British Journal of Mathematics & Computer Science
19(1): 1-19, 2016, Article no.BJMCS.29372
ISSN: 2231-0851

SCIENCEDOMAIN *international*
www.sciencedomain.org

Optimal Control of Ebola Transmission Dynamics with Interventions

F. T. Oduro[1], George Apaaboah[1*] and Joseph Baafi[1]

[1] *Department of Mathematics, Kwame Nkrumah University of Science and Technology, Kumasi Ghana.*

Authors' contributions

This work was carried out in collaboration between all authors. Authors FTO and GA initiated and directed the research study. Author GA implemented algorithms, conducted programming and drafted the manuscript. Authors GA, FTO and JB wrote introduction, collected parameters, ran simulations, analysed results, compared results with findings of other authors, and edited the manuscript. All authors read and approved the final version of the manuscript.

Article Information

DOI: 10.9734/BJMCS/2016/29372
Editor(s):
(1) Nikolaos Dimitriou Bagis, Department of Informatics and Mathematics, Aristotelian University of Thessaloniki, Greece.
(2) Paul Bracken, Department of Mathematics, The University of Texas-Pan American Edinburg, TX 78539, USA.
Reviewers:
(1) Jia-Bao Liu, Anhui Jianzhu University, Hefei, Anhui, China.
(2) Muhammad Altaf Khan, AbdulWali Khan University, Mardan, Khyber Pakhtunkhwa, Pakistan.
(3) Nita H. Shah, Gujarat University, Ahmedabad , Gujarat, India.
Complete Peer review History: http://www.sciencedomain.org/review-history/16542

Original Research Article

Received: 7th September 2016
Accepted: 3rd October 2016
Published: 13th October 2016

Abstract

In this paper, SEIR epidemic model is used to study Ebola transmission dynamics and compared with SIR model against World Health Organisation data from Sierra Leone. It was found that the constructed SEIR model was more representative of the situation in Sierra Leone. In addition, the impact of quarantine, vaccination and/ or both interventions on the transmission dynamics of the disease was studied. The introduction of interventions caused the disease free equilibrium to become stable. Finally, the optimal control problem was solved for the transmission dynamics of the disease using these interventions as control variables. It was observed that the best intervention strategy is to implement require a combination of both quarantine and vaccination.

**Corresponding author: E-mail: george.apaaboah@gmail.com;*
Co-author: E-mail: ftoduro@gmail.com;

Keywords: Ebola; optimal control; epidemic models.

1 Introduction

The World Health Organisation (WHO) describes Ebola virus disease as a severe and often fatal illness in humans [1]. It was first discovered in 1976 at Nzara in Sudan and Yambuku in DRC. The virus is transmitted to humans through contact with an infected person dead or alive [2]. [2] investigated the 1976 outbreak in Yambuku, Zaire and the 1995 outbreak in Kikwit, Zaire. Their objective was to understand the mathematical dynamics of a population infected by Ebola when an outbreak occurs. They proposed an SIR model for Kikwit and SEIR model for Yambuku. [3, 4] studied the Ebola outbreak in Democratic Republic of Congo (DRC) in 1995 and Uganda in 2000. Since the recent outbreak in West Africa in May 2014, there has been about 27,443 reported confirmed cases with about 11,207 reported deaths [1]. This is the first outbreak to reach epidemic level. Estimating the basic reproductive number or understanding the transmission dynamics and effective control measures has been studied by [5, 6, 7, 8, 9, 10]. Again, [11, 12, 13] have used optimal control to study the dynamics of the disease. [14] used an SEIR model type to study the spread of malaria in Ghana. [15] used optimal control to study the impact of intervention on malaria in Malawi. In this paper, we will construct an SEIR model for transmission dynamics of Ebola and perform stability analysis of model, determine the controllability of the dynamics near an equilibrium point with vaccination and quarantine as control variables and to obtain the optimal control of the system and perform simulations, study effects of vaccination, quarantine and or both on Ebola dynamics. We did not study the post-mortem effect of Ebola since it has been thoroughly studied by [16]. Currently, there exist an SIR model [11] and there is the need to investigate whether an SEIR model can be a significant improvement.

2 Methodology

Disease control has become a very complex problem for health officers. This is why mathematical models are used to predict and understand diseases. The practical use of models is based on the fact that they can be kept realistic depending on the assumptions given. The table below presents the parameter values used in our computation and their sources.

2.1 SIR model of Ebola

The SIR model of Ebola was described using compartmental model. At time t, there are susceptible humans $S(t)$, infected humans $I(t)$, quarantined human $Q(t)$ and removed human $R(t)$. The susceptible come into contact with an infected person at a rate β. The infective are removed at a rate ρ. It is assumed that without intervention every infected human will die. It is assumed that the latent period is insignificant to the epidemics dynamics. The equations below represent the SIR model of Ebola used by [11].

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \rho I \\ \frac{dR}{dt} &= \rho I \end{aligned} \tag{2.1}$$

with initial conditions $S(0) = S_0 > 0$, $I(0) = I_0 > 0$, $R(0) = 0$ and $\beta, \rho > 0$. The constant population size is obtained as $N(t) = S(t) + I(t) + R(t)$. From their differential equations

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

The basic reproductive number $R_0 = \beta/\rho = 1.867$.

2.2 Plot of I(t) of SIR model compared with real data

We plot $I(t)$ of SIR model comapred with real data. We plot the model without intervention against confirmed cases real data of Sierra Leone obtained from WHO. We used these parameter values: $\beta = 0.0003589$, $\epsilon = 0.000799$, $\delta = 0.0179$ and data in Table 1. We observed that Fig. 1 did not give a good representation of the real data of Sierra Leone.

Table 1. Parameter values for Ebola model and their sources

Parameter	Value	Source
N	160000	[17]
β	0.710	[7]
ε	0.089	[10]
δ	0.083	[9]
κ	0.5	[9]
ρ	0.1	[18]
μ	0.20	[18]
α	2.57	[19]
ψ	0.50	[9]
ω_I	0.10	[18]
ω_Q	0.50	[18]
σ	1.7	[18]
ω	0.073	[20]

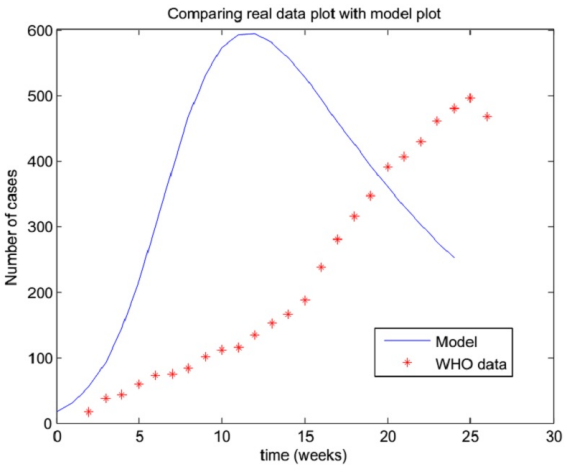

Fig. 1. Plotting real data with SIR model without intervention

2.3 SEIR model of Ebola

In this model, we introduce $E(t)$ which is the number of exposed humans at time t. The transmission rate due to contact with the dead is ε. There is an average incubation period δ. σ and ω natural birth and death rate respectively. We assume that without intervention all infected people eventually die. The compartmental SEIR diagram is presented below:

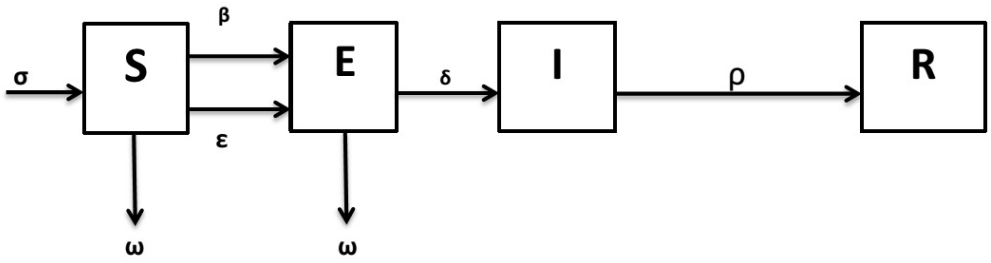

Fig. 2. Compartmental SEIR diagram of Ebola

The equations below represent SEIR model of Ebola.

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI - \varepsilon SR - \omega S + \sigma \\
\frac{dE}{dt} &= \beta SI + \varepsilon SR - \delta E - \omega E \\
\frac{dI}{dt} &= \delta E - \rho I \\
\frac{dR}{dt} &= \rho I
\end{aligned} \tag{2.2}$$

with initial conditions $S(0) = S_0 > 0$, $E(0) = E_0 > 0$, $I(0) = I_0 > 0$, $R(0) = 0$ and $\beta, \varepsilon, \delta, \rho, \omega > 0$. The constant population size is obtained as $N(t) = S(t) + E(t) + I(t) + R(t)$. From their differential equations

$$\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

2.3.1 Disease free equilibrium point of SEIR model

At the disease free equilibrium point there is no disease in the population. Therefore $E = 0, I = 0$ and we set equation (2.2) as below

$$\begin{aligned}
-\beta SI - \varepsilon SR - \omega S + \sigma &= 0 \\
\beta SI + \varepsilon SR - \delta E - \omega E &= 0 \\
\delta E - \rho I &= 0 \\
\rho I &= 0
\end{aligned} \tag{2.3}$$

Solving equation (2.3) with the natural birth rate and death rate not equal to zero, we obtained the disease free equilibrium point as:

$$E_0 = \left(\frac{\sigma}{\omega}, 0, 0, 0\right) \tag{2.4}$$

2.3.2 Basic reproductive number R_0 of SEIR model

Using the next generation matrix approach (G) developed by [21], we studied the basic reproductive number R_0 at the disease free equilibrium point. We obtained the R_0 as:

$$R_0 = \frac{\delta\beta}{\rho(\delta + \omega)} \tag{2.5}$$

2.3.3 Local stability analysis of SEIR model at disease free equilibrium point

We studied the local stability of the model at the disease free equilibrium point and obtained:

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0 \tag{2.6}$$

Using Routh-Hurwitz criteria from [22] to describe the polynomial, we realised the disease free equilibrium point was unstable.

2.4 Plot of I(t) of SEIR model (without intervention) compared with real data

We plot $I(t)$ of SEIR model compared with real data. Parameter values are $\beta = 0.0003589$, $\epsilon = 0.000799$, $\delta = 0.0179$. We observe from Fig. 3 that the model closely depicts the real data of Sierra Leone.

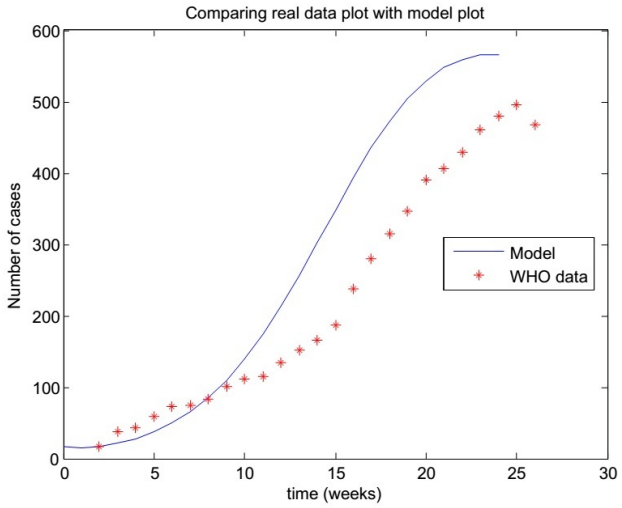

Fig. 3. Plotting real data with SEIR model without intervention

2.5 Simulation of SEIR model

We simulate the SEIR model without any intervention. We observe that the infected will continue to increase with time.

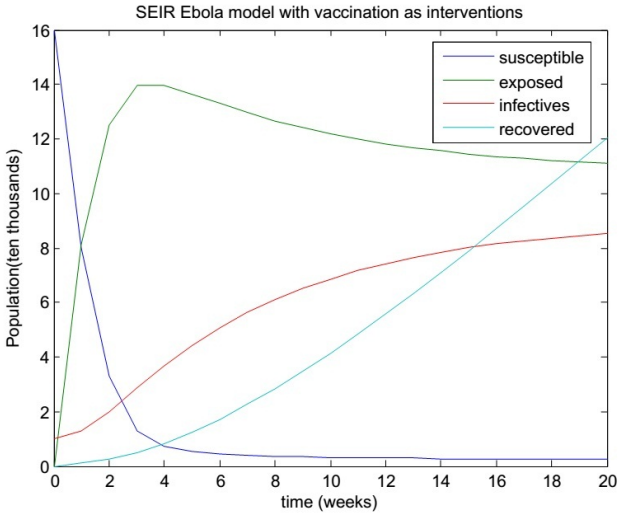

Fig. 4. Plotting Simulation of SEIR model without intervention. Parameters values N=160000, β=0.710, ϵ=0.089

2.6 SEIR model (with vaccination) as intervention

The SEIR model with vaccination as intervention is investigated. ψ is the vaccination rate and α is the rate at which the recovered return to the susceptible population. We assume that since vaccination is implemented as intervention, most people will not be infected with the disease. We also assume vaccination to be 100% effective. The compartmental model of the disease is represented below:

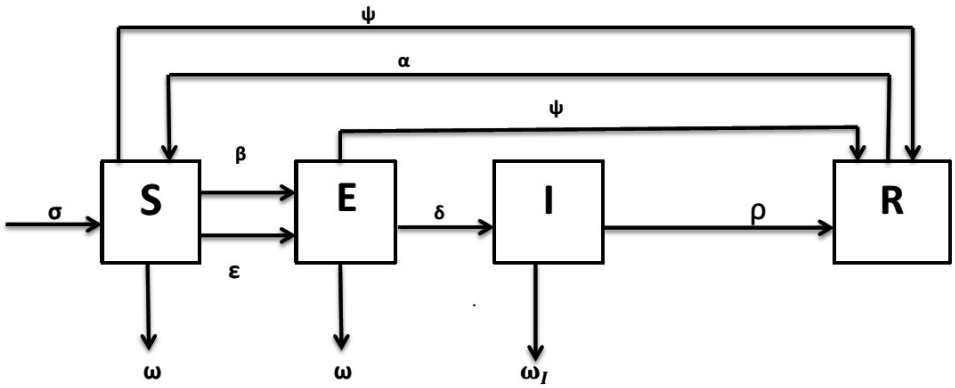

Fig. 5. Compartmental SEIR model of Ebola with vaccination

The equations of the SEIR model with vaccination is presented below:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI - \varepsilon SR - \omega S + \alpha R - \psi S + \sigma \\ \frac{dE}{dt} &= \beta SI + \varepsilon SR - \delta E - \omega E - \psi E \\ \frac{dI}{dt} &= \delta E - (\rho + \omega_I) I \\ \frac{dR}{dt} &= \rho I - \alpha R + \psi E + \psi S\end{aligned} \tag{2.7}$$

with initial conditions $S(0) = S_0 > 0$, $E(0) = E_0 > 0$, $I(0) = I_0 > 0$,, $R(0) = 0$ and $\beta, \varepsilon, \delta, \rho, \alpha, \psi, \sigma, \omega, \omega_I > 0$. The constant population size is obtained as $N(t) = S(t)+E(t)+I(t)+R(t)$. From their differential equations

$$\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

2.6.1 Disease free equilibrium point of SEIR model (with vaccination)

At the disease free equilibrium point, there is no disease in the population. Since Ebola happens for a short time, we do not study endemic equilibrium point. Therefore $E = 0, I = 0$ and we set equation (2.7) as below

$$\begin{aligned}-\beta SI - \varepsilon SR - \omega S + \alpha R - \psi S + \sigma &= 0 \\ \beta SI + \varepsilon SR - \delta E - \omega E - \psi E &= 0 \\ \delta E - (\rho + \omega_I) I &= 0 \\ \rho I - \alpha R + \psi E + \psi S &= 0\end{aligned} \tag{2.8}$$

Solving equation (2.8) with the natural birth rate and death rate not equal to zero, we obtained the disease free equilibrium point as:

$$E_0 = \left(\frac{\sigma}{\omega}, 0, 0, \frac{\psi\sigma}{\omega\alpha}\right) \tag{2.9}$$

2.6.2 Basic reproductive number R_0 of SEIR model (with vaccination)

Using the next generation matrix approach (G) developed by [21], we obtained the R_0 as:

$$R_0 = \frac{\delta\beta}{(\rho + \omega_I)(\delta + \omega + \psi)} \tag{2.10}$$

2.6.3 Local stability analysis of SEIR model (with vaccination) at disease free equilibrium point

We studied the local stability of the model at the disease free equilibrium point and obtained:

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0 \tag{2.11}$$

Using Routh-Hurwitz criteria to describe the polynomial, we realised the disease free equilibrium point was stable.

2.7 Herd immunity

According to [21], herd immunity r is the proportion of the population effectively vaccinated to control disease transmission.

$$\begin{aligned}r &> 1 - \frac{(\delta + \omega + \psi)(\kappa + \rho + \omega_I)}{\beta\delta} \\ &= 0.7353\end{aligned} \tag{2.12}$$

2.8 Simulation of SEIR model (with vaccination)

We simulate the SEIR model with vaccination as intervention. We assume that only 20% of the population is vaccinated. We observe that the infected decrease very fast and stays close to zero.

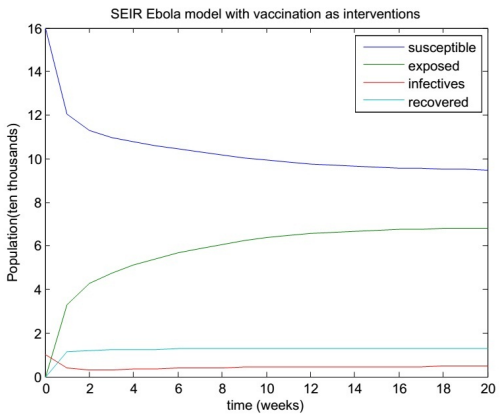

Fig. 6. Simulation of SEIR model with vaccination. Parameters have values N=160000, β=0.410, ϵ=0.049 and ψ=0.2

2.9 SEIQR model (with quarantine)

We used quarantine (Q) as a compartment to obtain SEIQR model. The probability of an infective being quarantined is κ, removal rate of quarantined is μ and ω_I, ω_Q are natural death rate. We assume that since quarantine is implemented as intervention, some infected people will recover. The diagram of the model is presented below:

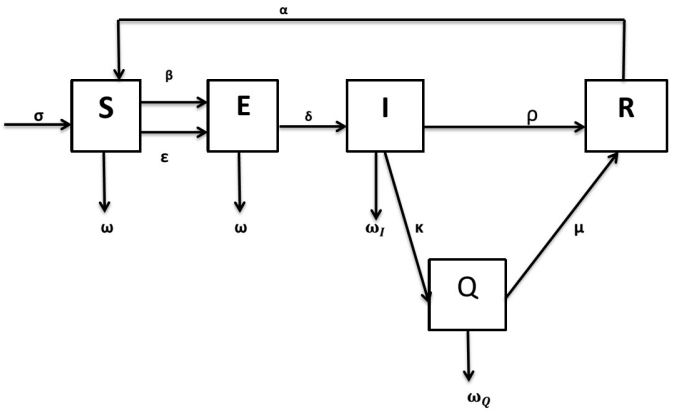

Fig. 7. Diagram for SEIQR model of Ebola with quarantine

The equations of the model with quarantine is presented below:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI - \varepsilon SR - \omega S + \alpha R + \sigma \\
\frac{dE}{dt} &= \beta SI + \varepsilon SR - \delta E - \omega E \\
\frac{dI}{dt} &= \delta E - (\kappa + \rho + \omega_I)I \\
\frac{dQ}{dt} &= \kappa I - \mu Q - \omega_Q Q \\
\frac{dR}{dt} &= \rho I + \mu Q - \alpha R
\end{aligned} \tag{2.13}$$

with initial conditions $S(0) = S_0 > 0$, $E(0) = E_0 > 0$, $I(0) = I_0 > 0$, $Q(0) = 0$, $R(0) = 0$ and $\beta, \varepsilon, \delta, \kappa, \rho, \mu, \alpha, \omega, \omega_I, \omega_Q > 0$. The constant population size is obtained as $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$. From their differential equations

$$\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} = 0$$

2.9.1 Disease free equilibrium point of SEIQR model (with quarantine)

At the disease free equilibrium point, there is no disease in the population. Therefore $E = 0, I = 0, Q = 0$ and we set equation (2.12) as below

$$\begin{aligned}
-\beta SI - \varepsilon SR - \omega S + \alpha R + \sigma &= 0 \\
\beta SI + \varepsilon SR - \delta E - \omega E &= 0 \\
\delta E - (\kappa + \rho + \omega_I)I &= 0 \\
\kappa I - \mu Q - \omega_Q &= 0 \\
\rho I + \mu Q - \alpha R &= 0
\end{aligned} \tag{2.14}$$

Solving equation (2.13) with the natural birth rate and death rate not equal to zero, we obtained the disease free equilibrium point as:

$$E_0 = \left(\frac{\sigma}{\omega}, 0, 0, 0\right) \tag{2.15}$$

2.9.2 Basic reproductive number R_0 of SEIQR model (with quarantine)

Using the next generation matrix approach (G) developed by [21],we obtained the R_0 as:

$$R_0 = \frac{\beta\delta}{(\delta + \omega)(\kappa + \rho + \omega_I)} \tag{2.16}$$

2.9.3 Local stability analysis of SEIQR model (with quarantine) at disease free equilibrium point

We studied the local stability of the model at the disease free equilibrium point and obtained:

$$\lambda^5 + a_1\lambda^4 + a_2\lambda^3 + a_3\lambda^2 + a_4\lambda + a_5 = 0 \tag{2.17}$$

Using Routh-Hurwitz criteria from [22] to describe the polynomial, we realised the disease free equilibrium point was stable.

2.10 Simulation of SEIQR model (with quarantine)

We simulate the SEIQR model with quarantine as intervention. We assume that only 30% of the infective is quarantined. We observe that the infected decrease very fast and stays close to zero.

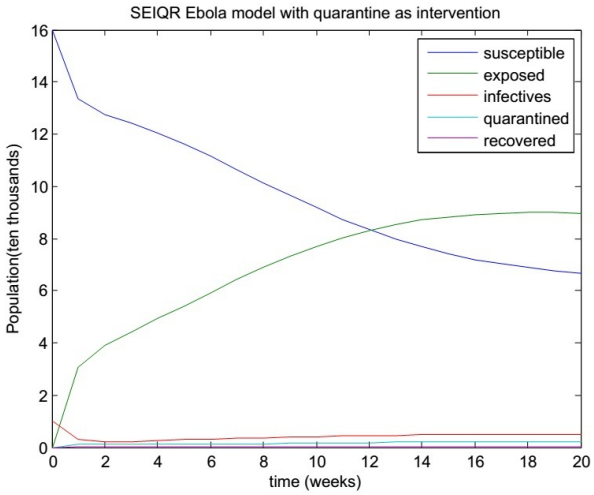

Fig. 8. Simulation of SEIQR model with quarantine. Parameter values N=160000, β=0.410, ϵ=0.049

2.11 SEIQR model (with quarantine and vaccination)

We investigate the SEIQR model with both quarantine and vaccination. We assume that since quarantine and vaccination are implemented as intervention, most infected people will recover. The compartmental diagram of the model is presented below:

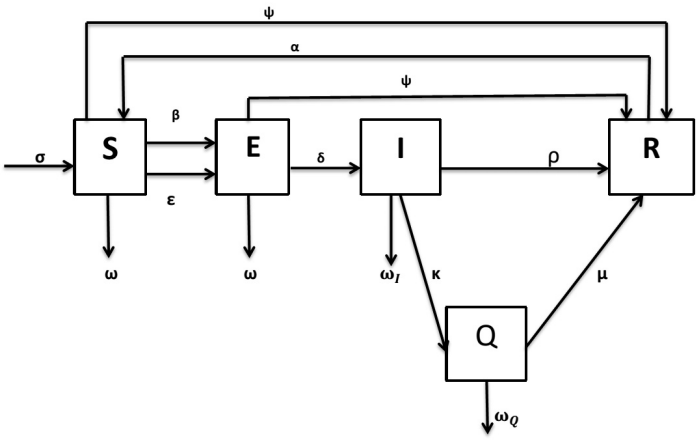

Fig. 9. Compartmental SEIQR model of Ebola with quarantine and vaccination

The equations of model for SEIQR model with both quarantine and vaccination is presented below:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI - \varepsilon SR - \omega S + \alpha R - \psi S + \sigma \\
\frac{dE}{dt} &= \beta SI + \varepsilon SR - \delta E - \omega E - \psi E \\
\frac{dI}{dt} &= \delta E - (\kappa + \rho + \omega_I) I \\
\frac{dQ}{dt} &= \kappa I - \mu Q - \omega_Q Q \\
\frac{dR}{dt} &= \rho I + \mu Q - \alpha R + \psi E + \psi S
\end{aligned} \tag{2.18}$$

with initial conditions $S(0) = S_0 > 0$, $E(0) = E_0 > 0$, $I(0) = I_0 > 0$, $Q(0) = 0$, $R(0) = 0$ and $\beta, \varepsilon, \delta, \kappa, \rho, \mu, \alpha, \psi, \sigma, \omega, \omega_I, \omega_Q > 0$. The constant population size is obtained as $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$. From their differential equations

$$\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt}\frac{dR}{dt} = 0$$

2.11.1 Disease free equilibrium point of SEIQR model (with quarantine and vaccination)

At the disease free equilibrium point, there is no disease in the population. Therefore $E = 0, I = 0, Q = 0$ and we set equation (2.17) as below

$$\begin{aligned}
-\beta SI - \varepsilon SR - \omega S + \alpha R - \psi S + \sigma &= 0 \\
\beta SI + \varepsilon SR - \delta E - \omega E - \psi E &= 0 \\
\delta E - (\kappa + \rho + \omega_I) I &= 0 \\
\kappa I - \mu Q - \omega_Q Q &= 0 \\
\rho I + \mu Q - \alpha R + \psi E + \psi S &= 0
\end{aligned} \tag{2.19}$$

Solving equation (2.18) with the natural birth rate and death rate not equal to zero, we obtained the disease free equilibrium point as:

$$E_0 = \left(\frac{\sigma}{\omega}, 0, 0, 0, \frac{\psi\sigma}{\omega\alpha}\right) \tag{2.20}$$

2.11.2 Basic reproductive number R_0 of SEIQR model (with quarantine and vaccination)

Using the next generation matrix approach (G) developed by [21], we obtained the R_0 as:

$$R_0 = \frac{\beta\delta}{(\delta + \omega + \psi)(\kappa + \rho + \omega_I)} \tag{2.21}$$

2.11.3 Local stability analysis of SEIQR model (with quarantine and vaccination) at disease free equilibrium point

We studied the local stability of the model at the disease free equilibrium point and obtained:

$$\lambda^5 + a_1\lambda^4 + a_2\lambda^3 + a_3\lambda^2 + a_4\lambda + a_5 = 0 \tag{2.22}$$

Using Routh-Hurwitz criteria from [22] to describe the polynomial, we realised the disease free equilibrium point was stable.

2.12 Simulation of SEIQR model (with quarantine and vaccination)

We simulate the SEIQR model with both quarantine and vaccination as intervention. We observe that the infected decrease very fast and stays very close to zero.

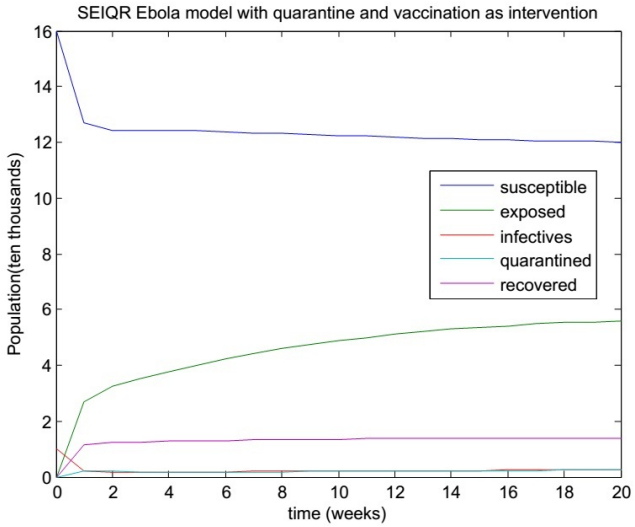

Fig. 10. Simulation of SEIQR model with quarantine and vaccination. Parameters values N=160000, β=0.410, ϵ=0.049, κ=0.7, ψ=0.2

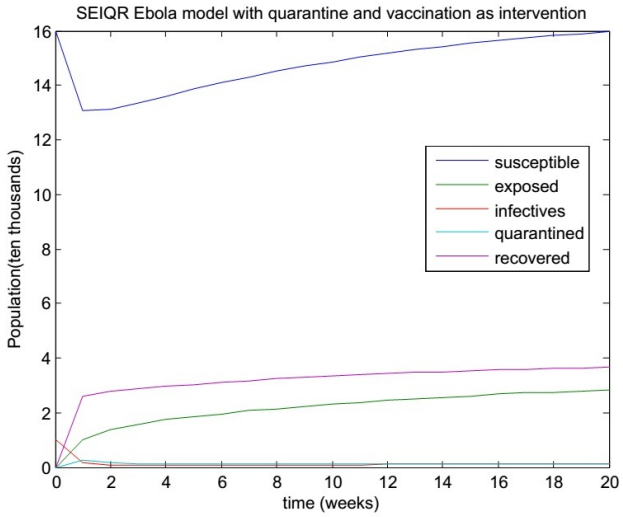

Fig. 11. Simulation of SEIQR model with quarantine and vaccination. Parameters values N=160000, β=0.112, ϵ=0.029, κ=0.9, ψ=0.5

2.13 Optimal control

We studied the optimal control problem using Pontryagin Maximum Principle. u_1, u_2 are the control variables representing vaccination and quarantine respectively.

2.13.1 Optimal control problem

An optimal control problem can be written as

$$MinJ[x(t),u(t)] = \int_{t_0}^{t_f} f(t,x(t),u(t))dt \tag{2.23}$$

subject to

$$\dot{x}(t) = g(t,x(t),u(t)) \tag{2.24}$$

where x is the state vector and u is the control vector.

$J[x(t),u(t)]$ is the objective functional.
x_{t_0} is the initial state.
x_{t_f} is the target state.

2.13.2 Optimal control problem with vaccination and quarantine

$$J(u_1,u_2) = \int_0^{t_f} \left[I(t) + \frac{c_1}{2}u_1^2(t) + \frac{c_2}{2}u_2^2(t) \right] dt \tag{2.25}$$

subject to

$$\begin{aligned}
\frac{dS}{dt} &= -\beta SI - \varepsilon SR - \omega S + \alpha R - u_1 S + \sigma \\
\frac{dE}{dt} &= \beta SI + \varepsilon SR - \delta E - \omega E - u_1 E \\
\frac{dI}{dt} &= \delta E - \rho I - \omega_I I - u_2 I \\
\frac{dQ}{dt} &= u_2 I - \mu Q - \omega_Q Q \\
\frac{dR}{dt} &= \rho I + \mu Q - \alpha R + u_1 E + u_1 S
\end{aligned} \tag{2.26}$$

where $u_1(t), u_2(t)$ are bounded Lebesgue integrable functions with time interval $[0, t_f]$ and c_1, c_2 are weights for vaccination and quarantine respectively.

2.13.3 Pontryagin's maximum principle

We will use Pontryagin's Maximum Principle to find a solution for the optimal control variables u_1^*, u_2^*. Let $p_i(t)$ be the co-state variables. Using the optimal control problem, the Hamiltonian H is given as:

$$\begin{aligned}
H\left(I,u_1,u_2,p_1,p_2,p_3,p_4,p_5\right) = I &+ \frac{c_1}{2}u_1^2 + \frac{c_2}{2}u_2^2 \\
&+ p_1[\sigma - \beta SI - \varepsilon SR - \omega S + \alpha R - u_1 S] \\
&+ p_2[\beta SI + \varepsilon SR - \delta E - \omega E - u_1 E] \\
&+ p_3[\delta E - \rho I - \omega_I I - u_2 I] \\
&+ p_4[u_2 I - \mu Q - \omega_Q Q] \\
&+ p_5[\rho I + \mu Q - \alpha R + u_1 E + u_1 S]
\end{aligned} \tag{2.27}$$

Solving the Hamiltonian, we obtained the solution of the optimal control problem as:

$$\begin{aligned}
u_1^* &= min\left\{1, max\left\{0, \frac{(p_1 - p_5)S + (p_2 - p_5)E}{c_1}\right\}\right\} \\
u_2^* &= min\left\{1, max\left\{0, \frac{(p_3 - p_4)I}{c_2}\right\}\right\}
\end{aligned} \tag{2.28}$$

The necessary condition for the Pontryagin's maximum principle shows that the adjoint variables satisfy the following:

$$\begin{aligned}
\frac{dp_1}{dt} &= -\frac{\partial H}{\partial S} = p_1\beta I + p_1\varepsilon R + p_1\omega + p_1u_1 - p_2\beta I - p_2\varepsilon R - p_5u_1 \\
\frac{dp_2}{dt} &= -\frac{\partial H}{\partial E} = p_2\delta + p_2\omega + p_2u_1 - p_3\delta - p_5u_1 \\
\frac{dp_3}{dt} &= -\frac{\partial H}{\partial I} = -1 + p_1\beta S - p_2\beta S + p_3\rho + p_3\omega_I + p_3u_2 - p_4u_2 - p_5\rho \\
\frac{dp_4}{dt} &= -\frac{\partial H}{\partial Q} = p_4\mu + p_4\omega_Q - p_5\mu \\
\frac{dp_5}{dt} &= -\frac{\partial H}{\partial R} = p_1\varepsilon S - p_1\alpha - p_2\varepsilon S + p_5\alpha
\end{aligned} \tag{2.29}$$

with transversality conditions

$$p_1(t_f) = p_2(t_f) = p_3(t_f) = p_4(t_f) = p_5(t_f) = 0 \tag{2.30}$$

where u_1^*, u_2^* satisfy the optimality condition. The solution to the optimal control problem was obtained numerically.

We performed simulations of the models using forward backward sweep for the optimal control problem.

Using the values $c_1 = 0.6, c_2 = 0.4$, $y_0 = (16, 0, 1, 0, 0)$, initial state $t_0 = 0$ and target state $t_f = 20$ weeks. Then we have:

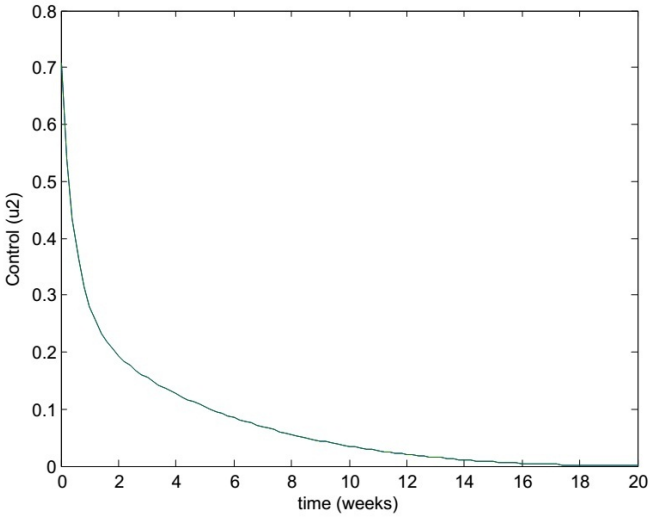

Fig. 12. Simulation of control state

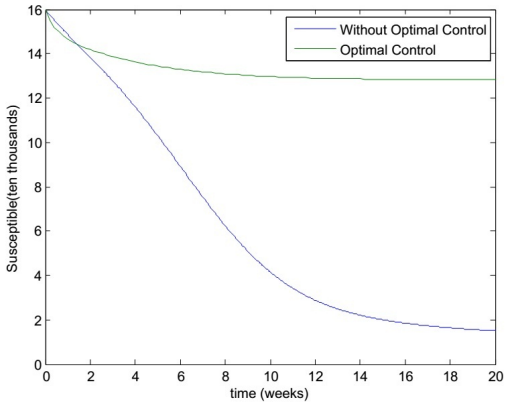

Fig. 13. Simulation of optimal control with quarantine (Susceptible)

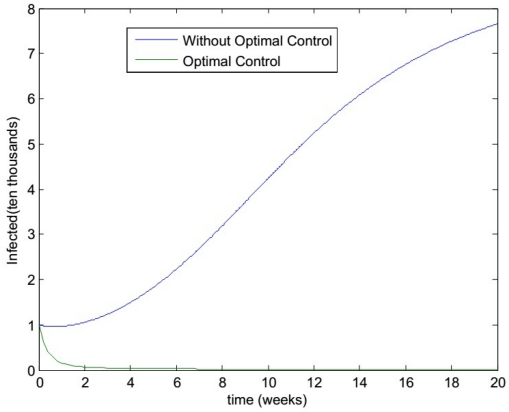

Fig. 14. Simulation of optimal control with quarantine (Infective)

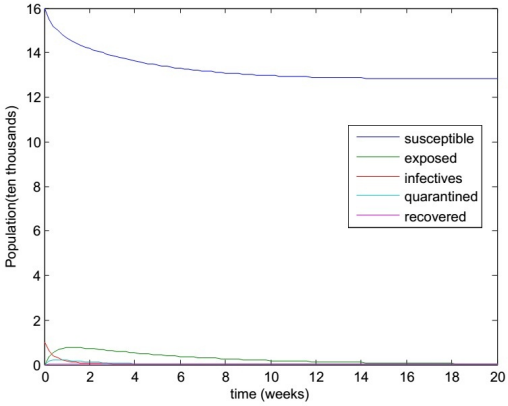

Fig. 15. Simulation of optimal control with quarantine

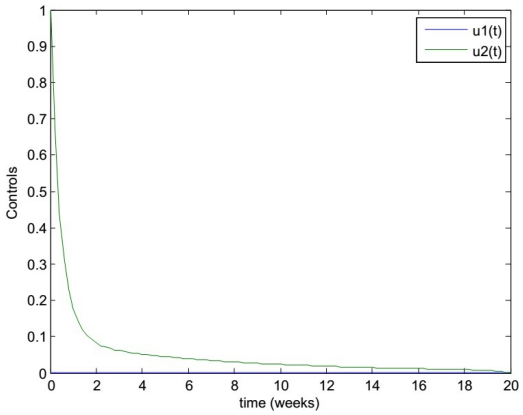

Fig. 16. Simulation of control states

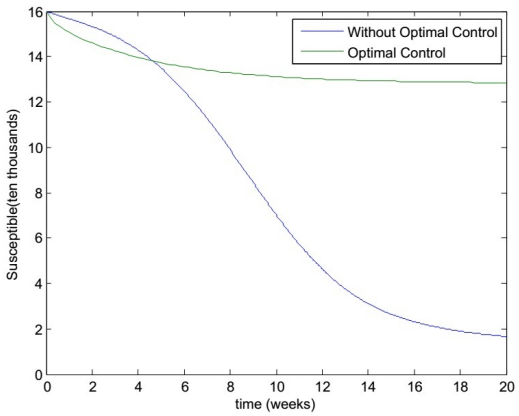

Fig. 17. Simulation of optimal control with quarantine and vaccination (Susceptible)

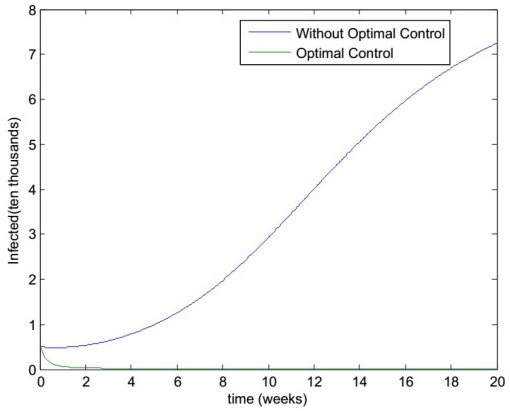

Fig. 18. Simulation of optimal control with quarantine and vaccination (Infective)

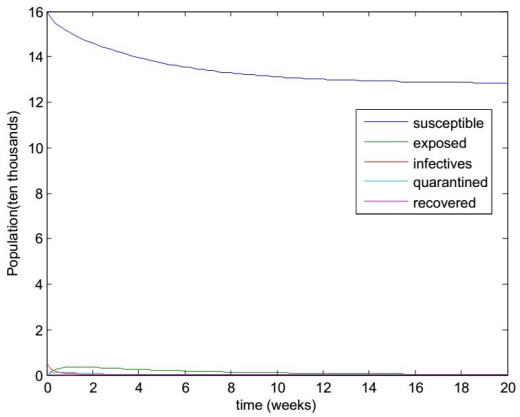

Fig. 19. Simulation of optimal control with quarantine and vaccination

3 Conclusion

We derived a mathematical model for Ebola virus disease considering quarantine and vaccination as intervention strategies and performed stability analysis of the models. We analysed the model to understand the transmission dynamics of the disease in Sierra Leone and Liberia. The basic reproductive number for our model without intervention is $R_0 = 3.7775$, this shows that there is an epidemic. For the model with quarantine, $R_0 = 0.5502$, this shows the epidemic will eventually die out when quarantine is implemented. For the model with vaccination, $R_0 = 0.4492$, this shows the epidemic will eventually die out when vaccination is implemented. For the model with quarantine and vaccination, $R_0 = 0.1283$, this shows the epidemic will eventually die out and this is more faster than the former. The stability analysis of the disease free equilibrium showed that, the disease without intervention was unstable but when quarantine, vaccination and/both was implemented the system was stable meaning the epidemic can be controlled. If the proportion of the population vaccinated exceeds the herd immunity, the disease will be eliminated. We realised from Figs. $(8-12)$ that the best intervention strategy is to implement both quarantine and vaccination immediately the disease is discovered.

Using optimal control, we observed that when both quarantine and vaccination are implemented the disease dies out in the first three weeks. The approximated solution of the optimal control problem is given as 0.002473 and 0.003355 for u_1^*, u_2^* respectively. This is aimed at reducing $R_0 < 1$.

Finally, we did not use an SIR model because without exposed class it does not represent the real data in Sierra Leone well this is also observed from Figs. $(6, 7)$. Hence SEIR model is an improved method for Ebola. We recommend that future research should investigate more intervention strategies such as contact tracing.

Acknowledgements

The authors would like to acknowledge WHO for providing data used in this research.

Competing Interests

Authors have declared that no competing interests exist.

References

[1] WHO. Ebola virus disease; 2015.
Available: http://who.int/mediacentre/factsheets/fs103/en/
(Accessed: 2015-5-8).

[2] Jaime Astacio, DelMar Briere, Milton Guillen, Josue Martinez, Francisco Rodriguez, Noe Valenzuela-Campos. Mathematical Models to Study the Outbreaks of Ebola; 1996.

[3] Judith Legrand, Rebecca Freeman Grais, Pierre-Yves Boelle, Alain-Jacques Valleron, and Antoine Flahault. Understanding the dynamics of ebola epidemics. Epidemiology and Infection. 2007;135(04):610-621.

[4] Gerardo Chowell, Nick W Hengartner, Carlos Castillo-Chavez, Paul W Fenimore, and JM Hyman. The basic reproductive number of ebola and the effects of public health measures: The cases of congo and uganda. Journal of Theoretical Biology. 2004;229(1):119-126.

[5] Caitlin M. Rivers, Eric T. Lofgren, Madhav Marathe, Stephen Eubank, Bryan L Lewis. Modeling the impact of interventions on an epidemic of ebola in sierra leone and liberia. PLoS Currents. 2014;6.

[6] Glenn Webb, Cameron Browne, Xi Huo, Ousmane Seydi, Moussa Seydi, and Pierre Magal. A model of the 2014 ebola epidemic in west africa with contact tracing. PLoS Currents. 2014;7.

[7] Christian L Althaus. Estimating the reproduction number of ebola virus (ebov) during the 2014 outbreak in west africa. PLoS Currents. 2014;6.

[8] Abdulrahman Ndanusa, Sirajo Abdulrahman, and Abdulrazaq Abdulmalik. A Mathematical Model for Controlling the Spread of Ebola Virus Disease in Nigeria. 9

[9] Jim Morrow. Modeling the spread of ebola; 2015.
Available: www.math.washington.edu/ morrow/mcm /mcm15/38725paper.pdf
(Accessed: 2015-11-1).

[10] Constantinos Siettos, Cleo Anastassopoulou, Lucia Russo, Christos Grigoras, Eleftherios Mylonakis. Modeling the 2014 Ebola Virus Epidemic–Agent-Based Simulations, Temporal Analysis and Future Predictions for Liberia and Sierra Leone; 2014.

[11] Doracelly Hincapie-Palacio, Juan Ospina, and Delfim FM Torres. Approximated Analytical Solution to an Ebola Optimal Control Problem; 2015.arXiv preprint arXiv:1512.02843.

[12] Amira Rachah and Delfim FM Torres. Mathematical modelling, simulation, and optimal control of the 2014 ebola outbreak in west africa. Discrete Dynamics in Nature and Society; 2015.

[13] Ellina Grigorieva, Evgenii Khailov. Analytical study of optimal control intervention strategies for ebola epidemic model; 2015.

[14] Francis Oduro, Gabriel A Okyere, George Theodore Azu-Tungmah. Transmission dynamics of malaria in ghana. Journal of Mathematics Research. 2012;4(6):22.

[15] Peter M. Mwamtobe, Shirley Abelman, Michel Tchuenche J, Ansley Kasambara. Optimal (control of) intervention strategies for malaria epidemic in karonga district, malawi. Abstract and Applied Analysis. volume 2014. Hindawi Publishing Corporation; 2014.

[16] Francis T Oduro, Joseph Baafi, and George Apaaboah. Modelling the effect of post-mortem contact on the spread of ebola with quarantine as an intervention. Journal of Mathematics Research. 2016;8(4):176.

[17] Amenaghawon C Osemwinyen and Aboubakary Diakhaby. Mathematical modelling of the transmission dynamics of ebola virus. Applied and Computational Mathematics. 2015;4(4):313-320.

[18] Adnan Khan, Mahim Naveed, Muhammad Dur-e Ahmad, and Mudassar Imran. Estimating the basic reproductive ratio for the ebola outbreak in liberia and sierra leone. Infectious Diseases of Poverty. 2015;4(1):13.

[19] World Health Organization et al. Who: Ebola response roadmap situation report 24 december 2014; 2014.

[20] UNICEF et al. Who, world bank, un desa/population division: Levels and trends in child mortality: report 2012. Estimates developed by the UN Inter-agency Group for Child Mortality Estimation; 2012.

[21] Odo Diekmann, JAP Heesterbeek, and Johan AJ Metz. On the definition and the computation of the basic reproduction ratio r 0 in models for infectious diseases in heterogeneous populations. Journal of Mathematical Biology. 1990;28(4):365-382.

[22] Juan M. Pena. Characterizations and stable tests for the routh–hurwitz conditions and for total positivity. Linear Algebra and its Applications. 2004;393:319-332.

Peer-review history:
The peer review history for this paper can be accessed here (Please copy paste the total link in your browser address bar)
http://sciencedomain.org/review-history/16542