A MODIFICATION OF APPROXIMATE RANDOM CHARACTERISTICS FOR A MODEL OF ZIKA VIRUS TRANSMISSION

by

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In this study, a theoretical model of Zika virus transmission is investigated with random parameters. The parameters of a deterministic model are transformed to random variables to obtain a system of random differential equations. The approximate solutions of the model are analyzed with modified random differential transformation method. It is seen that modified random differential transformation method performs better than random differential transformation method on long time intervals.

Key words: *random effect, random differential equations, Zika virus, differential transformation method*

Introduction

Mathematical models of disease transmission have become an especially popular research area in the twentieth century with the emergence of diseases such as AIDS and Hepatitis C. Epidemics such as the Ebola virus and the Coronavirus pandemic have also increased the number of studies in this field. Transmission dynamics of such diseases can be analyzed through the modelling of disease spread. Hence, numerous infectious diseases have been studied mathematically using compartmental models. One such study was given for Zika virus which causes an infectious disease that is spread by the Aedes mosquitoes. Most people infected with the Zika virus do not show any symptoms [1]. Zika virus infection can become an extremely dangerous scenario during pregnancy since it can cause Microcephaly or brain malformations in infants. Infection during pregnancy can also cause miscarriages or preterm birth as well [1].

Zika virus disease has been modeled many times using compartmental models to analyze different aspects of the disease. Bonyah *et al.* [2] have given a SIIIRR type model for the co-infection of dengue fever and Zika virus. Rezapour *et al*. [3] have given a SISI type model with Caputo derivative. Khan *et al*. [4] have given a SEIAR type based model for analyzing the dynamics of the case with asymptomatic Zika virus carriers. Biswas *et al*. [5] have used a seven-compartment model for analyzing the effects of vector control. Alzahrani *et al*. [6] have given a model for optimal control strategies. Kumar *et al*. [7] have given a SEIR type based model for temperature and rainfall dependent modelling of Zika progression. The current trend

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in modelling Zika virus transmission is the use of SEIR type based models with additional compartments for vector and host populations. Another perspective for analyzing the spread of Zika virus is to model the transmission considering the random dynamics of infection. Deterministic models neglect the random nature of disease transmission although it is known that the spread of diseases are affected by environmental factors such as temperature. Random effects can be implemented into the system to model the variations in disease dynamics. The motivation for such an analysis is the previous studies of the authors [8, 9]. Using a random framework, it is possible to analyze various random disease characteristics such as expected time for disease eradication or expected spread of disease in the total population as well as other concepts in engineering [10].

In this study, the deterministic model of Khan *et al*. [4] will be analyzed under random effects to model the theoretical random spread of Zika virus. Although recent studies on modelling mainly focus on the use of fractional calculus [11-13], our approach will transform the parameters of the deterministic differential equation system to random variables to obtain random equations. The obtained random model will be analyzed with modified random differential transformation method (MRDTM) to investigate the random dynamics of disease transmission. The MRDTM is the modification of DTM in the random framework using Laplace-Pade modification technique. Random DTM has been used to analyze random differential equations by many researchers [14, 8]. Its modification, MRDTM, is an improved method for obtaining approximate characteristics of random equations. This method will be applied to investigate the approximate random dynamics of Zika virus transmission.

Model of Zika virus transmission

The deterministic model used in this study is a theoretical model given by Khan *et al*. [4]. The system of ordinary differential equations is given:

$$\begin{aligned}
&\frac{\mathrm{d}S_H}{\mathrm{d}t} = \Lambda_H - \beta_H S_H (I_V + \rho I_H) - \mu_H S_H, \quad \frac{\mathrm{d}E_H}{\mathrm{d}t} = \beta_H S_H (I_V + \rho I_H) - (\mu_H + \chi_H) E_H \\
&\frac{\mathrm{d}I_H}{\mathrm{d}t} = \chi_H \varphi E_H - (\mu_H + \gamma + \eta) I_H, \quad \frac{\mathrm{d}R_H}{\mathrm{d}t} = \gamma I_H - \mu_H R_H, \quad \frac{\mathrm{d}A_H}{\mathrm{d}t} = \chi_H (1-\varphi) E_H - \mu_H A_H \\
&\frac{\mathrm{d}S_V}{\mathrm{d}t} = \Lambda_V - \beta_V S_V I_H - \mu_V S_V, \quad \frac{\mathrm{d}E_V}{\mathrm{d}t} = \beta_V S_V I_H - (\mu_V + \delta_V) E_V, \quad \frac{\mathrm{d}I_V}{\mathrm{d}t} = \delta_V E_V - \mu_V I_V
\end{aligned} \tag{1}$$

In eq. (1), the total host population N_H and the total vector population N_V are divided into compartments similar to the SEIR model with an additional compartment for asymptomatic humans. The S_H is the susceptible humans, E_H – the exposed humans, I_H – the infected humans, R_H – the recovered humans, and A_H – the asymptomatic carriers. Similarly S_V is the susceptible mosquitoes, E_V – the exposed mosquitoes, and I_V – the infected mosquitoes. The parameters of equation system (1) and their deterministic values for the numerical analysis are given: Λ_H – the human recruitment rate (100 day^{-1}), β_H – the human infection probability (0.02 day^{-1}), ρ – the effective contact rate (0.02 day^{-1}), μ_H – the human natural death rate [1/(365×67.7) day^{-1}], χ_H – the rate of humans becoming infectious (0.02 day^{-1}), φ – the proportion of humans to I_H or A_H (0.013 day^{-1}), γ – the human recovery rate (0.001 day^{-1}), η – the human treatment rate (0.002 day^{-1}), Λ_V – the mosquito recruitment rate (0.02 day^{-1}), β_V – the mosquito infection probability (0.0002 day^{-1}), μ_V – the mosquito natural death rate (1/21), and δ_V – the rate of exposed mosquitoes becoming infectious (0.1 day^{-1}). The initial conditions are given as $S_H(0) = 40$, $E_H(0) = 12$, $I_H(0) = 5$, $R_H(0) = 1$, $A_H(0) = 2$, $S_V(0) = 40$, $E_V(0) = 7$, and $I_V(0) = 0.5$. The values of the parameters have been obtained from the referred study [4].

Random parameters for Zika virus transmission

The equation system (1) neglects the random nature of disease transmission by assuming that the parameters Λ_H, β_H, ρ, μ_H, χ_H, φ, γ, η, Λ_V, β_V, μ_V, and δ_V are constant values. These parameters are transformed into the following random variables:

$$\Lambda_H^* = \Lambda_H + s_1 z_1,\ \beta_H^* = \beta_H + s_2 z_2,\ \rho^* = \rho + s_3 z_3,\ \mu_H^* = \mu_H + s_4 z_4,\ \chi_H^* = \chi_H + s_5 z_5$$

$$\varphi^* = \varphi + s_6 z_6,\ \gamma^* = \gamma + s_7 z_7,\ \eta^* = \eta + s_8 z_8,\ \Lambda_V^* = \Lambda_V + s_9 z_9,\ \beta_V^* = \beta_V + s_{10} z_{10}$$

$$\mu_V^* = \mu_V + s_{11} z_{11},\ \delta_V^* = \delta_V + s_{12} z_{12}$$

Here, $s_i, i = \overline{1,12}$ denote the standard deviations of the random parameters whereas $z_i, i = \overline{1,12}$ are independent standard normal random variables. Standard normally distributed z_i means that the random parameters have normal distribution with their mean values equal to the values given previously and their variances equal to s_i^2. If these random parameters are replaced with the deterministic ones in system (1), a random model is obtained. The random model enables the analysis of random disease dynamics such as the expected value for the time until disease eradication or the expected value of maximum number of infected humans.

Modified random differential transformation method

The modified random DTM has been recently introduced and the method relies upon the Laplace-Pade modification of the random DTM [8]. Assume that the fourth order stochastic process $u(t)$, $t \in T$ has a mean fourth derivative of a non-negative integer order k at $t \in T$ denoted by $u^{(k)}(t)$. The random differential transform of $u(t)$ is given:

$$U(k) = \frac{1}{k!}\left[\frac{\mathrm{d}^k(u(t))}{\mathrm{d}t^k}\right]_{t=t_0} \tag{2}$$

where $U(k)$ is the transformed process. The inverse transform of U is given:

$$u(t) = \sum_{k=0}^{\infty} U(k)(t-t_0)^k \tag{3}$$

where eqs. (2) and (3) are well-defined [15] and the derivative is in the mean-square sense.

Theorem 1. [15] Assume that $f^{(k)}(t)$ and $g^{(k)}(t)$, which are the k^{th} order mean fourth derivatives of the fourth order stochastic processes $f(t)$, $t \in T$ and $g(t)$, $t \in T$, respectively, exist at $t \in T$. The transformations of some operations under random DTM are given as follows. Note that here, F and G are the transformed processes for $f(t)$ and $g(t)$:

(i) If $u(t) = f(t) \pm g(t)$, then the random differential transform of $u(t)$ is given as $U(k) = F(k) \pm G(k)$.
(ii) If λ is a fourth order random variable and $u(t) = \lambda f(t)$, then $U(k) = \lambda F(k)$.
(iii) If

$$u(t) = \frac{\mathrm{d}^m[g(t)]}{\mathrm{d}t^m},\ \text{then}\ U(k) = (k+1)...(k+m)G(k+m)$$

(iv) If $u(t) = f(t)g(t)$, then its random differential transform is given:

$$U(k) = \sum_{n=0}^{k} F(n)G(k-n)$$

Deterministic and random DTM are generally used in applications with the selection of $t_0 = 0$. Also, the series solution (3) is truncated for a finite series representation:

$$u(t) = \sum_{k=0}^{n} U(k)t^k \tag{4}$$

The remainder term is known to be negligibly small [16]. The expected value and variance of $u(t)$ are given [14]:

$$E[u(t)] = \sum_{k=0}^{n} E[U(k)]t^k, \; Var[u(t)] = \sum_{i=0}^{n}\sum_{j=0}^{n} Cov[U(i),U(j)]t^{i+j} \tag{5}$$

where

$$Cov[U(i),U(j)] = E[U(i)U(j)] - E[U(i)]E[U(j)] \quad \text{for } i, j = 0,1,...,n$$

Since expected value and variance are non-random functions, the following Laplace-Pade modification can be applied to the approximate expected value and variance of a random variable. Consider the power series representation of a function $f(t)$ given as

$$f(t) = \sum_{k=0}^{\infty} f_k t^k$$

The Pade approximant is a polynomial fraction:

$$\left[\frac{L}{M}\right] = \frac{P_L(t)}{Q_M(t)}$$

where P_L and Q_M are polynomials of degrees up to L and M, respectively [17]. Hence, the approximation for $f(t)$ can be shown:

$$f(t) = \sum_{k=0}^{\infty} f_k t^k = \frac{p_0 + p_1 t + p_2 t^2 + p_3 t^3 + \ldots + p_L t^L}{q_0 + q_1 t + q_2 t^2 + q_3 t^3 + \ldots + q_M t^M} + \mathcal{O}(t^{L+M+1}) \tag{6}$$

It is known that the orders L and M are uniquely determined [18, 19] and every selection leads to a new approximation.

Approximate random dynamics of Zika transmission

Using model (1) with random parameters and *Theorem 1*, we obtain the random differential transform of Zika model as follows. Here, we use a theoretical 5% coefficient of variation for the random parameters, meaning the standard deviations $s_i, i = \overline{1, 12}$ are appointed values that are 5% of their deterministic quantities. Note that $\delta(k) = 1$ for $k = 0$ and $\delta(k) = 0$ elsewhere:

$$(k+1)S_H(k+1) = \Lambda_H^*\delta(k) - \beta_H^*\sum_{m=0}^{k} I_V(m)S_H(k-m) - \beta_H^*\rho^*\sum_{m=0}^{k} I_H(m)S_H(k-m) - \mu_H^* S_H(k)$$

$$(k+1)E_H(k+1) = \beta_H^*\sum_{m=0}^{k} I_V(m)S_H(k-m) + \beta_H^*\rho^*\sum_{m=0}^{k} I_H(m)S_H(k-m) - (\mu_H^* + \chi_H^*)E_H(k)$$

$$(k+1)I_H(k+1) = \chi_H^*\varphi^* E_H(k) - (\mu_H^* + \gamma^* + \eta^*)I_H(k)$$

$$(k+1)R_H(k+1) = \gamma^* I_H(k) - \mu_H^* R_H(k), \; (k+1)A_H(k+1) = \chi_H^*(1-\varphi^*)E_H(k) - \mu_H^* A_H(k) \tag{7}$$

$$(k+1)S_V(k+1) = \Lambda_V^*\delta(k) - \beta_V^*\sum_{m=0}^{k} I_H(m)S_V(k-m) - \mu_V^* S_V(k)$$

$$(k+1)E_V(k+1) = \beta_V^*\sum_{m=0}^{k} I_H(m)S_V(k-m) - (\mu_V^* + \delta_V^*)E_V(k)$$

$$(k+1)I_V(k+1) = \delta_V^* E_V(k) - \mu_V^* I_V(k)$$

The numbers of infected people and recovered people will be monitored since these two quantities are the most important signs of the course of the disease. Deterministic DTM, using a 5-term approximation, gives the following approximate results for $I_H(t)$ and $R_H(t)$:

$$\begin{aligned} I_H(t) &= 5 + 0.01599765686t - 0.002520951497t^2 + 0.0009210499217t^3 + 0.0002314389370t^4 \\ R_H(t) &= 1 + 0.004959531373t + 0.000007898475720t^2 - (8.404237123t^3 + 2.302709831t^4)\cdot 10^{-7} \end{aligned} \tag{8}$$

The result for $R_H(t)$ with the random DTM is obtained as follows for a 5-term approximation (from now on, the random variables are shown without the stars to overcome further complexity):

$$R_H(t) = 1 - (\mu_H + 5\gamma)t + \left(\frac{1}{2}\mu_H^2 - \frac{5}{2}\eta\gamma - 5\gamma\mu_H - \frac{5}{2}\gamma^2 + 6\chi_H\gamma\varphi\right)t^2 + \ldots \tag{9}$$

Thus, the expected value of eq. (9) becomes:

$$E(R_H) = E\left[1 - (\mu_H + 5\gamma)t + (0.5\mu_H^2 - 2.5\eta\gamma - 5\gamma\mu_H - 2.5\gamma^2 + 6\chi_H\gamma\varphi)t^2 + \ldots\right] \tag{10}$$

Note that the random variables are assumed to be independent from each other. Up to fourth moments are present in eq. (10) for the random variables. Since these are normally distributed random variables, we use the moment generating function (MGF) of a normal random variable $X(m, n^2)$ to obtain these higher moments given as $M_X(t) = e^{mt+}(n^2t^2)/2$. Using this function, the necessary moments for $\gamma \sim N(1000, 50^2)$ are calculated as: $E(\gamma) = 0.001$, $E(\gamma^2) = 1.0025\cdot 10^{-6}$, $E(\gamma^3) = 1.0075\cdot 10^{-9}$, and $E(\gamma^4) = 1.01501875\cdot 10^{-12}$. Higher moments for the other random variables are calculated similarly using the MGF. If the expected value operator is distributed in eq. (10) we get:

$$E(R_H) = 1 - \left[E(\mu_H) + 5E(\gamma)\right]t +$$
$$\left[\frac{1}{2}E(\mu_H^2) - \frac{5}{2}E(\eta)E(\gamma) - 5E(\gamma)E(\mu_H) - \frac{5}{2}E(\gamma^2) + 6E(\chi_H)E(\gamma)E(\varphi)\right]t^2 + \ldots$$

which gives:

$$\begin{aligned} E(R_H) = 1 &+ 0.004959531373303t + 7.892227768524795\cdot 10^{-6}t^2 - \\ &- 8.430135329197320\cdot 10^{-7}t^3 + 2.306362034574825\cdot 10^{-7}t^4 \end{aligned} \tag{11}$$

for a 5-term approximation. Similarly for $I_H(t)$, we get:

$$\begin{aligned} I_H(t) = 5 &+ \left(12\chi_H\varphi - 5\eta - 5\gamma - 5\mu_H\right)t + \left(10\chi_H\varphi\beta_H + 100\beta_H\rho\chi_H\varphi - 12\chi_H\varphi\mu_H - 6\chi_H^2\varphi - \right. \\ &\left. - 6\chi_H\eta\varphi - 6\chi_H\gamma\varphi + \frac{5}{2}\eta^2 + 5\eta\gamma + 5\eta\mu_H + \frac{5}{2}\gamma^2 + 5\gamma\mu_H + \frac{5}{2}\mu_H^2\right)t^2 + \ldots \end{aligned} \tag{12}$$

Similar calculations yield:

$$\begin{aligned} E(I_H) = 5 &+ 0.015997656866514t - 0.002528720237242t^2 + \\ &+ 9.225086766503972\cdot 10^{-4}t^3 + 2.311805261542818\cdot 10^{-4}t^4 \end{aligned} \tag{13}$$

The approximate expected values for recovered humans eq. (11) and infected humans eq. (13) are polynomials and contain growing errors as $t \to \infty$. Modifications of eqs. (11) and (13) give better approximations depending on the selection of $[L, M]$ in eq. (6). The modified approximate expected value for the recovered humans is obtained for $[L, M] = [3, 2]$:

$$E(R_H) = 2.198303839 - 1.198312090\mathrm{e}^{(-0.5402141375t)}\sinh(0.5360716536t) - \\ -1.198303839\mathrm{e}^{(-0.5402141375t)}\cosh(0.5360716536t) \tag{14}$$

The deterministic solution of model obtained by MATLAB, the approximate expected value eq. (11) and the modified approximate expected value eq. (14) are shown in fig. 1(a).

It is seen that the modified approximate expected value (14) performs better than the approximate expected value (11). Considering the value of the deterministic result for the recovered humans is 4.835 whereas eq. (11) gives 23.8 at $t = 100$, the relative error of the approximate expected value (11) is obtained as

$$100 \times \frac{|23.8 - 4.835|}{4.835} = 392.2441\%$$

at $t = 100$. The result for the modified approximate expected value eq. (14) at $t = 100$ is 1.406, resulting in the relative error:

$$100 \times \frac{|1.406 - 4.835|}{4.835} = 70.9204\%$$

It is seen that MRDTM decreases the relative error at $t = 100$ from 392.2441% to 70.9204%, more than five times for the selection of $[L, M] = [3, 2]$.

The modified approximate expected value for R_H is obtained for $[L, M] = [4, 2]$:

$$E(R_H) = 0.004926460403t + 0.00007222916466\mathrm{e}^{(-0.1239331706t)}\sin(0.5058567270t) + \\ +0.00002797161940\mathrm{e}^{(-0.1239331706t)}\cos(0.5058567270t) + 0.9999720284 \tag{15}$$

The modified expected value eq. (15) for recovered humans is shown in fig. 1(b).

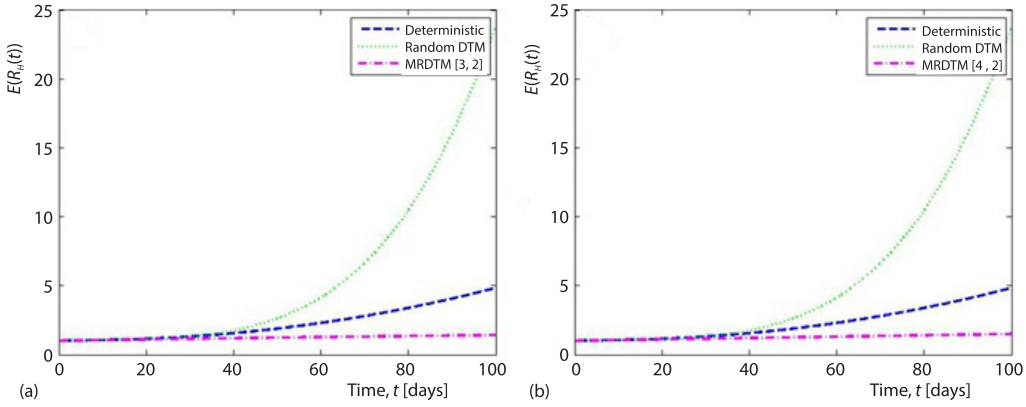

Figure 1. Approximate expected value eq. (11) its modification eq. (14) obtained with $[L, M] = [3, 2]$ (a) and eq. (15) obtained by using with $[L, M] = [4, 2]$ (b)

Since eq. (15) gives 1.493 at $t = 100$, the relative error is obtained:

$$100 \times \frac{|1.493 - 4.835|}{4.835} = 69.1210\%$$

The selection of [L, M] = [4, 1] gives the following modified approximate expected value for recovered humans:

$$E(R_H) = 0.004963754946t + 0.000003859805296\mathrm{e}^{(-1.094341642t)} - \\ -0.00001020324336t^2 + 0.9999961402 \tag{16}$$

Equation (16) gives 1.394 at t = 100, resulting in the following relative error

$$100 \times \frac{|1.394 - 4.835|}{4.835} = 71.1686\%$$

The selection of [L, M] = [2, 1] yields:

$$E(R_H) = 2.558302178 - 1.558302178\mathrm{e}^{(-0.003182650607t)} \tag{17}$$

Equation (17) gives 1.425 (t = 100), hence the relative error for eq. (17) is obtained as

$$100 \times \frac{|1.425 - 4.835|}{4.835} = 70.5274\%$$

Even the selection of [L, M] = [1, 1] gives the modified expected value $E(R_H) = \mathrm{e}^{(0.004959531374t)}$ which gives 1.642 at t = 100, resulting in the following relative error

$$100 \times \frac{|1.642 - 4.835|}{4.835} = 66.0393\%$$

The results of recovered humans for the deterministic case, the approximate expected value of recovered humans eq. (11) and the modified approximate expected values have been given in tab. 1.

Table 1. Comparison of the results for the modified expected values

t	Deterministic	Random DTM	[3, 2]	[4, 2]	[4, 1]	[2, 1]	[1, 1]
0.0	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
0.5	1.0025	1.0025	1.0025	1.0025	1.0025	1.0025	1.0025
1.0	1.0050	1.0050	1.0049	1.0050	1.0050	1.0050	1.0050
1.5	1.0075	1.0075	1.0074	1.0074	1.0074	1.0074	1.0075
2.0	1.0099	1.0099	1.0099	1.0099	1.0099	1.0099	1.0100
2.5	1.0124	1.0124	1.0123	1.0123	1.0123	1.0123	1.0125
3.0	1.0149	1.0149	1.0148	1.0148	1.0148	1.0148	1.0150
3.5	1.0175	1.0175	1.0172	1.0173	1.0172	1.0173	1.0175
4.0	1.0200	1.0200	1.0197	1.0197	1.0197	1.0197	1.0200
4.5	1.0225	1.0225	1.0221	1.0222	1.0221	1.0222	1.0226
5.0	1.0250	1.0250	1.0246	1.0246	1.0246	1.0246	1.0251

It is seen that all of the modifications produce similar results to the approximate expected value (11) for $t \in [0, 5.]$ Hence, it can be concluded that MRDTM works as effectively as random DTM for small values of t. However, fig. 1 and the relative error percentages show that for growing values of t, MRDTM works approximately up to 5-6 times better than random DTM for recovered humans.

Similar results can be seen for the results of infected humans $I_H(t)$. The modified approximate expected value for the infected humans is obtained for $[L, M] = [2, 2]$:

$$E(I_H) = 0.6000000000\left[8.347623190\sinh(0.5455836518t) + \right.$$
$$\left. + 8.333333335\cosh(0.5455836518t)\right]\mathrm{e}^{(-0.5433196780t)} \tag{18}$$

The deterministic result for the infected humans is 83.05 at $t = 100$, whereas the approximate expected value eq. (13) gives 24020 at $t = 100$. Hence, the relative error for the approximate expected value eq. (13) is obtained:

$$100 \times \frac{|24020 - 83.05|}{93.05} = 28822\%$$

which means that there is a *huge* amount of error in eq. (13) for large values of t. This situation can be seen in fig. 2(a). The result for the modified expected value eq. (18) is obtained as 6.276 ($t = 100$), resulting in the relative error:

$$100 \times \frac{|6.276 - 83.05|}{93.05} = 92.4431\%$$

It is seen that MRDTM decreases the relative error a $t = 100$ from 28822% to 92.4431%, about more than approximately 300 times for the selection of $[L, M] = [2, 2]$. The modified approximate expected value for the infected humans is obtained for $[L, M] = [3, 1]$:

$$E(I_H) = -0.004222298907\mathrm{e}^{(-1.094437411t)} + 0.01137661557t + 5.004222299 \tag{19}$$

The modified expected value eq. (19) for infected humans is shown in fig. 2(b), eq. (19) gives 6.142 at $t = 100$, hence, the relative error is obtained:

$$100 \times \frac{|6.142 - 83.05|}{93.05} = 92.6045\%$$

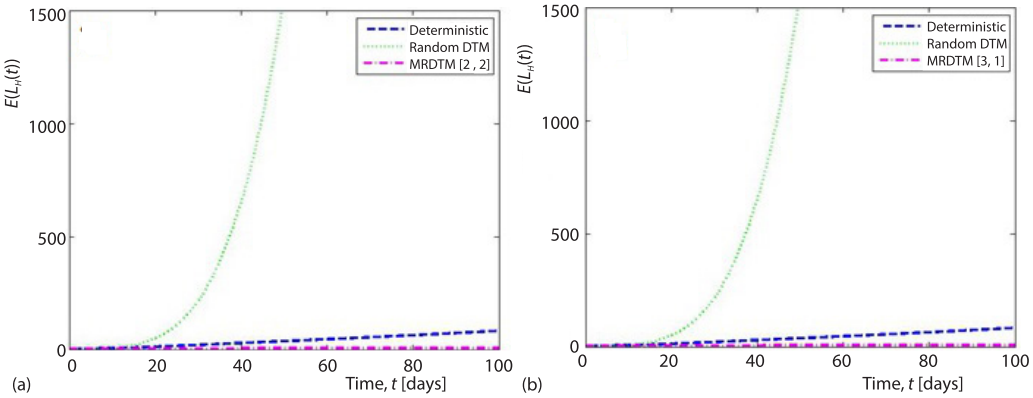

Figure 2. Approximate expected value eq. (13) and its modification eq. (18) obtained with $[L, M] = [2, 2]$ (a) and eq. (19) obtained with $[L, M] = [3, 1]$ (b)

The selection of $[L, M] = [2, 1]$ gives the following modified approximate expected value for I_H:

$$E(I_H) = -0.05060366577\mathrm{e}^{(-0.3161363264t)} + 5.050603666 \tag{20}$$

Equation (20) gives 5.051 at $t = 100$, meaning that the relative error is obtained:

$$100 \times \frac{|5.051 - 83.05|}{93.05} = 93.9181\%$$

The selection of $[L, M] = [1, 1]$ gives the following modified approximate expected value for infected humans: $E(I_H) = 5e^{(0.0031995313741)}$ which gives 6.885 at $t = 100$, meaning that the relative error is obtained:

$$100 \times \frac{|6.885 - 83.05|}{93.05} = 91.7098\%$$

The results of infected humans for the deterministic case, the approximate expected value of infected humans eq. (13) and the modified approximate expected values have been given in tab. 2.

Table 2. Comparison of the results for the modified expected values

t	Deterministic	Random DTM	[2, 2]	[3, 1]	[2, 1]	[1, 1]
0.0	5.0000	5.0000	5.0000	5.0000	5.0000	5.0000
0.5	5.0075	5.0075	5.0075	5.0075	5.0074	5.0080
1.0	5.0146	5.0146	5.0142	5.0142	5.0137	5.0160
1.5	5.0226	5.0226	5.0205	5.0205	5.0191	5.0241
2.0	5.0330	5.0330	5.0265	5.0265	5.0237	5.0321
2.5	5.0477	5.0476	5.0324	5.0324	5.0276	5.0402
3.0	5.0689	5.0689	5.0382	5.0382	5.0310	5.0482
3.5	5.0993	5.0993	5.0440	5.0439	5.0339	5.0563
4.0	5.1419	5.1418	5.0498	5.0497	5.0363	5.0644
4.5	5.1998	5.1996	5.0555	5.0554	5.0384	5.0725
5.0	5.2767	5.2766	5.0612	5.0611	5.0402	5.0806

Once again, it is seen that the modified approximate expected values produce similar results to the approximate expected value eq. (13) within $t \in [0, 5]$. This time interval is a purely hypothetical choice and it can be shown that MRDTM works as effectively as random DTM for small values of t. However, fig. 2 and the relative error percentages show that for large values of t, MRDTM works approximately up to 300 times better than random DTM for infected humans. It is seen that MRDTM dramatically reduces the error in random DTM for large values of t. This case can be applied to the other compartments to obtain similar results.

Conclusion

In this study, a model of Zika virus transmission with asymptomatic carriers has been investigated under random effects. The parameters of the deterministic system have been transformed into random variables to obtain a system of random equations. The random model has been analyzed by using MRDTM. The MRDTM is a modification of random DTM and the modification is done by the use of Laplace-Pade method. The random model has been transformed under random DTM and approximate expected values have been obtained for recovered humans and infected humans. The approximate expectations for R_H and I_H have been modified for different orders of approximants. Several modifica-

tions have been obtained for both variables. It is seen that for small values of t, MRDTM performs similarly. The modifications produce much better results for growing t since Laplace-Pade is based on removing the growing error amount in the approximation as $t \to \infty$. It is seen that for large values of t, MRDTM provides much better results. It should also be noted that the study framework can be extended to include the other compartments as well. The MRDTM improves the approximate expected value for R_H up to 5-6 times for $t = 100$. Note that $t = 100$ is a large amount for this method and the improvement through Laplace-Pade technique is noticeable. A similar case has been seen for the approximate expected value of I_H, where MRDTM improves the approximation about 300 times for $t = 100$. It should be noted that variances and confidence intervals can also be analyzed. As a conclusion, it can be said that MRDTM is a much better technique for analyzing random approximate transmission dynamics of Zika virus for growing values of t. This study can also be used to analyze other compartmental models for disease transmission dynamics.

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