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Stochastic modeling of spreading an infection with standard incidence rate

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Abstract

This paper studies and models the random spread of an infection in a population. It extends the traditional deterministic modeling approach by incorporating discrete-time stochastic modeling using Markov chains. The probability of extinction and disease persistence is then investigated using the branching chain method, with a focus on a quantity in the non-random model, which is called the basic reproductive number. Moreover, the random model is transformed into a system of stochastic differential equations by approximating the probability distribution function using the forward Kolmogorov equation. An equivalent stochastic differential system is also introduced and examined for the stochastic model. Finally, numerical simulations of the stochastic models are conducted to evaluate the theoretical findings presented in the paper.

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1. Introduction

Infectious diseases have always been a challenge for human societies, causing significant mortality even in developed countries. It is crucial to study the factors contributing to their spread and explore control strategies, as new infections can emerge or previous ones can resurface and peak. Epidemic compartmental models with the aid of computer implementations are tools to study an infection in the population. These models, known as epidemic models, can be continuous or discrete [18, 27], using either differential equations or difference equations [28, 32], respectively, to describe the dynamics of infectious diseases in a population. In addition, the infection propagation in epidemic models may be in the form of standard, bi-linear, or a non-linear incidence rate [6, 17, 19, 33].

In epidemic modeling, according to the progress of the disease, the population is partitioned into some smaller population groups such as susceptible, recovered, removed, exposed, infected, quarantined individuals, etc. [1, 5, 30, 31]. The movements and transitions between these sub-populations, as well as demographic changes like birth, death, and migration are related to each other by mathematical equations. This creates a dynamic system that captures the behavior of that population during an epidemic [7, 9, 23]. One well-known epidemic model is the susceptible-infectious-susceptible (SIS) model, where infectious individuals can become susceptible after period of infection. This model has been extensively studied and as a framework to examine the impact of interventions like treatment, quarantine, or vaccination on the population under investigation [8, 12, 14, 16, 29, 36]. Vaccination, in particular, is a practical, highly effective, and affordable method, and its impact has been explored in various works by incorporating it into the SIS model. Some studies have formulated the model by considering some ordinary differential equations as a dynamical system [27, 35] while others have presented it as a set of difference equations [25, 26].

To capture the inherent randomness in the spread of infections, stochastic models offer a more realistic description of the phenomenon, as it has been used by many authors to describe real world phenomena. For instance, in [4] the severity of a global risk has been interpreted by formulating a stochastic model in which some random variables have been incorporated. In many stochastic SIS models, randomness is introduced by inserting a noise term into each of the ordinary differential equations or perturbing the model parameters. [10, 21, 37]. The diffusion coefficient in these models typically involves a diagonal matrix with non-

zero elements. However, other works have focused on discrete stochastic models formulated as Markov chain processes [11, 13, 22]. These models are obtained by stochastic extension of the deterministic modeling approach of a dynamical system. Allen and Burgin [3] analyzed and compared the dynamics of discrete stochastic and deterministic SIS models with constant and variable populations. The authors showed that when the extinction time of the disease is long and $\mathcal{R}_0 > 1$, there is a quasi-stationary distribution with a mean equal to the endemic steady state of the non-stochastic (deterministic) model. In [2], Allen explored two well-known epidemic models: SIS and SIR (Susceptible-Infectious-Removed) models with a constant population size. The stochastic extensions of these models were presented using Markov chains and stochastic differential equations (SDEs). The SDE model for the SIS model consisted of a single differential equation with one Wiener process, while the stochastic model for the SIR model involved a system of two stochastic differential equations with two independent Wiener processes. A study by Lismawati [20] introduced a stochastic model for a SIS model with two pathogens in two patches. The model was investigated using Markov chain processes, and the transition probabilities for the infection and dispersal processes were determined. Another paper [34] extended a deterministic SIV (Susceptible-Infectious-Vaccinated) epidemic model by incorporating noise terms in the equations and considering a saturated function for treatment. The near-optimal control for the stochastic SIV epidemic model using Markovian switching was studied, along with the sufficient and necessary conditions for near-optimality. The estimation of the error boundary of near-optimality was also provided.

In this study, we examine a population affected by an infectious disease and investigate the effect of the vaccination program within the context of an SIS epidemic model using the standard incidence rate. Our initial focus is on analyzing the extinction and persistence of the infection through a discrete stochastic model represented by a Markov chain process. Subsequently, we develop and discuss two stochastic differential systems for the model. The structure of this paper is as follows; The next section describes the deterministic model and its formulation and then gives some information about the model such as the equilibria and the basic reproductive ratio. Section 3 introduces the Markov chain model and establishes the conditions for extinction. In Section 4, we derive three stochastic models formulated as stochastic differential equations (SDEs). Following that, in the subsequent section, we examine and discuss the stochastic models through various examples, utilizing simulations,

diagrams, and histograms. Lastly, we conclude the paper in the final section by summarizing the obtained results and drawing conclusions.

2. Description of the deterministic model

Consider a population at a specific time t consisting of N individuals. Based on the disease status, the pepople can be divided into the three categories as follows: susceptible individuals, infected individuals, and vaccinated individuals. Each person in the population belongs to one of these classes and S, I, and V respectively denote the size of (number of individuals in) each sub-population at time t. The demographic changes include natural death with the rate φ, infection-induced death with the rate σ, and recruitment with entering λ individuals per unit of time. A proportion ν of newcomers are vaccinated as well as susceptible individuals, those are vaccinated with the rate ω. The vaccine is assumed to be temporary, and a vaccinated individual loses its immunity at a rate of δ, although the vaccine is perfect and vaccinated individuals do not get infected. The infection captures only susceptible individuals with standard incidence rate $\frac{\beta SI}{N}$ where β is contact rate, while individual recover from infection with rate η and return to the susceptible category. The described population can be modeled according to system (1) by a set of ordinary differential equations. This model is referred to as SIVS model, which indeed stands for an epidemic model that consists of the Susceptible, Infected, and Vaccinated compartments.

$$\begin{aligned} \dot{S} &= (1-\nu)\lambda - \frac{\beta SI}{N} - (\varphi+\omega)S + \eta I + \delta V, \\ \dot{I} &= \frac{\beta SI}{N} - (\varphi+\eta+\sigma)I, \\ \dot{V} &= \nu\lambda + \omega S - (\varphi+\delta)V. \end{aligned} \tag{1}$$

This model has been examined in previous studies [24, 27], where it was demonstrated that if we consider positive values for λ and φ, the region $\Lambda = \{[S,I,V] \in \mathbb{R} : S,I,V \geq 0, S + I + V \leq \frac{\lambda}{\varphi}\}$ serves as a positively invariant set for the system (1). When the initial values of the system lie within Λ, the solution of (1) remains within Λ for all times, since $\limsup_{t\to\infty} N(t) \leq \frac{\lambda}{\varphi}$. The basic reproduction number of (1) was provided as

$$\mathcal{R}_0 = \frac{\beta(\varphi(1-\nu)+\delta)}{(\varphi+\eta+\sigma)(\varphi+\delta+\omega)}, \tag{2}$$

and it was proved that the system always has the infection-free equilibrium

$$E^0 = [S^0, I^0, V^0] = \left[\frac{\lambda(\varphi(1-\nu)+\delta)}{\varphi(\varphi+\delta+\omega)}, 0, \frac{\lambda(\varphi\nu+\omega)}{\varphi(\varphi+\delta+\omega)}\right], \tag{3}$$

which is globally stable when $\mathcal{R}_0 < 1$. When $\mathcal{R}_0 > 1$, the infection-free equilibrium is unstable, and there exists a unique infected equilibrium. Furthermore, under some conditions, this infected equilibrium is globally stable:

$$E^* = [S^*, I^*, V^*] = \left[\frac{\lambda(\varphi+\eta+\sigma)}{\beta\varphi}\left(1-\frac{\sigma(\mathcal{R}_0-1)}{\varphi\mathbf{R}+\sigma(\mathbf{R}-1)}\right), \frac{\lambda(\mathcal{R}_0-1)}{\varphi\mathbf{R}+\sigma(\mathbf{R}-1)}, \frac{\nu\lambda}{\varphi+\delta}\left(1+\frac{\frac{\omega(\varphi+\sigma\nu+\delta)}{\nu(\varphi+\omega+\delta)}}{\varphi\mathbf{R}+\sigma(\mathbf{R}-1)}\right)\right], \tag{4}$$

in which

$$\mathbf{R} = \frac{\beta(\varphi+\delta)}{(\varphi+\eta+\sigma)(\varphi+\delta+\omega)}. \tag{5}$$

3. The Markov chain model

Consider that all demographic changes and interactions between compartments of the model occur probabilistically, despite the certain transitions in the deterministic model (1). As a result, a stochastic model

Table 1

All events in model (1) during the time interval $\hbar$ and their probabilities.

event	notation	population change	probability
recruitment	$b_S = (1-\nu)\lambda$	$\Delta Z^{(1)} = (1,0,0)$	$p_1 = b_S\hbar$
death in S	$d_S = \varphi S$	$\Delta Z^{(2)} = (-1,0,0)$	$p_2 = d_S\hbar$
infection	$m_{SI} = \frac{\beta SI}{N}$	$\Delta Z^{(3)} = (-1,1,0)$	$p_3 = m_{SI}\hbar$
vaccinating susceptible members	$m_{SV} = \omega S$	$\Delta Z^{(4)} = (1,0,-1)$	$p_4 = m_{SV}\hbar$
treatment	$m_{IS} = \eta I$	$\Delta Z^{(5)} = (1,-1,0)$	$p_5 = m_{IS}\hbar$
vaccine immunity lost	$m_{VS} = \delta V$	$\Delta Z^{(6)} = (1,0,-1)$	$p_6 = m_{VS}\hbar$
death in I	$d_I = (\varphi+\sigma)I$	$\Delta Z^{(7)} = (0,-1,0)$	$p_7 = d_I\hbar$
death in V	$d_V = \varphi V$	$\Delta Z^{(8)} = (0,0,-1)$	$p_8 = d_V\hbar$
vaccinating new members	$b_V = \nu\lambda$	$\Delta Z^{(9)} = (0,0,1)$	$p_9 = b_V\hbar$
no change		$\Delta Z^{(10)} = (0,0,0)$	$p_{10} = 1-\sum_{k=1}^{9} p_k$

arises. In this section, we examine the impact of randomness on the aforementioned model.

Let $Z=(S,I,V)$ denotes the number of susceptible, infected, and vaccinated individuals at time t, respectively, same as we considered in the deterministic SIVS model. Also, suppose the vector $\Delta Z = (\Delta S, \Delta I, \Delta V)$ shows the changes in the size of each sub-populations during time increment $\hbar$. From the system of ODEs (1) for deterministic SIVS model, we extract all possible changes. We list all such events in the unit of time $\hbar$ together with their probabilities according to Table 1.

The process $\{S(t), I(t), V(t)\}$ can be considered as a three-dimensional stochastic process in which the state at time t is determined by the vector $Z=(S,I,V)$ and the non-null transition probabilities between time t to time $t+\hbar$ can be obtained from Table 1:

$$\begin{aligned} p_{Z,Z+\Delta Z^{(n)}}(\hbar) &= \text{Probability}\{Z(t+\hbar)=Z+\Delta Z^{(n)} \mid Z\}=p_n, n=1,\ldots,9, \\ p_{Z,Z}(\hbar) &= \text{Probability}\{Z(t+\hbar)=Z \mid Z\}=p_{10}. \end{aligned} \tag{6}$$

In this section, we utilize the branching method to determine the probabilities of extinction and persistence for Markov chain $\{S(t), I(t), V(t)\}$. This method involves considering the dynamics of I near the infection-free equilibrium of the deterministic model and assuming the process $I(t)$ to be independent. At the infection-free equilibrium E^0 of the deterministic model, we have: $S^0=\frac{\lambda(\varphi(1-\nu)+\delta)}{\varphi(\varphi+\delta+\omega)}$ and $N^0=\frac{\lambda}{\varphi}$. We also notice that $\mathcal{R}_0 = \frac{\beta(\varphi(1-\nu)+\delta)}{(\varphi+\eta+\sigma)(\varphi+\delta+\omega)} = \frac{\beta S^0}{N^0(\varphi+\eta+\sigma)}$.

Therefore by letting $S(t)=S^0$, $V(t)=V^0$, the offspring probabilities of branching chain $\{I(t)\}$ is as follows (see Figure 1):

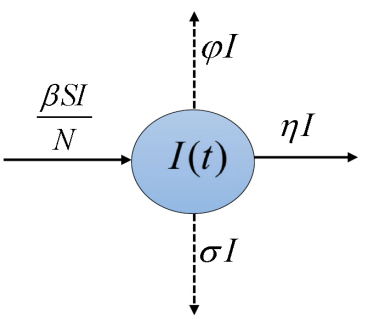

Figure 1

Process $I(t)$ with its possible transitions.

$$f(0)=\frac{\varphi+\eta+\sigma}{\frac{\beta S^0}{N^0}+(\varphi+\eta+\sigma)}=\frac{1}{\mathcal{R}_0+1},$$
$$f(2)=\frac{\frac{\beta S^0}{N^0}}{\frac{\beta S^0}{N^0}+(\varphi+\eta+\sigma)}=\frac{\mathcal{R}_0}{\mathcal{R}_0+1}, \tag{7}$$
$$f(k)=0, \text{for } k\in\mathbb{Z}^+ \text{ and } k\neq 0,2.$$

Thus the probability generation function of the offspring distribution can be found as

$$\begin{aligned}\phi(u)&=\sum_{n=0}^{\infty} f(n)u^n\\&=f(0)+f(2)u^2=\frac{\mathcal{R}_0}{\mathcal{R}_0+1}u^2+\frac{1}{\mathcal{R}_0+1},\end{aligned}$$

for $u\in[0,1]$. We obtain:

$$m=\phi'(1)=\frac{2\mathcal{R}_0}{\mathcal{R}_0+1},$$

and thus, $m\leq 1$ if and only if $\mathcal{R}_0\leq 1$ and $m>1$ if and only if $\mathcal{R}_0>1$. Therefore, the process $\{I(t)\}$ is absorbed to zero with probability 1 if and only if $\mathcal{R}_0\leq 1$, and with probability $\tilde{p}$ if and only if $\mathcal{R}_0>1$, in which $\tilde{p}$ is the smallest value in $(0,1]$ such that $\phi(\tilde{p})=\tilde{p}$. By solving the equation $\mathcal{R}_0u^2-(1+\mathcal{R}_0)u+1=0$, we find that $\tilde{p}=\frac{1}{\mathcal{R}_0}$. Thus,The above discussions lead to the following conclusion:

Theorem 3.1: *The discrete-time markov chain presentation of the stochastic SIVS epidemic model with transition probabities in Table 1,*

(I) *the necessary and sufficient condition for the extinction of infection with a probability equal to one is that* $\mathcal{R}_0\leq 1$.

(II) *assuming* $I(0)$ *as the initial number of infected individuals, the probability of infection extinction is obtained by*

$$\lim_{t\to\infty}\text{Probability}\{I(t)=0\}=\left(\frac{1}{\mathcal{R}_0}\right)^{I(0)},$$

if and only if $\mathcal{R}_0>1$.

4. The stochastic differential equation model

In this section, we will present the Markov chain model from the previous section as a system of stochastic differential equations. Let we show the state probability of the process $\{S(t),I(t),V(t)\}$ at time t as

$$P(t;Z)=P(t;z_1,z_2,z_3)=\text{Probability}\{S(t)=z_1,I(t)=z_2,V(t)=z_3\}.$$

Therefore, by considering all possible changes in the model according to Table 1, the state probability at $t+\hbar$ can be obtained as

$$P(t+\hbar;Z)=P(t;Z)+\hbar\sum_n C_n, \tag{8}$$

where

$$\begin{aligned}
C_1&=P(t;Z-\Delta Z^{(1)})\,b_S(t;Z-\Delta Z^{(1)})=P(t;z_1-1,z_2,z_3)b_S(t;z_1-1,z_2,z_3),\\
C_2&=P(t;Z-\Delta Z^{(2)})\,d_S(t;Z-\Delta Z^{(2)})=P(t;z_1+1,z_2,z_3)d_S(t;z_1+1,z_2,z_3),\\
C_3&=P(t;Z-\Delta Z^{(3)})\,m_{SI}(t;Z-\Delta Z^{(3)})=P(t;z_1+1,z_2-1,z_3)m_{SI}(t;z_1+1,z_2-1,z_3),\\
C_4&=P(t;Z-\Delta Z^{(4)})\,m_{SV}(t;Z-\Delta Z^{(4)})=P(t;z_1+1,z_2,z_3-1)m_{SV}(t;z_1+1,z_2,z_3-1),\\
C_5&=P(t;Z-\Delta Z^{(5)})\,m_{IS}(t;Z-\Delta Z^{(5)})=P(t;z_1-1,z_2+1,z_3)m_{IS}(t;z_1-1,z_2+1,z_3),\\
C_6&=P(t;Z-\Delta Z^{(6)})\,m_{VS}(t;Z-\Delta Z^{(6)})=P(t;z_1-1,z_2,z_3+1)m_{VS}(t;z_1-1,z_2,z_3+1),\\
C_7&=P(t;Z-\Delta Z^{(7)})\,d_I(t;Z-\Delta Z^{(7)})=P(t;z_1,z_2+1,z_3)d_I(t;z_1,z_2+1,z_3),\\
C_8&=P(t;Z-\Delta Z^{(8)})\,d_V(t;Z-\Delta Z^{(8)})=P(t;z_1,z_2,z_3+1)d_V(t;z_1,z_2,z_3+1),\\
C_9&=P(t;Z-\Delta Z^{(9)})\,b_V(t;Z-\Delta Z^{(9)})=P(t;z_1,z_2,z_3-1)b_V(t;z_1,z_2,z_3-1),\\
C_{10}&=P(t;Z)(-b_S-d_S-m_{SI}-m_{SV}-m_{IS}-m_{VS}-d_I-d_V-b_V)(t;Z).
\end{aligned}$$

By approximating these terms via their Taylor expansion about the point (z_1,z_2,z_3), up to the second derivative, we find

$$\begin{aligned}
C_1&=\left(1-\frac{\partial}{\partial z_1}+\frac{\partial^2}{2\partial z_1^2}\right)Pb_S(t;Z),\\
C_2&=\left(1+\frac{\partial}{\partial z_1}+\frac{\partial^2}{2\partial z_1^2}\right)Pd_S(t;Z),\\
C_3&=\left(1+\frac{\partial}{\partial z_1}-\frac{\partial}{\partial z_2}+\frac{\partial^2}{2\partial z_1^2}+\frac{\partial^2}{2\partial z_2^2}-\frac{\partial^2}{\partial z_1\partial z_2}\right)Pm_{SI}(t;Z),\\
C_4&=\left(1+\frac{\partial}{\partial z_1}-\frac{\partial}{\partial z_3}+\frac{\partial^2}{2\partial z_1^2}+\frac{\partial^2}{2\partial z_3^2}-\frac{\partial^2}{\partial z_1\partial z_3}\right)Pm_{SV}(t;Z),\\
C_5&=\left(1-\frac{\partial}{\partial z_1}+\frac{\partial}{\partial z_2}+\frac{\partial^2}{2\partial z_1^2}+\frac{\partial^2}{2\partial z_2^2}-\frac{\partial^2}{\partial z_1\partial z_2}\right)Pm_{IS}(t;Z),\\
C_6&=\left(1-\frac{\partial}{\partial z_1}+\frac{\partial}{\partial z_3}+\frac{\partial^2}{2\partial z_1^2}+\frac{\partial^2}{2\partial z_3^2}-\frac{\partial^2}{\partial z_1\partial z_3}\right)Pm_{VS}(t;Z),\\
C_7&=\left(1+\frac{\partial}{\partial z_2}+\frac{\partial^2}{2\partial z_2^2}\right)Pd_I(t;Z),\\
C_8&=\left(1+\frac{\partial}{\partial z_3}+\frac{\partial^2}{2\partial z_3^2}\right)Pd_V(t;Z),\\
C_9&=\left(1-\frac{\partial}{\partial z_3}+\frac{\partial^2}{2\partial z_3^2}\right)Pb_V(t;Z).
\end{aligned} \tag{9}$$

By substituting (9) into (8), we obtain

$$\begin{aligned}P(t+\hbar;Z) = P(t;Z) + \{&-\frac{\partial}{\partial z_1}\{P(b_S - d_S - m_{SI} - m_{SV} + m_{IS} + m_{VS})\}\\ &-\frac{\partial}{\partial z_2}\{P(m_{SI} - m_{IS} - d_I)\} - \frac{\partial}{\partial z_3}\{P(m_{SV} - m_{VS} - d_V + b_V)\}\\ &+\frac{1}{2}\frac{\partial^2}{\partial z_1^2}\{P(b_S + d_S + m_{SI} + m_{SV} + m_{IS} + m_{VS})\}\\ &+\frac{1}{2}\frac{\partial^2}{\partial z_2^2}\{P(m_{SI} + m_{IS} + d_I)\} + \frac{1}{2}\frac{\partial^2}{\partial z_3^2}\{P(m_{SV} + m_{VS} + d_V + b_V)\}\\ &+\frac{1}{2}\frac{\partial^2}{\partial z_1 \partial z_2}\{P(-2m_{SI} - 2m_{IS})\} + \frac{1}{2}\frac{\partial^2}{\partial z_1 \partial z_3}\{P(-2m_{SV} - 2m_{VS})\}\\ &+\frac{1}{2}\frac{\partial^2}{\partial z_2 \partial z_3}\{P(0)\}\}\hbar, \end{aligned} \tag{10}$$

where all calculations are at $(t;Z)$.

On the other hand, the expected value of random vector ΔZ is obtained as

$$\begin{aligned}\mathbb{E}[\Delta Z^T] &= \sum_{n=0}^{9} p_n (\Delta Z^{(n)})^T = \begin{bmatrix} b_S - d_S - m_{SI} - m_{SV} + m_{IS} + m_{VS} \\ m_{SI} - m_{IS} - d_I \\ m_{SV} - m_{VS} - d_V + b_V \end{bmatrix}\hbar\\ &= \begin{bmatrix} (1-\nu)\lambda - \dfrac{\beta SI}{N} - (\varphi+\omega)S + \eta I + \delta V \\ \dfrac{\beta SI}{N} - (\varphi+\eta+\sigma)I \\ \nu\lambda + \omega S - (\varphi+\delta)V \end{bmatrix}\hbar\\ &= \mathrm{M}\hbar. \end{aligned} \tag{11}$$

Moreover, the covariance matrix is given by

$$\begin{aligned}\mathbb{E}[\Delta Z^T \Delta Z] &= \sum_{n=0}^{9} p_n (\Delta Z^{(n)})^T Z^{(n)}\\ &= \begin{bmatrix} b_S + d_S + m_{SI} + m_{SV} + m_{IS} + m_{VS} & -m_{SI} - m_{IS} & -m_{SV} - m_{VS} \\ -m_{SI} - m_{IS} & m_{SI} + m_{IS} + d_I & 0 \\ -m_{SV} - m_{VS} & 0 & m_{SV} + m_{VS} + d_V + b_V \end{bmatrix}\hbar\\ &= \begin{bmatrix} (1-\nu)\lambda + \dfrac{\beta SI}{N} + (\varphi+\omega)S + \eta I + \delta V & -\dfrac{\beta SI}{N} - \eta I & -\omega S - \delta V \\ -\dfrac{\beta SI}{N} - \eta I & \dfrac{\beta SI}{N} + (\varphi+\eta+\sigma)I & 0 \\ -\omega S - \delta V & 0 & \omega S + (\varphi+\delta)V + \nu\lambda \end{bmatrix}\hbar\\ &= \Sigma\hbar, \end{aligned} \tag{12}$$

It is worth noting that $\mathbb{E}[\Delta Z^T]\mathbb{E}[\Delta Z]$ is of order $\hbar^2$ and can be considered negligible. Consequently, the equation (10) is stated in the following form:

$$\frac{\partial P(t;Z)}{\partial t} \approx \frac{P(t+\hbar;Z)-P(t;Z)}{\hbar} = -\sum_{r=1}^{3}\frac{\partial}{\partial z_r}\{P(t;Z)\mathrm{M}_r\} + \frac{1}{2}\sum_{r=1}^{3}\sum_{l=1}^{3}\frac{\partial^2}{\partial z_r \partial z_l}\{P(t;Z)\Sigma_{rl}\}, \tag{13}$$

where $(t;Z) = (t;z_1, z_2, z_3)$.

Now, let's assume that the matrix Σ can be expressed as $\Sigma = \Phi\Phi^T$, where Φ is an arbitrary matrix. By expanding Σ_{rl}, we have $\Sigma_{rl} = \sum_u \Phi_{ru}\Phi_{ul}^T = \sum_u \Phi_{ru}\Phi_{lu}$. Substituting this expression into equation (13), we obtain the modified form as follows:

$$\frac{\partial P(t;Z)}{\partial t} \approx -\sum_{r=1}^{3}\frac{\partial}{\partial z_r}\{P(t;Z)\mathrm{M}_r\} + \frac{1}{2}\sum_{r=1}^{3}\sum_{l=1}^{3}\frac{\partial^2}{\partial z_r \partial z_l}\{P(t;Z)\sum_u \Phi_{ru}\Phi_{lu}\}. \tag{14}$$

This relation indicates that $P(t;Z)$ approximately satisfies the Fokker-Planck equation, also known as forward Kolmogorov equation. Moreover, it can be demonstrated the probability distribution function $P(t;Z)$ which exactly satisfies the Fokker-Planck equation (14), and the distribution of solutions of system of SDEs

$$\mathrm{d}Z(t) = \mathrm{M}(t;Z)\mathrm{d}t + \Phi(t;Z)\mathrm{d}W(t), \tag{15}$$

with initial size of compartments as $Z(0)$, are identical. Here, $W(t)$ is a vector of three independent Wiener processes and matrices $\mathrm{M}(t;Z)$ and $\Phi(t;Z)$ can be obtained from (11) and (12), respectively. Consequently, the probability distribution of Markov chain $\{S(t), I(t), V(t)\}$ is approximately identical with distribution of solutions of SDE (15). Thus, in practical terms, our objective is to identify a matrix Φ such that $\Sigma = \Phi\Phi^T$:

Case 1: Consider a 3×9 matrix Υ in which k-th column is replaced by multiplication of $\Delta Z^{(k)}$ and the square root of multiple of $\hbar$ in p_k presented in Table 1:

$$\Upsilon = \begin{bmatrix} \sqrt{(1-\nu)\lambda} & -\sqrt{\varphi S} & -\sqrt{\frac{\beta SI}{N}} & -\sqrt{\omega S} & \sqrt{\eta I} & \sqrt{\delta V} & 0 & 0 & 0 \\ 0 & 0 & \sqrt{\frac{\beta SI}{N}} & 0 & -\sqrt{\eta I} & 0 & -\sqrt{(\varphi+\sigma)I} & 0 & 0 \\ 0 & 0 & 0 & \sqrt{\omega S} & 0 & -\sqrt{\delta V} & 0 & -\sqrt{\varphi V} & \sqrt{\nu\lambda} \end{bmatrix}. \tag{16}$$

We observe that $\Sigma = \Upsilon\Upsilon^T$, indicating that the matrix Υ can be employed in place of the matrix Φ within the stochastic differential equation (SDE) (15).

Case 2: The covariance matrix Σ is a positive definite symmetric matrix, and thus its unique Cholesky decomposition is of the form $\Sigma = LL^T$, where L is a lower-triangular matrix [15]. Consequently, the matrix Φ in (15) could be replaced by a the lower-triangular matrix L, whose components are:

$$\begin{aligned} L_{11} &= \sqrt{\Sigma_{11}}, \\ L_{21} &= \frac{\Sigma_{21}}{\sqrt{\Sigma_{11}}}, \quad L_{22} = \sqrt{\Sigma_{22} - \frac{\Sigma_{21}^2}{\Sigma_{11}}}, \\ L_{31} &= \frac{\Sigma_{31}}{\sqrt{\Sigma_{11}}}, \quad L_{32} = -\frac{\Sigma_{31}\Sigma_{21}}{\sqrt{\Sigma_{11}^2\Sigma_{22} - \Sigma_{11}\Sigma_{21}^2}}, \quad L_{33} = \sqrt{\Sigma_{33} - \frac{\Sigma_{31}^2\Sigma_{22}}{\Sigma_{11}\Sigma_{22} - \Sigma_{21}^2}}. \end{aligned} \tag{17}$$

5. Simulations

Example 5.1: We consider the following values for parameters in model (1): $\lambda = 60$, $\nu = 0.3$, $\beta = 0.7$, $\varphi = 0.05$, $\omega = 0.25$, $\sigma = 0.1$, $\eta = 0.2$, $\delta = 0.08$. With these values, we calculate $\mathcal{R}_0 = 0.61 < 1$, indicating that and the disease disappears in the deterministic model at the infection-free equilibrium E^0 = (363.16, 0, 836.84). Supposing $S(0) = 500$, $I(0) = 300$, and $V(0) = 50$ for initial population size in each category, the solution of system (1) using Euler scheme with a step size of $\hbar = 0.001$ is shown in Figure 2.

By choosing the contact rate as $\beta = 0.5$ we have $\mathcal{R}_0 = 0.43 < 1$. For this value for β and initial values for individuals close to the equilibrium, specifically as $S(0) = 360$, $I(0) = 10$, and $V(0) = 830$, the solution of the deterministic model is represented by the dashed lines in Figure 2. It can be observed that for various values for β and intial number of individuals, the solutions tend to converge towards the infection-free equilibrium E^0.

To obtain solutions for the stochastic counterparts of deterministic model (1) with the given parameter values and starting values for sub-populations similat to this example, we perform $10{,}000$ independent trials of stochastic methods using a step size of $\hbar = 0.01$. Then the approximate solution is given by the mean of these solutions.

To simulate the stochastic models described by SDE (15), we consider two cases: one with the matrix Υ and the other with the matrix L as the

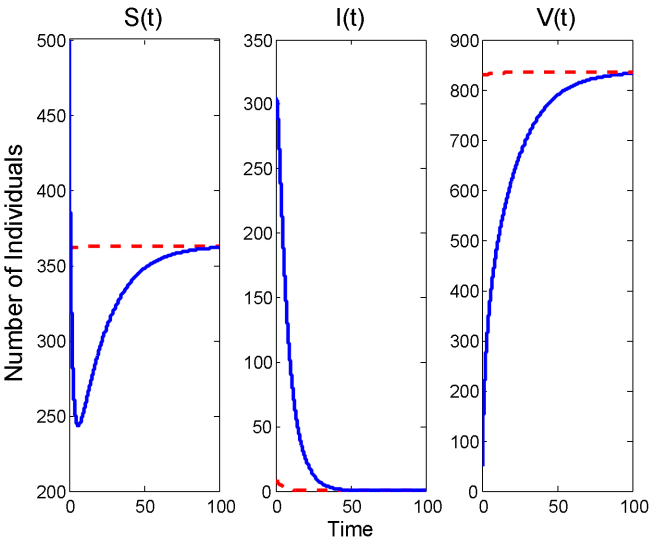

Figure 2

Solution of system (1) was derived as $(361.87, 0, 832.81)$ **with parameters values in Example 5.1 using Euler scheme with** $\hbar = 0.001$ **and initial values** $S(0) = 500$, $I(0) = 300$, **and** $V(0) = 50$ **by the time** $T = 100.$**. Here,** $\mathcal{R}_0 < 1$ **and the number of infectious individuals vanishes. Dashed lines show the solution for** $\beta = 0.5$ **and** $S(0) = 360$, $I(0) = 10$, **and** $V(0) = 830$.

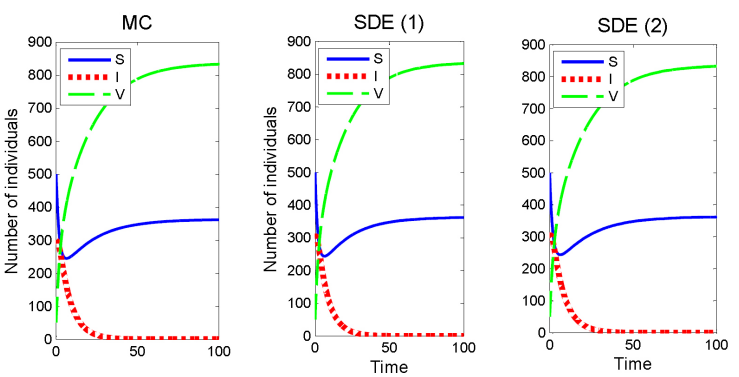

Figure 3

Solutions of stochastic SIVS models with parameters values same as in Example 5.1 over $10,000$ **independent trials with** $\hbar = 0.01$ **and starting values** $S(0) = 500$, $I(0) = 300$, **and** $V(0) = 50$. **From left to right: SDE model using matrix** Υ **in (16), and SDE model using matrix** L **in (17).**

diffusion matrix. In Case 1, where the matrix Υ is used as the matrix Φ, a nine-dimensional wiener process with mean zero and variance $\hbar$ is needed in each step. In contrast, in Case 2, where the matrix L is employed, a three-dimensional wiener process need to be generated at each step.

We utilize the Euler-Maruyama scheme to solve the SDEs for each trial. The averages solutions are labeled as **SDE (1)** and **SDE (2)** in the figures representing Case 1 and Case 2, respectively.

Table 2

Mean value (first column) and standard deviation (second column) for solutions of two stochastic models SDE (1) and SDE (2) for values considered for paremeters in Example 5.1 at time T = 100.

	stochastic model			
	SDE (1)		SDE (2)	
Variable	m.	s. d.	m.	s. d.
$S(T)$	361.85	18.89	361.44	19
$I(T)$	0	0	0	0
$V(T)$	832.92	29.24	832.43	29.19

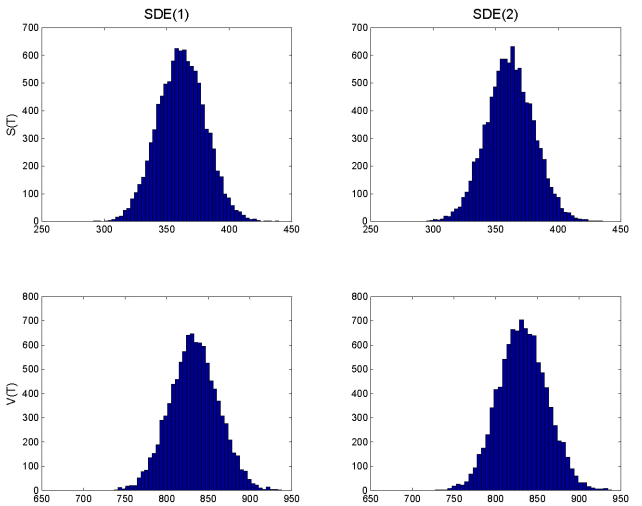

Figure 4

Histograms of S and V at time T = 100 for 10,000 independent simulations for stochastic models SDE (1) and SDE (2).

For two stochastic models, **SDE (1)** and **SDE (2)**, the mean value and the standard deviation of the solutions are displayed in Table 2. Also, Figure 3 presents the solutions of stochastic models for parameter values in Example 5.1. By examining these values along with the histograms illustrating the probability distribution of variables S and V at time $T = 100$ for all $10,000$ trajectories in Figure 4, it becomes evident that the solutions of these two stochastic models share the same distribution. Therefore, we can conclude that the two stochastic models, **SDE (1)** and **SDE (2)**, are equivalent.

Now, by setting the contact rate in Example 5.1 to $\beta = 0.5,$ and utilizing initial values for individuals close to E^0 such as $S(0) = 360,$ $I(0) = 10,$ and $V(0) = 830,$ we compare the solutions of the SDE models with those obtained by Monte Carlo simulations.

For simulating the Markov chain model, we employ the transition probabilities (6). In each trial, starting with the initial number of individuals, we assess the occurrence of all possible events in Table 1 during time intervals $\hbar$. An event is considered to occur if the generated uniform random variable is less than its corresponding probability. This procedure is repeated until the end time is reached, yielding the solution for a single trial. The average of all simulated trials is then regarded as the solution of the stochastic model (6), which is denoted as **MC** (solution for Markov Chain model) in the figures (see Figure 3).

In our calculations for each stochastic model, We utilize a total of 5000 independent paths. A path is considered to end, indicating the occurrence of extinction, when the number of infected individuals drops below one. The mean number of the number of individuals at the end of all paths is then taken as the solution of the stochastic model, while the mean of exit times provide insight into the duration of epidemic. Furthermore, we

Table 3

Mean value (first column) and standard deviation (second column) for stochastic models with $\beta = 0.5$ and other parameter valuse as in Example 5.1, starting from $S(0) = 360,$ $I(0) = 10,$ and $V(0) = 830.$

	stochastic model					
	MC		SDE (1)		SDE (2)	
Variable	m.	s. d.	m.	s. d.	m.	s. d.
$S(T)$	362.95	17.85	363.02	18.62	363.13	18.52
$I(T)$	0	0	0	0	0	0
$V(T)$	833.09	24.00	833.09	23.79	832.67	23.57

adjust the time interval $\hbar$ by halving it as long as the durations of epidemics in two last computations are sufficiently close.

Table 3 shows the mean value and standard deviation of simulations for the stochastic models, demonstrating a significant agreement between the calculations. It is worth noting that with the given parameter values, namely $\mathcal{R}_0 = 0.43 < 1$, the calculations indicate that the number of infected individuals vanishes in %100 of the paths, thus confirming Part (1) of Theorem 3.1.

Example 5.2: Let's modify the parameter values ν, β, and ω of model (1) in Example 5.1 to 0.125, 0.8, and 0.1, respectively. Consequently, we obtain $\mathcal{R}_0 = 1.23 > 1$, indicating that the disease persists in the deterministic model at the endemic equilibrium E^* = (369.36, 147.02, 362.53). Similar to Example 5.1, we present the results of simulations of Example 5.2 as follows. Figure 5 depicts the solutions of deterministic model with starting values for sub-populations as $S(0) = 500$, $I(0) = 300$, and $V(0) = 50$. The solutions of stochastic models **SDE (1)** and **SDE (2)**, along with the histograms of the solutions (at the final time $T = 100$) are shown in Figures 6 and 7, respectively. Moreover, the mean and standard deviation of solutions are given in Table 4. These results verify that two stochastic differential models are equivalent.

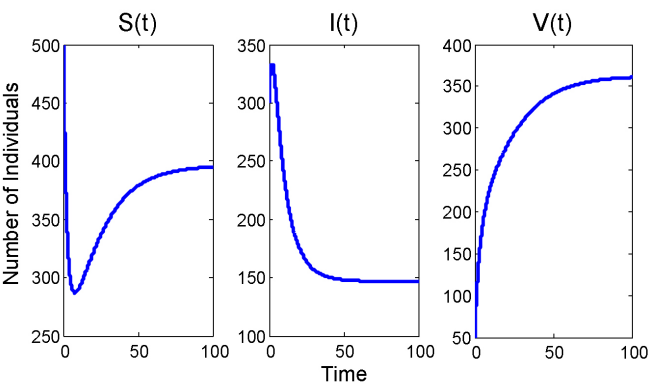

Figure 5

Solution of system (1) with parameters values in Example 5.2 was obtained as (394.96, 146.98, 360.80) by using Euler scheme with $\hbar = 0.01$ and starting size for sub-populations $S(0) = 500$, $I(0) = 300$, and $V(0) = 50$ until the final time $T = 100$. Here, $\mathcal{R}_0 > 1$ and the number of infectious individuals remains at a positive level.

Figure 4

Mean value (first column) and standard deviation (second column) for solutions of two stochastic models SDE (1) and SDE (2) at time $T = 100$ and for values of parameters as in Example 5.2.

	stochastic model			
	SDE (1)		SDE (2)	
Variable	m.	s. d.	m.	s. d.
$S(T)$	401.48	31.50	401.12	32.00
$I(T)$	143.03	24.71	142.94	24.85
$V(T)$	365.81	26.57	365.17	26.81

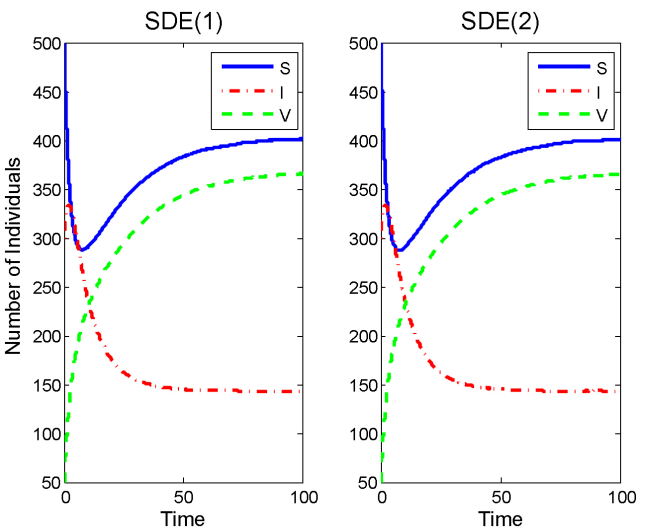

Figure 6

Solutions of stochastic SIVS models with parameters values same as in Example 5.2 over $10,000$ independent trials with $\hbar = 0.01$ and initial values $S(0) = 500$, $I(0) = 300$, and $V(0) = 50$. From left to right: SDE model using matrix Υ in (16), and SDE model using matrix L in (17).

Now, by setting the initial values for the number of individuals close to the endemic equilibrium of the deterministic model as $S(0) = 396$, $I(0) = 147$, and $V(0) = 363$, we simulate three stochastic models up to time $T = 50$ using 1000 independent paths. The mean value and standard deviation of the solutions, presented in Table 5, demonstrate that the stochastic models yield very similar results.

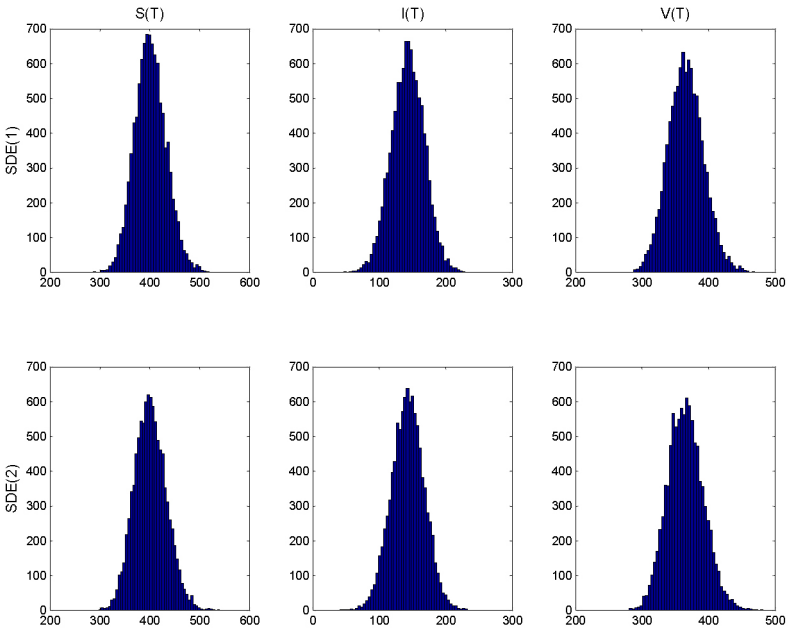

Figure 7

Histograms of S, I, and V at time $T = 100$ for $10,000$ independent simulations in stochastic differential models.

Table 5

Mean value (first column) and standard deviation (second column) for stochastic models at time T = 50 and parameter values in Example 5.2.

	stochastic model					
	MC		SDE (1)		SDE (2)	
Variable	m.	s. d.	m.	s. d.	m.	s. d.
$S(T)$	401.33	31.33	401.72	30.87	402.30	31.62
$I(T)$	143.53	24.99	142.91	24.88	142.59	24.97
$V(T)$	366.17	26.61	367.46	26.84	366.73	25.92

6. Summary and conclusions

We conducted a study on an SIS epidemic model that incorporates a vaccination program. This model accounts for the spread of infection in a population of varying size, following the standard incidence rate. Our

approach involved examining the stochastic aspects of the model through the introduction of a Markov chain as a stochastic process. We explored the extinction and persistence of this stochastic model by relating it to the basic reproduction number of the deterministic model. It was established that when the reproduction number is less than or equal to unity, extinction occurs with a probability of one. However, when the reproduction number exceeds unity, there is a positive probability of extinction. Furthermore, we expressed the stochastic model using a system of stochastic differential equations. We found that the probability distribution function of the Markov chain model closely approximates the distribution of solutions from the stochastic differential equation model. To ensure equivalence between the two systems, we introduced two diffusion matrices for the stochastic differential system. To validate our findings, we conducted simulations of the deterministic model and the stochastic models in various numerical examples. The deterministic model was solved using the Euler method, while the Markov chain model was solved using the Monte Carlo approach. Solutions for the stochastic differential models were obtained using the Euler-Maruyama method. Through these simulations and the corresponding histograms of the solutions, we confirmed that the two stochastic differential models are numerically equivalent, supporting our theoretical proof of equivalence.

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