Generalized beta parameters for a SVEIR-type random model of Polio transmission

Article *in* AIP Conference Proceedings · January 2018

DOI: 10.1063/1.5078459

3 authors:

Zafer Bekiryazici
Recep Tayyip Erdoğan Üniversitesi
27 PUBLICATIONS **81** CITATIONS
SEE PROFILE

Tülay Kesemen
Karadeniz Technical University
41 PUBLICATIONS **136** CITATIONS
SEE PROFILE

Mehmet Merdan
Gümüshane Üniversitesi
43 PUBLICATIONS **669** CITATIONS
SEE PROFILE

Generalized beta parameters for a SVEIR-type random model of Polio transmission

Zafer Bekiryazici, Mehmet Merdan, and Tulay Kesemen

Citation: AIP Conference Proceedings **2037**, 020004 (2018); doi: 10.1063/1.5078459
View online: https://doi.org/10.1063/1.5078459
View Table of Contents: http://aip.scitation.org/toc/apc/2037/1
Published by the American Institute of Physics

Generalized Beta Parameters for a SVEIR-Type Random Model of Polio Transmission

Zafer Bekiryazici[1,a)], Mehmet Merdan[2,b)] and Tulay Kesemen[3,c)]

[1]*Recep Tayyip Erdogan University, Department of Mathematics, Rize, Turkey,*
[2]*Gumushane University, Department of Mathematical Engineering, Gumushane, Turkey*
[3]*Karadeniz Technical University, Department of Mathematics, Trabzon, Turkey.*

[a)]Corresponding Author: zafer.bekiryazici@erdogan.edu.tr
[b)]mmerdan@gumushane.edu.tr
[c)]tkesemen@gmail.com

Abstract. In this study, a SVEIR-type compartmental model of Poliomyelitis transmission is examined under random effects. We introduce Generalized Beta and normal distributed random parameters into the equation system to investigate the random dynamics of the disease. The approximate analytical solution of the model under random effects is obtained by using Random Differential Transformation Method (RDTM). Results from simulations and RDTM are analyzed to comment on the randomness of the compartments and disease transmission. It is seen that the random model successfully provides similar results that can be obtained through the deterministic model while providing additional information on the random behavior of the disease, such as the standard deviations and the variation coefficients.

Keyword: Random Differential Equation, Generalized Beta Distribution, Random Effect, Poliomyelitis, Random Differential Transformation Method.
AMS 2010: 34F05, 92B05.

INTRODUCTION

Polio (or Poliomyelitis) is a highly contagious disease caused by the Poliovirus (PV). Children under the age of five are primarily affected by the disease. Polio affects the central nervous system and can sometimes cause paralysis within hours [1]. The epidemic in America caused more than 21000 paralysis cases in 1952 [2], however, the actions taken against the disease worldwide within the leadership of the World Health Organization (WHO) in 1988 has resulted in a serious decrease in the number of cases around the globe. The preventive Polio vaccine has caused the number of Polio cases to decrease from around 350000 worldwide in 1988 to 37 reported cases in 2016 [1]. However, WHO has reported an increase in Polio in Cameroon since 2013 [3]. Hence, a new approach to the mathematical modeling of the disease transmission is valuable for battling the disease.

Several Polio models exist in the literature analyzing various aspects of the disease such as; disease transmission [4], the effects of vaccination for eradication and transmission of the disease [5] and response scenarios to potential outbreaks [6]. It is seen that almost all of the modeling studies are performed by using deterministic quantities and equations. However, an overall analysis of the existing Polio transmission models shows that the parameters used in these models are assigned different values for each study according to the conditions of the region or the case being investigated. For instance, the parameter β in the model of Browne et al. denotes the transmission rate of the disease and an approximate daily value of 0.88 (319.655 yearly) has been used in the study [5]. Similarly, the parameter β_i in the model of Dénes and Székely similarly denotes the disease transmission rate and an approximate daily value of 0.29 (2.05 weekly) has been used in the study [7]. Another recent model by Nkamba et al. uses a daily value of 0.10 for the parameter β which denotes the effective contact rate for disease transmission [3]. Similarly, the parameters values for recovery rates in these three studies, denoted by γ, are as follows: 0.06 daily ($\frac{365}{16} = 22.8125$

7th International Eurasian Conference on Mathematical Sciences and Applications (IECMSA-2018)
AIP Conf. Proc. 2037, 020004-1–020004-12; https://doi.org/10.1063/1.5078459
Published by AIP Publishing. 978-0-7354-1763-2/$30.00

yearly) in [5], 0.08 daily (0.58 weekly) in [7] and 0.05 daily in [3]. Such variability in the dynamics of disease is a sign of the randomness of Polio transmission. It is clear that the disease transmission, recovery, birth/death rates and etc. occur randomly in different countries, regions or climates. Hence, a model consisting of random differential equations may prove more useful for analyzing disease dynamics. There are several statistical studies in the literature on random aspects of the disease. A recent study in 2017 states a mean of 1.3413 and a variance of 3.5153 for the number of monthly Polio cases in USA [8] whereas other random studies can also be found for monthly disease counts and incidence data for Polio [9], [10]. The study by Noori et al. investigates demographic, socio-economic and environmental factors using disease incidence data from several countries and comments on the geographical variation of Polio transmission with a random analysis [11]. Studies on the changes in Polio dynamics for various countries such as Pakistan, Afghanistan and etc. can be found in the literature [12]. Due to the unignorable randomness of the disease components, we propose a random transmission model for Polio disease using random differential equations.

Using the deterministic model of Nkamba et al. [3] we obtain a random model by transforming the coefficients into random variables. The coefficients of the deterministic system are the parameters of the model which describe the disease transmission dynamics, such as the recovery rate, vaccination efficacy and the disease transmission rate. Transforming these coefficients to random variables allows the equation system to model disease transmission on a wider range of conditions rather than just a single case in a single country. There are several methods to analyze random differential equations such as Homotopy Analysis Method (HAM) [13], Variational Iteration Method (VIM) [14] along with some other approximate schemes. In this study, random Differential Transformation Method (DTM) [15] will be used to obtain approximate solutions to the random model of Polio transmission. Random DTM [16] is a generalization of the Differential Transformation Method [17], [18] to random equations using mean-square calculus. Random DTM has been used to analyze differential equations with random components [19], linear random differential equations [15] and parabolic diffusion equation with uncertainty [20]. Both the random and ordinary DTM have been proven to be efficient for analyzing mathematical models used in a variety of areas. Hence, random DTM will be used to obtain approximate-analytical solutions of the model under random effects. The approximate solutions will be used to obtain approximate expected values and approximate variances of disease transmission. Using results from simulations of the model and numerical results from the deterministic model, the random model will be interpreted for its validity in modeling the disease transmission accurately. This approach can be generalized to investigate the random behavior of many diseases or other biological models in the future.

THE DETERMINISTIC MODEL

The Polio transmission model used in this study has been given in [3] by Nkamba et al. in 2017. The compartmental model presents a new SVEIR type equation system for investigating the effects of vaccination for controlling disease transmission. The model is given as:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (d_S + p)S - \beta S I, \\
\frac{dV}{dt} &= pS - d_V V - \theta\beta V I, \\
\frac{dE}{dt} &= \beta I(S + \theta V) - (d_E + \varepsilon)E, \\
\frac{dI}{dt} &= \varepsilon E - (d_I + \gamma)I, \\
\frac{dR}{dt} &= \gamma I - d_R R.
\end{aligned} \tag{1}$$

Here, the compartments are as follows: $S(t)$ denotes the number of susceptible individuals, $V(t)$ denotes the number of vaccinated individuals with a small chance of infection, $E(t)$ denotes the number of individuals which have been exposed, $I(t)$ denotes the number of individuals which have been infected and $R(t)$ denotes the number of recovered individuals at any time t. The daily values $(1/day)$ of the parameters of (1) are presented in Table 1. The values have been obtained from the referred study while possible other values can also be found in the literature supporting the random nature of the disease transmission [21], [22].

TABLE 1. Parameters, values and descriptions of the model

Parameter	Description	Value
d_S	S - natural death rate	0.0551
d_V	V - natural death rate	0.0551
d_E	E - natural death rate	0.0551
d_I	I - natural death rate	0.08
d_R	R - natural death rate	0.0551
Λ	Susceptible recruitment rate	2.5
p	Vaccination rate	1
β	Interaction rate	0.1
θ	Vaccine efficacy (1-θ)	0.1
ε	Expected incubation period rate	0.05
γ	Recovery rate	0.005

The initial values of the model are given as $S(0) = 20$, $V(0) = 15$, $E(0) = 5$, $I(0) = 5$, $R(0) = 0$, which means the initial population is depicted as a group of 45 people with 20 susceptibles. The positivity of the solutions of (1) and the region where the solutions are biologically meaningful can be found in the deterministic study. Using this model as a basis, we will investigate the random behavior of the disease transmission.

POLIO TRANSMISSION MODEL WITH RANDOM PARAMETERS

Random differential equations can be obtained from ordinary differential equations by using random initial values, random coefficients or random inhomogeneous parts [23]. Since the coefficients of the equation system (1) are the parameters that describe the dynamics of the disease, we will use random variables for the coefficients to obtain a random equation system that models the random nature of disease transmission. Two random models will be formed where the parameters have Generalized Beta probability distribution and Normal (Gaussian) probability distribution. The exact real life probability distribution of the parameters are unknown for Polio. The disease transmission can be affected by environmental, geographical or climatic factors and hence we will use Normal distribution for modeling the variability of the parameters. Generalized Beta distributed random parameters will also be produced with similar statistical properties to the Normally distributed case to investigate the effects of the probability distributions. The motivation for a random modeling study is a previous study by Merdan et al. [24] where random antibiotic resistance dynamics are analyzed with random and stochastic models.

If we transform the parameters of (1), $d_S, d_V, d_E, d_I, d_R, \Lambda, p, \beta, \theta, \varepsilon, \gamma$ to random variables (denoted with an asterisk superscript), we obtain the following random model (the death rates for the compartments S, V, E, R are all shown as d^* since they have the same deterministic value and their random counterpart will be determined such that they have the same expectation):

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda^* - (d^* + p^*)S - \beta^* S I, \\
\frac{dV}{dt} &= p^* S - d^* V - \theta^* \beta^* V I, \\
\frac{dE}{dt} &= \beta^* I(S + \theta^* V) - (d^* + \varepsilon^*)E, \\
\frac{dI}{dt} &= \varepsilon^* E - (d_I^* + \gamma^*)I, \\
\frac{dR}{dt} &= \gamma^* I - d^* R.
\end{aligned} \tag{2}$$

with the same initial conditions $S(0) = 20,\ V(0) = 15,\ E(0) = 5,\ I(0) = 5,\ R(0) = 0$. The random parameters $\Lambda^*, d^*, p^*, \beta^*, \theta^*, \varepsilon^*, d_I^*, \gamma^*$ in (2) are defined as follows:

$$\begin{aligned} &\Lambda^* = c_1 + d_1 Z_1,\ d^* = c_2 + d_2 Z_2,\ p^* = c_3 + d_3 Z_3,\ \beta^* = c_4 + d_4 Z_4, \\ &\theta^* = c_5 + d_5 Z_5,\ \varepsilon^* = c_6 + d_6 Z_6,\ d_I^* = c_7 + d_7 Z_7,\ \gamma^* = c_8 + d_8 Z_8. \end{aligned} \tag{3}$$

Here, $c_i,\ i = \overline{1,8}$ are the location parameters and $d_i,\ i = \overline{1,8}$ are the scale parameters of the Generalized Beta distribution while $Z_i,\ i = \overline{1,8}$ are independent random variables with standard Beta distribution. The statistical properties of the random parameters will be assigned similarly for both cases with Beta and Normal distributions to compare and comment on the results. Hence the location and scale parameters are assigned such that the expected values of the parameters equal their deterministic values, while standard deviations are 5% of their expectations. It is known that for a generalized Beta distributed random variable X, i.e. $X \sim gBeta(c, d, a, b)$, where c, d are the location and scale parameters and a, b are the left and right shape parameters, respectively, the expectation and variance are given as [25]:

$$E(X) = c + d\frac{a}{a+b},\ Var(X) = d^2\frac{ab}{(a+b)^2(a+b+1)}. \tag{4}$$

The following random variables are used:

$$\begin{aligned} &\Lambda^* \sim gBeta\left(\frac{17}{8}, \frac{3}{4}, 4, 4\right),\ d^* \sim gBeta(0.046835, 0.01653, 4, 4),\ p^* \sim gBeta\left(\frac{17}{20}, \frac{3}{10}, 4, 4\right) \\ &\beta^* \sim gBeta\left(\frac{17}{200}, \frac{3}{100}, 4, 4\right), \theta^* \sim gBeta\left(\frac{17}{200}, \frac{3}{100}, 4, 4\right),\ \varepsilon^* \sim gBeta\left(\frac{17}{400}, \frac{3}{200}, 4, 4\right), \\ &d_I^* \sim gBeta\left(\frac{17}{250}, \frac{3}{125}, 4, 4\right),\ \gamma^* \sim gBeta\left(\frac{17}{4000}, \frac{3}{2000}, 4, 4\right). \end{aligned} \tag{5}$$

The parameters are assigned identical left and right shape parameters a, b to obtain a bell-shaped generalized Beta distribution similar to the Normal distribution. Using (4), the expected value, variance and variation coefficient (CV) for Λ^* are obtained as:

$$E(\Lambda^*) = c_1 + d_1\frac{a}{a+b} = 2.5,\ Var(\Lambda^*) = d_1^2\frac{ab}{(a+b)^2(a+b+1)} = \frac{1}{64},\ CV = 100 \times \frac{\sqrt{1/64}}{2.5} = 5\%. \tag{6}$$

All of the random parameters (5) are randomized to have 5% variation coefficients to model a hypothetical 5% randomness in their real life behaviors. This value could be altered according to real data.

Similarly, the random parameters $\Lambda^*, d^*, p^*, \beta^*, \theta^*, \varepsilon^*, d_I^*, \gamma^*$ in (2) can be defined as the following Normally distributed parameters:

$$\begin{aligned} &\Lambda^* = \Lambda + s_1\eta_1,\ d^* = d + s_2\eta_2,\ p^* = p + s_3\eta_3,\ \beta^* = \beta + s_4\eta_4, \\ &\theta^* = \theta + s_5\eta_5,\ \varepsilon^* = \varepsilon + s_6\eta_6,\ d_I^* = d_I + s_7\eta_7,\ \gamma^* = \gamma + s_8\eta_8. \end{aligned} \tag{7}$$

Here, $\Lambda, d, p, \beta, \theta, \varepsilon, d_I, \gamma$ denote the deterministic values given in Table 1, $s_i,\ i = \overline{1,8}$ denote the standard deviations of the Normally distributed random parameters and $\eta_i,\ i = \overline{1,8}$ are independent random variables with standard Normal distribution. The expected value and the variance of a random variable X with Normal distribution ($X \sim N(\mu, \sigma^2)$) are known to be $E(X) = \mu$ and $Var(X) = \sigma^2$. The standard deviations are defined as follows to obtain a set of random parameters with 5% variation coefficients to match the previous case with generalized Beta distributed parameters:

$$\begin{aligned} &\Lambda^* = 2.5 + 0.125\eta_1,\ d^* = 0.0551 + 0.002755\eta_2,\ p^* = 1 + 0.05\eta_3,\ \beta^* = 0.1 + 0.005\eta_4, \\ &\theta^* = 0.1 + 0.005\eta_5,\ \varepsilon^* = 0.05 + 0.0025\eta_6,\ d_I^* = 0.08 + 0.004\eta_7,\ \gamma^* = 0.005 + 0.00025\eta_8. \end{aligned} \tag{8}$$

In particular, $\Lambda^* = 2.5 + 0.125\eta_1 \Rightarrow \Lambda^* \sim N(2.5, 0.125^2)$ since $\eta_1 \sim N(0, 1)$. Hence, it is seen that $E(\Lambda^*) = \mu = 2.5$ and $Var(\Lambda^*) = 0.125^2$ and thus $CV = \frac{\sqrt{0.125^2}}{2.5} = 5\%$.

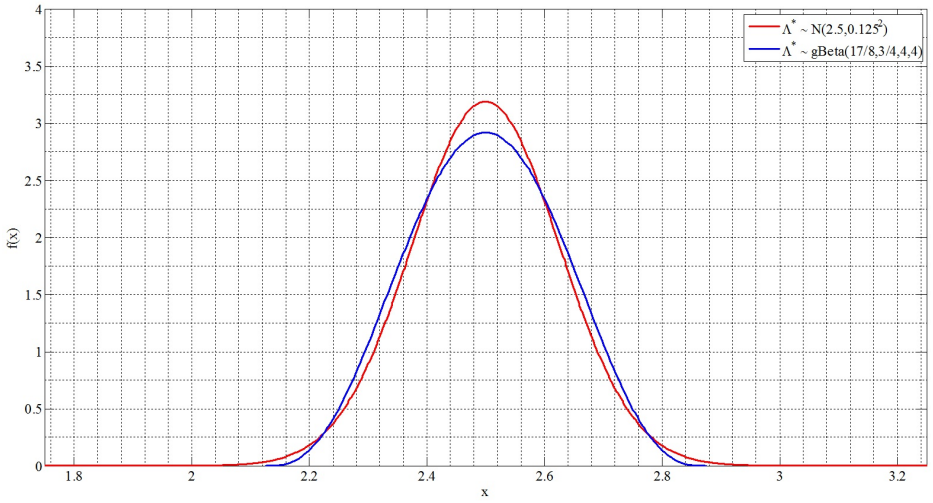

FIGURE 1. Distributions for the random parameter Λ^*

This similarity of the distributions for the parameters can be seen for Λ^* in Figure 1. The random Λ^* takes values in within a range whereas the deterministic Λ can only assume the value $\Lambda = 2.5$.

RANDOM DIFFERENTIAL TRANSFORMATION METHOD

The random model (2) with Generalized Beta parameters (5) or Normal parameters (8) is too complex to be solved analytically. Random Differential Transformation Method (DTM) is one of the approximate analytical methods that can be used to obtain approximate solutions of the model. We initially summarize the method and its modification via Laplace-Padé technique.

Let k be a non-negative integer, $u(t), t \in T$ be a fourth-order stochastic process and $u^{(k)}(t)$ denote the $k-th$ derivative of this process at $t \in T$ in the mean-fourth sense. The random differential transform of $u(t)$ is given as

$$U(k) = \frac{1}{k!}\left[\frac{d^k u(t)}{dt^k}\right]_{t=t_0}, \tag{9}$$

where U is the transformed stochastic process and the derivation is in the mean square sense [16]. The inverse transformation for U is similarly given as

$$u(t) = \sum_{k=0}^{\infty} U(k)(t-t_0)^k \tag{10}$$

Theorem 1 ([16]) *Let k be a non-negative integer and $f^{(k)}(t)$, $g^{(k)}(t)$ denote the $k-th$ derivatives of the fourth order stochastic processes $f(t), t \in T$ and $g(t), t \in T$ at $t \in T$ in the mean-fourth sense. The following hold for random Differential Transformation:*

(i) *If $u(t) = f(t) \pm g(t)$, then the random differential transform of $u(t)$ becomes $U(k) = F(k) \pm G(k)$,*

(ii) *For a fourth-order random variable λ, If $u(t) = \lambda f(t)$, then the random differential transform of $u(t)$ becomes $U(k) = \lambda F(k)$,*

(iii) *If $u(t) = d^m(g(t))/dt^m$, then $U(k) = (k+1)\ldots(k+m)G(k+m)$ is the random differential transformation of $u(t)$,*

(iv) *If $u(t) = f(t)g(t)$, then $U(k) = \sum_{n=0}^{k} F(n)G(k-n)$ is the random differential transformation of $u(t)$,*

where m is a non-negative integer and F, G are the transformed processes for f and g respectively.

In applications, $t_0 = 0$ is the popular choice for the power series solution in random Differential Transformation with finitely many terms

$$u(t) = \sum_{k=0}^{n} U(k)t^k \tag{11}$$

whereas the approximate expected value and variance of the solution process are given as

$$E(u(t)) = \sum_{k=0}^{n} E(U(k))t^k \tag{12}$$

$$Var(u(t)) = \sum_{i=0}^{n}\sum_{j=0}^{n} cov(U(i), U(j))t^{i+j}$$

for the covariance function $cov(U(i), U(j)) = E(U(i)U(j)) - E(U(i))E(U(j)), i, j = 1, \ldots, N$ [13], [26].

The approximate expected values and variances (12) can be modified by using Laplace-Padé technique for a better approximation. This modification has been applied to the deterministic DTM in several studies [27], [28]. The basic approach of the method lies on the principle of using a quotient of two polynomials $P_L(t)$ and $Q_M(t)$ of orders L and M, respectively, to obtain an approximation to a function $f(t)$. Hence, for the approximate solutions (11),(12) we can obtain better approximations by using Padé approximants of the form [29]

$$x(t) = \sum_{i=0}^{\infty} a_i t^i = \frac{p_0 + p_1 t + p_2 t^2 + p_3 t^3 + \ldots + p_L t^L}{q_0 + q_1 t + q_2 t^2 + q_3 t^3 + \ldots + q_M t^M} + O(t^{L+M+1}). \tag{13}$$

Optimum choices for the orders of the Padé approximants and the approximations to the solutions of the random model are found with mathematical softwares.

RESULTS

Using random DTM on (2), we obtain

$$(k+1)S(k+1) = \Lambda^*\delta(k) - (d^* + p^*)S(k) - \beta^*\sum_{m=0}^{k} I(m)S(k-m), \tag{14}$$

$$(k+1)V(k+1) = p^*S(k) - d^*V(k) - \theta^*\beta^*\sum_{m=0}^{k} I(m)V(k-m),$$

$$(k+1)E(k+1) = \beta^*\sum_{m=0}^{k} I(m)S(k-m) + \theta^*\sum_{m=0}^{k} I(m)V(k-m) - (d^* + \varepsilon^*)E(k),$$

$$(k+1)I(k+1) = \varepsilon^*E(k) - (d_I^* + \gamma^*)I(k),$$

$$(k+1)R(k+1) = \gamma^*I(k) - d^*R(k).$$

The approximate expected value for $I(t)$ with the Generalized Beta random parameters (5) is

$$E(I(t)) = 5 - 0.175t + 0.26307453125t^2 - 0.131148360545833t^3 + 0.054008208130904t^4, \tag{15}$$

whereas the approximate expectation for $R(t)$ with the Generalized Beta random parameters using 5 terms for the truncated power series solution becomes:

$$E(R(t)) = 0.025t - 0.00112640625t^2 + 0.00044183162198750 01t^3 - 0.000170264348747 6519t^4. \tag{16}$$

Note that the parameters and the random variables are assumed to be independent for these calculations. If the Normally distributed random parameters (8) are used, the approximate expectations for $I(t)$ and $R(t)$ become

$$E(I(t)) = 5 - 0.175t + 0.26307453125t^2 - 0.131148360545833t^3 + 0.054008971778864t^4 \tag{17}$$

and

$$E(R(t)) = 0.025t - 0.00112640625t^2 + 0.00044183162198750001t^3 - 0.00017026436283825 69t^4, \quad (18)$$

respectively. Using Laplace-Padé technique with orders [3, 2] for the polynomials in (13), the approximate expected number of infected population for Generalized Beta parameters (15) can be modified as

$$E(I(t)) = 4.355956053 + [0.2716410522sinh(0.9507440120t) + 0.6440439466cosh(0.9507440120t)]e^{(-0.6727197825t)}. \quad (19)$$

In the Normally distributed case, the approximate expectations (17) and (18) are modified by using polynomials of orders [3, 2] as:

$$E(I(t)) = 4.356046001 + [0.2715615205sinh(0.9507723071) + 0.643953998cosh(0.9507723071)]e^{(-0.6727082555t)} \quad (20)$$

and

$$E(R(t)) = 0.001626893221 + 0.02308555873t - 0.001626893221e^{(-11176746725t)}. \quad (21)$$

Monte-Carlo simulations of the random model (2) with the parameters (5) and (8) are also performed to compare the approximate results with long term disease dynamics. Results for the expected values and variances are given in Figures 2 and 3. Note that the simulations results are given for the variables $S(t)$, $V(t)$, $E(t)$, $I(t)$, similar to the referred study which omits $R(t)$ since it does not appear in other compartments of (1).

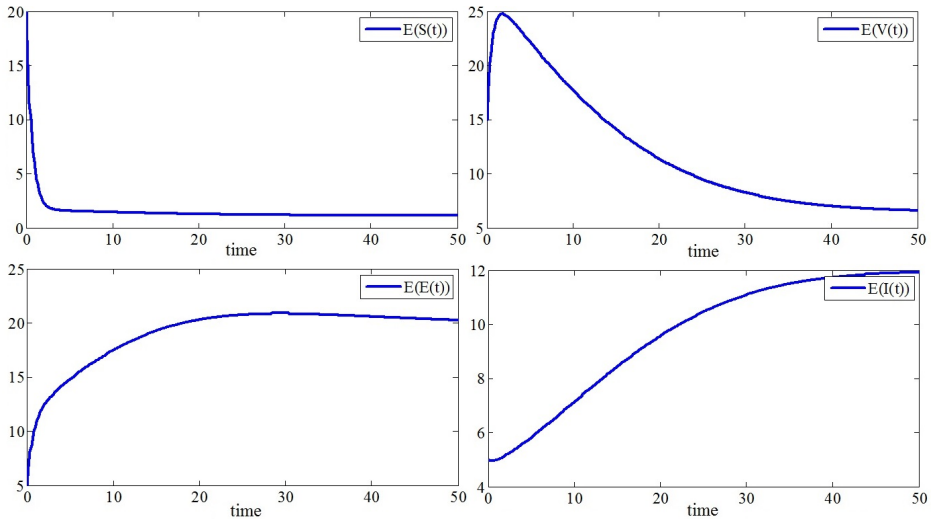

FIGURE 2. Expected values of the random model

For the case with Normally distributed parameters: $E(S(t))$ gets its minimum value 1.116 at $t = 50$ and its maximum value 20 at $t = 0$. $E(V(t))$ gets its minimum value 6.57 at $t = 50$ and its maximum value 24.77 at $t = 1.8$. $E(E(t))$ gets its minimum value 5 at $t = 0$ and its maximum value 20.88 at 28.1. $E(I(t))$ gets its minimum value 4.965 at $t = 0.1$ and its maximum value 11.91 at $t = 50$. Similarly for the case with Generalized Beta parameters the extremum values are as follows: the minimum for $E(S(t))$ is obtained at $t = 50$ with 1.117 while the maximum is the same. The minimum for $E(V(t))$ is obtained at $t = 50$ with 6.588 while maximum is obtained at $t = 1.9$ with 24.78. The minimum for $E(E(t))$ is the same while its maximum is obtained at $t = 28.2$ with 20.89. The minimum for $E(I(t))$ is the same at $t = 0.4$ while its maximum is also the same.

For the variances, it is seen that all of the minimum points are 0 at $t = 0$ for both cases. The maximum points for the case with Normally distributed parameters are 0.08246 at $t = 0.7$ for $Var(S(t))$, 1.637 at $t = 19.2$ for $Var(V(t))$, 2.689 at $t = 39.3$ for $Var(E(t))$ and 1.435 at $t = 50$ for $Var(I(t))$. For the case with Generalized Beta parameters, the maximum points are: 0.08114 at $t = 0.7$ for $Var(S(t))$, 1.637 at $t = 18.92$ for $Var(V(t))$, 2.756 at $t = 39.3$ for $Var(E(t))$ and 1.473 at $t = 50$ for $Var(I(t))$.

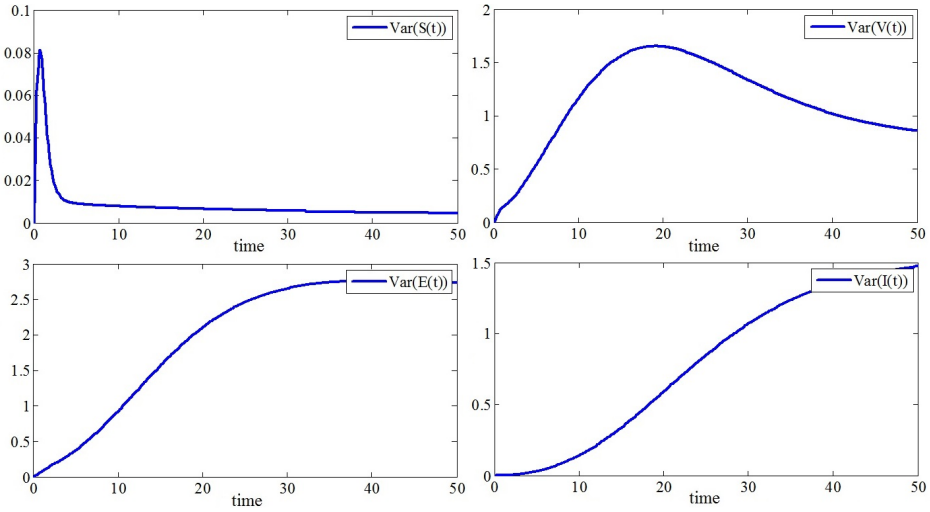

FIGURE 3. Variances of the random model

Using these results, the coefficients of variation (CV) for both distributions are calculated. Minimum CV for both cases are 0 as the minimal variances suggest. The results are shown in Figure 4.

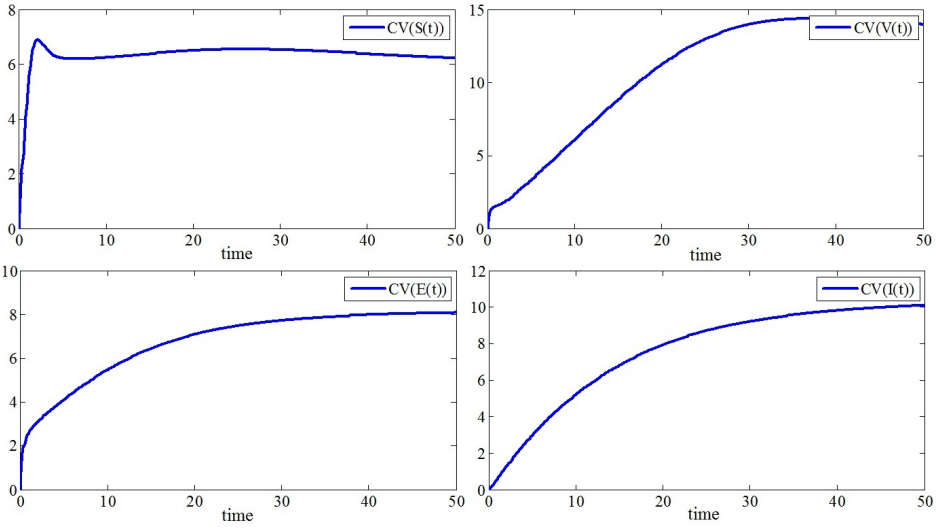

FIGURE 4. Variation coefficients of the random model

The maximum results for coefficients of variation are compared in Table 2 for both cases.

Figures 2, 3 and 4 and the numerical results of the simulations suggest that the expectations of the random model (2) are almost identical to the solutions of the deterministic model (1) meaning the random equation system is a sufficient tool for modeling the disease transmission. However, unlike the deterministic model, the random model also presents results for the variations and enables measurement of the variability between cases of the disease in various conditions.

Expected values indicate that the number of susceptible people decreases through the process, reaching a minimum at the end of the investigation period $t = 50$ (50th day). The number of vaccinated people increases in the beginning, reaching its maximum at around $t = 1.8 - 1.9$, i.e. before the second day of the investigation and then keeps decreasing. The number of exposed people increases until it reaches its maximum at $t = 28.1 - 28.2$, i.e. around

TABLE 2. Comparison of maximum variation coefficients

	Normal Distribution	Generalized Beta Distribution
$S(t)$	%6.902	%6.84
$V(t)$	%14.38	%14.53
$E(t)$	%8.051	%8.148
$I(t)$	%10.06	%10.19
$R(t)$	%12.1	%12.24

the 28th day and keeps approximately the same level until the end. However, the number of infected people is seen to increase through the process, reaching its maximum on day 50.

Since the distributions of the random variables are similarly defined, as seen in Figure 1, we see that the amounts of variations and the variation coefficients are very similar for Normally and Generalized Beta distributed parameters (Table 2 and Figure 4). However, although all of the random parameters were defined with a 5% coefficient of variation, we see that the CV differs for each compartment. The variability in the number of vaccinated people is the largest with an approximately 14.5% CV, meaning that the results of the deterministic studies could be 14.5% different from real life occurences. The results for both distributions are similar, due to the construction of the random parameters, and it is seen that the randomness in the comartments V, R and I are greater than the others.

The modification of the approximate expected value obtained with DTM through Laplace-Padé method is an original application for random differential equation systems, although similar examples exist for deterministic studies. The improvement of results through the modification can be seen in the tables below (Tables 3, 4).

TABLE 3. Numerical results for $I(t)$ (with Generalized Beta parameters (5))

t	Deterministic	DTM	Simulation	RDTM	Modified
0.0	5.000	5.000	5.000	5.000	5.000
0.1	4.985	4.985	4.985	4.985	4.985
0.2	4.975	4.975	4.975	4.975	4.975
0.3	4.968	4.968	4.968	4.968	4.968
0.4	4.965	4.965	4.965	4.965	4.965
0.5	4.965	4.965	4.965	4.965	4.965
0.6	4.967	4.968	4.967	4.968	4.967
0.7	4.972	4.974	4.972	4.974	4.972
0.8	4.978	4.983	4.978	4.983	4.979
0.9	4.986	4.995	4.986	4.995	4.987
1.0	4.996	5.011	4.996	5.011	4.997
1.1	5.007	5.030	5.007	5.030	5.009
1.2	5.020	5.054	5.020	5.054	5.022
1.3	5.033	5.083	5.033	5.083	5.036
1.4	5.047	5.118	5.047	5.118	5.051
1.5	5.062	5.160	5.062	5.160	5.067

Table 3 contains the values for $I(t)$ ($E(I(t))$ in the random case) from (i) the approximate solution of the deterministic model (1) obtained in MATLAB, (ii) the approximate solution of the deterministic model (1) obtained with deterministic DTM, (iii) the Monte-Carlo simulation of the random model (2), (iv) the approximate expected value obtained with random DTM, (v) the Laplace-Padé modification of the approximate expected value obtained with random DTM. Results show that for the random model with Generalized Beta random parameters, the modification

noticeably improves the approximations.

TABLE 4. Numerical results for $R(t)$ (with Normal parameters (5))

t	Deterministic	DTM	Simulation	RDTM	Modified
0.0	0	0	0	0	0
0.1	0.00249	0.00249	0.00249	0.00249	0.00249
0.2	0.00496	0.00496	0.00496	0.00496	0.00496
0.3	0.00741	0.00741	0.00742	0.00741	0.00741
0.4	0.00985	0.00985	0.00985	0.00984	0.00985
0.5	0.01227	0.01227	0.01228	0.01226	0.01227
0.6	0.01468	0.01467	0.01469	0.01467	0.01468
0.7	0.01707	0.01707	0.01708	0.01706	0.01707
0.8	0.01946	0.01945	0.01947	0.01944	0.01946
0.9	0.02184	0.02181	0.02185	0.02180	0.02184
1.0	0.02421	0.02416	0.02422	0.02415	0.02421
1.1	0.02657	0.02650	0.02658	0.02648	0.02658
1.2	0.02892	0.02882	0.02894	0.02879	0.02893
1.3	0.03127	0.03112	0.03129	0.03108	0.03129
1.4	0.03361	0.03340	0.03363	0.03335	0.03363
1.5	0.03595	0.03565	0.03597	0.03560	0.03598
1.6	0.03828	0.03788	0.03830	0.03781	0.03832
1.7	0.04060	0.04008	0.04063	0.03999	0.04065
1.8	0.04292	0.04224	0.04295	0.04214	0.04299
1.9	0.04524	0.04437	0.04527	0.04425	0.04532
2.0	0.04756	0.04645	0.04759	0.04631	0.04764
2.1	0.04987	0.04848	0.04990	0.04831	0.04997
2.2	0.05217	0.05045	0.05222	0.05026	0.05229
2.3	0.05448	0.05237	0.05451	0.05215	0.05462
2.4	0.05678	0.05422	0.05681	0.05397	0.05694
2.5	0.05907	0.05599	0.05911	0.05571	0.05926

The simulations have been performed 10^5 times in MATLAB. Considering the simulation values, which are in accordance with the deterministic results, the absolute error percentages of the random DTM and the modified method for $E(I(t))$ at $t = 1.5$ are as follows:

$$\begin{aligned} Random\ DTM &\rightarrow 100 \times \tfrac{|5.062-5.160|}{5.062} \simeq 1.94\% \\ Modified &\rightarrow 100 \times \tfrac{|5.062-5.067|}{5.062} \simeq 0.10\% \end{aligned} \tag{22}$$

It is seen that by using a 5-term approximate solution within the interval $t \in [0, 1.5]$ (the first 36 hours of the disease), the modified method decreases the error from 1.94% to 0.10%.

Similarly, Table 4 contains a comparison of the results for $R(t)$ in the deterministic model (1) and $E(R(t))$ in the random model (2) with Normally distributed parameters. The Laplace-Padé modification of the approximate expected value is once again considerably improved compared to the approximate expected value obtained with random DTM.

The error percentages of random DTM and the modification, compared to simulation results for $E(R(t))$ at $t = 2.5$ are given as follows:

$$\begin{aligned} Random\ DTM &\rightarrow 100 \times \tfrac{|0.05911-0.05571|}{0.05911} \simeq 5.75\% \\ Modified &\rightarrow 100 \times \tfrac{|0.05911-0.05926|}{0.05911} \simeq 0.25\% \end{aligned} \tag{23}$$

Once again, the modification dramatically decreases the error of random DTM from 5.75% to 0.25%.

CONCLUSION

In this study, a deterministic model of Polio transmission has been analyzed with Generalized Beta and Normally distributed random parameters to investigate the random behavior of disease transmission. The probability distributions of the random parameters have been constructed similarly to ensure similar statistical properties for the random parameters for both cases. The resulting random model has been analyzed by Monte-Carlo simulations, random Differential Transformation Method (DTM) and a modified version of the random DTM using Laplace-Padé technique. Simulation results of the model has proven that the expectations of the random model provides similar results to the deterministic model and can be used for analyzing long term disease transmission. However, unlike the deterministic model, the random model provides the ability to analyze possible variations in the disease transmission which could be caused by geographical, climatic or environmental factors affecting the disease and the population. The random model was also investigated by using random DTM and a modification of the approximate-analytical model was proposed to improve the approximations. Results for $E(R(t))$ and $E(I(t))$ were investigated by using both methods and it was shown that the modification reduces the error percentage considerably. The random model was also examined for the coefficients of variation of the compartments to show the randomness of the population groups and it was seen that the vaccinated population group has the most randomess in the equation system. The randomization of the parameters were hypothetically determined, however this could be done more accurately if data from health organizations are obtained for the disease transmission. Such data would provide a more accurate random modeling approach. Nevertheless, it was shown that our random approach to modeling disease transmission has advantages over the popular deterministic approach and the modified random DTM, along with other approximation techniques in the literature, could be used to investigate the models. This approach could be used for any compartmental model for a variety of diseases.

REFERENCES

[1] World Health Organization, Poliomyelitis, Mar 2018.
[2] J. Hamborsky, A. Kroger, *et al.*, *Epidemiology and prevention of vaccine-preventable diseases, E-Book: The Pink Book* (Public Health Foundation, 2015).
[3] L. Nkamba, J. Ntaganda, H. Abboubakar, J. Kamgang, and L. Castelli, Open Journal of Modeling and Simulation **5**, 98–112 (2017).
[4] D. A. Kalkowska, R. J. D. Tebbens, M. A. Pallansch, S. L. Cochi, S. G. Wassilak, and K. M. Thompson, BMC infectious diseases **15**, p. 66 (2015).
[5] C. J. Browne, R. J. Smith, and L. Bourouiba, Journal of mathematical biology **71**, 215–253 (2015).
[6] K. M. Thompson, R. J. Duintjer Tebbens, and M. A. Pallansch, Risk Analysis **26**, 1541–1556 (2006).
[7] A. Dénes and L. Székely, Mathematical biosciences **293**, 64–74 (2017).
[8] M. Awale, N. Balakrishna, and T. Ramanathan, Statistical Papers 1–25 (2017).
[9] J. Kang, Entropy **20**, p. 107 (2018).
[10] J. Kang and S. Lee, Journal of Time Series Analysis **30**, 239–258 (2009).
[11] N. Noori, J. M. Drake, and P. Rohani, Scientific reports **7**, p. 17362 (2017).
[12] R. J. Duintjer Tebbens, M. A. Pallansch, S. L. Cochi, D. T. Ehrhardt, N. H. Farag, S. C. Hadler, L. M. Hampton, M. Martinez, S. G. Wassilak, and K. M. Thompson, Risk Analysis (2018).
[13] A. Golmankhaneh, N. Porghoveh, and D. Baleanu, Romanian Reports in Physics **65**, 350–362 (2013).
[14] A. R. Khudair, A. A. Ameen, and S. L. Khalaf, Applied Mathematical Sciences **5**, 2505–2519 (2011).
[15] L. Villafuerte and J. Cortés, Advances in Dynamical Systems and Applications **8**, 413–425 (2013).
[16] L. Villafuerte and B. M. Chen-Charpentier, Applied Mathematics Letters **25**, 1490–1494 (2012).

[17] J. Zhou, Differential transformation and its applications for electrical circuits, 1986.
[18] G. G. Ev Pukhov, International Journal of Circuit Theory and Applications **10**, 265–276 (1982).
[19] A. R. Khudair, S. Haddad, and S. L. Khalaf, Open Journal of Applied Sciences **6**, p. 287 (2016).
[20] G. González-Parra, A. J. Arenas, and M. Cogollo, Ingeniería y Ciencia **11**, 49–72 (2015).
[21] H. Abboubakar, J. C. Kamgang, N. L. Nkamba, D. Tieudjo, and L. Emini, Biomath **4**, p. 1507241 (2015).
[22] H. Abboubakar, J. C. Kamgang, and D. Tieudjo, Mathematical biosciences **278**, 100–129 (2016).
[23] T. T. Soong, *Random differential equations in science and engineering* (Elsevier, 1973).
[24] M. Merdan, Z. Bekiryazici, T. Kesemen, and T. Khaniyev, Advances in Difference Equations **2017**, p. 133 (2017).
[25] C. Forbes, M. Evans, N. Hastings, and B. Peacock, *Statistical distributions* (John Wiley & Sons, 2011).
[26] J. Fakharzadeh, E. Hesamaeddini, and M. Soleimanivareki, Applied Mathematics in Engineering, Management and Technology **3**, 115–123 (2015).
[27] A. Gökdoğan, M. Merdan, and A. Yildirim, Communications in Nonlinear Science and Numerical Simulation **17**, 45–51 (2012).
[28] M. Mehdi Rashidi and E. Erfani, International Journal of Numerical Methods for Heat & Fluid Flow **21**, 864–883 (2011).
[29] M. M. Rashidi, Computer Physics Communications **180**, 2210–2217 (2009).