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Queueing Based Compartmental Models for Ebola Virus Disease Analysis

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Abstract Ebola Virus Disease (EVD) is a complex and unprecedented epidemic killer disease. Recently, the disease has caused serious loss of life, waste of economic and material resources in West African nations. The most prevalent countries are Guinea, Liberia and Sierra Leone. Compartmental models are traditional epidemiological mdels that try to explain epidemic problems through the use of specific compartments that are subsets of a given population. Analysis using the developed queueing based compartmental models for Ebola Virus Disease (EVD) resulted in estimates of R_0= (2.2550, 3.5264, 2.2325) for Guinea, Liberia and Sierra Leone. $R_0 > 1$ for each of the countries, implying that the transmission and control of the epidemic was unstable and needed urgent intervention. The developed SEI_LI_CDR model outperformed the existing SEIR model by 13.10%, 91.76%, and 83.14%, respectively on the basis of their RMSE. Finally, analysis using queueing in SEI_LI_CDR compartmental models led to the discovery that, at a probability of 0.4 in each compartment, the transmission of EVD can be controlled.

Keywords: *Ebola Virus Disease, epidemic, comparmental model, transmission, control, queueing*

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1. Introduction

Compartmental model is a traditional epidemiological analysis that is based on subdividing the population under consideration into various sections [1]. It tries to explain epidemic problems through the use of specific compartments that are subsets of a given population [2]. In compartmental model, persons in the population are allocated to smaller groups, each signifying a definite phase of the epidemic. It is mostly used to model in a large population the growth of an epidemic. Application of compartmental model to epidemic problems could be traced to the work of Kermack and Mckendrick on SIR epidemic model as cited by Bashar et al [1]. The work analysed epidemic problems using three compartments, namely: Susceptible, Infected and Removed. Subsequently, to make provision for the dynamics of epidemic diseases, other compartmental models were proposed namely: the SEIR (Susceptible, Exposed, Infected, Removed) model cited by Chowell et al [3], and the SEIS model of Hernandez-Suarez et al [4]. Other proposed models were: the $SEID_bD_IR$ (Susceptible, Exposed, Infected, Dead Buried, Dead Infected, Removed) model by Siettos et al [5], and the SEIHFR (Susceptible, Exposed, Infected, Hospitalized, Funeral, Removed) model cited by Legrand et al [6]. However, Ebola Virus Disease has unique transmission phases, namely: Susceptible, Exposed, Likely Infected, Confirmed Infected, Dead/Removed - SEI_LI_CDR [7]. In this paper, each EVD transmission phase is considered as a compartment within the confines of queueing theory. Queueing theory is the mathematical study of waiting lines, or queues [8]. This paper adopts the integration of the different compartments to analyse the EVD epidemic problem.

2. Deveopment of Models

2.1. SEI_LI_CDR Compartmental Model

The development process of the SEI_LI_CDR compartmental model followed the concept of SEIR compartmental model proposed by Chowell *et al*. [3] as illustrated in Figure 1.

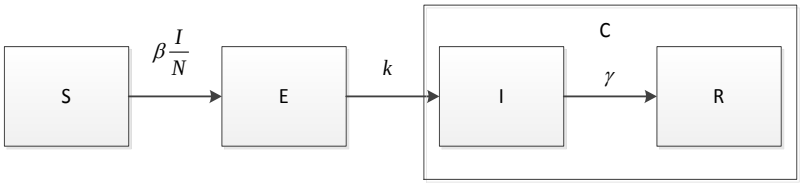

Figure 1. A Schematic of the Transitions between Different States of EVD for SEIR Model

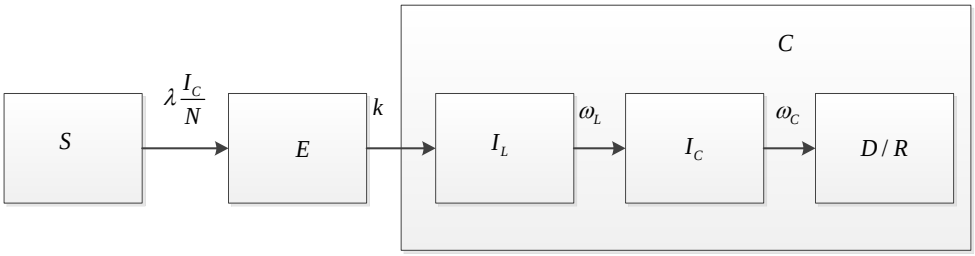

Figure 2. A Schematic of the Transitions between Different States of EVD for SEI_LI_CDR Model

In Figure 1, S denotes Susceptible, E represents Exposed, I signifies Infected and R means Removed, while in Figure 2, the proposed model, S denotes Susceptible, E equals Exposed, I_L signifies Likely Infected, I_C denotes Confirmed Infected, D equals Dead and R means Removed. It is obvious from Figure 1 that Chowell et al [3] did not incorporate the likely infected stage which is part of the phase of Ebola and cannot be ignored. In this regard, a better framework is developed which integrates likely infected stage. To this effect, the proposed model is from Susceptible (S) to Exposed (E) to Likely Infected (I_L) to Confirmed Infected (I_C) then finally to Dead/Removed (D/R) stage ($S \to E \to I_L \to I_C \to D/R$).

Assuming a fixed population,

$$N = S(t) + E(t) + I_L(t) + I_C(t) + D/R(t),$$

$$\frac{dS}{dt} = -\frac{\lambda S I_C}{N} \tag{1}$$

$$\frac{dE}{dt} = \frac{\lambda S I_L}{N} - kE \tag{2}$$

$$\frac{dI_L}{dt} = kE - \omega_L I_L \tag{3}$$

$$\frac{dI_C}{dt} = \omega_L I_L - \omega_C I_C \tag{4}$$

$$\frac{dD/R}{dt} = \omega_C I_C \tag{5}$$

$$\frac{dC}{dt} = kE. \tag{6}$$

In $SEI_L\ I_CDR$ model, the population is divided into five compartmental states, namely: S, E, I_L, I_C, D/R. Susceptible (S) persons in interaction with the virus move to the Exposed (E) state at a rate of $\lambda I_C/N$. Therefore, Exposed (E) persons experience mean incubation period of $1/k$ days before developing to the Likely Infectious (I_L) state and then to Confirmed Infectious (I_C) state. It is assumed that Exposed state is symptomless and un-infectious. Likely infectious (I_L) persons move to Confirmed infectious (I_C) state, then finally to D/R state, either Dead or Removed, at a rate of ω_L as well as ω_C respectively. The parameters are: λ, the rate of transmission per individual per day; N, the total effective size of population; and I_C/N, the probability that contact is made with a Confirmed Infected person. C is not a state of epidemiology, nevertheless, keeping track of the cumulative number of infected incidents from the time the outbreak started is beneficial.

The transmission rate λ was modelled as a function of time in order to model the influence of intervention on the transmission of the disease, in the above model. At the early phase of the outbreak, before intervention, λ is parameterized by λ_0. The value of λ transitions from λ_0 to λ_1 after intervention where $\lambda_0 > \lambda_1$ [1]. This means that as a result of intervention or control on Ebola, since it is a deadly disease, once intervention starts taking place the initial transmission rate will be greater than the subsequent one.

$$\lambda(t) = \begin{bmatrix} \lambda_0 \\ \lambda_1 + (\lambda_0 - \lambda_1)e^{(-\alpha[t-\tau])} \end{bmatrix}_{t \geq \tau}^{t < \tau} \tag{7}$$

where τ is the time when intervention starts and α controls how rapidly the rate of transmission fluctuates from λ_0 to λ_1. The SEI_LI_CDR model under consideration is a non-linear model with seven parameters. The model parameters are $\lambda_0, \lambda_1, k, \alpha, \omega_L, \omega_C, \tau$ in Eqs. 1-7.

Moreover, the spreading of the recent Ebola epidemic depended on the preventive measures taken, the underlying dynamics of the transmission changed radically at any time. It had affected both human and material resources drastically and therefore needed to be controlled especially for future occurrence. The Ebola data for the three most-affected countries in West Africa - Guinea, Liberia and Sierra Leone are denoted as (t_i, y_i), $i = 1, 2, ..., n$, where t_i denotes the *ith* reporting time and y_i the cumulative number of infective incidents from the commencement of the outbreak to time t_i. The model parameters $\lambda_0, \lambda_1, k, \alpha, \omega_L, \omega_C, \tau$ for these three countries were estimated using a non-linear technique by fitting these data to the cumulative number of incidents $C(t, \lambda_0, \lambda_1, k, \alpha, \omega_L, \omega_C, \tau)$ in Eqs. 1-7.

One of the parameters was fixed based on studies on former Ebola epidemics. The incubation time of the Ebola virus $1/k$ is found to vary between 1 and 21 days, with an average time of 6.3 days for former outbreaks of Ebola in Chowell et al [3]. To ease data fitting, the parameter value was set to the average value of 6.3 days. Other parameters are deduced, since the dynamics of the recent epidemic may be different from former ones, and therefore fixing

values based on the previous estimate may lead to some erroneousness. The process of choosing initial outbreak time t_0 and intervention time τ is difficult. Various sources namely WHO (World Health Organization) and CDC (Centre for Disease Control) websites were considered to study further the timeline of the transmission. The derivation of timeline of the recent spread for each country was done in Section 3.

Accordingly, optimization technique was employed to solve the problem. The optimization problem connecting the model fitting of the SEI_LI_CDR model is a non-linear (exponential) problem. The exponential function for the problem is given as

$$Y = e^{\lambda t} \tag{8}$$

The exponential function was applied to analyse the dynamic system of the Ebola outbreak.

2.2. Basic Reproduction Number, R_0

The basic reproduction number, denoted R_0, is the expected number of secondary incidents produced in a population that is completely susceptible, by a typical infectious person [9,10]. Numerous epidemiological models have a Disease Free Equilibrium (DFE) at which the population remains in the absence of disease. These models commonly have a threshold parameter, called the basic reproduction number, R_0, such that if $R_0 < 1$, then the DFE is locally asymptotically stable and the disease cannot infest the population, but if $R_0 > 1$, then the DFE is unstable and infestation is possible all the time. In essence, if $R_0 < 1$, then on average an infected person produces less than one new infected person over the course of its infective period, and the infection cannot grow. On the contrary, if $R_0 > 1$, then each infected person produces, on average, more than one new infection, and the disease can infest the population.

The application of compartmental model to Ebola Virus Disease (EVD) requires the derivation and estimation of the fundamental quantity called the basic reproduction number R_0 inorder to determine if an epidemic exists. This leads to decomposition of $f(x)$ into the components F and V using a simple transmission/control model as deduced from the work of Castillo-Chavez and Feng [11] and Blower et al [12]. F is the rate of appearance of new infections in compartment and V is the rate of transfer of persons into and out of compartment. The population is divided into five compartments, that is, persons Susceptible to Ebola (S), Exposed persons (E), Likely Infectious persons (I_L), Confirmed Infectious persons (I_C) and Controlled Individuals (D/R). The dynamics are shown in Figure 3. Susceptible and controlled persons move in the Exposed compartment at rates $\lambda_1 I_L/N$ and $\lambda_2 I_L/N$, where $N = E + I_L + I_C + S + D/R$. Exposed individuals progress to Likely Infectious individuals (I_L), then to Confirmed Infectious individuals (I_C) compartment at the rate υ_1 and υ_2. All newborns are susceptible, b is a constant fraction and all persons die at the rate $d > 0$. Hence, the core of the model is an $SEI_L\ I_C$ model using standard incidence. The control rates are η_1 for Exposed persons and η_2 for Confirmed Infectious persons. However, only a fraction q of the Control of Infectious persons is successful. Unsuccessfully Control Infectious persons re-enter the Exposed compartment $(p = 1 - q)$.

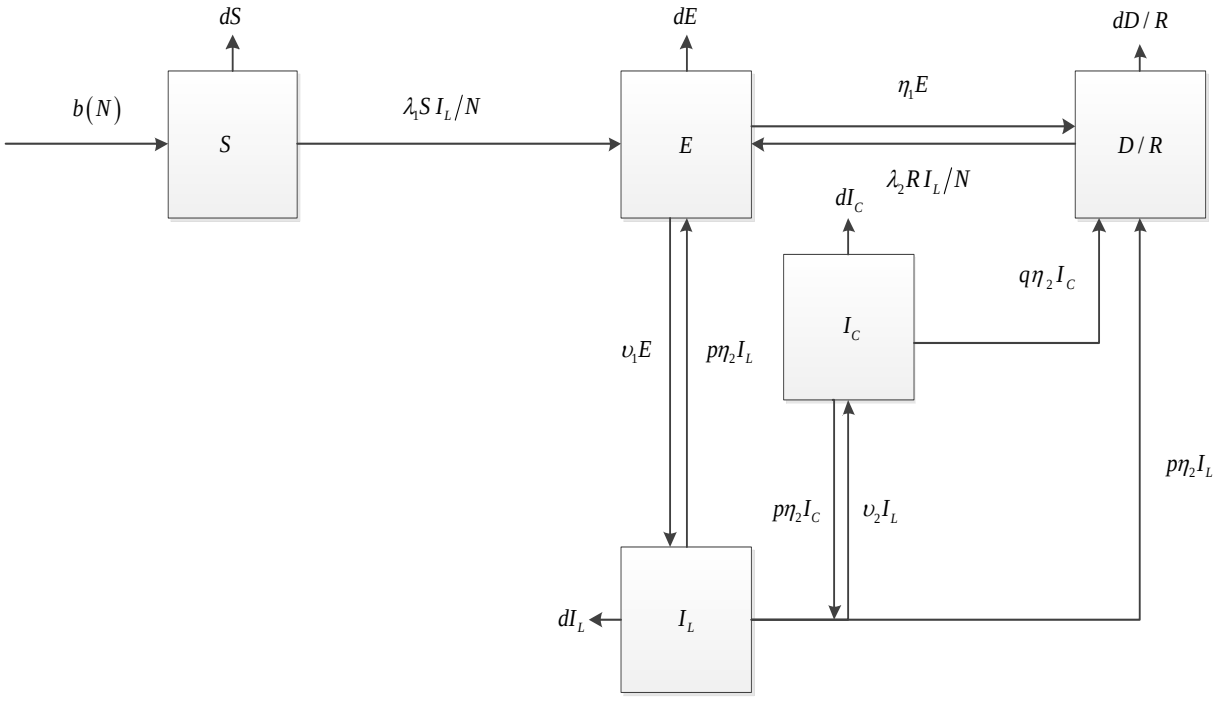

Figure 3. Progression of Infection for the Transmission/Control Model of Eqs. 9–13

The disease transmission model involves the following differential equations together with non-negative initial conditions:

$$\dot{E} = \frac{\lambda_1 S I_L}{N} + \frac{\lambda_2 D/R I_L}{N} - (d+\upsilon_1+\eta_1)E + P\eta_2 I_L \quad (9)$$

$$\dot{I_L} = \upsilon_1 E - (d+\eta_2) I_L \quad (10)$$

$$\dot{I_C} = \upsilon_2 I_L - (d+\eta_2) I_C \quad (11)$$

$$\dot{S} = b(N) - dS - \frac{\lambda_1 S I_L}{N} \quad (12)$$

$$\dot{R} = -dR + \eta_1 E + q\eta_2 I_L + q\eta_2 I_C - \frac{\lambda_2 R I_L}{N}. \quad (13)$$

Progression from E to I_L, then to I_C and failure of control are not considered to be new infections, but rather the progression of an infected person through the various compartments. Thus,

$$F = \begin{pmatrix} \frac{\lambda_1 S I_L}{N} + \frac{\lambda_2 D/R I_L}{N} \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} (d+\upsilon_1+\eta_1)E - P\eta_2 I_L \\ -\upsilon_1 E + (d+\eta_2) I_L \\ -\upsilon_2 I_L + (d+\eta_2) I_C \\ -b(N) + dS + \frac{\lambda_1 S I_L}{N} \\ dR - \eta_1 E - q\eta_2 I_L - q\eta_2 I_C + \frac{\lambda_2 R I_L}{N} \end{pmatrix}. \quad (14)$$

The infected compartments are E, I_L and I_C, giving $m=3$. An equilibrium solution with $E = I_L = I_C = 0$ has the form $x_0 = (0,0,0,S_0,0)^t$, where S_0 is any positive solution of $b(S_0) = dS_0$. This will be a DFE (Disease Free Equilibrium) if and only if $b^T S_0 < d$. Without loss of generality, assume $S_0 = 1$ is a DFE. Then,

$$F = \begin{pmatrix} 0 & \lambda_1 \\ 0 & 0 \end{pmatrix}, \quad (15)$$

$$V = \begin{pmatrix} d+\upsilon_1+\eta_1 & -p\eta_2 \\ -\upsilon_2 & d+\eta_2 \end{pmatrix} \quad (16)$$

giving

$$V^{-1} = \frac{1}{(d+\upsilon_1+\eta_1)(d+\eta_2) - \upsilon_2 p\eta_2} \begin{pmatrix} d+\eta_2 & p\eta_2 \\ \upsilon_2 & d+\upsilon_1+\eta_1 \end{pmatrix} \quad (17)$$

and

$$R_0 = \rho(FV^{-1}) \quad (18)$$

where V^{-1} is the mean length of time a person spends in compartment during its lifetime, assuming that the population remains near the DFE and barring reinfection. F is the rate at which infected persons in compartment produce new infections in compartment. FV^{-1} is the expected number of new infections in compartment produced by the infected individual originally introduced into compartment which is also known as the next generation matrix for the model, ρ represents the spectral radius of matrix FV^{-1}.

Driessche and Watmough [13] stated that DFE, x_0, is locally asymptotically stable if all the eigenvalues of the matrix $Df(x_0)$ have negative real parts, and not stable if any eigenvalue of $Df(x_0)$ has a positive real part. $Df(x_0)$ is the derivative $[\partial f/\partial x]$ evaluated at the DFE, x_0 (that is the Jacobian matrix).

2.3. Queueing in SEI_LI_CDR Compartmental Model

In queueing theory, queues tend to be modelled by stochastic processes, which are random functions based on probability distributions [8,14,15,16]. Accordingly, the following expressions based on SEI_LI_CDR compartmental model were used to explain the EVD problem:

$$P_E = \lim_{t\to\infty} P\begin{Bmatrix} \frac{\lambda_1 S I_L}{N} + \frac{\lambda_2 D/R I_L}{N} \\ -(d+\upsilon_1+\eta_1)E + P\eta_2 I_L \end{Bmatrix} \quad (19)$$

$$P_{I_L} = \lim_{t\to\infty} P\{\upsilon_1 E - (d+\eta_2) I_L\} \quad (20)$$

$$P_{I_C} = \lim_{t\to\infty} P\{\upsilon_2 I_L - (d+\eta_2) I_C\} \quad (21)$$

$$P_S = \lim_{t\to\infty} P\left\{b(N) - dS - \frac{\lambda_1 S I_L}{N}\right\} \quad (22)$$

$$P_{D/R} = \lim_{t\to\infty} P\begin{Bmatrix} -dD/R + \eta_1 E + q\eta_2 I_L \\ +q\eta_2 I_C - \frac{\lambda_2 D/R I_L}{N} \end{Bmatrix}. \quad (23)$$

Eqs. 19-23 explain the movements from $S \to E \to I_L \to I_C \to D/R$, which are in compartments, they represent waiting (queues) and the movement of random variables (phases) are based on probability distribution. Taking limit of the probability of each phase as t tends to infinity yields a normal distribution.

3 Timeline of Spread of Recent EVD Outbreak

3.1. Guinea

The manifestation incident was a two-year-old boy who lived in the village of Meliandou, Gueckedou situated in

the Nzerekore Region of Guinea. Later, the boy who was identified as Emile Ouamouno, fell ill on 2nd December 2013 and died four days later [17,18]. The Ministry of Health of Guinea alerted the World Health Organization (WHO), then on 23rd March 2014 the WHO broadcasted an outbreak of EVD [19,20,21,22]. The EVD affected districts in Guinea are presented in Figure 4.

From the above information, it could be observed that the index case of the recent Ebola outbreak was traced back to December 2, 2013, hence, t_0 was set to December 2. Again, Guinea government informed WHO concerning an Ebola epidemic possibility and affirmed a national health emergency on March 23, 2014; nevertheless, there was lack of reasonable data to the best of the researchers' knowledge until April 1, 2014. Therefore, this date, April 1 was considered as the intervention date and set τ to 120. The Estimated Cumulative Infected, Exposed, Likely Infected, Confirmed Infected, Number of Death and Removed are obtained by using EVD data from August 2014 to April 2015 and fixing all these information in Eq. 7 to obtain the model fit result for the SEI_LI_CDR model. The same explanation follows for Liberia and Sierra Leone. Consequently, the model fit result for the SEI_LI_CDR model is shown in Figure 5. The discussion of the results is presented in Section 4.

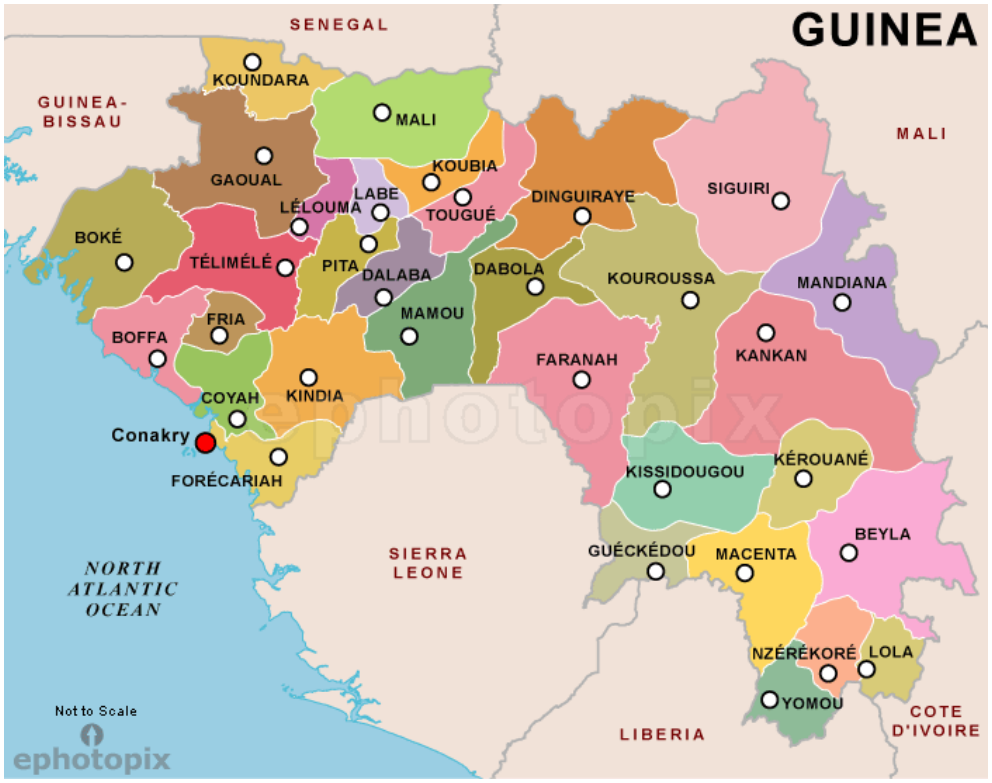

Figure 4. EVD affected districts in Guinea (https://www.google.com) [23]

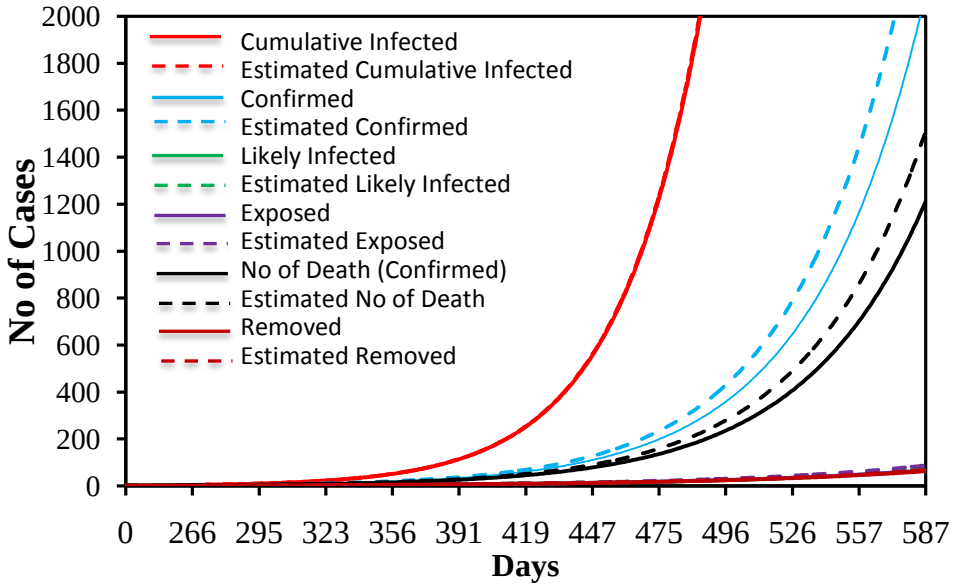

Figure 5. SEI_LI_CDR model fit result for 2014 Ebola epidemic data for Guinea

Figure 6. EVD affected districts in Liberia https://www.google.com [23]

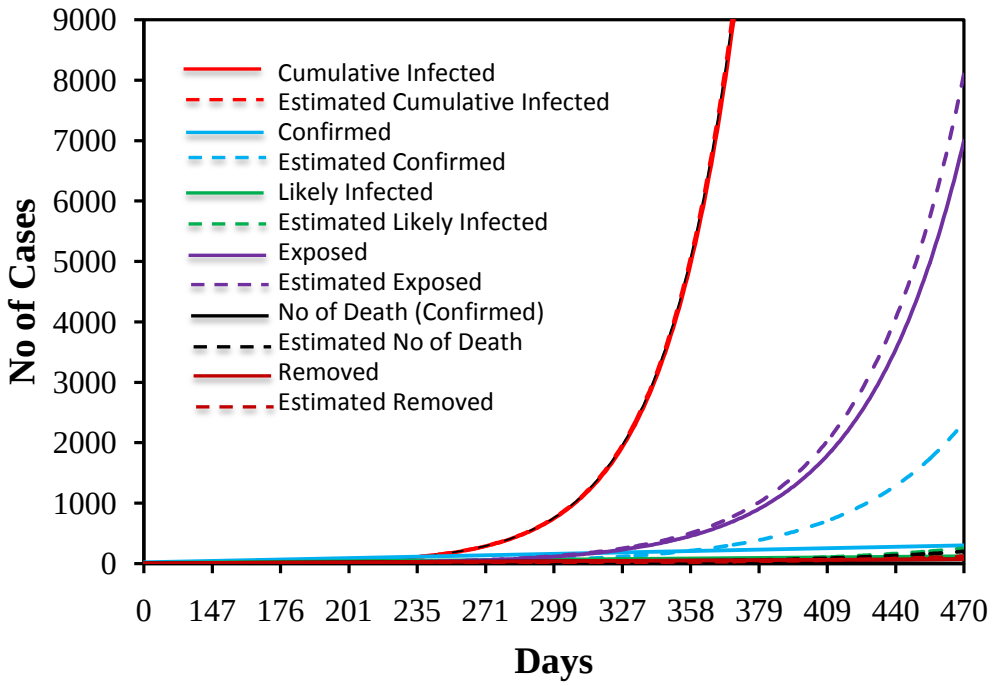

Figure 7. SEI_LI_CDR model fit result for 2014 Ebola epidemic data for Liberia

3.2. Liberia

An epidemic of Ebola Virus Disease was experienced by West African nation of Liberia, generally recognised as Ebola in 2014 and 2015, along with the neighbouring countries of Guinea and Sierra Leone. The first incidents of the virus were reported by late March 2014 [24]. Infected individuals by those early incidents, spread the disease to other villages in Guinea [25,26]. This also led to the spread of the disease in Liberia, since they are neighbouring countries [27]. The EVD affected districts in Liberia are presented in Figure 6.

On March 31, 2014 in Liberia there was authorized confirmation of two infected people with Ebola. This date was set as t_0 (initial time). On July 30, 2014 all schools were shut down by the government of Liberia. This date was considered as the date of intervention in Liberia and set τ to 120. Consequently, the model fit result for the SEI_LI_CDR model is shown in Figure 7. The discussion of the results is presented in Section 4.

3.3. Sierra Leone

Epidemic of EVD generally known as Ebola severely afflicted the West African nation of Sierra Leone, including Guinea and Liberia, the neighbouring countries. On March 23, 2014 Guinean health officials broadcast the outbreak of a mysterious haemorrhagic fever which strikes like lightning [28]. It was identified as EVD and spread to Sierra Leone by May 2014 [29]. The disease is believed to have initiated when a child in a bat-hunting family contacted the disease in Guinea in December 2013 [30]. The EVD affected districts in Sierra Leone are presented in Figure 8.

Figure 8. EVD affected districts in Sierra Leone https://www.google.com [23]

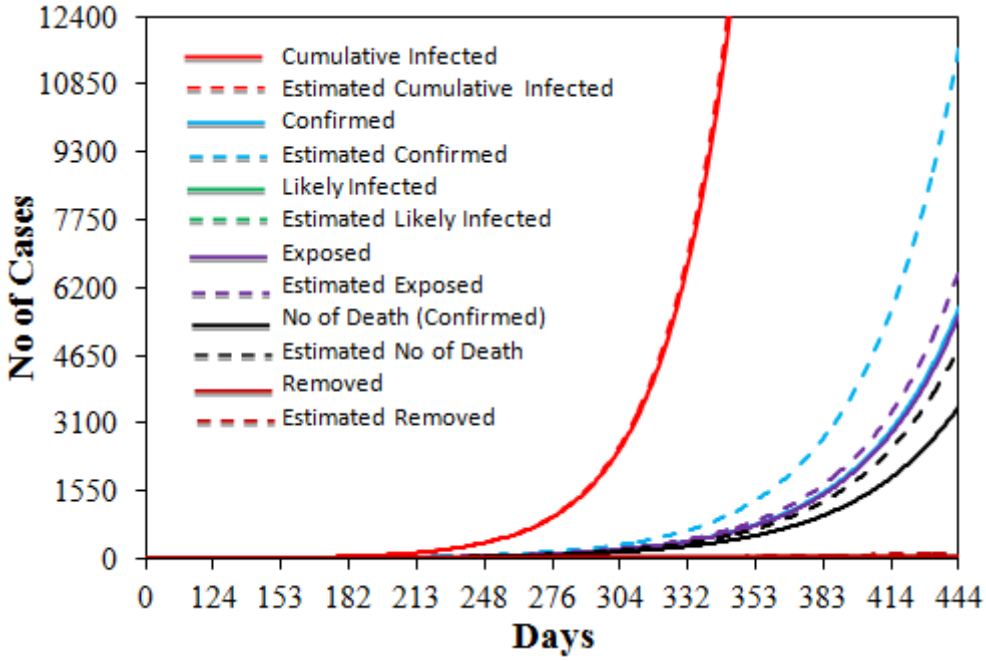

Figure 9. SEI_LI_CDR model fit result for 2014 Ebola epidemic data for Sierra Leone

In Sierra Leone, Ebola spread by May 1, 2014. The country declared an emergency and closed its borders with neighbouring Guinea and Liberia in June 12, 2014. The first date was considered as t_0 and second date as the intervention time, therefore τ was set to 42. Consequently, the model fit result for the SEI_LI_CDR model is shown in Figure 9. The discussion of the results is presented in Section 4.

4. Results and Discussion

4.1. Model Fit for the SEI_LI_CDR Model

In Figure 7, Figure 8 and Figure 9, the number of cases at different compartments of the SEI_LI_CDR model in Guinea, Liberia and Sierra Leone for observed and estimated cases were presented, likewise the cumulative number of infective incidents over time. The model fit was accomplished with the EVD data from August 2014 to April 2015. The solid lines represent observed cases while the dashed lines represent estimated cases. The model was found to be significantly fit because the solid lines representing observed cases are mostly close to the dashed lines representing estimated cases, which shows that the differences and errors between observed and estimated values are small.

Furthermore, the RMSE from the proposed SEI_LI_CDR model was compared to that of the SEIR model used by Bashar et al [1] for the same months (November and December, 2014). Accordingly, the RMSE results in Table 1, show that the proposed model performed better than the SEIR model by 13.10%, 91.76% and 83.14% in Guinea, Liberia and Sierra Leone respectively. It indicates that SEI_LI_CDR model predicted number of confirmed individuals better than the SEIR model.

Table 1. Comparative Analysis of RMSE

Country	Root Mean Square Error (RMSE)		
	SEIR	SEI_LI_CDR	% Difference
Guinea	218.9	190.217	13.10
Liberia	546.2	45	91.76
Sierra Leone	504.24	85	83.14

4.2. The Basic Reproduction Number

The results of the matrix gave the basic reproduction number for Guinea, Liberia and Sierra Leone. Disease Commencement days and Intervention Time is shown in Table 2.

Table 2. Disease Commencement days and Intervention Time

Country/Month	I_C	I_L	E	D/R	Cases
Guinea 2 Dec.2013-1Apr.2014	94	28	5	83	127
Liberia 31 Mar.2014-30 Jul.2014	79	23	5	65	107
Sierra Leone 1 May.2014-12 Jun. 2014	58	17	4	6	79

Eqs. 9-18 were applied to obtain the basic reproduction numbers: $R_0 = 2.2550$ for Guinea, 3.5264 for Liberia, and 2.2325 for Sierra Leone.

The R_0 for each of the three countries is greater than 1, with Liberia having the highest value. It implies that the disease was more severe in Liberia than Guinea and Sierra Leone before intervention. The result also shows that the transmission and control of the epidemic is unstable, and needs urgent intervention to avert danger. The finding is in line with Driessche and Watmough [13] who stated that an epidemic system is unstable when the basic reproduction number is greater than 1.

The basic reproduction number was integrated into Equations 9–13 for adequate solution of SEI_LI_CDR model according to their respective compartments. The results are shown in Figure 10 for Guinea, Liberia and Sierra Leone respectively.

The Figures (Figure 10) show the growth of the epidemic in the various compartments. It was discovered that the rate of transmission of the epidemic increased vigorously before intervention, and reduced gradually after intervention. The result shows that the epidemic growth/decay was 1.39 CS/s for Guinea, 0.61 CS/s for Liberia, and 0.58 CS/s for Sierra Leone, where CS/s means Compartment Size per second. It implies that the control of epidemic took more time in Sierra Leone than the other two countries, meaning that Guinea abided by the intervention method more than Liberia and Sierra Leone. The finding is in line with the report of Johnson [31]. The report showed that the number of death in the recent EVD epidemic as at July 2015 increased 28.90, 436, and 654.33 times for Guinea, Liberia, and Sierra Leone respectively.

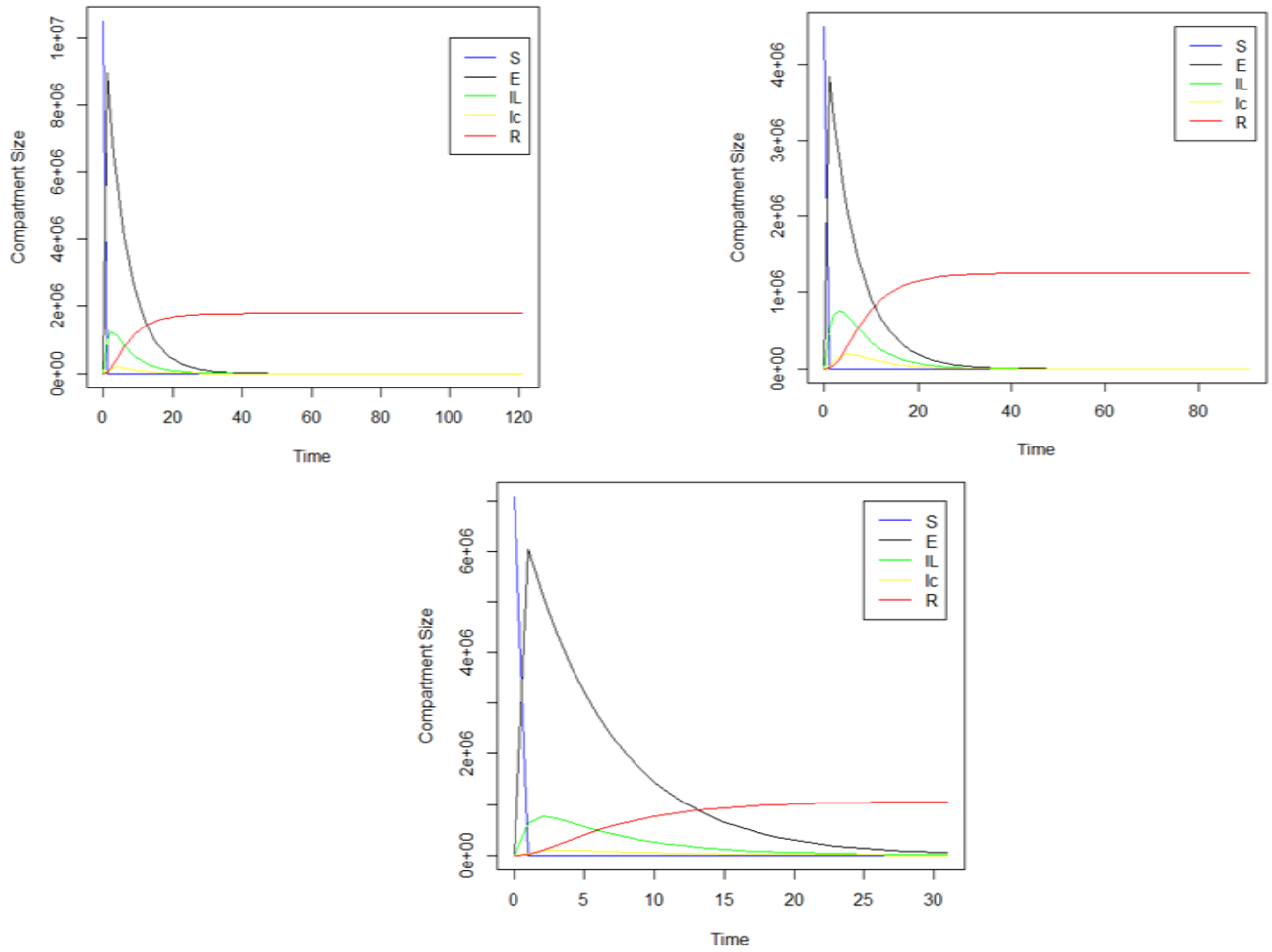

Figure 10. Trend of EVD Epidemic in SEI_LI_CDR Compartments for (a) Guinea (b) Liberia (c) Sierra Leone

4.3. Outcome of Queueing in SEI_LI_CDR Compartmental Model

The application of queueing theory to Compartmental model, Figure 11, Figure 12 and Figure 13 show the normal distribution curves and the probability of existence of individuals in the various compartments for the recent EVD epidemic in Guinea, Liberia and Sierra Leone respectively. The normal distribution curves also show that when probability is 0.4 in each compartment the transmission of EVD can be controlled.

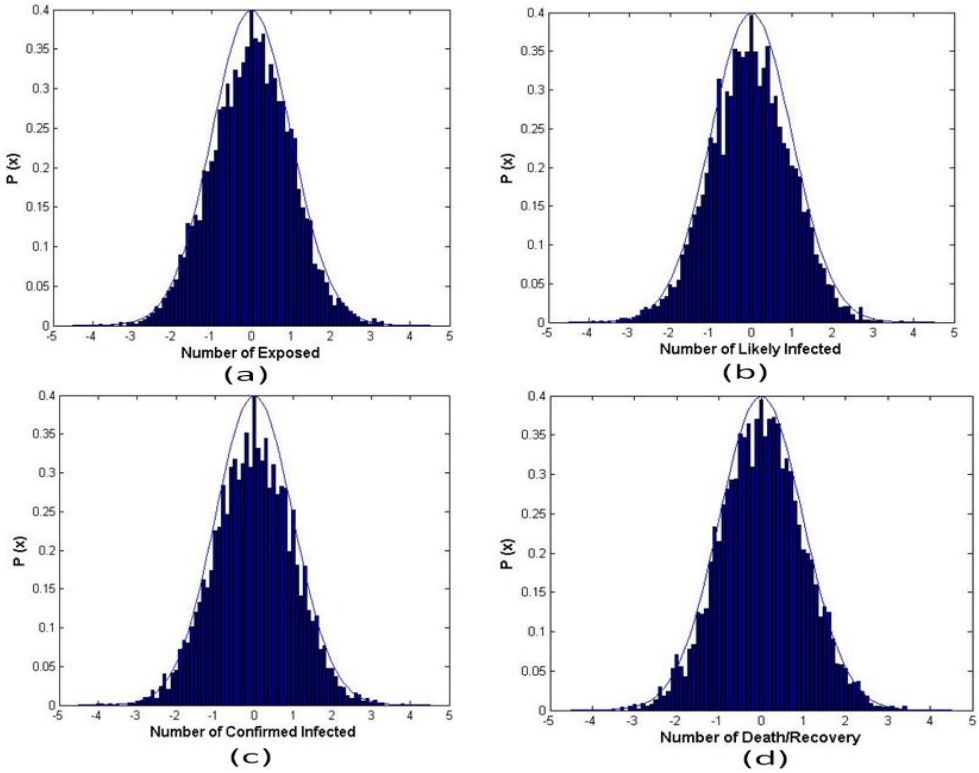

Figure 11. Normal Distribution Curve in Guinea for (a) Number of Exposed, (b) Number of Likely Infected, (c) Number of Confirmed Infected and (d) Number of Death/Recovery

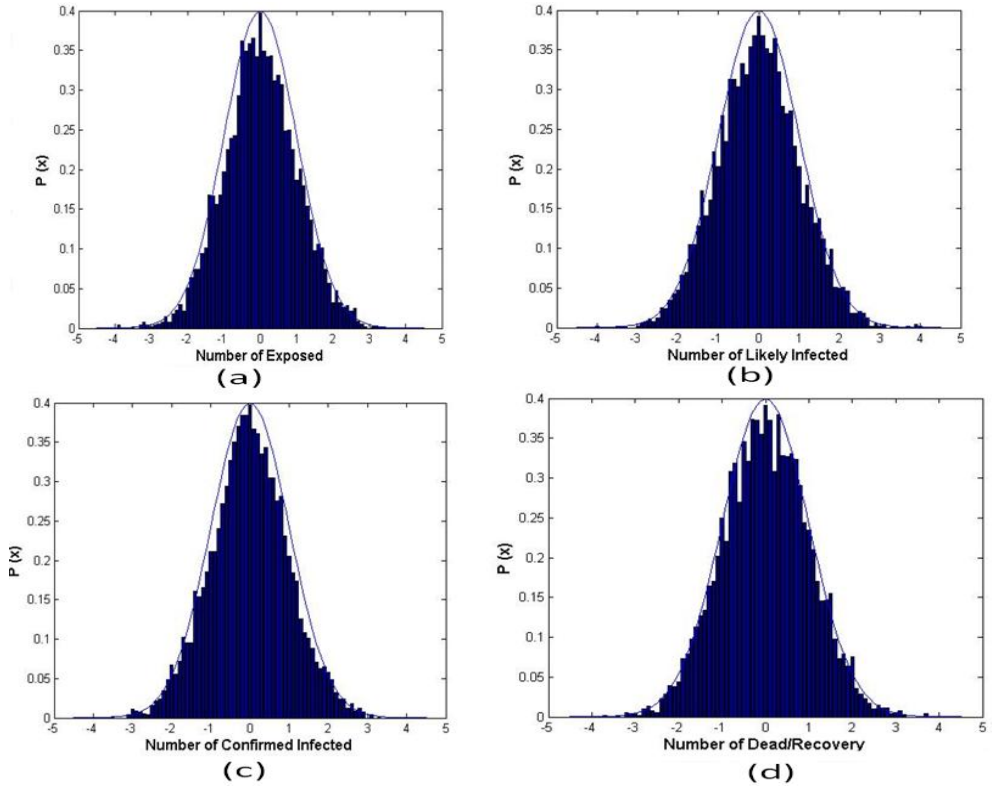

Figure 12. Normal Distribution Curve in Liberia for (a) Number of Exposed, (b) Number of Likely Infected, (c) Number of Confirmed Infected and (d) Number of Death/Recovery

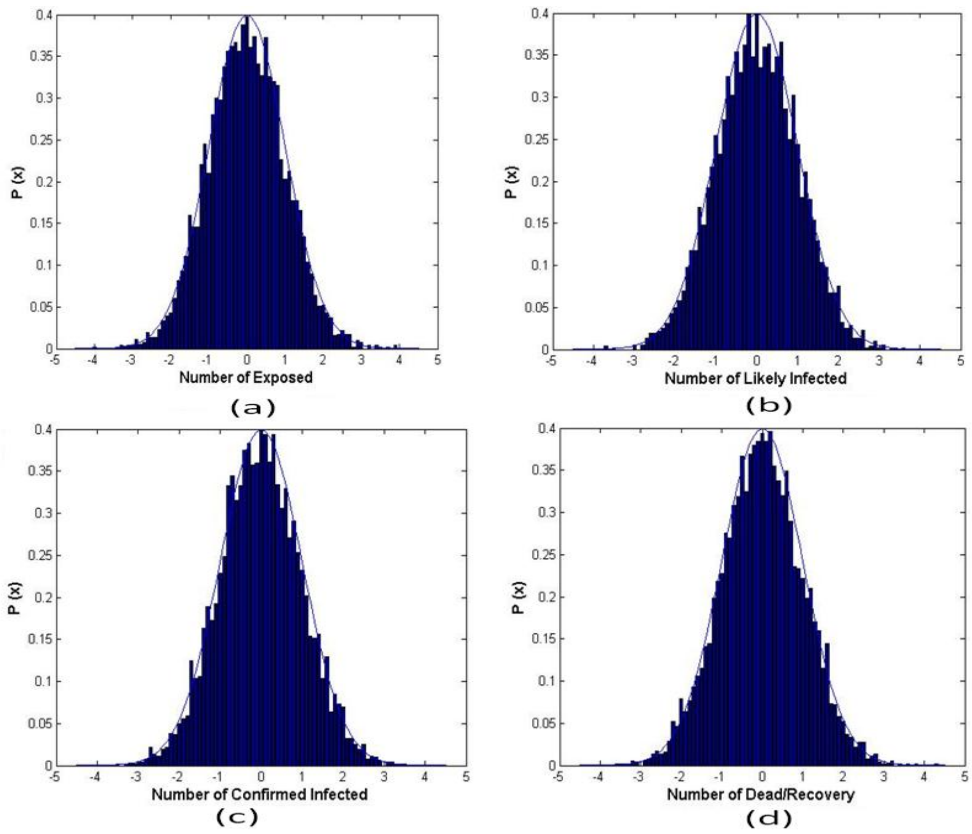

Figure 13. Normal Distribution Curve in Sierra Leone for (a) Number of Exposed, (b) Number of Likely Infected, (c) Number of Confirmed Infected and (d) Number of Death/Recovery

It was observed that the normal distribution curves of all the compartments are similar. This indicates that the SEI_LI_CDR compartment model using the queueing theory approach yielded better result, also it shows when the transmission of EVD can be controlled in each compartment. The finding agrees with the submission of Hernandiz-Suarez et al [4], Anderson and Britton [32], and Darroch and Seneta [33] who maintained that the limiting approximation is determined by the extent to which the normal distribution curves of the various compartments are similar.

5. Conclusion

This paper analysed the 2014 Ebola epidemic in three West African Countrie of Guinea, Liberia and Sierra Leone using queueing based compartmental models for Ebola virus disease. In section 2, the SEI_LI_CDR compartmental, the Basic Reproductive number, R_0, and queueing based compartmental models were developed. In section 3, the timeline of the spread of EVD outbreak in the three countries was presented. Section 4 presented the results and discussions. A comparison of the existing SEIR and the developed SEI_LI_CDR models shows that the developed model outperformed the existing model by 13.10%, 91.76%, and 83.14% for Guinea, Liberia and Sierra Leone on the basis of their RMSE. The R_0 for Guinea, Liberia and Sierra Leone are 2.2550, 3.5264 and 2.2325, respectively; indicating that the EVD was mor severe in Liberia. Analysis of the growth of the epidemic in the various compartments showed that the control of the epidemic took more time in Sierra Leone than in Guinea and Liberia. Finally, analysis using queueing in SEI_LI_CDR compartmental models show that at a probability of 0.4 in each compartment, the transmission of EVD can be controlled.

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