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Numerical study on a stochastic model for simulating the transmissibility of Zika virus

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Abstract

In this paper we develop and analyze a mathematical model for the transmission of Zika virus. Firstly we construct stochastic environment because of parameters random essence, and introduce Zika epidemic model in stochastic form. Moreover, the equilibria of the system is considered. Additionally, the disease-free equilibrium point of the model and biologically feasible region for this dynamical system are presented. Finally, using numerical simulations, we were able to illustrate the analytical results obtained herein.

Keywords: Zika virus, stochastic modeling, stochastic differential equation, transmission simulation
Mathematics Subject Classification [2010]: 92C60, 93A30, 60H10

1 Introduction

In recent years, One of the interesting topics in mathematical sciences is modeling the behavior of real phenomena, including chemistry [4,11], biology [5,6], mathematical finance [8,10] and physics [3,14]. Modeling of infectious diseases is considered as an important tool to describe dynamics of transmission. Mathematical models are powerful tools for achieving precise observation to the transmission and control of infectious diseases. Zika is a flavivirus transmitted to humans through either the bite of infected Aedes mosquitoes or sexual intercourse with infected individuals. The first large outbreak of disease caused by Zika infection was reported from the Island of Yap in 2007. Moreover the World Health Organization (WHO) declared that Zika virus is transmitted through infected blood as well as through sexual contact with an infected person. Many mathematical models and statistical methods have been employed to understand the transmission dynamics of Zika Virus. Recently, Zika virus gained a lot of attention due to its fast spread of associated diseases.(For example see [1,2,12,13,15]). One of the common methods for considering and to describing dynamics of transmission is the use of ordinary differential equations (ODE), but there are some restrictions compared to stochastic models. The deterministic models make assumptions about the expected value of parameters in future, but they ignore the variation and fluctuation about the expected value of parameters. In this paper, we establish a model for investigation of the Zika transmission based on stochastic version of the Zika model with additional degree of realism. This paper is organized as follows. In Section 2, preliminaries and notations are presented. In Section 3, the model of transmission of Zika virus and the process of the implementation stochastic form are presented. In Section 3, we present dynamical analysis of solution. In last part of this section, equilibria of the system is presented and finally, Section 4 is devoted to introducing some numerical simulation to validate our theoretical results.

[1]speaker

2 Stochastic Zika Virus Model

In this work, we consider a mathematical model for Zika virus transmission dynamics. This model consists of nine differential equations. In this section, we formulate a stochastic mathematical model for Zika virus transmission based on three populations. In human population, we use a sex-structured mathematical model. Based on their disease status, sexually active male (N_M) and female (NF) individuals are grouped into different disjoint classes. Classes of susceptible male and female individuals are denoted by S_M and S_F , respectively. The classes I_M and I_F stand for infectious male and female individuals, respectively. We grouped recovered male and female individuals from Zika virus in R_M and R_F classes,respectively. Thus,

$$N_H = N_M + N_F, \qquad N_M = S_M + I_M + R_M, \qquad N_F = S_F + I_F + R_F.$$

In the mosquito population (N_V), the susceptible, latent and infected classes of Zika virus are denoted by S_V, E_V and I_V ,respectively. Hence, we have

$$N_V = S_V + E_V + I_V.$$

Also, the model parameters and their definitions are given in Tab. 1. To describe the mechanism of the

Table 1: Description of parameters

β_1	Sexual transmission rate from infectious males to susceptible female individuals
β_2	Mosquito-to-human transmission rate
β_3	Human-to-mosquito transmission rate
β_4	Sexual transmission rate from infectious females to susceptible male individuals
γ	Human recovery rate
μ	Mosquito death rate
Λ	Mosquito recruitment rate
α	Mosquito transition rate from latent to infectious class

spread of Zika virus, we consider the deterministic mathematical model as follows [13]:

$$\begin{aligned}
dS_M &= -(\beta_2 I_v + \beta_4 I_F) S_M dt \\
dI_M &= ((\beta_2 I_v + \beta_4 I_F) S_M - \gamma I_M) dt \\
dR_M &= \gamma I_M dt \\
dS_F &= -(\beta_1 I_M + \beta_2 I_v) S_F dt \\
dI_F &= ((\beta_1 I_M + \beta_2 I_v) S_F - \gamma I_F) dt \\
dR_F &= \gamma I_F dt \\
dS_v &= (\Lambda - \beta_3 (I_M + I_F) S_v - M S_v) dt \\
dE_v &= (\beta_3 (I_M + I_F) S_v - (\alpha + \mu)) dt \\
dI_v &= (\alpha E_v - \mu I_v) dt
\end{aligned}$$

We can provide an additional degree of realism by defining the white noise and Brownian motion and introduce a stochastic model. Therefore, we implement this idea by replacing random parameters

$$\begin{cases} \beta_1 \to \beta_1 + \sigma_1 \dot{B}_1(t) \\ \beta_2 \to \beta_2 + \sigma_2 \dot{B}_2(t) \\ \beta_3 \to \beta_3 + \sigma_3 \dot{B}_3(t) \\ \beta_4 \to \beta_4 + \sigma_4 \dot{B}_4(t) \end{cases} \qquad \begin{cases} \gamma \to \gamma + \sigma_5 \dot{B}_5(t) \\ M \to M + \sigma_6 \dot{B}_6(t) \\ \Lambda \to \Lambda + \sigma_7 \dot{B}_7(t) \\ \alpha \to \alpha + \sigma_8 \dot{B}_8(t) \end{cases}$$

where $B_i(t)$ and σ_i, $i = 1, 2, \ldots, 6$ are the Brownian motions and the intensities of the white noises, respectively. These parameters are selected for implementation of stochastic environment because of their random

essence. So, we present the following modified model with stochastic approach for Zika virus:

$$\begin{aligned}
ds_M &= -(\beta_2 I_v + \beta_4 I_F)S_M dt - \sigma_2 I_v S_M dB_2(t) - \sigma_4 I_F S_M dB_4(t),\\
dI_M &= ((\beta_2 I_v + \beta_4 I_F)S_M - \gamma I_M)dt + \sigma_2 I_v S_M dB_2(t) + \sigma_4 I_F S_M dB_4(t)\\
&\quad -\sigma_5 I_M dB_5(t),\\
dR_M &= \gamma I_M dt + \sigma_5 I_M dB_5(t),\\
dS_F &= -(\beta_1 I_M + \beta_2 I_v)S_F dt - \sigma_1 I_M S_F dB_1(t) - \sigma_2 I_v S_F dB_2(t),\\
dI_F &= ((\beta_1 I_M + \beta_2 I_v)S_F - \gamma I_F)dt + \sigma_1 I_M S_F dB_1(t) + \sigma_2 I_v S_F dB_2(t)\\
&\quad -\sigma_5 I_F dB_5(t),\\
dR_F &= \gamma I_F dt + \sigma_5 I_F dB_5(t),\\
dS_v &= (\Lambda - \beta_3(I_M + I_F)S_v - \mu S_v)dt + \sigma_7 dB_7(t) - \sigma_3(I_M + I_F)S_v dB_3(t),\\
&\quad -\sigma_6 S_v dB_6(t),\\
dE_v &= (\beta_3(I_M + I_F)S_v - (\alpha + \mu)dt + \sigma_3(I_M + I_F)S_v dB_3(t) - \sigma_8 E_v dB_8(t),\\
&\quad -\sigma_6 E_v dB_6(t),\\
dI_v &= (\alpha E_v - M I_v)dt + \sigma_8 E_v dB_8(t) - \sigma_6 I_v dB_6(t).
\end{aligned} \tag{1}$$

3 Existence of the Solution

In this section, dynamical analysis of the solution of the introduced model in section 2 and the equilibria of system are presented.

Theorem 3.1. *The coefficient of stochastic differential equation* (1) *are locally Lipschitz.*

Proof. Now we define the following kernels

$$\nu(S_M, t) = -\beta_2 I_v S_M$$
$$\varepsilon(S_M, t) = -\beta_4 I_F S_M$$

So we shoud prove Lipschitz condition for the kernels ν and ε. We assume $\Phi(S_M(t), I_v(t)) = -\beta_2 I_v S_M$, first we set $d = (I_v, S_M)$. Then we have $\Phi(d) = -I_v(t).S_M(t)$ and $\Phi(d) \in C^1(\Omega, \mathbb{R})$.
Therefore we must prove

$$\forall d_1, d_2 \in \Omega, \exists K > 0 : \|\Phi(d_2) - \Phi(d_1)\| \leq K \|d_2 - d_1\| \tag{2}$$

Now we choose suitable subset of Ω and consider $N(x, r)$ as an open ball centered at x and with radius r, such that

$$N(x, r) = \{y| \ \|y - x\| \leq r\}$$

Then we continue our proof by applying: $d_1, d_2 \in N(x, r) \subset \Omega \subset \mathbb{R}^2$. Since $\Phi(d)$ is unbounded therefore, due to (2) , we replace K with K_x which depends on x.
So we define the path $\psi : [0, 1] \to N(x, r)$ such that $\psi(t) = (1 - t)d_1 + td_2$
So we consider following increment from d_1 to d_2:

$$\|\Phi(d_2) - \Phi(d_1)\| = \|\Phi(\psi(1)) - \Phi(\psi(0))\| = \int_0^1 \frac{d\Phi(\psi(t))}{dt} dt$$

Where $\dfrac{d\Phi(\psi(t))}{dt} = \nabla\Phi(\psi(t))\psi'(t) = \nabla\Phi(\psi(t))(d_2 - d_1)$

Then we have:

$$\begin{aligned}
\left\| \int_0^1 \frac{d\Phi(\psi(t))}{dt} dt \right\| &= \left\| \int_0^1 \nabla\Phi(\psi(t))(d_2 - d_1) dt \right\|\\
&\leq \int_0^1 \|\nabla\Phi(\psi(t))\| \, \|d_2 - d_1\| \, dt\\
&= \|d_2 - d_1\| \int_0^1 \|\nabla\Phi(\psi(t))\| \, dt\\
&\leq K_x \|d_2 - d_1\| .
\end{aligned}$$

where $K_x > \sup\{\|\nabla\Phi(d)|d \in N(x,r)\|\}$.
As a result, there is no global Lipschitz constant K valid on all of $\Omega = \mathbb{R}^2$ in this case ,thus $\Phi(d)$ is in fact locally Lipschitz. Therefore, we have local Lipschitz condition for the coefficient of $dB_1(t)$ and similarly this condition will be proved for the coefficient of dB_2, dB_3 and dB_4.
So our Model contains stochastic differential equations with Lipschitz coefficient and we can obtain strong solution and for each initial value, the solution will be unique. □

3.1 Equilibria of the System

Equilibrium is a state of system which does not change. Equilibria of the system can be estimated by setting the all derivatives equal to zero. In order to obtain the fixed points of Zika model (1), firstly we consider following system

$$\begin{aligned}
\frac{S_M}{1+(\beta_2 I_v+\beta_4 I_F)\phi} &= S_M\\
\frac{(\beta_2 I_v+\beta_4 I_F)\phi S_M + I_M}{1+\gamma\phi} &= I_M\\
\gamma\phi I_M + R_M &= R_M\\
\frac{S_F}{1+(\beta_1 I_M+\beta_2 I_v)\phi} &= S_F\\
\frac{(\beta_1 I_M+\beta_2 I_v)\phi S_F + I_F}{1+\gamma\phi} &= I_F\\
\gamma\phi I_F + R_F &= R_F\\
\frac{\Lambda\phi + S_v}{1+(\beta_3(I_M+I_F)+\mu)\phi} &= S_v\\
\frac{\beta_3(I_M+I_F)\phi S_v + E_v}{1+(\alpha+\mu)\phi} &= E_v\\
\frac{\alpha\phi E_v + I_v}{1+\mu\phi} &= I_v
\end{aligned}$$

and gives

$$(S_M^k, I_M^k, R_M^k, S_F^k, I_F^k, R_F^k, S_v^k, E_v^k, I_v^k) = (S_{M_0}, 0, 0, S_{F_0}, 0, 0, \frac{\Lambda}{\mu}, 0, 0).$$

Accorrding to [13], Zika virus model (1) is a dynamical system on the biologically feasible region

$$\begin{aligned}
\Omega = \{&(S_M, I_M, R_M, S_F, I_F, R_F, S_v, E_v, I_v) \in \mathbb{R}_+^9 :\\
&0 \le S_M + I_M + R_M + S_F + I_F + R_F = N_H = \text{const}, \text{ and } 0 \le S_v + E_v + I_v = N_v \le \Lambda/\mu\}.
\end{aligned}$$

4 Simulation Results

In order to illustrate our analytical results, we prepare a numerical simulation. The results of implementation are given by the following Euler–Maruyama method [7]. Consider the following discretization model for

$t = 0, \Delta t, 2\Delta t, \ldots, n\Delta t,$

$$\begin{aligned}
dS_M &= -(\beta_2 I_v + \beta_4 I_F)S_M\Delta t - \sigma_2 I_v S_M \Delta B_2(t) - \sigma_4 I_F S_M \Delta B_4(t),\\
dI_M &= ((\beta_2 I_v + \beta_4 I_F)S_M - \gamma I_M)\Delta t + \sigma_2 I_v S_M \Delta B_2(t) + \sigma_4 I_F S_M \Delta B_4(t)\\
&\quad -\sigma_5 I_M \Delta B_5(t),\\
dR_M &= \gamma I_M \Delta t + \sigma_5 I_M d\Delta_5(t),\\
dS_F &= -(\beta_1 I_M + \beta_2 I_v)S_F\Delta t - \sigma_1 I_M S_F \Delta B_1(t) - \sigma_2 I_v S_F \Delta B_2(t),\\
dI_F &= ((\beta_1 I_M + \beta_2 I_v)S_F - \gamma I_F)\Delta t + \sigma_1 I_M S_F \Delta B_1(t) + \sigma_2 I_v S_F \Delta B_2(t) -\\
&\quad \sigma_5 I_F \Delta B_5(t),\\
dR_F &= \gamma I_F \Delta t + \sigma_5 I_F \Delta B_5(t),\\
dS_v &= (\Lambda - \beta_3(I_M + I_F)S_v - \mu S_v)\Delta t + \sigma_7 \Delta B_7(t) - \sigma_3(I_M + I_F)S_v \Delta B_3(t),\\
&\quad -\sigma_6 S_v \Delta B_6(t),\\
dE_v &= (\beta_3(I_M + I_F)S_v - (\alpha + \mu)\Delta t + \sigma_3(I_M + I_F)S_v \Delta B_3(t) - \sigma_8 E_v \Delta B_8(t),\\
&\quad -\sigma_6 E_v \Delta B_6(t),\\
dI_v &= (\alpha E_v - \mu I_v)\Delta t + \sigma_8 E_v \Delta B_8(t) - \sigma_6 I_v \Delta B_6(t).
\end{aligned} \tag{3}$$

Where $\Delta B_i(t) \sim \sqrt{\Delta t} Z_i$ and $Z_i \sim \mathcal{N}(0,1)$, $i = 1, 2, \ldots, 4$. In the other words, Z is the Gaussian random variable. The source code has been carried out using MATLAB R2020a.

Example 4.1. In this section, using numerical results, we investigate the behavior of the solution of the transmission model of Zika virus obtained from system (2). In order to illustrate the adaptation and compatibility of the presented model with deterministic model. The numerical values of the model parameters are given in Tab. 2. The graphical representations demonstrated in Fig.1 exhibit the efficiency and adaptation

Table 2: The parameter values used in numerical simulations of model

α	β_1	β_2	β_3	β_4	γ	μ	λ
0.167	0.024	0.242	0.326	0.100	0.333	0.050	5000

of our model with the deterministic model.

5 Conclusion and Remarks

In this paper, we have analyzed a model for simulating transmissibility of the Zika virus. We use the white noise and Brownian motion to construct the corresponding stochastic model for the transmission of the Zika virus. We established a stochastic model for Zika virus with additional degree of realism. Finally, disease-free equilibrium point of the model and biologically feasible region for this dynamical system is presented. Finally, the numerical simulations are carried out to demonstrate efficiency of our model, and the possibility of comparability of the stochastic model with the deterministic model. This paper could lead to other studies that have included random and uncertainty of the model and may be more consistent with the reality of the transmission of the Zika virus.

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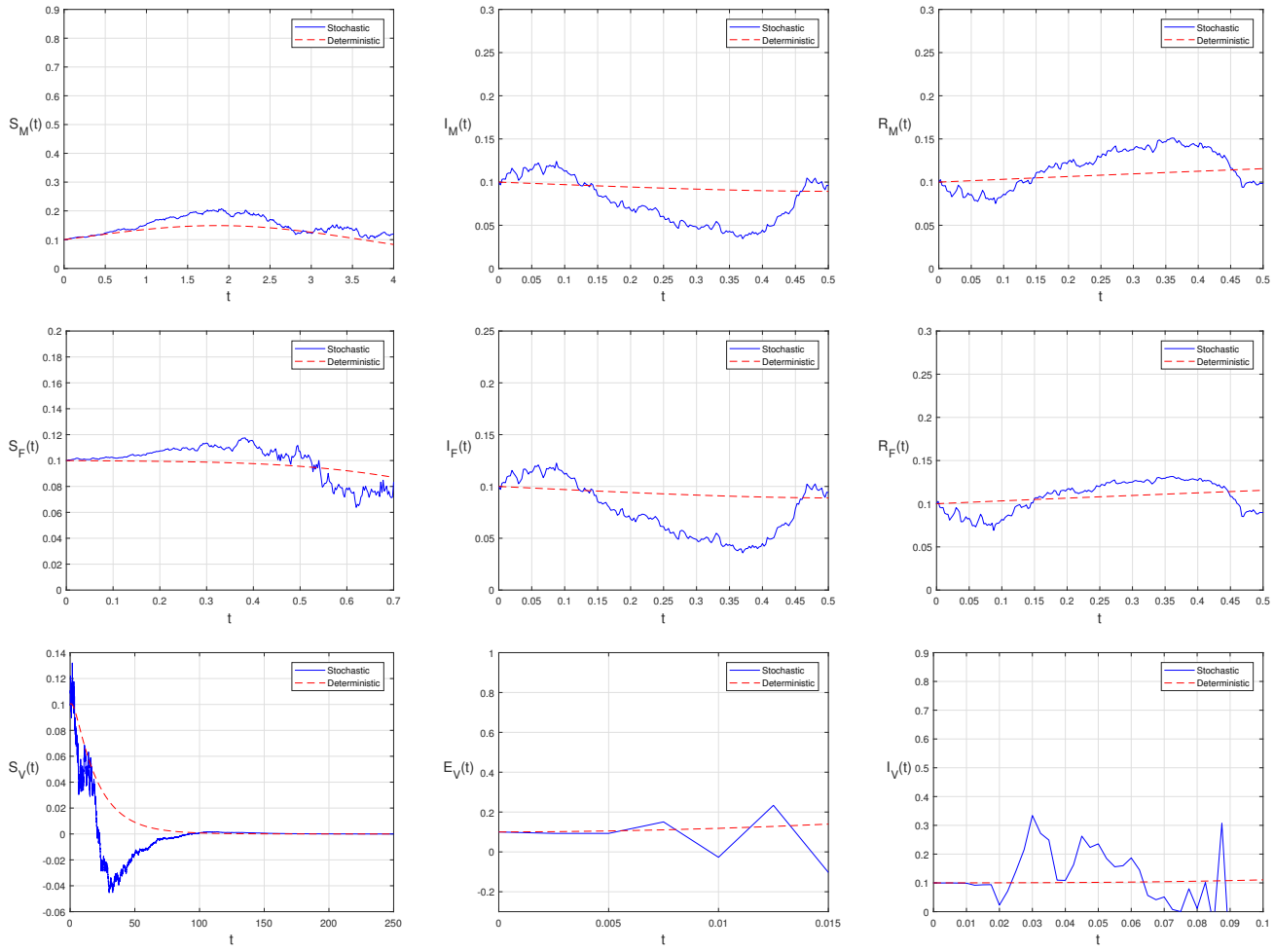

Figure 1: Comparison between the our presented stochastic model and deterministic model

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