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MODELING DISEASE TRANSMISSION DYNAMICS WITH RANDOM DATA AND HEAVY TAILED RANDOM EFFECTS: THE ZIKA CASE

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Abstract. In this study, we investigate a compartmental model of Zika Virus transmission under random effects. Random effects enable the analysis of random numerical characteristics of transmission, which cannot be modeled through deterministic equations. Data obtained from Zika studies in the literature are used along with heavy tailed random effects to obtain new random variables for the parameters of the deterministic model. Finally, simulations of the model are carried out to analyze the random dynamics of Zika Virus transmission. Deterministic results are compared with results from the simulations of the random system to underline the advantages of a random modeling approach. It is shown that the random model provides additional results for disease transmission dynamics such as results for standard deviation and coefficients of variation, making it a valuable alternative to deterministic modeling. Random results suggest around 90% - 120% coefficient of variation for the random model underlining the fact that the randomness should not be ignored for the transmission of this disease.

Keywords: Zika Virus, Pareto Distribution, Random Differential Equation, Random Effect, Simulation.

AMS Subject Classification: 34F05, 92D30.

1. Introduction

Mathematical modeling of disease transmission has been a popular research area for a couple decades. The developments in epidemiology have let scientists understand the

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spread of infectious diseases which has enabled the mathematical modeling of transmission. An important tool in epidemiological modeling is the classical SIR model of Kermack and McKendrick. This model and its versions containing additional parameters/compartments are extensively used in studies within a broad range from medicine to engineering (Kibona and Yang, 2017; Merdan et al., 2017, Cruz-Pacheco et al., 2019). Recent applications of compartmental models include the use of fractional order derivatives for the transmission of various diseases (Naik et al., 2020; Yavuz and Yokus, 2020; Naik et al., 2020b; Naik et al., 2020c; Owolabi and Atangana, 2019). A certain application of compartmental models has been given for the modeling of Zika virus transmission. Zika virus has been named after the Zika Forest in Uganda where it was first discovered in 1947 and is similar to West Nile and Dengue viruses (WHO, 2018). The virus causes abnormal brain development and birth defects if it is transmitted to the fetus during pregnancy and miscarriages, brain malformations in newborns and various other dangerous results of the disease have led World Health Organization and other health organizations to issue worldwide warnings in the last couple of years (WHO, 2018). This is one of the reasons for the increase in the number of modeling studies on Zika virus transmission (Hasan et al., 2019; González-Parra et al., 2019; Yogurtcu et al., 2019). However, it is seen that most of these modeling studies are carried out deterministically (Cai et al., 2019; Tang et al., 2019).

In this study, a recent mathematical model given by Cruz-Pacheco et al. will be analyzed for the spread of Zika virus with heavy-tailed random effects (Cruz-Pacheco et al., 2019). It is known that varying environmental conditions such as temperature have important effects on mosquito populations and hence disease transmission. Changes in temperature have non-negligible effects on rates of mosquito mortality, incubation rates and etc. (Pinho et al. 2010). Deterministic models neglect the possible variations of disease transmission parameters and accept these as constant values for the numerical analyses. Thus, a random modeling approach, which considers the deviations of these parameters, may be more suitable for modeling Zika virus transmission. In this regard, the parameters of the model given by Cruz-Pacheco et al. will be transformed into random variables. This approach is an alternative for the analysis of numerical characteristics for the random transmission of Zika virus such as the expected disease transmission rate and the standard deviation of disease spread. Another powerful approach for the random analysis of disease transmission would be to use stochastic differential equations instead of deterministic ones. Stochastic modeling is frequently used for various infectious diseases such as AIDS (Ding et al., 2008) and the novel coronavirus (Dordevic et al., 2021). However, in this study we make use of random differential equations which are more easily obtained from deterministic models using random effects on the parameters. Pareto distribution, which is a heavy tailed probability distribution, will be used to model the distribution of random effects. Heavy tailed distributions have tails that are not exponentially bounded, meaning their tails are heavier than exponential distribution. While a deterministic study neglects the possibility that a parameter will assume values that are different from its average value, we want to model the case where there is a considerable probability for the parameters to assume quantities that are farther than their mean values. Hence, we use Pareto distributed random variables as the parameters of the model. Pareto distribution follows the 80-20 rule which is used to describe many natural phenomena and is a suitable distribution to model the case where the values distributed in the range of parameters have considerable probabilities. Using a heavy-tailed probability distribution, namely Pareto distribution, allows us to model disease transmission scenarios where disease components have a considerable probability of deviating from their values used for deterministic studies. Studies suggest that heavy-tailed distributions may better for reflecting real data in some cases (Nair et al., 2013).

For instance, the original deterministic study given by Cruz-Pacheco et al. uses 0.5 for the value of the parameter b which denotes the biting rates of mosquitoes (Cruz-Pacheco et al., 2019). The use of a light-tailed distribution such as Normal distribution would also provide means for a random analysis, but the probability of the rate of mosquito bites being considerably different from 0.5 is very low in a light-tailed distribution. The use of Pareto distribution allows a non-negligible probability for mosquito biting rate to be distant from its deterministic value 0.5.

The outline of the study can be given as follows. In section 2, the deterministic model and the parameters are described. In section 3, Pareto distribution and the random model are presented. Section 4 contains the numerical characteristics and the random analysis of Zika transmission. Finally, comparison of the random and deterministic results and the concluding remarks are given.

2. Data and the Deterministic Model

In this study, a SIR-type based model of Zika given by Cruz-Pacheco et al. is (Cruz-Pacheco et al., 2019) used to model Zika transmission using real data and heavy-tailed random effects. The equation system is a SIR-based model for the populations of men, women and the vector and is given as follows:

$$\begin{aligned}
\frac{dS_M}{dt} &= q\mu - bm\beta_V S_M I_V - \beta_M S_M I_W - \mu S_M, \\
\frac{dI_M}{dt} &= bm\beta_V S_M I_V + \beta_M S_M I_W - (\gamma+\mu) I_M, \\
\frac{dS_W}{dt} &= (1-q)\mu - bm\beta_V S_W I_V - \beta_W S_W I_M - \mu S_W, \\
\frac{dI_W}{dt} &= bm\beta_V S_W I_V + \beta_W S_W I_M - (\gamma+\mu) I_W, \\
\frac{dI_V}{dt} &= b\alpha(1-I_V) I_M + b\alpha(1-I_V) I_W - \nu I_V.
\end{aligned} \tag{1}$$

where the variables $S_M(t), I_M(t), S_W(t), I_W(t)$, and $I_V(t)$ denote the ratio of susceptible and infected men (M), women (W) and vector (V) at any time t. This model is based on the SIR model where the compartments S and I have been used twice for men and women with an additional compartment for the infected vector. The model suggests that the disease spread is a result of the interaction between the susceptibles (S_M and S_W) and the infecteds (I_M, I_W and I_V). The variables S_M, S_W and I_M, I_W have been defined in a way to reflect the population structure (ratio of men to women) and the difference between these two groups. The descriptions of the parameters are given in Table 2.

The referred study uses deterministic values for the parameters of model (1) for analyzing Zika Virus transmission in men, women and the vector. The following initial values are also given in the referred study: $S_M(0) = 0.5, I_M(0) = 0, S_W(0) = 0.46, I_W(0) = 0.04$ and $I_V(0) = 0.06$ (Cruz-Pacheco et al., 2019). The inital values model a case where only a small fraction of the vector is infected and almost all of the human population is susceptible to the disease. In the next section we will introduce heavy-tailed random variables for some of the parameters to model the random transmission of Zika virus and microcephaly cases according to data obtained from the literature. Additionally, data for the ratio of men in the total population and rate of human mortality have been obtained from 2018 data of Turkish Statistical Institute for Turkey (TUIK, 2019). Since it has been reported that there is no Zika virus in Turkey, the use of Turkish household data can only serve as an indicator of a possible Zika scenario for Turkey (Ministry of Health, Turkey, 2018).

TABLE 1. 2018 data for Turkey's population

Data	Value
Total Population (2018)	82003882
Men	40863902
Women	41139980
Total Deaths in 2018	426106

This data corresponds to $\mu = 1.42 \times 10^{-5}$, $q = 0.5016$, $1 - q = 0.4984$ which are also given in Table 2. The original parameter values are given as follows: q is the ratio of men and has a value of 0.5, b is the biting rate of mosquitoes with a value of 0.5, m is the ratio of mosquitoes to people with a value of 1.4, β_V is the probability of disease transmission from vector to human and has a value of 0.5, ν is the rate of mosquito mortality and has a value of 0.25 and μ is the rate of human mortality with a value of 3.7×10^{-5}. The parameters have been defined to reflect the approach of distributing the human population into two groups: men and women. Different parameters have been assigned for the transmission probabilities and rates for these two groups. Note that some of the values for the parameters have been used as they were given in the original study (Cruz-Pacheco et al., 2019). The parameters associated with the population structure (men/women ratio and human mortality rate) and the mosquito population have been assigned new values as an alternative approach.

3. Pareto Distribution and Random Effects

Pareto distribution is one of the most popular Heavy-tailed distributions, named after the Italian economist Vilfredo Pareto. Its famous 80-20 distribution rule is known to fit a variety of natural phenomena, which makes it a suitable choice for modeling heavy-tailed random effects. A Pareto distributed random variable X is known to have the distribution function

$$F(x) = 1 - \left(\frac{b}{x}\right)^{\alpha}, x \in [b, \infty) \tag{2}$$

with the scale parameter $b \in (0, \infty)$ and the tail index $\alpha \in (0, \infty)$. Note that this version is also known as the General Pareto distribution or Pareto Type I distribution since there are other versions in the literature. The mean and variance of Pareto distribution are given as

$$\begin{aligned} E(X) &= \frac{\alpha}{\alpha - 1} b \, (\alpha > 1), \\ Var(X) &= \frac{\alpha}{(\alpha - 1)^2 (\alpha - 2)} b^2 \, (\alpha > 2). \end{aligned} \tag{3}$$

Another useful property of the Pareto distribution is that if the random variable U has the standard uniform distribution then the random variable $X = b/(1 - U)^{1/\alpha}$ is known to have the Pareto distribution. This property makes Pareto distribution easily applicable for modeling heavy-tailed events. Hence, we describe the new parameters under Pareto distributed random effects. The parameters b, m, ν and β_V denote the mosquito biting rates, ratio to humans, mortality rates and transmission rates to humans respectively. The deterministic model accepts these as constant quantities for the numerical analysis. However, it is known that changing climatic and environmental factors have effects on mosquito populations that cannot be ignored. Hence, we transform these parameters to Pareto distributed random variables to model the random effects of external factors on

disease transmission. The new random parameters are denoted as b^*,β_V^*,ν^* and m^*. We denote the general Pareto distributed random parameters as $b^* \sim Pareto(\alpha_1, \beta_1)$, $\beta_V^* \sim Pareto(\alpha_2, \beta_2)$, $\nu^* \sim Pareto(\alpha_3, \beta_3)$ and $m^* \sim Pareto(\alpha_4, \beta_4)$, where $\alpha_i, \beta_i, i = \overline{(1,4)}$ are the tail indexes and the scale parameters of the corresponding general Pareto distributions.

TABLE 2. Descriptions and values of the parameters of the deterministic model

Parameters	Descriptions	Value
q	Ratio of men in total population	0.5016
b	Rate of mosquito bites	Pareto$(3, \frac{1}{3})$
m	Ratio of vector to human	Pareto$(3, \frac{28}{30})$
β_V	Vector to human transmission probability	Pareto$(3, \frac{1}{3})$
α	Human to vector transmission probability	0.7
β_W	Man to woman transmission rate	0.55
β_M	Woman to man transmission rate	0.55
ν	Rate of mosquito mortality	Pareto$(3, \frac{1}{6})$
γ	Human infectious period (γ^{-1})	1/6
μ	Rate of human mortality	1.42×10^{-5}

These independently defined random parameters will be assigned tail indexes and scale parameters such that their expected values match their deterministic values. For instance, since $b = 0.5$ is the deterministic baseline value, we assign $E(b^*) = 0.5$. Moreover, the values are assigned identical tail indexes to model similarly distributed random effects for the equation system. Thus, $\alpha_i, \beta_i, i = \overline{(1,4)}$ given as:

$$\alpha_1, \beta_1 = 3, 1/3 \Rightarrow E(b^*) = \frac{\alpha_1}{\alpha_1 - 1} b_1 = 0.5,$$
$$\alpha_2, \beta_2 = 3, 1/3 \Rightarrow E(\beta_V^*) = \frac{\alpha_2}{\alpha_2 - 1} b_2 = 0.5,$$
$$\alpha_3, \beta_3 = 3, 1/6 \Rightarrow E(\nu^*) = \frac{\alpha_3}{\alpha_3 - 1} b_3 = 0.25,$$
$$\alpha_4, \beta_4 = 3, 28/30 \Rightarrow E(m^*) = \frac{\alpha_4}{\alpha_4 - 1} b_4 = 1.4.$$

These general Pareto distributed random parameters have the following probability distribution functions (Figure 1).

The above-mentioned scaling parameters and tail indexes result in the following variances for the new random parameters:

$$\alpha_1, \beta_1 = 3, 1/3 \Rightarrow Var(b^*) = \frac{\alpha_1}{(\alpha_1 - 1)^2(\alpha_1 - 2)} b_1^2 = 1/6,$$
$$\alpha_2, \beta_2 = 3, 1/3 \Rightarrow Var(\beta_V^*) = \frac{\alpha_2}{(\alpha_2 - 1)^2(\alpha_2 - 2)} b_2^2 = 1/6,$$
$$\alpha_3, \beta_3 = 3, 1/6 \Rightarrow Var(\nu^*) = \frac{\alpha_3}{(\alpha_3 - 1)^2(\alpha_3 - 2)} b_3^2 = 1/24,$$
$$\alpha_4, \beta_4 = 3, 28/30 \Rightarrow Var(m^*) = \frac{\alpha_4}{(\alpha_4 - 1)^2(\alpha_4 - 2)} b_4^2 = 98/25.$$

Using these newly defined random variables in (1), we obtain the random model:

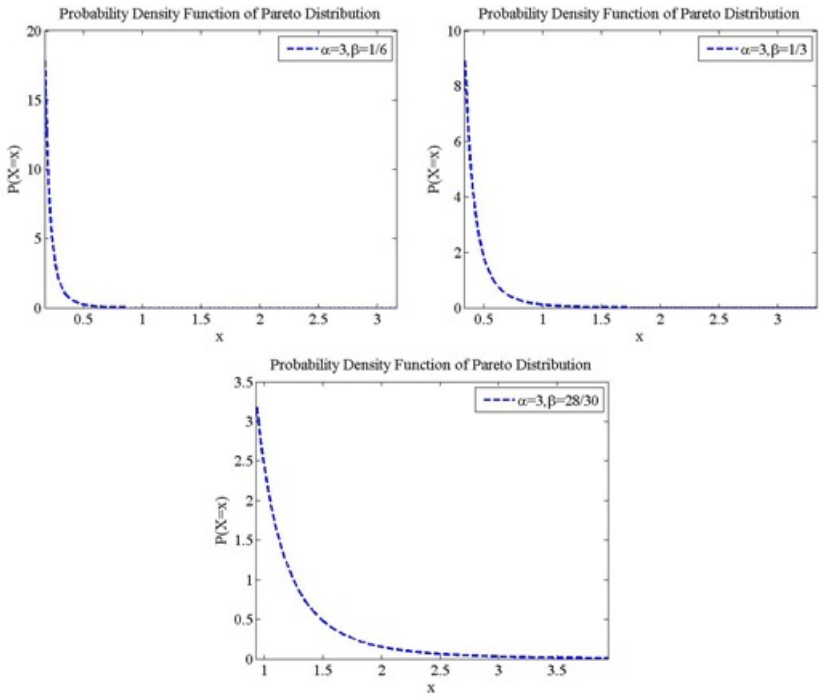

FIGURE 1. PDF for Pareto random variables with expected values equal to 0.25, 0.5 ve 1.4, respectively.

$$
\begin{aligned}
\frac{dS_M}{dt} &= q\mu - b^* m^* \beta_V^* S_M I_V - \beta_M S_M I_W - \mu S_M, \\
\frac{dI_M}{dt} &= b^* m^* \beta_V^* S_M I_V + \beta_M S_M I_W - (\gamma + \mu) I_M, \\
\frac{dS_W}{dt} &= (1-q)\mu - b^* m^* \beta_V^* S_W I_V - \beta_W S_W I_M - \mu S_W, \\
\frac{dI_W}{dt} &= b^* m^* \beta_V^* S_W I_V + \beta_W S_W I_M - (\gamma + \mu) I_W, \\
\frac{dI_V}{dt} &= b^* \alpha (1 - I_V) I_M + b^* \alpha (1 - I_V) I_W - \nu^* I_V.
\end{aligned} \tag{4}
$$

This equation system models the transmission dynamics of Zika virus under random effects. It is stated that changes in daily temperature, rainfall and several other environmental conditions affect the value of parameters, especially for the mosquito population (Pinho et al., 2010). For instance, Pinho et al. states that average mosquito mortality rate has a range of $0.02 - 0.09$ per day for temperatures in the interval of $T \in [10.54, 33.41]^\circ C$ (Pinho et al., 2010) whereas this range is considered as $0.028 - 0.25$ by Tang et al. (Tang et al., 2019). Both studies neglect the variability of this parameter and use its mean value for numerical investigations. Using the random parameters in (4) will enable the analysis of the numerical characteristics of the random system, which cannot be done with the deterministic model. Note that the values of the parameters of the deterministic model (1) containing information about the mosquito population have been transformed to random variables, the values of the parameters containing information about the total population

have been given values from Turkish household data and the other parameters have been left the same.

4. Numerical Characteristics of the Random Model

Simulations of the random system (4) have been done in MATLAB using 10^5 simulations. Results for the deterministic solutions of (1) and the expected values of the system (4) have been given in the figures below, respectively (Figures 2,3).

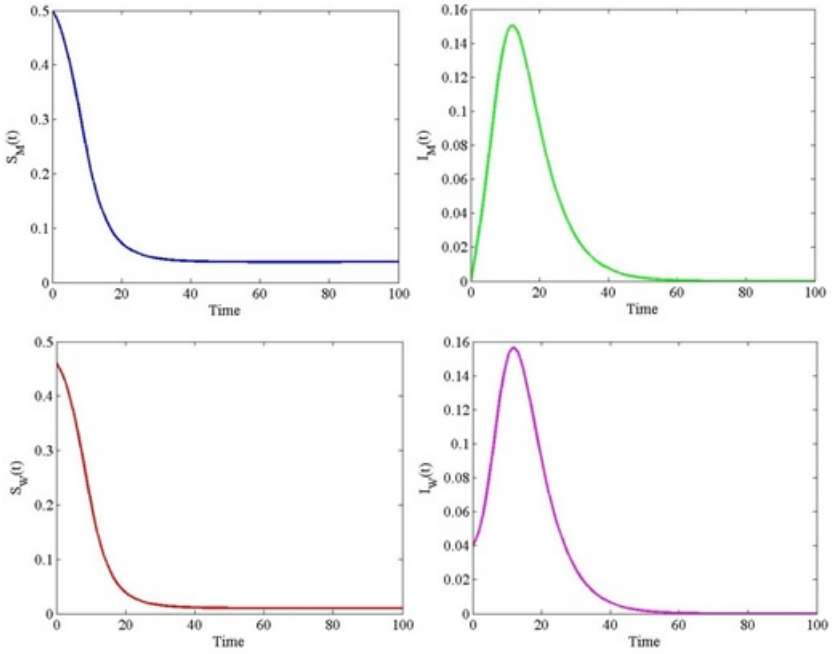

Figure 2. Solution curves for the human-associated compartments of the deterministic model

The maximum and minimum values for the deterministic solutions and expected values can be seen in the tables below (Tables 3 and 4).

Table 3. Extremum values for the numerical solution of the deterministic model

	$S_M(t)$	$I_M(t)$	$S_W(t)$	$I_W(t)$	$I_V(t)$
Minimum	0.03783	0	0.01015	1.737×10^{-6}	1.165×10^{-5}
Time	62.5	0	63.9	100	100
Maximum	0.5	0.1503	0.46	0.1563	0.2821
Time	0	11.9	0	11.7	14.8

The correspondence between extremum results for the deterministic and random models can be seen from the tables and figures (Tables 3-4 and Figures 2-4 and 7). This is a clear indication of the meaningfulness of the random model. The random system (4) can model the disease dynamics just as accurately as the deterministic system (1). However, unlike the deterministic system, the random model can express the variations and deviations for disease transmission as well. Examination of the standard deviations in the random results is an important tool for analyzing the variability in the dynamics of disease transmission.

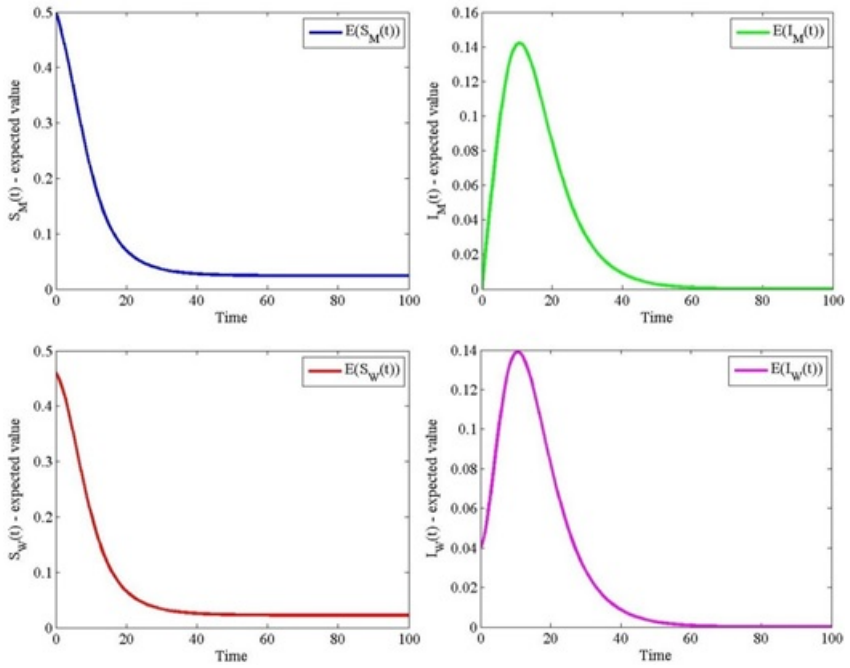

FIGURE 3. Expected values for the human-associated compartments of the random model

TABLE 4. Extremum values for the expectations of the random model

	$E(S_M(t))$	$E(I_M(t))$	$E(S_W(t))$	$E(I_W(t))$	$E(I_V(t))$
Minimum	0.02401	0	0.02232	8.535×10^{-6}	4.577×10^{-5}
Time	72.1	0	75.3	100	100
Maximum	0.5	0.1424	0.46	0.1393	0.272
Time	0	10.5	0	10.3	13.9

It is seen in these two figures (Figure 3 and Figure 4) that both in the deterministic and the random cases, the ratio of susceptibles (men and women) decrease to almost zero (varying between 0.01 to 0.04) in the first 30-40 days and remain at this level until the end of the process. The infecteds (men, women and vector) increase initially until they obtain their maximum value (about 0.14 for humans and 0.27 for vector) after which they decrease to almost zero around day 50-60.

The coefficients of variation, obtained as a percentage of the ratio of the standard deviation to the mean value, and the confidence interval for the expected values within three standard deviations reveal important results for the variability in the disease dynamics.

TABLE 5. Maximum values of the coefficients of variation in the random model

	$CV(S_M(t))$	$CV(I_M(t))$	$CV(S_W(t))$	$CV(I_W(t))$	$CV(I_V(t))$
Maximum	89.79	121.7	90.3	122.6	108
Time	44.8	100	44.4	100	100

Table 5 and Figure 5 show the maximum values for the coefficients of variation and the changes in the coefficients of variation, respectively. The main motivation of this

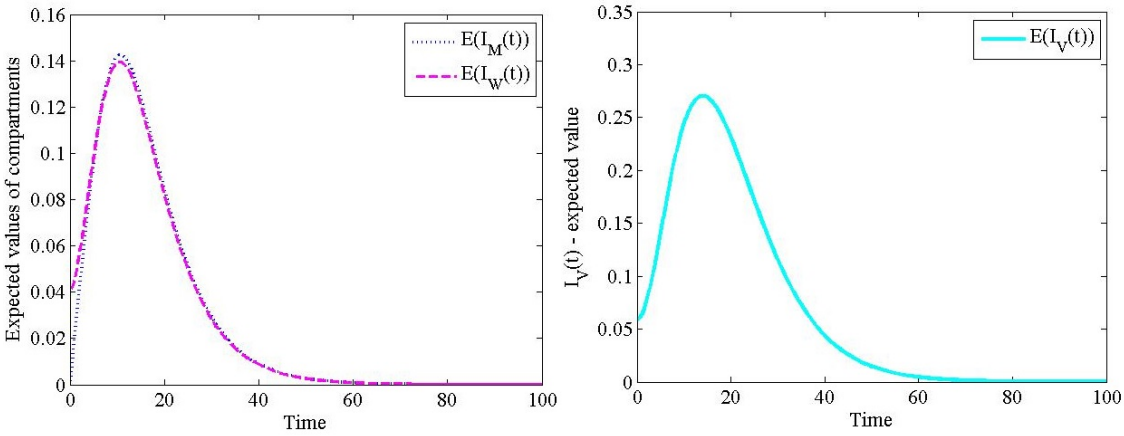

FIGURE 4. Expected values of infected compartments in the random model

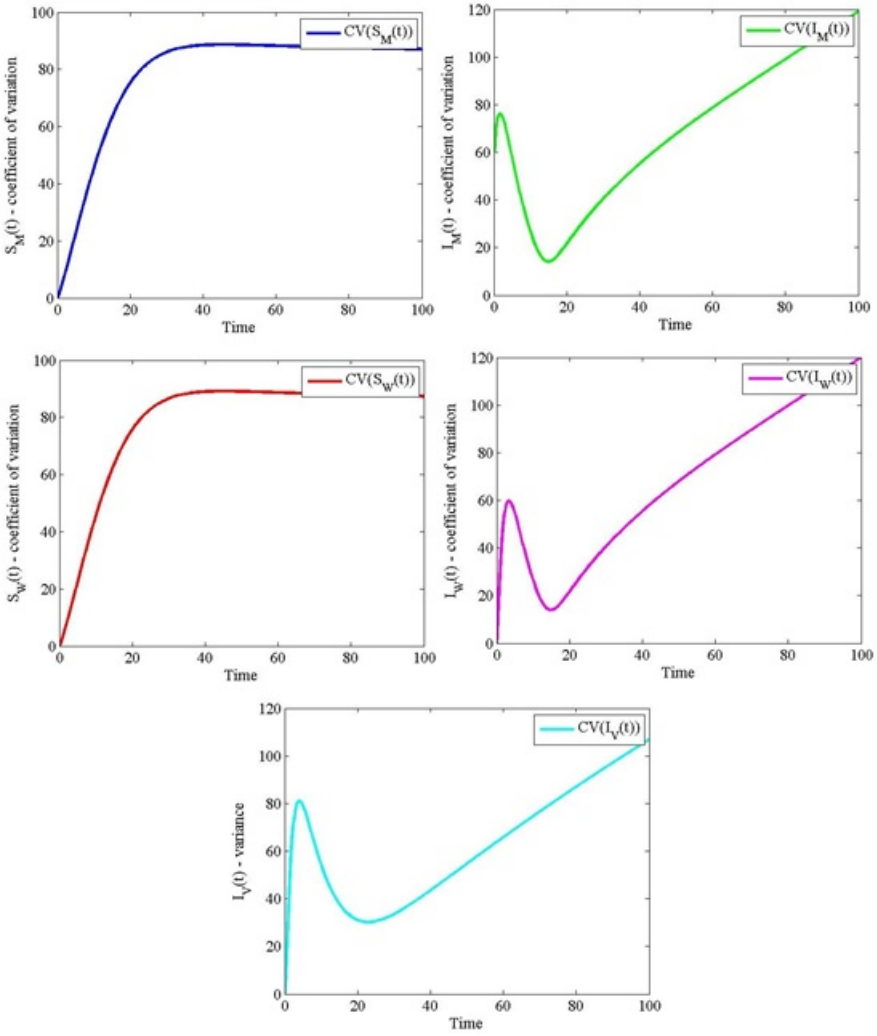

FIGURE 5. Coefficients of variation for the random model

study is that the real life dynamics of disease transmission shows that the parameters denoting certain aspects of the disease such as mosquito bite rate, vector to human ratio and etc. are not constant for every case of the disease and vary according to environmental conditions. This variation results in deviation of results from the deterministic outcomes of the original model. The coefficient of variation is a useful tool for analyzing this variation. The coefficient of variation for the Pareto distributed random parameters are about 81.65% for b, β_V and ν and 141.42% for m whereas the coefficient of variation for the compartments go up to 122.6%. This can be interpreted as a similarity of the deviation in the parameters and the deviation in the model results.

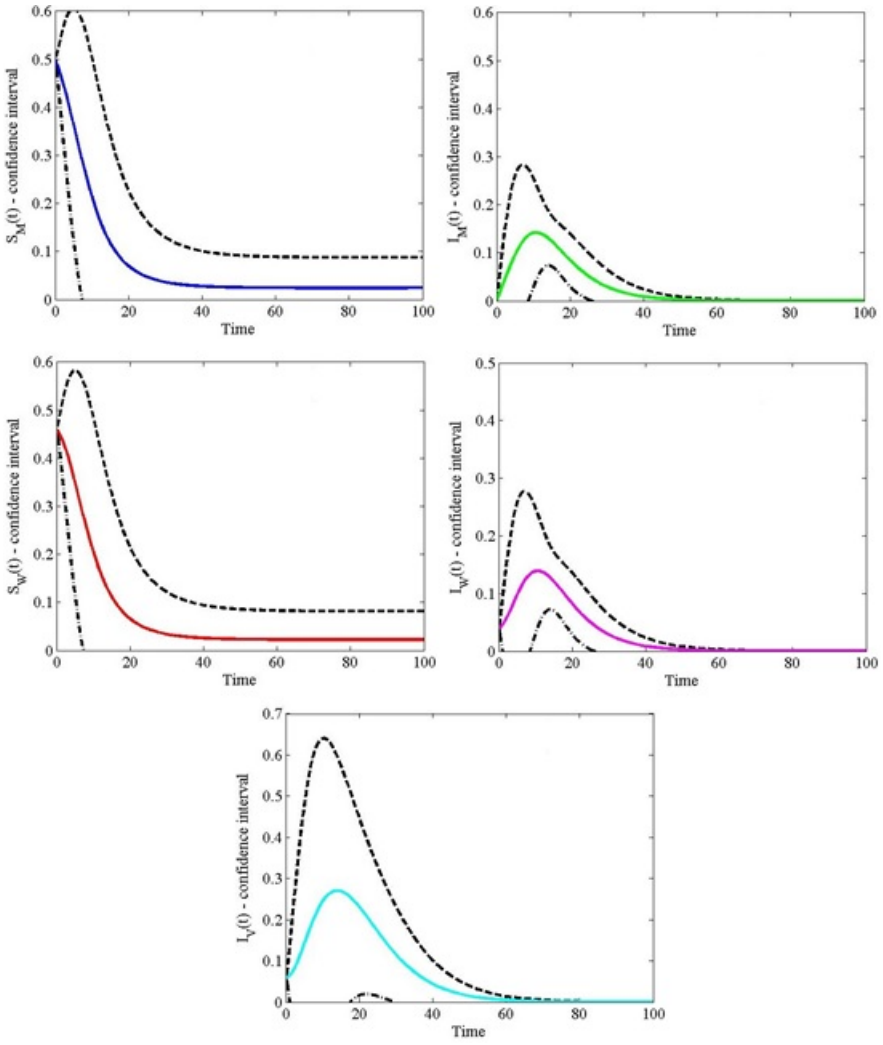

FIGURE 6. Confidence intervals for the expected values of the random model

Figure 6 shows the expected values of model compartments within three standard deviations of their mean value. The random results show that the ratio of susceptible men, $S_M(t)$, is expected to be about 2.411%, whereas the confidence interval suggests that this percentage could vary between 0% to 8.789% at $t = 100$ and the maximum ratio could go up to 60.775%. The ratio of infected men, $I_M(t)$, is expected to be 12.32% at $t = 7$ but the confidence interval suggests that the result could be anywhere between $[0\%, 28.57\%]$. The

results for the ratio of susceptible women, $S_W(t)$, says that at $t = 100$, the expectation is around 2.243% whereas the confidence interval for this expectation is $[0\%, 8.199\%]$. The expected value for the ratio of infected women, $I_W(t)$ is 12.23% at $t = 7$, however, the confidence interval suggests that this results could vary within $[0\%, 27.95\%]$. The expected value for infected mosquito ratio is 24.87% at $t = 10.2$ but the confidence interval suggest that this expectation could be anywhere within $[0\%, 64.83\%]$.

Coupled with the results for the variation coefficients, the results for confidence intervals denote that the deterministic results could provide some misleading information since the randomness of disease transmission is ignored for the deterministic analysis. Figures 5 and 6, along with the results in Table 5, denote that the difference between the random and deterministic results could go up to 122.6% at certain points of the interval. Hence, Figure 6 is a presentation of the possible deviation of real life results from the results suggested in a deterministic study.

The results for the case with Pareto distributed random effects can also be compared to the results of the simulations with exponentially distributed random effects. The extremum values for exponentially distributed random parameters are given below (Table 6).

TABLE 6. Extremum values for the random model with exponential random effects

	$S_M(t)$	$I_M(t)$	$S_W(t)$	$I_W(t)$	$I_V(t)$
Minimum	0.0246	0	0.02291	8.852×10^{-6}	4.779×10^{-5}
Time	65.8	0	64.8	100	100
Maximum	0.5	0.1421	0.46	0.139	0.2703
Time	0	10.6	0	10.4	14

Considering the deterministic extremal data in Table 3, extremum values of the case with Pareto distributed random effects in Table 4 and the results in Table 6, it can be said that all of the models enable similar predictions for the behavior of disease transmission. Note that the differences between the extremum values of the deterministic and random cases are results of the Pareto and exponential random effects added to the original model. An overall comparison of the deterministic results and the random expectations for Pareto distributed random effects have been presented in the figure below (Figure 7).

Although Turkish household data has been used for the study, it has been reported by the Turkish Ministry of Health in 2018 that there are actually no verified Zika cases in Turkey (Turkish Ministry of Health, 2018). In order to give reliability to the arguements of this study the data from Brazil has been used for a final simulation since the most recent major Zika virus outbreak began in Brazil in 2015 and spread to other countries in the Americas. Real data of yearly total infections from Brazil between 2016 and 2020 have been used to compare the simulation results of the model. The basic reproduction number for the outbreak in Brazil is estimated to be within the 95% confidence interval $(0.523, 6.3)$ around (Gao et al., 2016). The following parameter values have been used in the model in accordance with values from the literature (Wang et al., 2017). Additionally, demographic data about the population of Brazil has been obtained and used for the simulations and the calculations of the values of q and μ (World Bank, 2022): $q = 0.49228$, $E(b) = 1$, $E(m) = 1$, $E(\beta_V) = 0.3$, $\alpha = 0.3$, $\beta_W = 0.01$, $\beta_M = 0.01$, $E(\nu) = 0.3$, $\gamma = \frac{13}{49}$, $\mu = 1.71112 \times 10^{-5}$. These values result in $R_0 = 1.1524$ according to the original study, and this value is within the confidence interval given in the literature (Wang et al., 2017). The initial values have

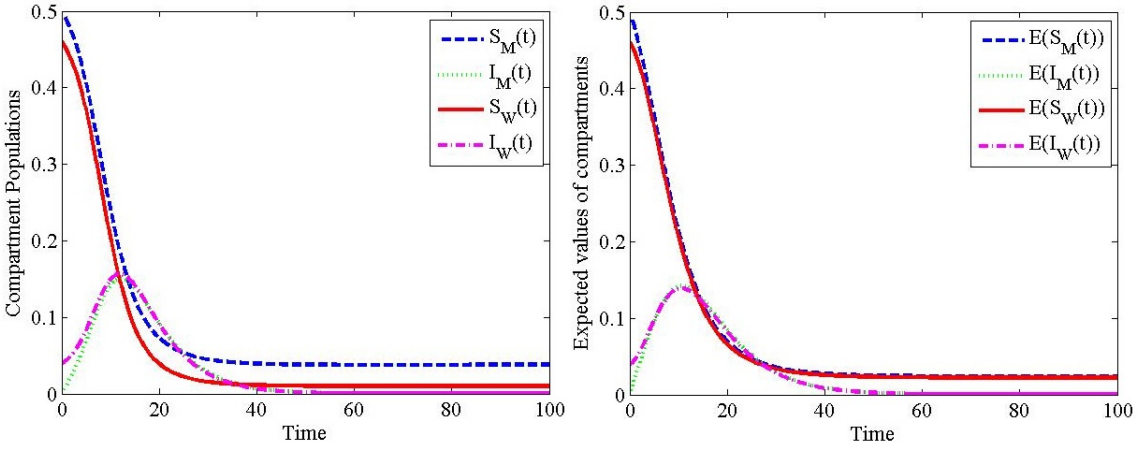

FIGURE 7. Overall comparison of the deterministic results and the random expectations for human population

been used as $S_M(0) = 0.49933, I_M(0) = 0.00067, S_W(0) = 0.49933, I_W(0) = 0.00067$ and $I_V(0) = 0.0005$ to simulate an initial infected population of 274700 people, approximately matching the real data. The compared real data on infection numbers have been obtained from Pan American Health Organization (PAHO) (PAHO, 2022) for Brazil between 2016 and 2020. The comparison can be seen in the figure below (Figure 8). In the figure, the green diamond shows the initial number of simulated infections (274700) that are defined through the initial values $I_M(0)$ and $I_W(0)$, whereas the others show the number of infected individuals in Brazil between 2016 to 2020. The equation system of Cruz-Pacheco et al. models a decrease in the number of total infections after the peak in 2016 until the end of the epidemic in 2020, approximately mimicking the dynamics of the spread in real life.

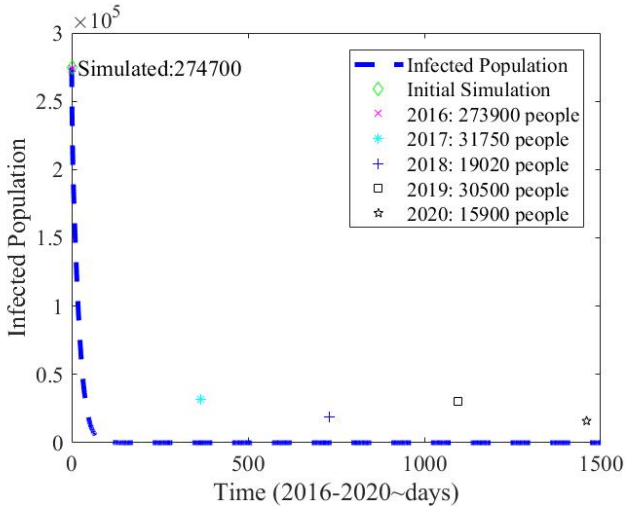

FIGURE 8. Random Model simulation vs Real Data for Brazil 2015-2020

5. CONCLUSION

In this paper, the deterministic Zika virus transmission model of Cruz-Pacheco et al. is used to analyze the random behavior of Zika transmission. Some of the deterministic

parameters of the model have been transformed to random variables with Pareto distribution, whereas other parameters have been assigned values suitable to Turkish household data. The random model, obtained by assigning random coefficients to the original ordinary differential equation system, was simulated with both Pareto and exponentially distributed random effects. Figures 2 and 3 suggest that the deterministic and Pareto distributed cases are very similar in modeling the behavior of disease transmission, whereas this similarity can also be seen in the extremum values of the three cases given in Tables 3, 4 and 6. In addition to modeling disease transmission, the random model also models the variability in disease transmission as well. Study of the standard deviations, variations, coefficients of variation and confidence intervals for expected values show how the disease transmission dynamics vary throughout the process. These results, which can be important for battling disease spread, cannot be achieved with the deterministic model. The distribution of disease transmission parameters could be determined using real life field data from Zika cases around the world which would lead to more precise results. These results would be beneficial for planning Zika virus disease battling scenarios. This study acts as a preliminary guide to overcoming the insufficiency of deterministic models for predicting the varying nature of real life disease transmission. Similar studies can be made for other diseases by using systems of random differential equations to model disease dynamics. Suitable probability distributions can be added for random effects and field data could be used to predict the randomness of the parameters. We believe this study will be an important component in the mathematical modeling studies for Zika virus transmission.

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