Solving Initial Value Problem by Using Simulation Technique

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Abstract:

The 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". The efficiency of simulation technique in the description of any real life system and through out extended time periods was obvious from the results.

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ملخص البحث :

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

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, (Giordano et al. 2003). 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. 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 (Uysal, 2003). To solve the disease problem we developed a method to generate sample path of the birth-and-death process as our objective.

Section (3) gives a review of the Markov renewal theory. The main results of this paper are presented in section 4.

Section (4) simulates the underlying stochastic process (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.

2. Differential Equations of a 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:

Popul = Susc + Sick + Cured

We shall use the approximate differential equation model (Korn and Wait, 1978):

$$\frac{dY_1}{dT} = -P_1 * Y_1 * Y_2$$

$$\frac{dY_2}{dT} = -P_1 * Y_1 * Y_2 - P_2 * Y_2 \qquad \qquad \qquad ...(1)$$

$$\frac{dY_3}{dT} = -P_2 * Y_2$$

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. Markov Renewal Theory:

The process $\{(X_n, T_n); n = 0, 1, 2, \ldots\}$ is a Markov renewal process with state space E if (Cinlar, 1975):

$$\Pr\{X_{n+1} = j, T_{n+1} - T_n \le t \mid X_o, X_1, \ldots, X_n = i, T_o, T_1, \ldots T_n\}$$

$$= \Pr\{X_{n+1} = j, T_{n+1} - T_n \le t \mid X_n = i\}; \text{ for all } n \ge 0 ; i, J \in E \text{ and } t > 0.$$

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

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

$$= \Pr\{X_{n+1} = j, \mid X_n = i\} . \Pr\{T_{n+1} - T_n \le t \mid X_{n+1} = J, X_n = i\}$$

$$= P_{ij} . F_{ij}(t) \qquad \ldots (2)$$

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

4. Numerical Simulation of a Disease Model:

We started by assuming the disease problem could be modeled as a Markov renewal 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. By (2) one would have to generate the state of a Markov chain using P_{ij} as the 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 continuos valued random variables $T_{n+1} - T_n$ from the distribution given by $F_{ij}(t)$. The transition function $P_{ij}(.)$ which describes the stochastic evolution of a birth-and-death process $\{X(t), t \ge 0\}$ (the spread of the disease in this case) satisfies

a system of difference differential equations know as the Chapman Kolmogorov equations given by (Heyman and Sobel, 1982):

$$\left.\begin{array}{l} \dfrac{d}{dt}P_n(t) = -\,(\lambda_n(t) + \mu_n(t))P_n(t) + \lambda_{n-1}(t)\,P_{n-1}(t) + \mu_{n+1}(t)\,P_{n+1}(t); \ n \geq 1 \\[4mm] \dfrac{d}{dt}P_o(t) = -\,\lambda_o(t)\,P_o(t) + \mu_1(t)\,P_1(t) \qquad\qquad\qquad\qquad\qquad ; \ n = 0 \end{array}\right\} \quad \dots (3)$$

In the following we present a simulation approximation of Markov renewal equations by providing a method of simulating birth-and-death process, by constructing sample paths of the process. Assignment to this set of paths a probability measure so that $P_{ij}(t)$ is determined as a simulation approximation of the solution of the Chapman Kolmogorov equations. Suppose $X(0)= i$, the process (disease) spends a random length of time, exponentially distributed with parameter $(\lambda_i + \mu_i)$ in a state i, and subsequently moves with probability $\lambda_i/(\lambda_i+\mu_i)$ to state (i+1) and with probability $\mu_i/(\lambda_i+\mu_i)$ to state (i-1), next the process (disease) sojourns a random length of time in the new state and then moves to one of neighboring states, and so on.

We observed a value T_1 from the exponential distribution with parameter $(\lambda_i+\mu_i)$ that fixes the initial sojourn time in state i. Then we toss a coin with probability of heads $P_i = \lambda_i / (\lambda_i + \mu_i)$. If heads (tails) appears we move the process to state i+1 (i-1). In state (i+1) we observed a value T_2 from the exponential distribution with parameter $(\lambda_{i+1} + \mu_{i+1})$ that fixed the sojourn time in the second state visited. If the process at the first transition enters, start (i-1) the subsequent sojourn time T_2 is an observation from the exponential distribution with parameter $(\lambda_{i-1} + \mu_{i-1})$.

After the second wait is completed, a binomial trial is performed that choose the next state to be visited and the process continues in the

same way. 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 $P_{ij}(t)$ is determined as a simulation approximation of the solution of (3) (Taylor and Karlin, 1984).

To implement the above method on a computer we first describe a procedure for sampling from the exponential distribution. Let X be the exponential random variable and F(x) be the distribution function, that is:

$$F(x) = Pr \{X \leq x\} = 1 - e^{-\lambda x}, X \geq 0 .$$

Set F(x) = U ; U is defined over the range 0 and 1. Now we show if U is a random variable uniformly distributed between 0 and 1, the variable X defined by $X = F^{-1}(U)$ has the commutative distribution F(x). Now

$$U = 1 - e^{-\lambda x} \quad \text{leads to} \quad X = - \ln (1-U) / \lambda$$

Since (1-U) is itself a random decimal number between 0 and 1 we use

$$X = - \frac{1}{\lambda} \ Ln \ U \qquad \qquad \dots(4)$$

as a generator of the sequence of random observations from the exponential distribution. The generation of uniformly distributed random numbers in the range [0,1) is based on the well-known congruential method (Taha, 2003):

$$x_i = a.x_{i-1} + c \ (mod \ m) ; \quad u_i = x_i / m$$

Rather than go into the theory of generation random numbers, we will merely state that all computer system have a subroutine available for generating random numbers. The constants in the procedure are (Naylor, 1971):

m = 2^{35} = 34359738368, a = 13493037709   and   c = 7261067085.

It will generate 2^{33} random numbers before repeating, for example we can generate n random numbers $x_1, x_2, \ldots, x_n$ 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 :

for i to n do

x = stats[random,uniform[0,1]]

The solution of (1) 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 Y3 = 70 is calculated by using the libraries of *Maple* so-called **RKF45** which use fourth and fifth order Runge-Kutta method (Burden et al., 2001). The results of this method are plotted in figure (1), while figure (2) shows the sample path of the disease.
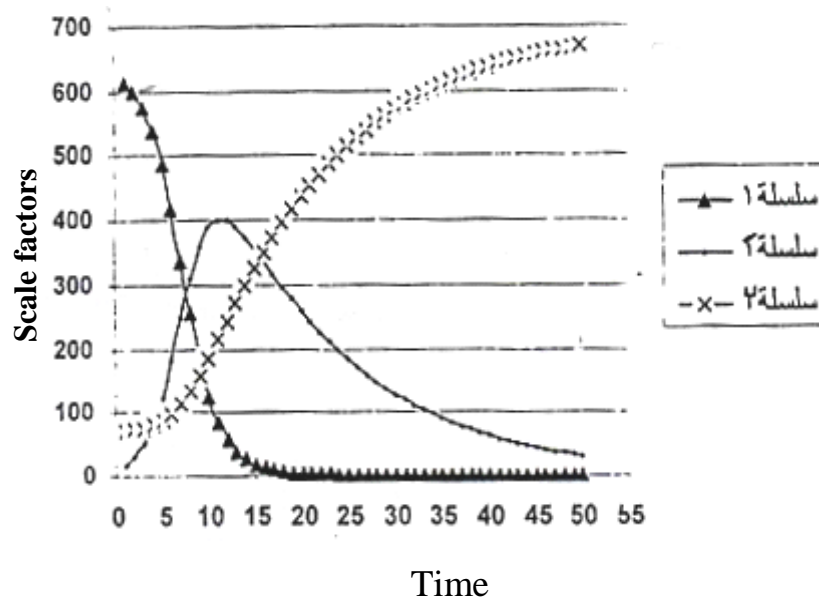
Fig. 1: Deterministic results of epidemic problem.

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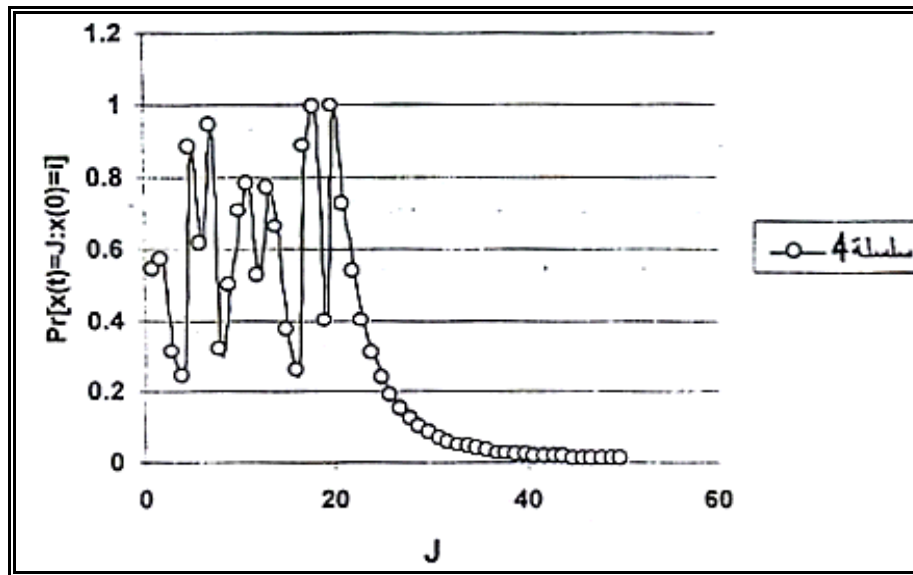
Fig. 2: Sample path of the epidemic behavior.

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. Notice that curve 1 represent the individuals susceptible to disease, curve 2 represent infectious carriers while curve 3 represent the individuals recovered and immune, finally curve 4 represent the behavior of the disease during time T.

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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