Dynamics of Ebola Virus

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Abstract: In this work a deterministic and stochastic model is developed to investigate the dynamics of Ebola epidemic. The model includes susceptible, exposed, infected, quarantined and removed or recovered individuals. The model used in this work is based on a deterministic model. The Chowel et. al (2015) work on early detection of Ebola is modified by introducing an assumption that the quarantined class is totally successful and cannot infect the susceptible class. The resulting model is transformed into a stochastic model and solved using the Euler Maruyama method. Data generated with the values assigned to the parameters are used for the simulation. We have been able to develop and analyse a model with an effective isolation of infected individuals and its effect to the basic reproductive number is analysed. In our simulation, the population of infectious individuals is shown over a period of time. It is seen that the disease will produce an epidemic and after some time, the infected class maintain a uniform increment.

INDEX TERMS: Jacobian, Steady State, Reproductive Number, Stochastic, Deterministic

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1. Introduction/Model Formulation:

The total population at time t, denoted by $N(t)$, is divided into the mutually exclusive compartments of susceptible individuals $S(t)$, exposed individuals $E(t)$, infectious individuals $I(t)$, quarantined or isolated individuals $Q(t)$ and recovered individuals $R(t)$, so that

$$N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$$

We formulate our model with the following assumptions:

i. The isolation is completely effective such that a successful contact with susceptible individuals is impossible.

ii. There can be a recovery for both infectious and quarantined class.

iii. It is assumed that individuals are recruited either by birth or by migration into the susceptible class at rate Λ.

iv. Susceptible individuals acquire Ebola virus as a result of interaction with only infectious individuals at a rate λ, where $\lambda = \beta I$

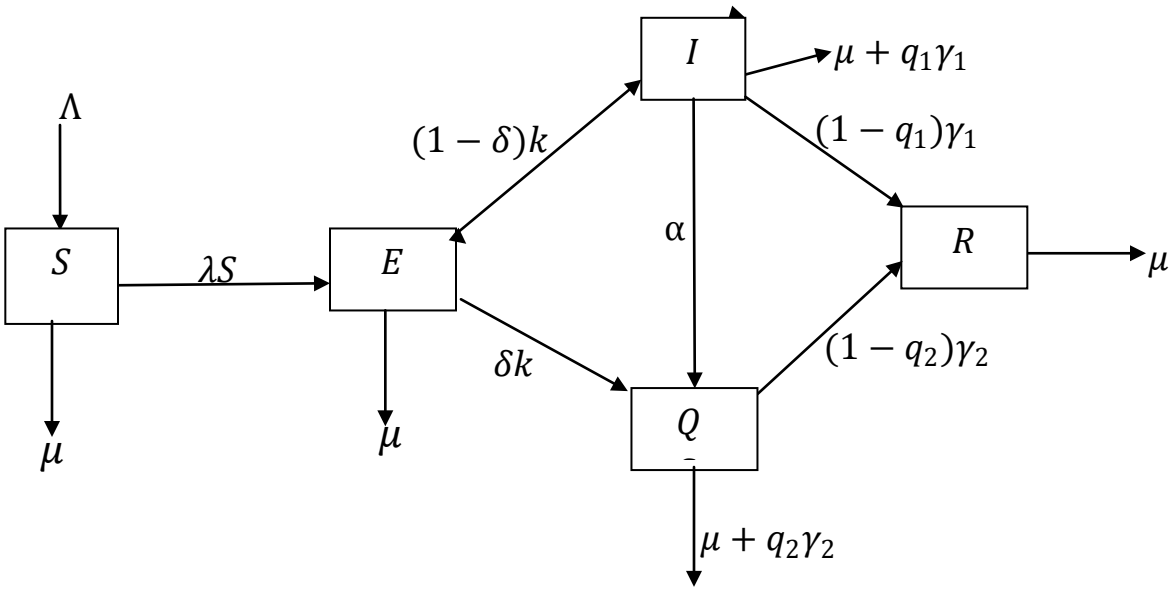

Figure 1: Schematic representation of the model

Table 1: Description of model variables

Variable	Description
$S(t)$	Susceptible individuals
$E(t)$	Exposed individuals
$I(t)$	Infectious individuals
$Q(t)$	Quarantined or isolated individuals
$R(t)$	Recovered individuals

Table 2: Description of model parameters

Parameter	Description
Λ	Recruitment rate
β	Effective contact rate
k	Transmission rate for exposed individuals
γ_1	Removal rate for infectious individuals either by recovery or Ebola induced death
γ_2	Removal rate for isolated individuals either by recovery or Ebola induced death
α	Rate at which an infectious individual gets isolated
δ	Fraction of latent detectable individuals who are diagnosed and get isolated

q_1	Probability that an infectious individual dies due to Ebola
q_2	Probability that an isolated individual dies due to Ebola

The model equations are therefore given by

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda - \lambda S - \mu S \\
\frac{dE}{dt} &= \lambda S - (k+\mu)E \\
\frac{dI}{dt} &= (1-\delta)kE - (\alpha + \gamma_1 + \mu)I \\
\frac{dQ}{dt} &= \delta kE + \alpha I - (\gamma_2 + \mu)Q \\
\frac{dR}{dt} &= (1-q_1)\gamma_1 I + (1-q_2)\gamma_2 Q - \mu R
\end{aligned}\right\} \qquad (1.1)$$

1.1 Basic Properties of the model

Theorem 1

Let the initial data for the model (1.1) be $S(0) > 0, E(0) > 0, I(0) > 0, Q(0) > 0,\ R(0) > 0$. Then, the solutions $\left(S(t), E(t), I(t), Q(t), R(t)\right)$ of the model (1.1) with positive initial data, will remain positive for all time $t > 0.$

Proof

Let

$$t_1 = \sup\left\{t > 0 : S(t) > 0, E(t) > 0, I(t) > 0, Q(t) > 0, R(t) > 0\right\} > 0$$

It follows from the first equation of the model (3.6) that

$$\frac{dS}{dt} = \Lambda - \lambda S - \mu S$$

which can be re-written as

$$\frac{d}{dt}\left\{S(t)\exp[\mu t + \int_0^t \lambda(\tau)d\tau]\right\} = \Lambda\left\{\exp[\mu t + \int_0^t \lambda(\tau)d\tau]\right\}$$

Thus,

$$S(t_1)\left\{\exp[\mu t_1 + \int_0^{t_1} \lambda(\tau)d\tau]\right\} - S(0) = \int_0^{t_1} \Lambda\left\{\exp[\mu y + \int_0^y \lambda(\tau)d\tau]\right\}dy$$

This implies

$$S(t) = S(0)\exp[-\mu t_1 - \int_0^{t_1} \lambda(\tau)d\tau]$$
$$+\left\{\exp[-\mu t_1 - \int_0^{t_1} \lambda(\tau)d\tau]\right\}$$
$$\times \int_0^{t_1} \Lambda \exp\left\{-\mu y - \int_0^{y} \lambda(\tau)d\tau\right\}dy > 0$$

Similarly, it can be shown that $E > 0, I > 0, Q > 0, R > 0$ for all time $t > 0$

Theorem 2

The closed set $\Omega = \left\{(S, E, I, Q, R) \in R_+^5 : N \le \frac{\Lambda}{\mu}\right\}$ is positively invariant

Proof

Adding all the equations of the model gives

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dR}{dt}$$
$$= \Lambda - \mu N - q_1\gamma_1 I - q_2\gamma_2 Q$$

In the absence of infection

$I = Q = 0$, so that

$$\frac{dN}{dt} \le \Lambda - \mu N$$

We now apply Birkhoff and Rota's Theorem on differential inequality.

By separation of variables of differential inequality, we obtain

$$\frac{dN}{\Lambda - \mu N} \le dt$$

Integrating both sides gives

$$\int \frac{dN}{\Lambda - \mu N} \le \int dt$$
$$\Rightarrow -\frac{1}{\mu}\ln(\Lambda - \mu N) \le t + c$$
$$\Rightarrow \ln(\Lambda - \mu N) \ge -\mu(t + c)$$

Therefore,

$\Lambda - \mu N \ge Be^{-\mu t}$, where B is a constant.

Now applying $N(0) = N_0$ we have

$$A = \Lambda - \mu N_0$$

Substituting gives

$$\Lambda - \mu N \geq (\Lambda - \mu N_0)e^{-\mu t}$$

Making μ the subject of the formula we have

$$N \leq \frac{\Lambda}{\mu} - \left[\frac{\Lambda - \mu N_0}{\mu}\right]e^{-\mu t}$$

As $t \to \infty$ in the population size, N approaches

$$0 \leq N \leq \frac{\Lambda}{\mu} \Rightarrow N \to \frac{\Lambda}{\mu}$$

Therefore, the feasibility solution set of the system of equations enters the region

$$\Omega = \left[(S, E, I, Q, R) \in R_+^5 : N \leq \frac{\Lambda}{\mu}\right]$$

In this case, whenever $N > \frac{\Lambda}{\mu}$, then $\frac{dN}{dt} < 0$ which means that the population reduces asymptotically to the carrying capacity. On the other hand, whenever $N \leq \frac{\Lambda}{\mu}$, every solution with initial condition in R_+^5 remains in that region for $t > 0$.

Thus, the region Ω is positively-invariant and the model is well posed and biologically meaningful.

1.2 STOCHASTIC MODEL EQUATIONS

Applying the method developed by Allen *et al.* (2008), we can get the stochastic model for the deterministic model above.
The drift vector is defined as

$\vec{f} = \sum_{i=1}^{14} p_i \vec{\lambda}_i$, where p_i and $\vec{\lambda}_i$ are the random changes and transition probabilities respectively, defined in Table 3 below.

Table 3

Change	Probability	Event
$[1\ 0\ 0\ 0\ 0]^T$	$p_1 = \Lambda\Delta t$	Birth of a susceptible
$[-1\ 0\ 0\ 0\ 0]^T$	$p_2 = \mu S\Delta t$	Susceptible dies natural death
$[-1\ 1\ 0\ 0\ 0]^T$	$p_3 = \beta SI\Delta t$	Susceptible becomes exposed
$[0\ -1\ 0\ 0\ 0]^T$	$p_4 = \mu E\Delta t$	Exposed individual dies natural death
$[0\ -1\ 1\ 0\ 0]^T$	$p_5 = (1-\delta)k\Delta t$	Exposed individual becomes infectious
$[0\ -1\ 0\ 1\ 0]^T$	$p_6 = \delta k\Delta t$	Exposed individual is quarantined
$[0\ 0\ -1\ 0\ 0]^T$	$p_7 = \mu I\Delta t$	Infectious individual dies natural death
$[0\ 0\ -1\ 1\ 0]^T$	$p_8 = \alpha I\Delta t$	Infectious individual is quarantined
$[0\ 0\ -1\ 0\ 1]^T$	$p_9 = (1-q_1)\gamma_1\Delta t$	Infectious individual recovers
$[0\ 0\ -1\ 0\ 0]^T$	$p_{10} = q_1\gamma_1\Delta t$	Infectious individual dies due to Ebola
$[0\ 0\ 0\ -1\ 0]^T$	$p_{11} = \mu Q\Delta t$	Quarantined dies natural death
$[0\ 0\ 0\ -1\ 0]^T$	$p_{12} = (1-q_2)\gamma_2\Delta t$	Quarantined individual recovers
$[0\ 0\ 0\ -1\ 1]^T$	$p_{13} = q_2\gamma_2\Delta t$	Quarantined individual dies due to Ebola

$[0\ 0\ 0\ 0\ -1]^T$	$p_{14} = \mu R \Delta t$	Recovered individual dies natural death

$$\vec{f} = \sum_{i=1}^{14} p_i \vec{\lambda}_i$$

$$\vec{f} = p_1 \begin{pmatrix} 1 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} + p_2 \begin{pmatrix} -1 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} + p_3 \begin{pmatrix} -1 \\ 1 \\ 0 \\ 0 \\ 1 \end{pmatrix} + p_4 \begin{pmatrix} 0 \\ -1 \\ 0 \\ 0 \\ 0 \end{pmatrix} + p_5 \begin{pmatrix} 0 \\ -1 \\ 1 \\ 0 \\ 0 \end{pmatrix} + p_6 \begin{pmatrix} 0 \\ -1 \\ 0 \\ 1 \\ 0 \end{pmatrix} + p_7 \begin{pmatrix} 0 \\ 0 \\ -1 \\ 0 \\ 0 \end{pmatrix}$$

$$+ p_8 \begin{pmatrix} 0 \\ 0 \\ -1 \\ 1 \\ 0 \end{pmatrix} + p_9 \begin{pmatrix} 0 \\ 1 \\ 0 \\ 0 \\ 1 \end{pmatrix} + p_{10} \begin{pmatrix} 0 \\ 0 \\ -1 \\ 0 \\ 0 \end{pmatrix} + p_{11} \begin{pmatrix} 0 \\ 0 \\ 0 \\ -1 \\ 0 \end{pmatrix} + p_{12} \begin{pmatrix} 0 \\ 0 \\ 0 \\ -1 \\ 0 \end{pmatrix} + p_{13} \begin{pmatrix} 0 \\ 0 \\ 0 \\ -1 \\ 1 \end{pmatrix} + p_{14} \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ -1 \end{pmatrix}$$

$$\vec{f} = \begin{pmatrix} \Delta \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} -\mu S \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} -\beta SI \\ \beta SI \\ 0 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ -\mu E \\ 0 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ -(1-\delta)k \\ (\delta-1)k \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ -\delta k \\ 0 \\ \delta k \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ -\mu I \\ 0 \\ 0 \end{pmatrix}$$

$$+ \begin{pmatrix} 0 \\ 0 \\ -\alpha I \\ \alpha I \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ (q_1-1)\gamma_1 \\ 0 \\ (1-q_1)\gamma_1 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ -q_1\gamma_1 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ 0 \\ -\mu Q \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ 0 \\ (q_2-1)\gamma_2 \\ 0 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ 0 \\ -q_2\gamma_2 \\ q_2\gamma_2 \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ -\mu R \end{pmatrix}$$

Hence, the drift vector $\vec{f}$ of order 5×1, is given by

$$\vec{f} = \begin{pmatrix} \Lambda - \lambda S - \mu S \\ \lambda S - (k+\mu)E \\ (1-\delta)kE - (\alpha + \gamma_1 + \mu)I \\ \delta kE + \alpha I - (\gamma_2 + \mu)Q \\ (1-q_1)\gamma_1 I + (1-q_2)\gamma_2 Q - \mu R \end{pmatrix}$$

where V is the covariance matrix, given as:

$$V = \sum_{i=1}^{14} p_i \vec{\lambda} \vec{\lambda}^T$$

$$V = p_1 \begin{pmatrix} 1 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} (1 \quad 0 \quad 0 \quad 0 \quad 0) + p_2 \begin{pmatrix} -1 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} (-1 \quad 0 \quad 0 \quad 0 \quad 0) + p_3 \begin{pmatrix} -1 \\ 1 \\ 0 \\ 0 \\ 0 \end{pmatrix} (-1 \quad 1 \quad 0 \quad 0 \quad 0)$$

$$+ p_4 \begin{pmatrix} 0 \\ -1 \\ 0 \\ 0 \\ 0 \end{pmatrix} (0 \quad -1 \quad 0 \quad 0 \quad 0) + p_5 \begin{pmatrix} 0 \\ -1 \\ 1 \\ 0 \\ 0 \end{pmatrix} (0 \quad -1 \quad 1 \quad 0 \quad 0) + p_6 \begin{pmatrix} 0 \\ -1 \\ 0 \\ 1 \\ 0 \end{pmatrix} (0 \quad -1 \quad 0 \quad 1 \quad 0)$$

$$+ p_7 \begin{pmatrix} 0 \\ 0 \\ -1 \\ 0 \\ 0 \end{pmatrix} (0 \quad 0 \quad -1 \quad 0 \quad 0) + p_8 \begin{pmatrix} 0 \\ 0 \\ -1 \\ 1 \\ 0 \end{pmatrix} (0 \quad 0 \quad -1 \quad 1 \quad 0) + p_9 \begin{pmatrix} 0 \\ 0 \\ -1 \\ 0 \\ 1 \end{pmatrix} (0 \quad 0 \quad -1 \quad 0 \quad 1)$$

$$+ p_{10} \begin{pmatrix} 0 \\ 0 \\ -1 \\ 0 \\ 0 \end{pmatrix} (0 \quad 0 \quad -1 \quad 0 \quad 0) + p_{11} \begin{pmatrix} 0 \\ 0 \\ 0 \\ -1 \\ 0 \end{pmatrix} (0 \quad 0 \quad 0 \quad -1 \quad 0) + p_{12} \begin{pmatrix} 0 \\ 0 \\ 0 \\ -1 \\ 0 \end{pmatrix} (0 \quad 0 \quad 0 \quad -1 \quad 0)$$

$$+ p_{13} \begin{pmatrix} 0 \\ 0 \\ 0 \\ -1 \\ 1 \end{pmatrix} (0 \quad 0 \quad 0 \quad -1 \quad 1) + p_{14} \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ -1 \end{pmatrix} (0 \quad 0 \quad 0 \quad 0 \quad -1)$$

$$V=\begin{pmatrix}\Lambda&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\end{pmatrix}+\begin{pmatrix}\mu S&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\end{pmatrix}+\begin{pmatrix}\beta SI&-\beta SI&0&0&0\\-\beta SI&\beta SI&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\-\beta SI&0&0&0&\beta SI\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&\mu E&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\end{pmatrix}$$

$$+\begin{pmatrix}0&0&0&0&0\\0&(1-\delta)k&(\delta-1)k&0&0\\0&(\delta-1)k&(1-\delta)k&0&0\\0&0&0&0&0\\0&0&0&0&0\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&\delta k&0&-\delta k&0\\0&0&0&0&0\\0&-\delta k&0&\delta k&0\\0&0&0&0&0\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&\mu I&0&0\\0&0&0&0&0\\0&0&0&0&0\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&\alpha I&-\alpha I&0\\0&0&-\alpha I&\alpha I&0\\0&0&0&0&0\end{pmatrix}$$

$$+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&(1-q_1)\gamma_1&0&(q_1-1)\gamma_1\\0&0&0&0&0\\0&0&(q_1-1)\gamma_1&0&(1-q_1)\gamma_1\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&q_1\gamma_1&0&0\\0&0&0&0&0\\0&0&0&0&0\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&\mu Q&0\\0&0&0&0&0\end{pmatrix}$$

$$+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&(1-q_2)\gamma_2&0\\0&0&0&0&0\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&0&q_2\gamma_2&-q_2\gamma_2\\0&0&0&-q_2\gamma_2&q_2\gamma_2\end{pmatrix}+\begin{pmatrix}0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&-\mu R\end{pmatrix}$$

Hence, the covariance matrix V of order 5×5 is given by

$$\begin{pmatrix}\Lambda+\mu S+\beta SI&-\beta SI&0&0&0\\-\beta SI&\beta SI+\mu E+(1-\delta)k+\delta k&(\delta-1)k&-\delta k&0\\0&-\delta k+(q_1-1)\gamma_1&-\delta k+(q_1-1)\gamma_1&\delta k+\mu I+(q_1-1)\gamma_1+q_1\gamma_1+2(1-q_2)\gamma_2&(q_1-1)\gamma_1\\0&-\delta k&-\alpha I&\delta k+\alpha I+\mu Q+q_2\gamma_2&0\\0&0&(q_1-1)\gamma_1&-q_2\gamma_2&(1-q_1)\gamma_1+q_2\gamma_2+\mu R\end{pmatrix}$$

The stochastic model is therefore given by

$$d(\overrightarrow{X}(t))=\overrightarrow{f}(X(t))dt+V^{1/2}(t,X(t))dW(t)$$

We have already seen the transition probabilities as shown above.

where the drift vector $\vec{f}$ of order 5×1,

p_i and $\vec{\lambda}_i$ $(i = 1, \ldots, 14)$ are random changes and transition probabilities represented in the above table.

The diffusion matrix is obtained from the entries $p_i\vec{\lambda}_i$. It is given by

$$\begin{pmatrix} \sqrt{(\Delta)} & -\sqrt{(\mu S)} & -\sqrt{(\beta SI)} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \sqrt{(\beta SI)} & -\sqrt{\mu E} & -\sqrt{(\delta-1)k} & -\sqrt{\delta k} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sqrt{(1-\delta)k} & 0 & -\sqrt{(\mu I)} & -\sqrt{(\alpha I)} & -\sqrt{[(1-q_1)\gamma_1]} & -\sqrt{(q_1\gamma_1)} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sqrt{\delta k} & 0 & \sqrt{\alpha I} & 0 & 0 & -\sqrt{(\mu Q)} & -\sqrt{[(1-q_2)\lambda_2]} & -\sqrt{(q_2\gamma_2)} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sqrt{[(1-q_1)\gamma_1]} & 0 & 0 & 0 & \sqrt{(q_2\gamma_2)} & -\sqrt{(\mu R)} \end{pmatrix}$$

where $\overrightarrow{W} = [W_1, W_2, W_3, W_4, W_5, W_6, W_7, W_8, W_9, W_{10}, W_{11}, W_{12}, W_{13}, W_{14}]^T$ is a vector of fourteen independent Wiener processes. In addition, $d\overrightarrow{W}(t)$ has order

14×1 while $d\overrightarrow{X}$ is a 5×1 dimensional vector.

f_i are given below:

$$f_1 = \Lambda - \lambda S - \mu S$$
$$f_2 = \lambda S - (k+\mu)E$$
$$f_3 = (1-\delta)kE - (\alpha + \gamma_1 + \mu)I$$
$$f_4 = \delta kE + \alpha I - (\gamma_2 + \mu)Q$$
$$f_5 = (1-q_1)\gamma_1 I + (1-q_2)\gamma_2 Q - \mu R$$

The elements of the diffusion matrix

$$g_{1,1} = \sqrt{\Lambda}, g_{1,2} = -\sqrt{\mu S}, g_{1,3} = -g_{2,3} = \sqrt{\beta SI}, g_{3,5} = -g_{2,5} = \sqrt{(1-\delta)}$$
$$g_{2,4} = -\sqrt{\mu E}, g_{4,6} = -g_{2,6} = \sqrt{\delta k}, g_{4,8} = -g_{3,8} = \sqrt{[\alpha I}$$
$$g_{3,7} = -\sqrt{\mu I}, g_{4,8} = -g_{3,8} = \sqrt{\alpha I}, g_{5,9} = -g_{3,9} = (1-q_1)\gamma_1$$
$$g_{4,11} = -\sqrt{\mu Q}, g_{4,12} = \sqrt{(q_2-1)\gamma_2}, g_{5,13} = -g_{4,13} = \sqrt{q_2\gamma_2}$$
$$g_{5,14} = -\sqrt{\mu R}$$
$$g_{1,4} = g_{1,5} = g_{1,6} = g_{1,7} = g_{1,8} = g_{1,9} = g_{1,10} = g_{1,11} = g_{1,12} = g_{1,13} = g_{1,14} = 0$$
$$g_{2,1} = g_{2,2} = g_{2,7} = g_{2,8} = g_{2,9} = g_{2,10} = g_{2,11} = g_{2,12} = g_{2,13} = g_{2,14} = 0$$
$$g_{3,1} = g_{3,2} = g_{3,3} = g_{3,4} = g_{3,6} = g_{3,11} = g_{3,12} = g_{3,13} = g_{3,14} = 0$$
$$g_{4,1} = g_{4,2} = g_{4,3} = g_{4,4} = g_{4,5} = g_{4,7} = g_{4,9} = g_{4,10} = g_{4,14} = 0$$
$$g_{5,1} = g_{5,2} = g_{5,3} = g_{5,4} = g_{5,5} = g_{5,6} = g_{5,7} = g_{5,8} = g_{5,10} = g_{5,11} = 0$$

$$\|f\| = \sqrt{\sum_{i=1}^{5} f_i(x)^2} \text{ and } , \|G\| = \sqrt{\sum_{i=1}^{4}\sum_{j=1}^{9} g_{ij}(x)^2}$$

where

$$\|f\| = \sqrt{[f_1]^2 + [f_2]^2 + [f_3]^2 + [f_3]^2 + [f_4]^2 + [f_5]^2}$$

$$\|G\| = \sqrt{\Lambda + \mu S + 2\beta SI + 3(1-\delta) + \delta k + (1-q_1) + q_1\gamma_1 + 2(1-q_{2)})\gamma_2 + \mu R}$$

Both f_i and g_{ij} are continuously differentiable at S, E, I, Q *and* R and hence satisfy the

Lipschitz condition (by the Mean value theorem for calculus). Since the norms exist, they are bounded. The drift and the diffusion matrices are therefore bounded. Hence, they satisfy the conditions for existence and uniqueness of solution.

1.3 Basic reproduction number (R_0)

The basic reproductionnumber (R_0) is calculated from the disease compartments i.e

those classes that have the disease (E, I, Q).

The basic reproductionnumber (R_0) is calculated as follows:

$\mathcal{F}$: Rate of appearance of new infection $= \begin{pmatrix} \beta SI \\ 0 \\ 0 \end{pmatrix}$

$\mathcal{V}_i^-$: Rate of transfer of disease out of the disease compartment $= \begin{pmatrix} \mu E + (1-\delta)kE + \delta kE \\ \alpha I + (\mu + q_1\gamma_1)I + (1-q_1)\gamma_1 I \\ (\mu + q_2\gamma_2)Q + (1-q_2)\gamma_2 Q \end{pmatrix} = \begin{pmatrix} (\mu + k)E \\ (\mu + \alpha + \gamma_1)I \\ (\mu + \gamma_2)Q \end{pmatrix}$

$\mathcal{V}_i^+$: Rate of transfer of infection into the disease compartment by other means

$$\mathcal{V}_i^+ = \begin{pmatrix} 0 \\ (1-\delta)kE \\ \alpha I + \delta kE \end{pmatrix}$$

$$\mathcal{V}_i = \mathcal{V}_i^- - \mathcal{V}_i^+ = \begin{pmatrix} (\mu + k)E \\ (\mu + \alpha + \gamma_1)I - (1-\delta)kE \\ (\mu + \gamma_2)Q - \alpha I - \delta kE \end{pmatrix}$$

$F = \frac{\partial \mathcal{F}(E_0)}{\partial x_j}$: The Jacobian of $\mathcal{F}$with respect to disease compartments(x_j)evaluated at D.F.E i.e $E_0 = (S_0, E_0, I_0, Q_0,$

$$V = \begin{pmatrix} (\mu + k) & 0 & 0 \\ -(1-\delta)k & (\mu + \alpha + \gamma_1) & 0 \\ -\delta k & -\alpha & (\mu + \gamma_2) \end{pmatrix}$$

$$V^{-1} = \frac{1}{Det(v)}(Adjoint\ of\ V)$$

$$= \frac{1}{(\mu + k)(\mu + \alpha + \gamma_1)(\mu + \gamma_2)} \begin{pmatrix} (\mu + \alpha + \gamma_1)(\mu + \gamma_2) & 0 & 0 \\ (\mu + \gamma_2)(1-\delta)k & (\mu + \gamma_2)(\mu + k) & 0 \\ \alpha(1-\delta)k + \delta k(\mu + \alpha + \gamma_1) & \alpha(\mu + k) & (\mu + \alpha + \gamma_1)(\mu + k) \end{pmatrix}$$

$$= \begin{pmatrix} \frac{1}{(\mu + k)} & 0 & 0 \\ \frac{(1-\delta)k}{(\mu + k)(\mu + \alpha + \gamma_1)} & \frac{1}{(\mu + \alpha + \gamma_1)} & 0 \\ \frac{\alpha(1-\delta) + \delta k(\mu + \alpha + \gamma_1)}{(\mu + k)(\mu + \alpha + \gamma_1)(\mu + \gamma_2)} & \frac{\alpha}{(\mu + \alpha + \gamma_1)(\mu + \gamma_2)} & \frac{1}{(\mu + \gamma_2)} \end{pmatrix}$$

The basic reproductive number

$$R_0 = FV^{-1} = \begin{pmatrix} 0 & \beta\frac{\Lambda}{\mu} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\mu+k)} & 0 & 0 \\ \frac{(1-\delta)k}{(\mu+k)(\mu+\alpha+\gamma_1)} & \frac{1}{(\mu+\alpha+\gamma_1)} & 0 \\ \frac{\alpha(1-\delta)k+\delta k(\mu+\alpha+\gamma_1)}{(\mu+k)(\mu+\alpha+\gamma_1)(\mu+\gamma_2)} & \frac{\alpha}{(\mu+\alpha+\gamma_1)(\mu+\gamma_2)} & \frac{1}{(\mu+\gamma_2)} \end{pmatrix}$$

$$= \frac{\beta\Lambda(1-\delta)k}{\mu(\mu+k)(\mu+\alpha+\gamma_1)}$$

1.4 ENDEMIC STEADY STATE

Endemic state equilibrium at this state the differential equations of the model is set to zero but $I \neq 0, Q \neq 0$

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S = 0 \qquad 1.2$$

$$\frac{dE}{dt} = \beta SI - (k+\mu)E = 0 \qquad 1.3$$

$$\frac{dI}{dt} = (1-\delta)kE - (\alpha+\gamma_1+\mu)I = 0 \qquad 1.4$$

$$\frac{dJ}{dt} = \delta kE + \alpha I - (\gamma_2+\mu)Q = 0 \qquad 1.5$$

$$\frac{dR}{dt} = (1-q_1)\gamma_1 I + (1-q_2)\gamma_2 Q - \mu R = 0 \qquad 1.6$$

On putting the derivatives in the left hand side and equating it to zero and solving the resulting differential equation with respect to the variables S, E, I, Q and R, we obtain

$$\Lambda - \beta SI - \mu S = 0 \Rightarrow S = \frac{\Lambda}{\mu+\beta I}$$

$$\mathrm{E} = \frac{\frac{\Lambda}{\mu+\beta I}\beta I}{k+\mu} = \frac{\Lambda}{\mu+\beta I}\cdot\frac{\beta \mathrm{I}}{k+\mu}$$

$$I = \frac{(1-\delta)\mathrm{k}}{\alpha+\gamma_1+\mu}\cdot\frac{\Lambda}{\mu+\beta I}\cdot\frac{\beta \mathrm{I}}{k+\mu} \qquad 1.7$$

$$Q = \frac{\delta k\Lambda}{\mu+\beta I}\cdot\frac{\beta \mathrm{I}}{k+\mu}\cdot\frac{(1-\delta)\alpha \mathrm{k}}{\alpha+\gamma_1+\mu}\cdot\frac{\Lambda}{\mu+\beta I}\cdot\frac{\beta \mathrm{I}}{k+\mu}$$

$$R = \frac{1}{\mu}[(1-q_1)\gamma_1 I + (1-q_2)\gamma_2 Q]$$

We obtain the endemic steady state at $U_1 = (S^1, E^1, I^1, Q^1, R^1)$

Evaluating J at U_1

$$J_1=\begin{pmatrix} -(\beta I+\mu) & 0 & -\beta S & 0 & 0 \\ \beta I & -(k+\mu) & \beta S & 0 & 0 \\ 0 & (1-\delta)k & -(\alpha+\gamma_1+\mu) & 0 & 0 \\ 0 & \delta k & \alpha & -(\gamma_2+\mu) & 0 \\ 0 & 0 & (1-q_1)\gamma_1 & (1-q_2)\gamma_2 & -\mu \end{pmatrix}$$

Compute the eigenvalues, we solve

$|cI - J_1|$ =0

$$\Rightarrow \begin{pmatrix} c+(\beta I+\mu) & 0 & \beta S & 0 & 0 \\ -\beta I & c+(k+\mu) & -\beta S & 0 & 0 \\ 0 & -(1-\delta)k & c+(\alpha+\gamma_1+\mu) & 0 & 0 \\ 0 & -\delta k & -\alpha & c+(\gamma_2+\mu) & 0 \\ 0 & 0 & -(1-q_1)\gamma_1 & -(1-q_2)\gamma_2 & c+\mu \end{pmatrix} = 0$$

$$\Rightarrow c = -(\mu-\beta I), -(k+\mu), -(\alpha+\gamma_1+\mu), -(\gamma_2+\mu), -\mu$$

The endemic state is locally asymptotically stable $\mu > \beta I$

Numerical Simulation

Parameter	values	unit	Reference
Λ	70	day^{-1}	Chowel, *et al.*(2015)
β	0.91	day^{-1}	Ebenezer, *et al.*(2016)
k	0.2	day^{-1}	Chowel, *et al.*(2015)
γ_1	0.17	day^{-1}	Ebenezer, *et al.*(2016)
γ_2	0.2	day^{-1}	Chowel, *et al.*(2015)
α	0.08	day^{-1}	Ebenezer, *et al.*(2016)
δ	0.6	day^{-1}	Chowel, *et al.*(2015)
q_1	0.7	day^{-1}	Chowel, *et al.*(2015)
q_2	0.63	day^{-1}	Chowel, *et al.*(2015)
μ	0.000498	day^{-1}	Ebenezer, *et al.*(2016)

The initial populations were assumed to be $(S(t), E(t), I(t), Q(t), R(t)) = (20, 25, 15, 25, 15)$

Deterministic model analysis

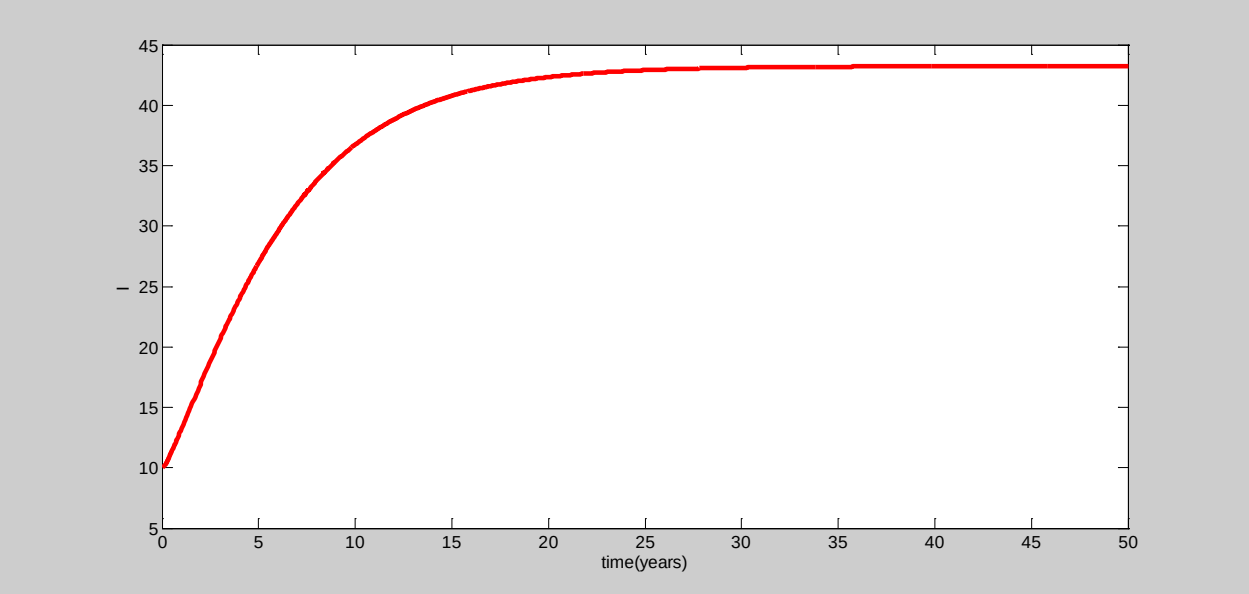

Fig. 2: Graph of Infected against time

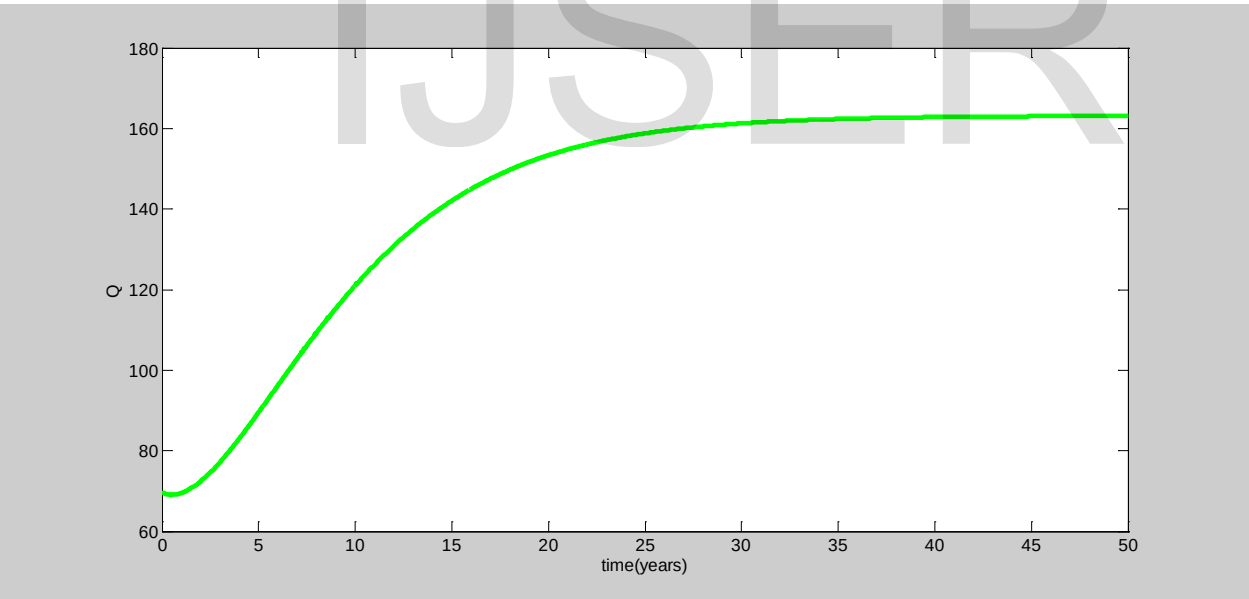

Fig. 3: Graph of Quarantined against time

From Fig. 2, the population of infectious individuals is shown over a period of time. It is seen that the disease will produce an epidemic and after some time, the infected class maintains a uniform increment. The quarantined population is also shown to behave in a similar manner over a period of time.

Stochastic model Analysis

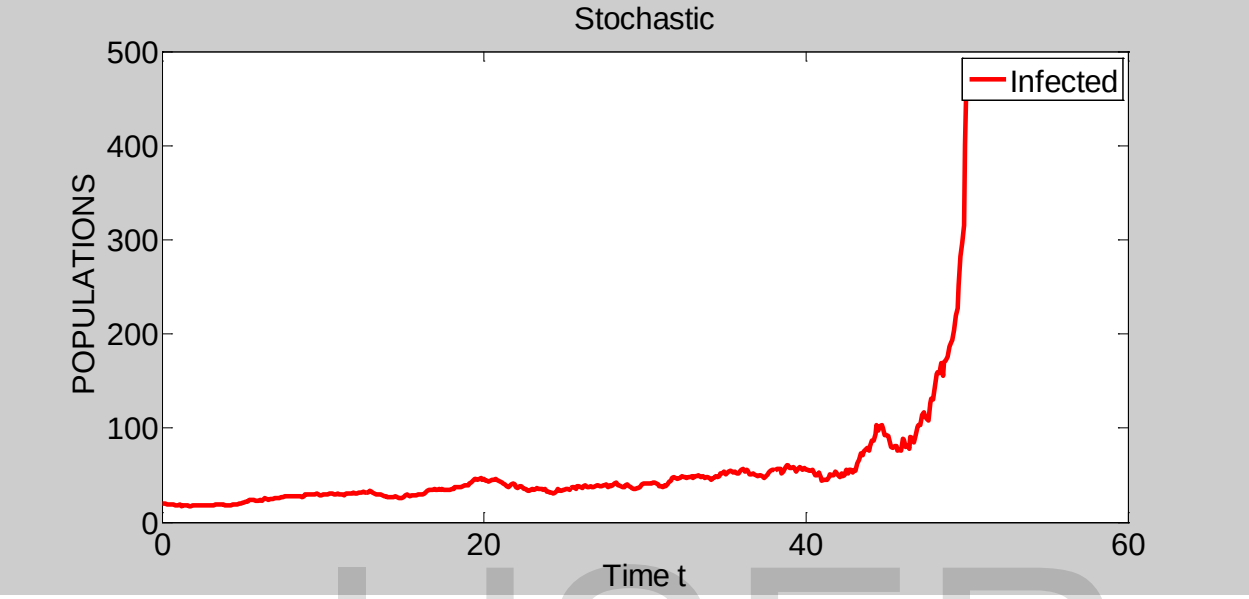

Fig. 4: Graph of Infected against time

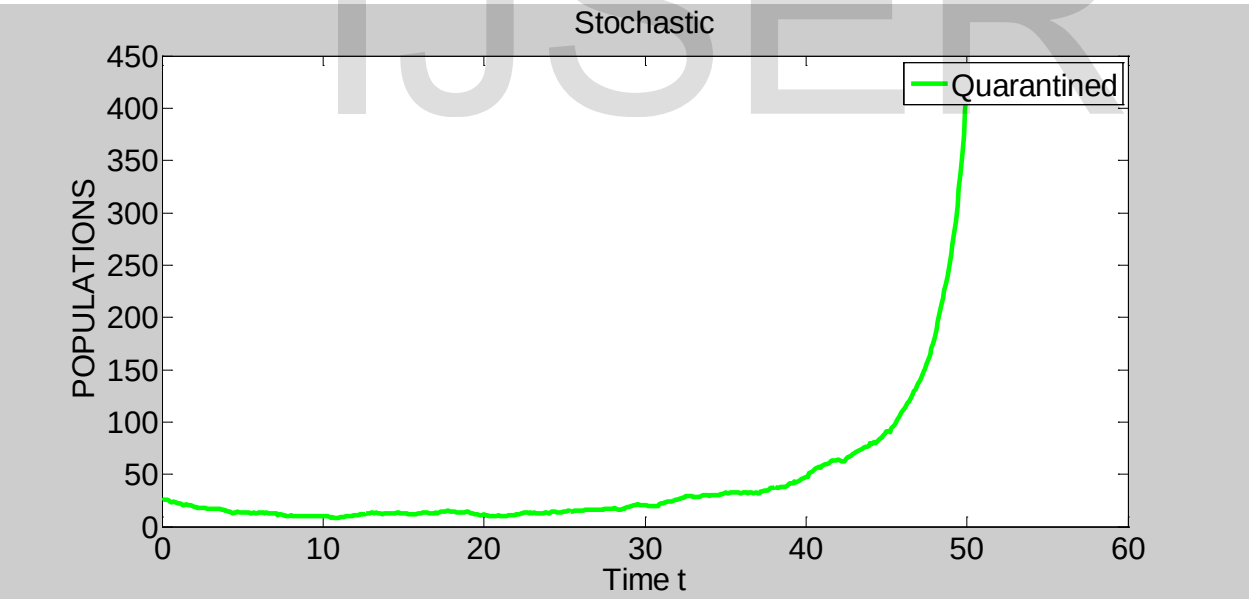

Fig. 5: Graph of Quarantined against time

The populations of infectious and quarantined individuals over a period of time are shown in figures 4 and 5 here, the two populations have below 50 individuals for a long period of time, but after 40 years. The result seem a contrast to what is obtainable in the deterministic model when the infected and quarantined populations increase rapidly at the onset of the disease. The deterministic gives a better description of the model. It considered environmental fluctuations which were not captured by the deterministic model.

2. Results And Conclusion

In this work, Chowell et. al (2015) work on modeling the case of early detection of Ebola virus is reviewed and extended to Stochastic model. A deterministic and Stochastic differential equation model is developed and investigated for the transmission dynamics of Ebola virus. The model, which is a multidimensional diffusion process, includes susceptible, exposed, infected and quarantined classes. This model is developed with an assumption that there can be a recovery for the infected population and after recovery the recovered individual do not stood the chance of been re-infected. We were able to see that the disease free steady state of our model is globally asymptotically stable. We also observed that there should be a bound at which Susceptible become infected. The endemic steady state showed that the disease will persist in the population if there is no bound on the interactions between the susceptible and infected population. It is also important to place the infected population in a quarantine, since removing the infected population will stop the susceptible from been infected.

Not only should mass vaccination exercise be encouraged to cover the majority of the population whenever there is an outbreak of the disease but also, measles prevention must be a public health priority. As a mathematical epidemiologist, I can tell you there is some good news in the Ebola epidemic ravaging West Africa. This Ebola is not spreading nearly as fast as some scourges of the past. Ebola was an interesting case study for our mathematical modeling of the spread of disease, as there were two relatively large and well-documented outbreaks in which the impact of efforts to control the virus was evident (the 1995 outbreak in Congo — formerly known as Zaire — and the 2000 outbreak in Uganda). It was intriguing — not to mention scary — to work on a disease that produced such horrific symptoms with a fatality rate above 50 percent. But I learned then that Ebola isn't the fastest-spreading disease in human history. The good news is that Ebola has a lower reproductive rate than measles in the pre-vaccination days or the Spanish flu. Our 2004 work, which produced the first estimates for Ebola's reproductive rate by using mathematical modeling and epidemiological data from the Central African outbreaks, found that each case of Ebola produced 1.3 to 1.8 secondary cases on average. This ongoing outbreak, a colleague and I recently found, has a reproductive rate that is about the same as the last one. It hasn't become more transmissible in the more than 10 years it was lying low — and humankind has experience in dealing with it. And the time that elapses between the first Ebola case and the generation of secondary cases is about two weeks. This should allow plenty of time to identify those who are sick and protect people who might come in contact with them. People with Ebola are contagious and able to transmit the virus only when they are showing symptoms, which occurs about a week after they are exposed to the virus. To break the chain of the current Ebola epidemic, our numbers show that health-care workers need to stop about 50 percent of infectious contacts by effectively isolating people who are infectious. (Vaccinating at least some of the population would be another option, but no licensed vaccine is available.) The trouble is that the countries suffering from outbreaks have weak health-care systems – perhaps too weak to halve the number of infectious contacts. These countries lack gloves, gowns, face masks and other essential supplies to protect nurses and doctors from infection, and they don't have an adequate surveillance system to catch and identify Ebola cases in a timely way. The number of doctors and health centers is small as well.

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Appendix

Deterministic Code:

```
clearall
global alpha Lambda beta k gamma_1 gamma_2 delta q_1 q_2 mu
alpha=0.2;
Lambda=40;
beta=0.91;
k=0.2;
%gamma_1=0.17;
gamma_2=0.2;
delta=0.6;
q_1=0.7;
q_2=0.63;
mu=0.0000498;
for gamma_1=0.1:0.1:0.9;
tspan =[0,50];
yzero = [50;40;10;75;20];
 [t,y]=ode45(@ebolatk,tspan,yzero);
plot(t,y(:,3),'r')
xlabel('time(years)'),ylabel('I')
holdon
end
```

Stochastic Code:

```
% A program for Ebola Model
% The Euler-Maruyama method is used for solving the SDEs
% y1 y2 y3 y4 and y5 are the different populations
% y10 y20 y30 y40 and y50 are the initial populations
% Problem-dependent statements are marked with a %***
% icase=1 corresponds to the deterministic problem
% nt is the number of steps
% h is the step size
% Accuracy generally increases as h decreases
clf
clear
foricase=2
cleartt
clearyp1
clearyp2
clearyp3
clearyp4
clearyp5
nsamp=100; %***
tmax=50; %***
nt=500; %***
y10=20; %***
```

```
y20=25; %***
y30=15; %***
y40=25; %***
y50=15; %***
if(icase==1) nsamp=1; end
h=tmax/nt;
hs=sqrt(h);
randn('state',20); %initiates the random number generator
te1=zeros(nsamp,1);
te2=zeros(nsamp,1);
te3=zeros(nsamp,1);
te4=zeros(nsamp,1);
te5=zeros(nsamp,1);
te6=zeros(nsamp,1);
jj1=0;
jj2=0;
jj3=0;
jj4=0;
jj5=0;
jj6=0;
forjj=1:nsamp
y1=y10;
y2=y20;
y3=y30;
y4=y40;
y5=y50;
yp1(1)=y1;
yp2(1)=y2;
yp3(1)=y3;
yp4(1)=y4;
yp5(1)=y5;
r=randn(nt+1,14);
nchk1=0;
nchk2=0;
nchk3=0;
nchk4=0;
nchk5=0;
n=0;
t=0;
chk=0;
tt(1)=0;
while (chk==0)
n=n+1;
t=t+h;
if(jj==nsamp) tt(n+1)=t; end
Lambda=0.070;
mu=0.0048;
alpha=0.03;
beta=0.01;
delta=0.2;
q_1=0.7;
q_2=0.63;
gamma_1=0.17;
gamma_2=0.2;
lambda_1=0.71;
lambda_2=0.82;
k=0.5;
f1=Lambda-beta*y3*y1-mu*y1;
f2=beta*y3*y1-(k+mu)*y2;
f3=(1-delta)*k*y2-(alpha+gamma_1+mu)*y3;
```

```
f4=delta*k*y2+alpha*y3-(gamma_2+mu)*y4;
f5=(1-q_1)*gamma_1*y3+(1-q_2)*gamma_2*y4-mu*y5;
g1=sqrt(delta)*r(n,1)-sqrt(mu*y1)*r(n,2)-sqrt(beta*y1*y3)*r(n,1);
g2=sqrt(beta*y1*y3)*r(n,4)-sqrt(mu*y2)*r(n,5)-sqrt((1-delta)*k)*r(n,6)-
sqrt(delta*k)*r(n,7);
g3=sqrt((1-delta)*k)*r(n,5)-sqrt(mu*y3)*r(n,7)-sqrt(alpha*y3)*r(n,8)-sqrt((1-
q_1)*gamma_1)*r(n,9);
g4=sqrt(delta*k)*r(n,6)+sqrt(alpha*y3)*r(n,8)-sqrt(mu*y4)*r(n,11)-sqrt((1-
q_2)*lambda_2)*r(n,12)-sqrt(q_2*gamma_2)*r(n,13);
g5=sqrt((1-q_1)*gamma_1)*r(n,9)+sqrt(2-q_2*gamma_2)*r(n,13)-sqrt(mu*y5)*r(n,14);
if(icase==1) g1=0; end
if(icase==1) g2=0; end
if(icase==1) g3=0; end
if(icase==1) g4=0; end
if(icase==1) g5=0; end
y1=y1+h*f1+hs*g1;
y2=y2+h*f2+hs*g2;
y3=y3+h*f3+hs*g3;
y4=y4+h*f4+hs*g4;
y5=y5+h*f5+hs*g5;
if(jj==nsamp) yp1(n+1)=y1; end
if(jj==nsamp) yp2(n+1)=y2; end
if(jj==nsamp) yp3(n+1)=y3; end
if(jj==nsamp) yp4(n+1)=y4; end
if(jj==nsamp) yp5(n+1)=y5; end
% This is Euler's approximation to the SDE
if (y1 < 1)
chk=1;
jj1=jj1+1;
te1(jj1)=t;
end
if (y2 < 1)
chk=1;
jj2=jj2+1;
te2(jj2)=t;
end
if (y3 < 1)
chk=1;
jj3=jj3+1;
te3(jj3)=t;
end
if (y4 < 1)
chk=1;
jj4=jj4+1;
te4(jj4)=t;
end
if (y5 < 1)
chk=1;
jj5=jj5+1;
te5(jj5)=t;
end
if (t >tmax)
chk=1;
jj6=jj6+1;
te6(jj6)=t;
chk=1;
end
end% end of while (chk==0) loop
end% end of for jj=1:nsamp loop
tp=0; tp1=0; tp2=0; tp3=0; tp4=0; tp5=0; tp6=0;
```

```
if(jj1 ~= 0) tp1=sum(te1)/jj1; end
if(jj2 ~= 0) tp2=sum(te2)/jj2; end
if(jj3 ~=0)  tp3=sum(te3)/jj3;end
if(jj4 ~= 0) tp4=sum(te4)/jj4; end
if(jj5 ~= 0) tp5=sum(te5)/jj5; end
if(jj6 ~= 0) tp6=sum(te6)/jj6; end
if(jj1+jj2+jj3+jj4+jj5~=0)tp=(sum(te1)+sum(te2)+sum(te3)+sum(te4)+sum(te4))/(jj1+jj2+jj3+
jj4+jj5); end
p1=jj1/nsamp;
p2=jj2/nsamp;
p3=jj3/nsamp;
p4=jj4/nsamp;
p5=jj5/nsamp;
p6=jj6/nsamp;
disp(' ')
if(icase==1) disp(' Deterministic Calculational Results'); end
if(icase==2) disp(' Stochastic Calculation Results'); end
disp(' icasensamp h tmax')
disp((sprintf(' %12.0f %12.0f %12.5f %12.2f',icase,nsamp,h,tmax)));
disp(' tp1 p1')
disp((sprintf(' %12.6f %12.6f', tp1, p1)));
disp(' tp2 p2')
disp((sprintf(' %12.6f %12.6f', tp2, p2)));
disp(' tp3 p3')
disp((sprintf(' %12.6f %12.6f', tp3, p3)));
disp(' tp4 p4')
disp((sprintf(' %12.6f %12.6f', tp4, p4)));
disp(' tp5 p5')
disp((sprintf(' %12.6f %12.6f', tp5, p5)));
disp(' tp6 p6')
disp((sprintf(' %12.6f %12.6f', tp6, p6)));
disp(' tp p1+p2+p3+p4+p5')
disp((sprintf(' %12.6f %12.6f', tp, p1+p2+p3+p4+p5)));
if(icase==1) title('Deterministic'); end
if(icase==2) title('Stochastic'); end
set(gca,'fontsize',18,'linewidth',1.5);
plot(tt,yp1,'r-')%,tt,yp2,'k-', tt,yp4,'r-',tt,yp3,'y-',tt,yp5,'g-')
xlabel('Time t')
ylabel(' POPULATIONS')
legend('Infected'),% 'Exposed','Infected','Quarantined','Recovered')
if(icase==2) title('Stochastic'); end
holdon
end% end of for icase=1:2 loop
holdoff
```