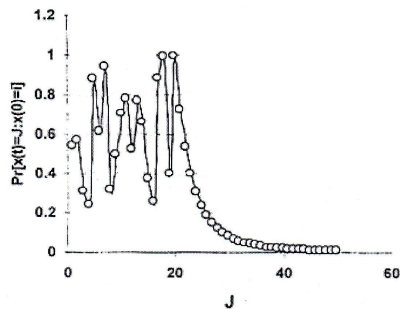


Fig. 2: Sample path of the epidemic behavior.

where the curve representing the behavior of the disease during time T .

From Fig. 1 and Fig. 2 we see that the results obtained by using numerical simulation is more easy and accuracy than the deterministic results.

5- Conclusion

As concluding remarks we mention that to predict sample path behavior of the spread of the disease we do not need to solve the approximate differential equations of the disease model, but instead, simply simulate the underlying process of the Markov renewal equations through generating sample paths of the process.

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Appendix

Markov Renewal Process: A survey

1. A short outline of Markov Renewal Process

The Poisson process has the property that the times between transitions are identically independent distributed with an exponential distribution function [4], [10]:

$$F(t) = 1 - e^{-\lambda t} \quad (1)$$

Continuous time Markov chain (CTMC) is a process that goes from state to state according to a Markov chain, and each time a state is visited the process stays a random time that is independent of the past behavior of the process and has an exponential distribution .

The Markov renewal process generalizes CTMC by allowing the time between transitions to be arbitrarily distributed nonnegative random variable which may depend on the current state and the next state during the time interval $(0, t]$

The process $\{(X_n, T_n); n = 0, 1, 2, \dots\}$ is a Markov renewal process with state space E if [4], [10]:

$\Pr \{X_{n+1} = j, T_{n+1} - T_n \leq t \mid X_0, X_1, \dots, X_n = i, T_0, T_1, \dots, T_n\}$
 $= \Pr \{X_{n+1} = j, T_{n+1} - T_n \leq t \mid X_n = i\}$; for all $n \geq 0$; $i, j \in E$ and $t > 0$.

The given data for a Markov renewal process is the semi-Markov kernel Q defined by:

$$Q(i, j, t) = \Pr \{X_{n+1} = j, T_{n+1} - T_n \leq t \mid X_n = i\}, \text{ for } i, j \in E \text{ and } t \geq 0$$

$$= \Pr \{X_{n+1} = j, \mid X_n = i\} \cdot \Pr \{T_{n+1} - T_n \leq t \mid X_{n+1} = j, X_n = i\}$$

$$= P_{ij} \cdot F_{ij}(t) \quad (2)$$

Where P_{ij} is the one-step transition probability of the Markov chain $\{X_n; n = 0, 1, 2, \dots\}$, and $F_{ij}(t) = \Pr \{T_{n+1} - T_n \leq t \mid X_{n+1} = j, X_n = i\}$.

2. Markov Renewal Equations

The Markov renewal equation is the generalization of a renewal equation where the distribution function in stead of being numerical is matrix valued based on the fact that the theory of Markov renewal process generalizes renewal process and Markov chain, and is a blend of the two. Recall that the renewal process generalizes the Poisson process by allowing the distribution function $F(t)$ to be any distribution function corresponding to a nonnegative random variable [4], [10].

2.1 Birth Equations

The transition function

$$P_{ij}(t) = \Pr \{X(t+s) = j \mid X(s) = i\} \quad (3)$$

from state i to state j which describes the stochastic evolution of a birth process $\{X(t); t \geq 0\}$ with birth rate $\lambda \geq 0$ satisfies a system of differential equations known as the forward kolmogorov equations given by [4], [10]:

$$P_j'(t) = \lambda P_{j-1}(t) - \lambda P_j(t); \quad j \geq 1 \quad (4)$$

$$P_0'(t) = -\lambda P_0(t) \quad (5)$$

with initial conditions

$$P_0(0) = 1; \quad P_j(0) = 0 \quad \text{for } j \geq 1$$

where

$$P_j(t) = \Pr \{X(t) = j\} \quad (6)$$

2.2 Birth and Death Equations

The transition function $P_{ij}(\cdot)$ defined above which describes the stochastic evolution of a birth-and-death process $\{X(t), t \geq 0\}$ (the

spread of the disease in this case) satisfies a system of difference differential equations known as the Chapman Kolmogorov equations given by [4], [10]:

$$P_n'(t) = -(\lambda_n(t) + \mu_n(t))P_n(t) + \lambda_{n-1}(t)P_{n-1}(t) + \mu_{n+1}(t)P_{n+1}(t); \quad n \geq 1$$

$$P_0'(t) = -\lambda_0(t)P_0(t) + \mu_1(t)P_1(t); \quad n = 0$$

2.3 Continuous Time Markov Chain Equations

Let $\{X(t); t \geq 0\}$ be a Continuous time Markov chain with state space $E \subset \{0, 1, 2, \dots\}$, recall that the transition function $P_{ij}(t)$ define by equation (2) represent the probability that a Continuous time Markov chain presently in state i at time t will be in state j at time $(t + s)$ [4], [10]. Define

$$q_j = \lim_{t \rightarrow 0} \frac{1 - P_{jj}(t)}{t}, \quad (8)$$

$$q_{kj} = \lim_{t \rightarrow 0} \frac{P_{kj}(t)}{t}; \quad k \neq j \quad (9)$$

According to [9], we have for all states i, j and time $t \geq 0$:

$$P_{ij}'(t) = \sum_{k \neq j} q_{kj} \cdot P_{ik}(t) - q_j \cdot P_{ij}(t) \quad (10)$$

This system of differential equations for $P_{ij}(t)$ is known as the forward kolmogorov equations for the Continuous time Markov chain $\{X(t); t \geq 0\}$. A complete discussion of uniqueness and limiting behavior solution of this system is given in [11].

المخلص

يعد أسلوب محاكاة المونت كارلو من الأدوات الحاسوبية الشائعة لتقليد وتتبع سلوك الأنظمة الحياتية المعقدة عبر تطورها مع الزمن. لقد تم تعريف متغيرات مسألة مرضية وبناء النموذج الرياضي لهذه المسألة، أما الحل العددي لهذا النموذج فقد تمت مقارنته مع المحاكاة الحاسوبية لعملية ماركوف التجديدية من نوع ولادة ووفاء، وتبين من خلال تفحص النتائج كفاءة أسلوب محاكاة المونت كارلو في وصف سلوك الأنظمة الواقعية الحياتية وعلى فترات زمنية ممتدة.