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ANALYZING THE DYNAMICS OF EBOLA TRANSMISSION WITH RANDOM EFFECTS

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Abstract. In this study, a deterministic mathematical model of Ebola transmission is analyzed under random effects. A recent compartmental model of Berge et al. incorporates both direct and indirect transmission in the model. We assume the parameters of this model are normally distributed random variables to investigate the random behavior of disease transmission. Random differential transformation method is used to obtain the approximate expectation of disease recovery. Furthermore, the approximation for expected recovery is modified by using Laplace-Padé method. Comparison of results indicate that the Laplace-Padé modification provides a better approximation. We also interpret the long term random behavior of the disease dynamics using simulation results.

Keywords: random differential equation; random differential transform method; random effect; normal distribution; Ebola.

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1. Introduction

Mathematical models play an important role in many fields of science as they have become an essential part of the scientific analysis method. Analyzing an unknown event through the use of equation systems to understand the nature of the phenomena as well as to predict the possible future dynamics of the event is a vital component of todays scientific investigations. Epidemiology, medicine and biochemistry are among some of the fields which mathematical models are extensively used in. Results from models consisting of systems of deterministic differential equations constitute a considerable part of the studies that are carried out in these fields. The parameters of the models are assumed to be constant values for these deterministic analyses. However, some components of the events being modelled may have random behavior in real life. For instance, Ebola Virus Disease has been modeled by using deterministic systems ([1], [2]) although there are various studies in the literature which present the random nature of some disease dynamics ([3], [4], [5], [6]).

Ebola Virus Disease (EVD), which passes to humans from animals, is a fatal disease. It was first discovered in 1976 in Africa. The 2014-2016 Ebola outbreak in West Africa has become the most deadly Ebola epidemic since the discovery of the virus ([7]), resulting in the death of 2544 out of 3814 cases in Guinea alone ([8]). However, the experimental rVSV-ZEBOV vaccine has proven to be successful in a trial led by World Health Organization (WHO) in 2015 ([7]).

The random nature of certain components for Ebola Virus Disease can be found in the recent modeling studies. The study of J. Bartlett et al. presents various values for disease infection rates ranging from 0 to 0.153 and death rates ranging from 0 to 0.0032 in a SIR based model for EVD ([3]). The study of WHO Ebola response team gives random results for the basic reproduction number of EVD for different countries, such as a mean value of 1.85 for Liberia with a 95% confidence interval $(1.72, 1.94)$ ([4]). A 2014 report on the epidemiological dynamics of Ebola by T. House gives a mean value of 1.49 years for the time period between consecutive Ebola outbreaks ([5]). Similarly, a study by G. Chowell and H. Nishiura states that the proportion of death in the first 9 months of the epidemic in West Africa has a mean value of 70.8% with a 95% confidence interval $(68.6, 72.8)$ ([6]).

In light of these random dynamics for various components of EVD, we propose a random model for EVD based on the deterministic model of T. Berge et al. ([2]). We transform the parameters of the deterministic equation system into random variables using random effect terms. This approach for obtaining systems of random differential equations for modeling infectious disease dynamics has been presented and used by the authors for various diseases ([9], [10]). The predictions based on the results of deterministic studies, which ignore the random nature of certain aspects of epidemics, can cause serious problems in battling the disease. A report in 2015 from WHO experts in Guinea states that the scale of the Ebola outbreak was underestimated by offical data ([11]). Using random differential equations for modeling disease dynamics enables us to model the random behavior of the disease in the equation system. We investigate the new random system by using approximate results obtained by random Differential Transformation Method (rDTM) ([12], [13]) along with simulations to interpret the randomness of the event. The approximations from rDTM are also modified by using Padé approximants to improve the results ([14],[15]). Results show that the random model is an efficient tool for modeling both the disease dynamics and the variations in disease behavior.

2. Ebola Disease Model

The system of deterministic nonlinear ordinary differential equations (1) given by T. Berge et al. is used in this study ([2]).

$$
\begin{aligned}
\frac{dS(t)}{dt} &= \pi - (\beta_1 I + \beta_2 D + \lambda P)S - \mu S, \\
\frac{dI(t)}{dt} &= (\beta_1 I + \beta_2 D + \lambda P)S - (\mu + \delta + \gamma)I, \\
\frac{dR(t)}{dt} &= \gamma I - \mu R, \\
\frac{dD(t)}{dt} &= (\mu + \delta)I - bD, \\
\frac{dP(t)}{dt} &= \sigma + \xi I + \alpha D - \eta P.
\end{aligned} \tag{1}
$$

This system is an original model for EVD since it incorporates both direct and indirect Ebola transmission in a single equation system. The variables of this system are as follows: $S(t)$ denotes the number of susceptible human individuals, $I(t)$ denotes the number of infectious human individuals, $R(t)$ denotes the number of recovered human individuals, $D(t)$ denotes the number of Ebola infected and deceased human individuals and $P(t)$ denotes the number of Ebola virus pathogens. Overall, this system models the change of the compartment populations in time, which is denoted by t (in days). The model is based on the basic SIR model with the additional compartments D and P to model indirect disease transmission caused by environmental factors and etc.

TABLE 1. Parameter values and descriptions

Parameter	Description	Value
π	Susceptible human recruitment rate	10
η	Ebola virus decay rate	0.03
ξ	Infectious human shedding rate	0.04
α	Deceased human shedding rate	0.04
δ	Human death-by-disease rate	0.9
β_1	Infectious human contact rate	0.006
β_2	Deceased human contact rate	0.012
λ	Ebola virus contact rate	0.01
γ	Human recovery rate	0.06
μ	Human natural death rate	0.02
b	Deceased human caring duration	0.8
σ	Ebola virus recruitment rate	variable

We will obtain random parameters for (1) by using the deterministic values of the parameters. This way, the random parameters will model the random nature of Ebola transmission in the equation system. Therefore the parameters of the equation system and their values for the numerical analysis are of great importance to our study. There are a number of possible choices for the values of the parameters in the referred study. Since we want to present the idea of a

random model for Ebola transmission, we arbitrarily choose the presented value set ([2]) (Table 1). Note that any of the other values for the original parameters can be used for obtaining the random model.

The following set of initial values will be used for the numerical investigation of the model dynamics: $S(0) = 15$, $I(0) = 10$, $R(0) = 0$, $D(0) = 10$, $P(0) = 0$. The values of the initial values, just like the parameter values, have been chosen according to the reference study ($\sigma = 0$ will be used) ([2]). The deterministic system, as mentioned before, neglects the randomness of the parameters. Therefore, the parameters of the equation system (1) will be added random effect terms that model the neglected randomness in the deterministic system. There are also several stochastic modeling studies in the literature where stochastic differential equations are used in modeling studies for various fields ([9], [16], [17], [18], [19]). Stochastic models could also be considered for modeling the volatility of results in Ebola transmission models.

3. Parameters under Random Effects

The parameters of system (1) will be transformed into random variables to obtain a system of random nonlinear differential equations. The parameters are assumed to be normally (Gaussian) distributed for this study. The motivation for considering random parameters in this system is to model the possible variations of the disease dynamics. It is known that certain aspects of the disease such as the infection rate, recovery rate and etc. can change for different places/populations. Hence, normally distributed parameters will be used to model these changes in the equation system. Normal distribution is widely used in scientific research for random variables for which the exact distribution is unknown. Since we know there are many factors that affect the values of these parameters and that the exact measure of their variation is not known, normal distribution is the most reasonable choice. Additionally, normal distribution is symmetric around its mean, which allows us to let the random parameters assume values below or above their deterministic values with equal probability.

The parameters of the system (1), $\pi, \eta, \xi, \alpha, \delta, \beta_1, \beta_2, \lambda, \gamma, \mu, b, \sigma$, are transformed into random variables with normal distribution as follows:

$$\pi^* = \pi + s_1\chi_1,\ \eta^* = \eta + s_2\chi_2,\ \xi^* = \xi + s_3\chi_3,\ \alpha^* = \alpha + s_4\chi_4,$$
$$\delta^* = \delta + s_5\chi_5,\ \beta_1^* = \beta_1 + s_6\chi_6,\ \beta_2^* = \beta_2 + s_7\chi_7,\ \lambda^* = \lambda + s_8\chi_8,$$
$$\gamma^* = \gamma + s_9\chi_9,\ \mu^* = \mu + s_{10}\chi_{10},\ b^* = b + s_{11}\chi_{11},\ \sigma^* = \sigma + s_{12}\chi_{12}.$$

Here, the coefficients $s_i, i = \overline{(1,12)}$ are the standard deviations of the newly formed random parameters $\pi^*, \eta^*, \xi^*, \alpha^*, \delta^*, \beta_1^*, \beta_2^*, \lambda^*, \gamma^*, \mu^*, b^*, \sigma^*$ and $\chi_i, i = \overline{(1,12)}$ are independent random variables with standard normal distribution. The standard deviations of the random variables, $s_i, i = \overline{(1,12)}$, are determined to be 5% of their corresponding deterministic values, so that the coefficient of variation (CV) is 5% for each random parameter. We use this specific CV for each parameter so that we can comment on the CV of each compartment using the numerical results of the system. The resulting new parameters are rewritten in the system (1) to obtain the new random system (2):

$$\begin{aligned}
\frac{dS(t)}{dt} &= (10 + 0.5\chi_1) - ((0.006 + 0.0003\chi_6)I + (0.012 + 0.0006\chi_7)D \\
&\quad + (0.01 + 0.0005\chi_8)P)S - (0.02 + 0.001\chi_{10})S, \\
\frac{dI(t)}{dt} &= ((0.006 + 0.0003\chi_6)I + (0.012 + 0.0006\chi_7)D \\
&\quad + (0.01 + 0.0005\chi_8)P)S - ((0.02 + 0.001\chi_{10}) + (0.9 + 0.045\chi_5) \\
&\quad + (0.06 + 0.003\chi_9))I, \\
\frac{dR(t)}{dt} &= (0.06 + 0.003\chi_9)I - (0.02 + 0.001\chi_{10})R, \\
\frac{dD(t)}{dt} &= ((0.02 + 0.001\chi_{10}) + (0.9 + 0.045\chi_5))I - (0.8 + 0.04\chi_{11})D, \\
\frac{dP(t)}{dt} &= (0.04 + 0.002\chi_3)I + (0.04 + 0.002\chi_4)D - (0.03 + 0.0015\chi_2)P.
\end{aligned} \tag{2}$$

Note that since $\sigma = 0$, this term in (1) does not appear in (2). This is a result of our selection for the value of σ and this term would take its place in the random model (2) for any other value of the parameter. The numerical solutions of the system (2) are used to determine the random behavior of Ebola disease. The approximate random dynamics are investigated by using

tools of mean square analysis while the long-term dynamics are investigated by Monte-Carlo simulations.

3.1. **Approximate Expectations for Recovery.** The first days of the epidemic are important as they are the initial signs of how wide the infection will spread through the population. The random model (2) will be used to obtain the approximate expectation of recovery and thus comment about the future of the epidemic using the initial results for this compartment. The details of the mean square and mean fourth calculus necessary for obtaining approximate analytical solutions can be found in the literature ([12],[20]).

Random Differential Transformation Method (rDTM) was used to obtain an approximate solution for the equations in truncated series form. Basically, the truncated series solution for any stochastic process $x(t)$ is obtained as

$$x(t) = \sum_{k=0}^{n} X(k)t^k,$$

using $X(k)$, the transformed process for the original process $x(t)$, along with its inverse transform about $t_0 = 0$ ([12], [13]). Random Differential Transform (rDTM) is the random version of the deterministic DTM and the theorems for the convergence of the approximations have been well established in the literature ([21], [22]). A list of some of the fundamental operations of DTM has been given in the literature along with the basic definition of the method ([15]). The approximate solution obtained with random DTM will also be modified through Laplace transforms and Padé approximants for a better approximation ([14], [15]). Using the tools of mean-square calculus and DTM, the expectation and the variance of any random process can be obtained as ([23], [24]):

$$E[x(t)] = \sum_{k=0}^{n} E[X(k)]t^k,$$

$$Var[x(t)] = \sum_{j=0}^{n}\sum_{i=0}^{n} cov(X(i),X(j))t^{i+j},$$

as given by Khudair, Haddad and Khalaf ([25]). Note that the use of random DTM with Laplace-Padé method for analyzing the statistical properties of a disease model is an original application of these methods.

In particular, the approximate solution for the third equation of system (2) obtained by Differential Transform Method ($\frac{dR(t)}{dt} = \gamma^* I - \mu^* R$) is found as

$$\begin{aligned} R(t) &= 10\gamma^* t + \left(\frac{1}{2}\gamma^*(150\beta_1^* + 150\beta_2^* - 10\mu^* - 10\delta^* - 10\gamma^*) - 5\mu^*\gamma^*\right)t^2 \\ &= 10\gamma^* t + (75\gamma^*\beta_1^* + 75\gamma^*\beta_2^* - 10\gamma^*\mu^* - 5\gamma^*\delta^* - 5(\gamma^*)^2)t^2 \end{aligned}$$

using iterations up to $n = 2$. Here, $R(1) = 10\gamma^*$ and $R(2) = 75\gamma^*\beta_1^* + 75\gamma^*\beta_2^* - 10\gamma^*\mu^* - 5\gamma^*\delta^* - 5(\gamma^*)^2$ for the series solution. While iterations for $n = 2$ may not be enough for an accurate approximation, this example is used for a better understanding of the methodology. Assuming that the random parameters $\pi^*, \eta^*, \xi^*, \alpha^*, \delta^*, \beta_1^*, \beta_2^*, \lambda^*, \gamma^*, \mu^*, b^*, \sigma^*$ are independent, we use this truncated series approximate solution of $R(t)$ to obtain its expectation as:

$$\begin{aligned} E[R(t)] = &\quad E[10\gamma^* t + (75\gamma^*\beta_1^* + 75\gamma^*\beta_2^* - 10\gamma^*\mu^* - 5\gamma^*\delta^* - 5(\gamma^*)^2)t^2] \\ = &\quad E[10\gamma^*]t + E[75\gamma^*\beta_1^* + 75\gamma^*\beta_2^* - 10\gamma^*\mu^* - 5\gamma^*\delta^* - 5(\gamma^*)^2]t^2. \end{aligned}$$

Higher moments such as $E[(\gamma^*)^2]$ are needed for all of the parameters, especially for series solutions with containing $n > 2$ terms. It is known that for a normally distributed random variable X with parameters $X \sim N(m, n^2)$, these moments can be obtained through the moment generation function of normal distribution ([26]):

$$M_X(t) = E[e^{tX}] = e^{mt + \frac{1}{2}n^2t^2}.$$

Thus, the first and second moments of the random variable $X \sim N(m, n^2)$ are:

$$E[X] = m,\ E[X^2] = m^2 + n^2.$$

Using these moments and the fact that $E[XY] = E[X]E[Y]$ for independent random variables X and Y, the approximate formulas for the expectations can be calculated since

$$\gamma^* = \gamma + s_9\chi_9 = 0.06 + 0.003\chi_9 \Rightarrow \gamma^* \sim N(0.06, (0.003)^2).$$

Similar calculation for other random parameters and the expectation formula are used to obtain the expectations of the random variables. For instance, using $n = 2$, the approximate formula

for the expectation of $R(t)$ given above can be rearranged as follows:

$$E[R(t)] = 10E[\gamma^*]t + (75E[\gamma^*\beta_1^*] + 75E[\gamma^*\beta_2^*] - 10E[\gamma^*\mu^*] - 5E[\gamma^*\delta^*] - 5E[(\gamma^*)^2])t^2. \tag{3}$$

Since the accuracy of the formulas increase with the iterations, the expectation of $R(t)$ obtained by random DTM with iterations for $n = 4$ can be found as below for a higher accuracy (t denotes the number of days):

$$E[R(t)] = 0.6t - 0.219045t^2 + 0.080833275t^3 - 0.02282931889739t^4.$$

This formula is modified for a better approximation to the expected value of the variable. The details of Laplace-Padé method which was used for the modification has been given by ([14]). The modified approximate expectation formula of $R(t)$, calculated in Maple software is obtained as:

$$E[R(t)] = 5.483588512 - 4.812982790\exp(-0.5867596092t) \times sinh(0.5438515717t) - 5.483588512\exp(-0.5867596082t) \times cosh(0.5438515717t).$$

Numerical results for $R(t)$ for the deterministic case is compared with the results of the rDTM and modified rDTM in Table 2. Note that the calculations for the expectation formulas are obtained under the assumption of independency for random variables.

The results (Table 2) clearly show that the modified algorithm produces results which successfully converge to the expected value of $R(t)$ in the interval $[0,2]$, i.e. the first two days of infection. The difference between the deterministic results and the modified expected values indicate the deviations caused by the random effects.

It is possible to find expected values and variances for all of the variables $S(t), I(t), R(t), D(t)$ and $P(t)$ using mean square calculus and the corresponding formulas. However, it should be noted that the assumption of independent variables, the nonlinearity of the equations and similar other factors may decrease the accuracy of the method in large intervals. Therefore, using a higher number of iterations for various cases may increase the accuracy of the results.

TABLE 2. Deterministic results for $R(t)$ compared with its approximate expectation formulas obtained by rDTM and modified rDTM (Simulation results are also included).

t	Deterministic	rDTM	Modified	Simulation
0.1	0.0579	0.0579	0.0579	0.0579
0.2	0.1119	0.1118	0.1118	0.1119
0.3	0.1623	0.1623	0.1623	0.1623
0.4	0.2097	0.2095	0.2096	0.2096
0.5	0.2542	0.2539	0.2541	0.2541
0.6	0.2961	0.2956	0.2960	0.2960
0.7	0.3358	0.3349	0.3357	0.3357
0.8	0.3735	0.3718	0.3733	0.3733
0.9	0.4092	0.4065	0.4091	0.4091
1.0	0.4434	0.4390	0.4433	0.4432
1.1	0.4761	0.4691	0.4760	0.4759
1.2	0.5074	0.4969	0.5073	0.5072
1.3	0.5375	0.5222	0.5375	0.5374
1.4	0.5666	0.5448	0.5666	0.5664
1.5	0.5947	0.5644	0.5947	0.5945
1.6	0.6218	0.5807	0.6220	0.6217
1.7	0.6483	0.5934	0.6484	0.6481
1.8	0.6740	0.6021	0.6741	0.6738
1.9	0.6990	0.6062	0.6992	0.6988
2.0	0.7234	0.6052	0.7237	0.7233

3.2. **Long Term Random Dynamics.** The random behavior of the model components can be accurately estimated for the first days using the modified algorithm above. However, Monte-Carlo simulations provide better results for the long term analyses of the random system (2). By

simulating the numerical results of the random model, we obtain the following characteristics for the variables.

3.2.1. *Expected Values with Deterministic Results.* As the figures suggest, the results of the random model (Figure 1) are very similar to the results of the deterministic model. The deterministic results for the model (1) can be shown on a graph as well to underline the similarity of the behaviors of the systems.

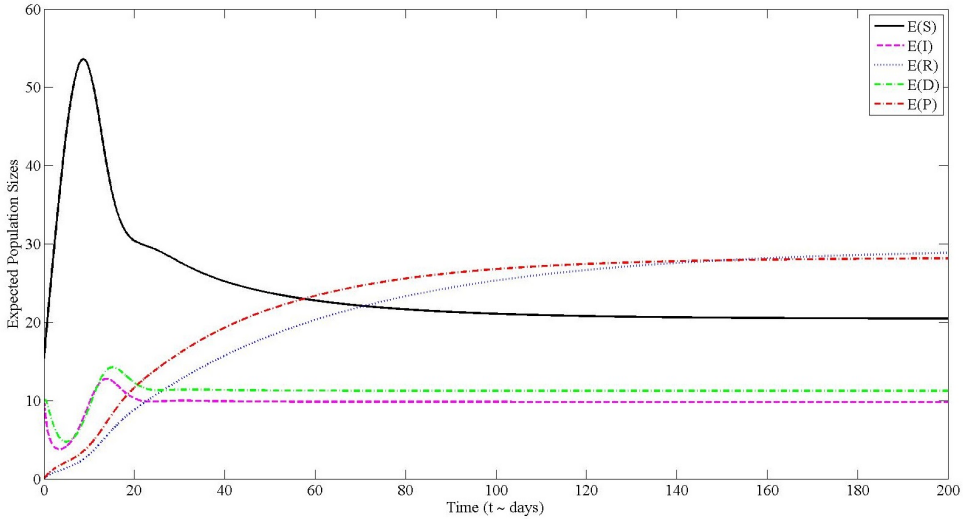

FIGURE 1. Expected values of the random variables.

The deterministic results (Figure 2) show that number of susceptible humans gets its maximum value 53.11 at $t = 8.689$ and its minimum value 15 at $t = 0$ (t denotes the number of days). It is also seen that the change in this variable almost stops after $t = 100$ since $S(t) = 20.84$ for $t = 100$ and $S(t) = 20.25$ for $t = 200$. The number of infectious humans, $I(t)$ gets its maximum and minimum values 12.79 and 3.801 at $t = 13.86$ and 3.442, respectively. The change in $I(t)$ almost stops after $t = 40$, since $I(t) = 9.882$ at $t = 40$ and $I(t) = 9.792$ at $t = 200$. The number of recovered humans begins from its minimum value 0 at $t = 0$ and reaches its maximum value 28.84 at $t = 200$. The number of Ebola-infected and deceased humans, $D(t)$, gets its minimum value 4.782 at $t = 4.902$ and its maximum value 14.34 at $t = 15.28$. The change in $D(t)$ almost stops around $t = 40$ too, since $D(t) = 11.38$ at $t = 40$ and $D(t) = 11.26$ at $t = 200$. Finally, $P(t)$, the number of Ebola pathogens, starts from 0 at $t = 0$ and reach its maximum 28.01 at $t = 200$.

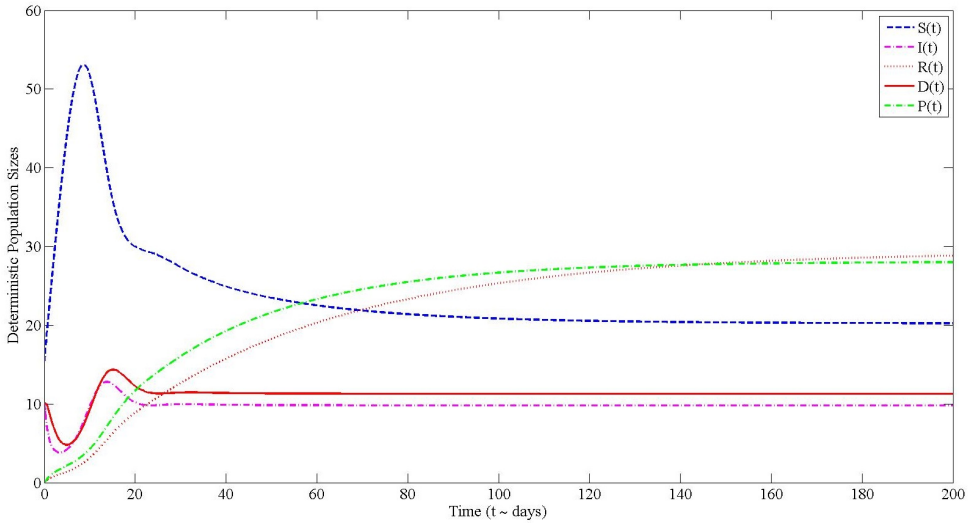

FIGURE 2. Deterministic results of model (1).

It is seen that the extremum values for the expectations of the random model are very similar to the deterministic values. This indicates that the dynamics of the model under random effects are in accordance with the deterministic model and thus the random model is meaningful. The difference between the random and deterministic results shows the effects of the random parameters on the disease dynamics.

$max(E(S(t)) = 52.88$ at $t = 8.667$ and $min(E(S(t)) = 15$ at $t = 0$. $max(E(I(t)) = 12.73$ at $t = 13.67$ and $min(E(I(t)) = 3.827$ at $t = 3.333$. $max(E(R(t)) = 29.01$ at $t = 200$ and $min(E(R(t)) = 0$ at $t = 0$. $max(E(D(t)) = 14.27$ at $t = 15$ and $min(E(D(t)) = 4.82$ at $t = 5$. $max(E(P(t)) = 28.1$ at $t = 200$ and $min(E(P(t)) = 0$ at $t = 0$. The correspondence between the extremum values and the times of these values should also be noted.

3.2.2. *Standard Deviations, Confidence Intervals and Variation Coefficients.* The results for the confidence intervals (for the expected values) of the random variables are used along with the coefficient of variations to interpret the randomness of these variables. For this study, approximately 99% confidence intervals have been used for the random variables $(K = 3)$ with the form

$$[E(X(t)) - K.\sigma(X(t)), E(X(t)) + K.\sigma(X(t))]$$

where $\sigma(X(t))$ denotes the standard deviation of an arbitrary random process $X(t)$. Here, K determines how many standard deviations will be used to form the confidence interval around the mean and $K = 3$ is used. The following graphs are obtained for the 99% confidence intervals of the random variables $S(t), I(t), R(t), D(t), P(t)$ (Figure 3). The confidence intervals show the maximum and minimum values that the expectations of the population groups can get through the infection period.

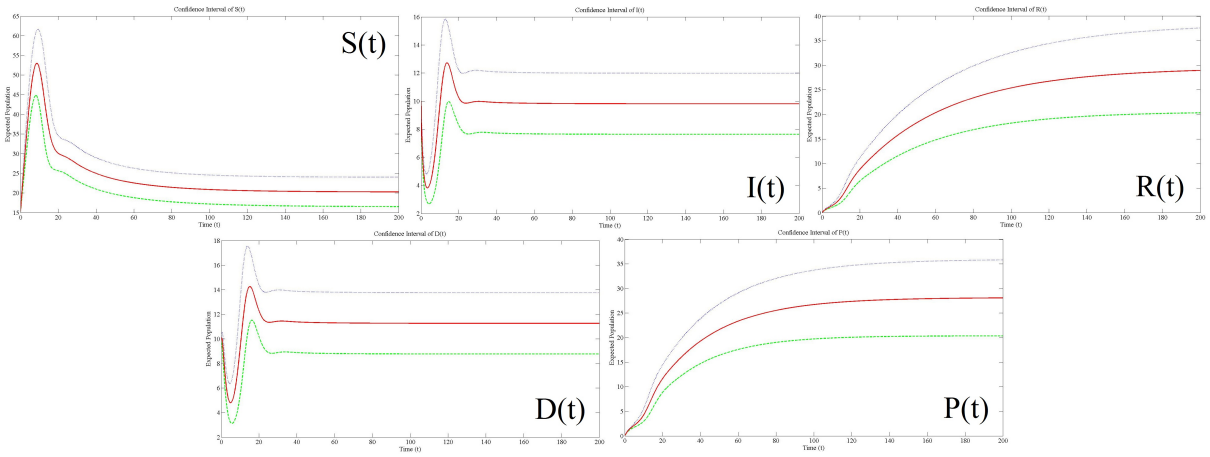

FIGURE 3. Confidence intervals of the random variables.

The maximum standard deviation of $S(t)$ is obtained at $t = 12$ with a value of 3.51 ($E(S(t)) = 46.06$ at $t = 12$). The standard deviation of $I(t)$ gets its maximum value 1.215 at $t = 10.67$ ($E(I(t)) = 10.52$ at $t = 10.67$). The standard deviation of $R(t)$ gets its maximum value 2.833 at $t = 200$ ($E(R(t)) = 28.84$ at $t = 200$). The standard deviation of $D(t)$ gets its maximum value 1.397 at $t = 11.67$ ($E(D(t)) = 11.69$ at $t = 11.67$). The standard deviation of $P(t)$ gets its maximum value 2.53 at $t = 200$ ($E(P(t)) = 28.1$ at $t = 200$).

Hence the maximum values of the coefficient of variations (CV) for the random variables are (CV=$\frac{100 \times std.deviation}{expectation}$):

$$CV(S(t)) = 7.6\%,\ CV(I(t)) = 11.5\%,\ CV(R(t)) = 9.8\%,$$

$$CV(D(t)) = 12.0\%,\ CV(P(t)) = 9.0\%.$$

These values, along with the confidence intervals and the standard deviations, show that the randomness in the variables are similar to each other, with the randomness of $S(t)$ being lower

than the others. The coefficient of variation shows the expected deviation in the results as a percentage, for instance on day twelve ($t = 12$), the expected value shows that we should expect 46 susceptible people in the population ($E(S(12)) = 46.06$), however this number may change by 7.6% in some cases since $CV(S(12)) = 7.6\%$. Standard deviation for $S(t)$ denotes that at $t = 12$, the expected number of susceptibles could change by more than 3 people ($std(S(12)) = 3.51$). This day sees the highest deviation for the susceptibles meaning the results of the deterministic study would be least accurate at $t = 12$. The expected number of infectious $I(t) = 10.52$ at $t = 10.67$ could also vary by 11.5% since the standard deviation shows that results could change by more than 1 person ($std(I(10.67)) = 1.215$). Similar conclusions can be obtained for all the compartments using the results of expectations and standard deviations. In this study, a 5% randomness has been assumed for all the parameters to model a small volatility in the disease dynamics. However, more precise data on the random nature of the disease could provide accurate results on the deviations of the disease dynamics. This means that the same random equation system could be used with a different set of parameters which have different probability distributions and standard deviations to model the random transmission of the disease.

4. Concluding Remarks

In this study, a deterministic model of Ebola Virus Transmission (EVD) presented by T. Berge et al. was used to investigate the random transmission dynamics of EVD. The random model was obtained by adding random effects to the parameters of the original deterministic model. The resulting system of random differential equations has proven to be useful for both modeling the transmission dynamics of EVD and representing the random behaviour of the disease components. The random model was analyzed by using both numerical and approximate analytical methods to investigate the random behavior of the model. The approximate analytical solution obtained by random DTM was used to obtain the approximate expectation of disease recovery. The approximate recovery formula was modified by using the Laplace-Padé algorithm. Comparison or results for random DTM and the modification suggests that the modified expectation converges to the deterministic results on a larger interval.

The results for the recovered population in the first two days of the disease obtained by random DTM could be improved by calculating more terms for the truncated series solution. Similar approximate expectation, variance and confidence interval formulas can be obtained and modified for all of the compartments in (2). There are also other modification algorithms for DTM that can be applied to improve the approximations. Formulas for the early random dynamics of the disease could provide useful results for epidemiological studies on various other models.

The random model was also simulated to analyze the long term random dynamics of the model. It was seen that the results of the random model matched the results of the deterministic model. The minor differences in between these two sets of results showed the effects of the random parameters. Finally, the confidence intervals and the coefficients of variations were analyzed for the variables to investigate the individual randomness of the variables of the model. It was seen that the results for $S(t)$ had smaller deviation. These analyses can be made for any model and provide valuable results for the investigation of event both on short and long terms. The results can be improved by using real life data to determine the amount and distributions of the random effects. Note that modification of the random approximate statistical properties for the disease through Laplace-Padé technique is an original application and just like the random modeling approach, could be used to obtain accurate results for numerical characteristics of various disease models.

It should be noted that the random model can be used instead of the deterministic model since its expected values obtained from simulation results are almost identical to the deterministic results. However, in addition, the random model also provides information about the random behavior of the compartments. The variation coefficients and confidence intervals for the expected values provide results for the possible deviations in the disease dynamics which can not be modeled through deterministic equations. These results are meaningful and also crutial for battling infections. Hence, this approach to modeling infectious diseases would be more practical for many other diseases. The use of random DTM and the modified algorithm along with the random modeling approach enables a random investigation of almost all epidemiological events. The random modeling approach could also be improved by determining the standard

deviations of the random parameters from real life data, instead of the hypothetical 5% selection. Various other probability distributions could also be used for the random effects other than normal distribution, whenever necessary.

Conflict of Interests

The authors declare that there is no conflict of interests.

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