International Journal of Science and Research (IJSR)
ISSN: 2319-7064
Index Copernicus Value (2016): 79.57 | Impact Factor (2017): 7.296

Sensitivity Analysis of the SEIR Epidemic Compartment Model

Affi Osei, P

University of Ghana, Department of Statistics, P .O .Box LG25, Legon-Ghana

Abstract: ***In this paper, the SEIR epidemic compartment model was explored. The model showed two equilibria namely the disease - free equilibrium point (DFEP) and the endemic equilibrium point (EEP). The stability of these points was investigated into. It was shown that whenever the basic reproduction number was greater than unity ($R_0 > 1$) then the endemic equilibrium point is stable but if otherwise that is $R_0 \leq 1$ then the disease –free equilibrium point is stable. Sensitivity analysis was employed to investigate into the effect of the various parameters used in the model on the model output and it was revealed that the infection rate (α) and the recovery rate (d) has the most significant effect on the SEIR epidemic model output in relation to the rate at which the latent individual moves to the infectious class. This was evidenced by the value of the basic reproduction number and the proportions of the classes at the endemic equilibrium point when the parameters: infection rate(α), rate at which the latent individual moves to the infectious class(β) and the recovery rate were varied(d).***

Keywords: Disease – free equilibrium point, Endemic equilibrium point, Sensitivity analysis, Basic reproduction number, SEIR

1. Introduction

The transmission of infectious disease has always been of concerns and public health threat. As a result of this several authors have investigated the epidemic models in many ways. Many mathematicians (authors) focus their attention on the dynamics of the infectious diseases transmission in order to find condition to eradicate them [1]. For example, Greenhalgh considered the SEIR epidemic model that included density incidence in the rate of death [2]. Castillo – Chavez and Feng, also looked into global stability of an age – structure SEIR model for infectious disease and it application to optimal vaccination strategies by formulating an age – structure model for infectious disease transmission dynamics in a population subjected to a vaccination program [3]. In addition to the examples by the authors above sever mathematical models have been developed to study the spread of infectious disease such as measles, influenza, rubeola, and chicken pox[4]-[10].These infectious diseases cause recurrent epidemic out- breaks, and their associated transmission rates depend strongly on age-specific contact rates.

Very little or no work has been done to find out the effect of the parameters they used in their respective epidemic models, hence this paper seeks to employ a one way sensitivity analysis to investigate into the effect these parameters have on the output of the SEIR epidemic compartment model.

2. Methodology

SEIR compartment model is developed by dividing the host population into four (4) subgroups: Susceptible (S), Exposed (E), Infectious (I) and Recovery (R). Hence the total population in mathematical terms is: N = S + E+I+R.

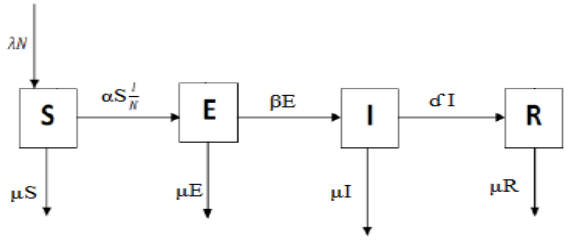

Figure 2.1: Flow chart of the SEIR model.

"λ" is the birth rate, "μ" is the death rate, "α" is the infection rate, "β" is the rate at which an individual moves from the exposed class to the infection class and "ɗ" is the recovery rate of the infectious individual. Assumptions of constant population (λ= μ) and permanent immunity was considered which resulted in the following ordinary differential equation:

$$\begin{aligned} \frac{ds}{dt} &= \lambda N - \mu S - \alpha S\frac{I}{N} \\ \frac{dE}{dt} &= \alpha S\frac{I}{N} - (\mu+\beta)E \\ \frac{dI}{dt} &= \beta E - (\mu+ɗ)I \\ \frac{dR}{dt} &= ɗI - \mu R \end{aligned} \qquad (2.1)$$

Re-scale the equation above by representing

$s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$ and $r = \frac{R}{N}$ where

s = susceptible proportion of the population, e= exposed proportion, i = infectious proportion and r= recovery proportion. The scaled equations are given below:

$$\begin{aligned} \frac{ds}{dt} &= \lambda - \mu s - \alpha si \\ \frac{de}{dt} &= \alpha si - (\mu+\beta)e \\ \frac{di}{dt} &= \beta e - (\mu+ɗ)i \end{aligned} \qquad (2.2)$$

$$\frac{dr}{dt} = \text{ɗ} i - \mu r$$

Where $s + e + i + r = 1 \Rightarrow r = 1 - s - e - i$ hence it is ok to study the system below instead of the systems in (2.2) [1].

$$\begin{aligned} \frac{ds}{dt} &= \lambda - \mu s - \alpha s i \\ \frac{de}{dt} &= \alpha s i - (\mu + \beta) e \\ \frac{di}{dt} &= \beta e - (\mu + \text{ɗ}) i \end{aligned} \quad (2.3)$$

2.1 Basic Reproduction Number (R_0)

Basic reproduction number (R_0) is the average number of secondary infections produce by one infective individual in a completely susceptible population at the disease – free equilibrium point. That is:

(R_0) = (Rate of secondary infections) × (Duration of infection) [11], [12]. Employing the next generation matrix approach resulted in the matrix below:

$$H - K = \begin{bmatrix} 0 & \alpha \\ 0 & 0 \end{bmatrix} - \begin{bmatrix} (\mu + \beta) & 0 \\ -\beta & (\mu + \text{ɗ}) \end{bmatrix}$$

"H" represents the matrix of infection rates and "K" also the matrix of transition rates.

$$H = \begin{bmatrix} 0 & \alpha \\ 0 & 0 \end{bmatrix} \text{ and } K = \begin{bmatrix} (\mu + \beta) & 0 \\ -\beta & (\mu + \text{ɗ}) \end{bmatrix}$$

But $|K| = (\mu + \beta)(\mu + \text{ɗ}) + 0$

$$\Rightarrow |K| = (\mu + \beta)(\mu + \text{ɗ})$$

$$K^{-1} = \frac{1}{(\mu + \beta)(\mu + \text{ɗ})} \begin{bmatrix} (\mu + \text{ɗ}) & 0 \\ \beta & (\mu + \beta) \end{bmatrix}$$

Hence $K^{-1} = \begin{bmatrix} \frac{1}{(\mu+\beta)} & 0 \\ \frac{\beta}{(\mu+\beta)(\mu+\text{ɗ})} & \frac{1}{(\mu+\text{ɗ})} \end{bmatrix}$

Multiplying the inverse of "K" above by the matrix "H" result in:

$$HK^{-1} = \begin{bmatrix} 0 & \alpha \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{(\mu+\beta)} & 0 \\ \frac{\beta}{(\mu+\beta)(\mu+\text{ɗ})} & \frac{1}{(\mu+\text{ɗ})} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{\alpha\beta}{(\mu+\beta)(\mu+\text{ɗ})} & \frac{\alpha}{(\mu+\text{ɗ})} \\ 0 & 0 \end{bmatrix}$$

Basic reproduction number(R_0) is defined as the spectral radius of HK^{-1} [1]. We denote this by $\rho(HK^{-1})$ hence:

$$R_0 = \rho(HK^{-1}) = \frac{\alpha\beta}{(\mu + \beta)(\mu + \text{ɗ})}$$

2.2 The Equilibrium Point

Two equilibrium points are considered in the study: the disease – free equilibrium (DFEP) where " i" = 0 and the endemic equilibrium (EEP) also i≠0. . To achieve this set the system of differential equations in (2.3) to zero and then solve for the values of s, e and i.

$$\begin{aligned} \frac{ds}{dt} = 0 &\Rightarrow \lambda - \mu s - \alpha s i = 0 \\ \frac{de}{dt} = 0 &\Rightarrow \alpha s i - (\mu + \beta) = 0 \\ \frac{di}{dt} = 0 &\Rightarrow \beta e - (\mu + \text{ɗ}) i = 0 \end{aligned} \quad (2.4)$$

2.2.1 Disease – Free Equilibrium Point

At the disease – free equilibrium point it is assumed that there is no infection or disease in the system hence $i = 0$.

$$\lambda - \mu s - \alpha s(0) = 0$$
$$\alpha s(0) - (\mu + \beta)(0) = 0$$
$$\beta(0) - (\mu + \text{ɗ})(0) = 0$$

These equations at the DFE reduces to

$$\lambda - \mu s = 0$$
$$\lambda = \mu s \Rightarrow s = \frac{\lambda}{\mu}$$

Hence at the DFEP $(s, e, i) = \left\{\frac{\lambda}{\mu}, 0, 0\right\} = \{1, 0, 0\}$ since the host population is constant and $\lambda = \mu$.

2.2.2 The Endemic Equilibrium point

The endemic equilibrium point shows that the disease will persist in the system in the steady state. Here solve the equations (3.4) to obtain s,e and i. But for easy identification s,e,i are represented by (s^*, e^*, i^*) at the steady state of the endemic respectively.

From $\beta e - (\mu + \text{ɗ}) i = 0 \Rightarrow i = \frac{\beta e}{u + \text{ɗ}}$

Similarly from $\alpha s i - (\mu + \beta) e = 0 \Rightarrow s = \frac{(\mu+\beta)}{\alpha i}$

Putting i above into s above gives

$$s = \frac{(\mu+\beta)e}{\alpha\left(\frac{\beta e}{u+\text{ɗ}}\right)} = \frac{(u+\beta)(\mu+\text{ɗ})e}{\alpha\beta e}$$

The e will cancel out to give $s^* = \frac{(\mu+\beta)(\mu+\text{ɗ})}{\alpha\beta}$

Also from $\alpha s i - (\mu + \beta) e = 0 \Rightarrow \alpha s i = (\mu + \beta) e$ and putting this into

$\lambda - \mu s - \alpha s i = 0$ yields $\lambda - \mu s - (\mu + \beta) e = 0$

$$\lambda - \mu s - (\mu + \beta) e = 0$$
$$\lambda - \mu s + (-\mu - \beta) e = 0$$
$$(-\mu - \beta) e = -\lambda + \mu s$$

But since $s = \frac{(\mu+\beta)(\mu+\text{ɗ})}{\alpha\beta}$ then

$$-(\mu + \beta) e = -(\lambda - \mu s)$$
$$\Rightarrow -(\mu + \beta) e = -\left\{\lambda - \mu \frac{(\mu + \beta)(\mu + \text{ɗ})}{\alpha\beta}\right\}$$

Dividing both sides by $-(\mu + \beta)$ gives

$$e^* = \frac{\lambda\alpha\beta - \mu(\mu+\beta)(\mu+\text{ɗ})}{\alpha\beta(\mu+\beta)}$$

Also since $i = \frac{\beta e}{\mu+\text{ɗ}}$ and e^* above then

$$i = \frac{\beta}{(\mu+\text{ɗ})}\left(\frac{\lambda\alpha\beta - \mu(\mu+\beta)(\mu+\text{ɗ})}{\alpha\beta(\mu+\beta)}\right)$$ β and $(\mu + \text{ɗ})$ will cancel out to result in $i^* = \frac{\lambda\alpha\beta - \mu(\mu+\beta)}{\alpha(\mu+\beta)}$ hence at the endemic equilibrium point we have:

$$(s^*, e^*, i^*) = \left(\frac{(\mu+\beta)(\mu+\text{ď})}{\alpha\beta}, \frac{\lambda\alpha\beta - \mu(\mu+\beta)(\mu+\text{ď})}{\alpha\beta(\mu+\beta)}, \frac{\lambda\alpha\beta - \mu(\mu+\beta)}{\alpha(\mu+\beta)}\right)$$

2.3 Stability of the Equilibrium Points

To study the stability of the equilibrium points obtained above consider the linearization of the system of equation (3.3) about the DFE by taking the Jacobian of them [1].

$$J(s,e,i) = \begin{bmatrix} -\mu - \alpha i & 0 & -\alpha s \\ \alpha i & -(\mu+\beta) & \alpha s \\ 0 & \beta & -(\mu+\text{ď}) \end{bmatrix}$$

2.3.1 Stability of the Disease – free Equilibrium Point

Theorem 2.1: the disease – free equilibrium point of the system (3.3) is asymptotically stable if and only if $R_0 \leq 1$ and unstable if $R_0 > 1$.

Proof:
We obtained the Jacobian at DFEP that is (s,e,i) = (1,0,0).

$$J(s,e,i) = \begin{bmatrix} -\mu & 0 & -\alpha \\ 0 & -(\mu+\beta) & \alpha \\ 0 & \beta & -(\mu+\text{ď}) \end{bmatrix}$$

We let $J(s,e,i)_{DFE} = J(s,e,i)$ the Jacobian matrix at the disease – free equilibrium and solve the characteristics equation of $J(s,e,i)_{DFE}$. This can be achieved by solving the relation: $J(s,e,i)_{DFE} - I\lambda$ where "I" is a unit matrix and it has order 3 by 3 since $J(s,e,i)_{DFE}$ also has same order.

$$I\lambda = \lambda\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} = \begin{bmatrix} \lambda & 0 & 0 \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{bmatrix}$$

$$J(s,e,i)_{DFE} - I\lambda = \begin{bmatrix} -\mu & 0 & -\alpha \\ 0 & -(\mu+\beta) & \alpha \\ 0 & \beta & -(\mu+\text{ď}) \end{bmatrix} - \begin{bmatrix} \lambda & 0 & 0 \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{bmatrix}$$

$$J(s,e,i)_{DFE} - I\lambda = \begin{bmatrix} -(\mu+\lambda) & 0 & -\alpha \\ 0 & -\{(\mu+\beta)+\lambda\} & \alpha \\ 0 & \beta & -\{(\mu+\text{ď})+\lambda\} \end{bmatrix}$$

From this we obtained characteristics equation by finding the determinant of the above matrix and equate it to zero.

$$|J(s,e,i)_{DFE} - I\lambda| = \begin{vmatrix} -(\mu+\lambda) & 0 & -\alpha \\ 0 & -\{(\mu+\beta)+\lambda\} & \alpha \\ 0 & \beta & -\{(\mu+\text{ď})+\lambda\} \end{vmatrix}$$

$$= -(\mu+\lambda)\begin{vmatrix} -(\mu+\beta+\lambda) & \alpha \\ \beta & -(\mu+\text{ď}+\lambda) \end{vmatrix} - 0\begin{vmatrix} 0 & \alpha \\ 0 & -(\mu+\text{ď}+\lambda) \end{vmatrix} - \alpha\begin{vmatrix} 0 & -(\mu+\beta+\lambda) \\ 0 & \beta \end{vmatrix}$$

$$= -(\mu+\lambda)[(\mu+\beta+\lambda)(\mu+\text{ď}+\lambda) - \alpha\beta]$$

But since $|J(s,e,i)_{DFE} - I\lambda| = 0$ then

$$-(\mu+\lambda)[(\mu+\beta+\lambda)(\mu+\text{ď}+\lambda) - \alpha\beta] = 0$$

Expanding the relation above results in:

$$-(\mu+\lambda)[\mu^2 + \mu\text{ď} + \mu\lambda + \mu\beta + \beta\text{ď} + \beta\lambda + \lambda\mu + \lambda\text{ď} + \lambda^2 - \alpha\beta] = 0$$

Expanding the above equation again and grouping like terms gives:

$$\lambda^3 + (3\mu+\beta+\text{ď})\lambda^2 + (3\mu^2 + 2\mu\text{ď} + 2\beta\mu + \beta\text{ď} - \alpha\beta)\lambda + (\mu^2 + \mu^2\text{ď} + \mu^2\beta + \mu\beta\text{ď} - \mu\alpha\beta) = 0$$

Let Y, Z be the coefficients of λ^2, λ and A be the constant term hence

$$Y = 3\mu + \beta + \text{ď}$$

$$Z = 3\mu^2 + 2\mu\text{ď} + 2\beta\mu + \beta\text{ď} - \alpha\beta$$

$$A = \mu^2 + \mu^2\text{ď} + \mu^2\beta + \mu\beta\text{ď} - \mu\alpha\beta$$

And the characteristic equation becomes:

$$\lambda^3 + Y\lambda^2 + Z\lambda + A$$

From Routh-Hurwitz Stability criterion analysis if $Y > 0, A > 0$ and $YZ - A > 0$ holds then all the roots of the characteristic equation has negative real part and hence the equilibrium point (DFE) point is stable.

2.3.2 Stability of the Endemic equilibrium

Theorem 2.2: The endemic equilibrium of system (3.3) is also asymptotically stable when $R_0 > 1$ and unstable when $R_0 \leq 1$.

Proof: At the endemic equilibrium it has been shown that: $s^* = \frac{(\mu+\beta)(\mu+\text{ď})}{\alpha\beta}$, $e^* = \frac{\lambda\alpha\beta - \mu(\mu+\beta)(\mu+\text{ď})}{\alpha\beta(\mu+\beta)}$ and $i^* = \frac{\lambda\alpha\beta - \mu(\mu+\beta)}{\alpha(\mu+\beta)}$ hence the Jacobian matrix at the endemic equilibrium point is

$$J(s^*, e^* i^*) = \begin{bmatrix} -\mu - \alpha i^* & 0 & -\alpha s^* \\ \alpha i^* & -(\mu+\beta) & \alpha s^* \\ 0 & \beta & -(\mu+\text{ď}) \end{bmatrix}$$

Let $J(s^*, e^*, i^*)EE$ be the Jacobian matrix at the endemic equilibrium and then solved the characteristic equation of $J(s^*, e^*, i^*)EE$ by finding the determinant of $J(s^*, e^*, i^*)EE - \lambda I$ and setting the results to zero. I is a three by three unit matrix hence $I = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$ and

$$I\lambda = \lambda\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} = \begin{bmatrix} \lambda & 0 & 0 \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{bmatrix}$$

$$J(s^*, e^*, i^*)EE - \lambda I = \begin{bmatrix} -\mu - \alpha i^* & 0 & -\alpha s^* \\ \alpha i^* & -(\mu+\beta) & \alpha s^* \\ 0 & \beta & -(\mu+\text{ď}) \end{bmatrix} - \begin{bmatrix} \lambda & 0 & 0 \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{bmatrix}$$

$$= \begin{bmatrix} -(\mu+\alpha i^*+\lambda) & 0 & -\alpha s^* \\ \alpha i^* & -(\mu+\beta+\lambda) & \alpha s^* \\ 0 & \beta & -(\mu+\text{ď}+\lambda) \end{bmatrix}$$

$$|J(s^*, e^*, i^*)EE - \lambda I| = \begin{vmatrix} -(\mu+\alpha i^*+\lambda) & 0 & -\alpha s^* \\ \alpha i^* & -(\mu+\beta+\lambda) & \alpha s^* \\ 0 & \beta & -(\mu+\text{ď}+\lambda) \end{vmatrix}$$

$$= -(\mu+\alpha i^*+\lambda)\begin{vmatrix} -(\mu+\beta+\lambda) & \alpha s^* \\ \beta & -(\mu+\text{ď}+\lambda) \end{vmatrix} - 0\begin{vmatrix} \alpha i^* & \alpha s^* \\ 0 & -(\mu+\text{ď}+\lambda) \end{vmatrix} - \alpha s^*\begin{vmatrix} \alpha i^* & -(\mu+\beta+\lambda) \\ 0 & \beta \end{vmatrix}$$

$$= -(\mu+\alpha i^*+\lambda)[(\mu+\beta+\lambda)(\mu+\text{ď}+\lambda) - \beta\alpha s^*] - \alpha s^*\beta\alpha i^*$$

Expanding the equation above and setting it to zero gives:

$$\lambda^3 + (3\mu + \alpha i^* + \beta + \text{d})\lambda^2 + \begin{pmatrix} 2\mu^2 + 2\mu\beta + \mu\text{d} + 2\alpha i^*\mu + \alpha i^*\beta \\ +\alpha i^*\text{d} + \beta\text{d} - \beta\alpha s^* \end{pmatrix}\lambda + \mu^2 + \beta\mu^2 + \mu\beta\text{d}$$
$$-\mu\beta\alpha s^* + \alpha i^*\mu^2 + \alpha i^*\beta\mu + \alpha i^*\beta\text{d} = 0$$

Let Y, Z represents the coefficient of λ^2 and λ respectively and A is the constant term in the polynomial above.
Then

$$Y = 3\mu + \alpha i^* + \beta + \text{d}$$
$$Z = 2\mu^2 + 2\mu\beta + \mu\text{d} + 2\alpha i^*\mu + \alpha i^*\beta + \alpha i^*\text{d} + \beta\text{d} - \beta\alpha s^*$$
$$A = \mu^2 + \beta\mu^2 + \mu\beta\text{d} - \mu\beta\alpha s^* + \alpha i^*\mu^2 + \alpha i^*\beta\mu + \alpha i^*\beta\text{d}$$

The polynomial (characteristics equation) above then becomes $\lambda^3 + Y\lambda^2 + Z\lambda + A = 0$.

Using the Routh-Hurwitz stability analysis if the conditions $Y > 0, A > 0$ and $YZ - A > 0$ holds then all the zeros of the characteristics equation have negative real part and hence the equilibrium (endemic) point is stable.

3. Sensitivity Analysis

This analysis helps to determine among which of the parameters used in the model is or are most responsible for generating the variability in the value of the mode's outputs over time. One way sensitivity analysis was employed. That is each parameter is varied one at a time to investigate the impact on the results. But since we considered a closed system that is the vital dynamics (birth and death) were assumed to be the same we will not consider the two in the sensitivity analysis. Only the following parameters: α, β, d were considered.

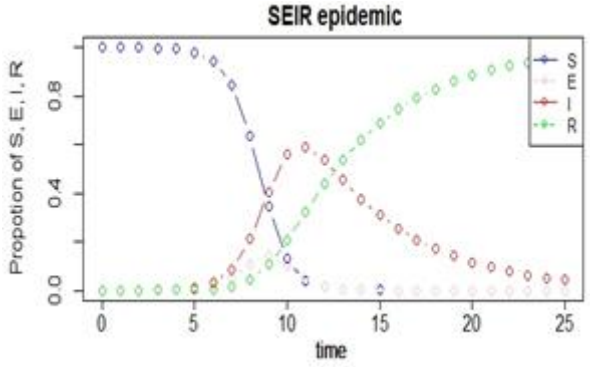

Figure 1: SEIR curves with λ=μ= 0.03, α=0.2, β=2, d=0.2, and R_0 = 10 with

$$(s^*, e^*, i^*, r^*)$$
$$= (6.997^{-05}, 3.4977e^{-06}, 0.04241, 0.95753)$$

The initial values of the classes are:
{S(0), E(0), I(0), R(0) }= {9990, 9, 1, 0}.

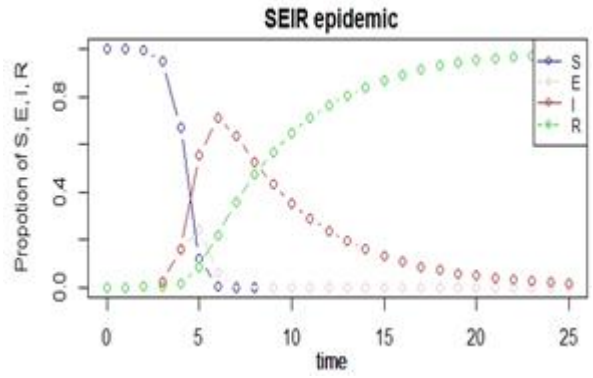

Figure 2: the SEIR curves with the infection rate increased from 0.2 to 0.5. That is λ=μ= 0.03, α=0.5, β=0.2, d=2, and R_0 = 25 was presented

with (s^*, e^*, i^*, r^*)
$= (2.355e^{-11}, 4.899e^{-08}, 0.01763, 0.98237)$

The initial values of the classes are:
{S(0), E(0), I(0), R(0) }= {9990, 9, 1, 0}.

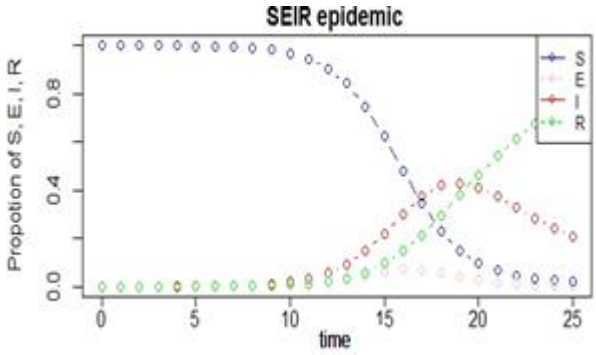

Figure 3: this figure shows the SEIR epidemic curve when the infection rate was reduced from 0.2 to 0.1. Parameter values for the curves above λ=μ= 0.03, α=0.5, β=0.2, d=2, and R_0 = 5.

$$(s^*, e^*, i^*, r^*)$$
$$= (0.0211, 2.6889e^{-03}, 0.20403, 0.7723)$$

The initial values of the classes are:
{S(0), E(0), I(0), R(0) }= {9990, 9, 1, 0}.

Using figure 1 as the basis for the sensitivity analysis it was observed that there was a significant change between figure 1 and figure 2, 3. Hence figure 2 and 3 are compared in relation to figure 1. It was observed that increasing the infection rate reduces the proportion of the susceptible population as early as possible (figure 2) as compared to when it was increased (figure 3). The proportion of the infectious class peaks early and very steep when the infection rate was increased (figure 2) compared to when it was reduced (figure 3).Also the recovery proportion rosed early in figure 2 when the infection rate was increased in relation to figure 3 when the infection rate was reduced.

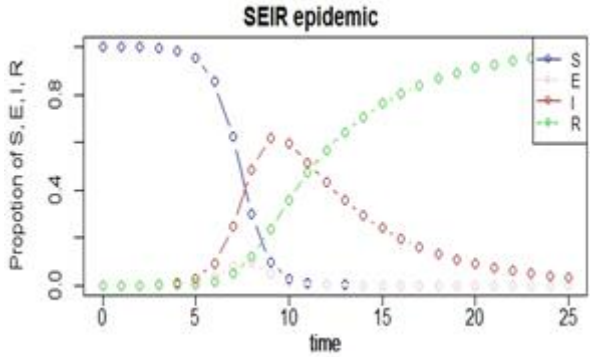

Figure 4: increasing the rate at which the latent individuals move to the infectious class. T hat is from 2 to 3.3. SEIR curves with λ=μ= 0.03, α=0.2, β=3.3, ḋ=0.2, and R_0 = 10 with

$$(s^*, e^*, i^*, r^*) = (6.3428^{-05}, 1..29252e^{-06}, 0.03245, 0.967482)$$

The initial values of the classes are:
{S(0), E(0), I(0), R(0) }= {9990, 9, 1, 0}.

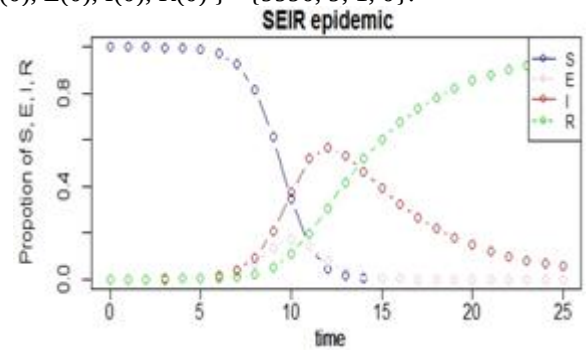

Figure 5: reducing the rate at which the latent individuals move to the infectious class. T hat is from 2 to 1.4. SEIR curves with λ=μ= 0.03, α=0.2, β=1.4, ḋ=0.2, and R_0 = 10 with

$$(s^*, e^*, i^*, r^*) = (7.8559^{-05}, 7.93623e^{-06}, 0.05396, 0.945938)$$

Comparing figure 4 and 5 to figure 1, it was realized that there was no significant changes in the proportions of the classes. The basic reproduction number is an evidence of that. The only insignificant changes which occurred were the proportion of the infectious. It increased slightly when the rate at which the individual move from latent class to infectious class was increased and reduced when the rate was reduced. The proportions at the endemic equilibrium indicate that.

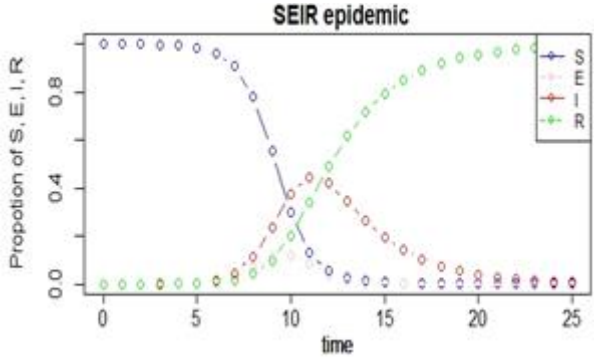

Figure 6: increasing the rate at which the infectious individuals move to the recovery class. That is from o.2 to 0.33 hence SEIR curves with λ=μ= 0.03, α=0.2, β=2, ḋ=0.33, and R_0 = 6 with

$$(s^*, e^*, i^*, r^*) = (0.00265, 2.484e^{-06}, 0.00775, 0.98957)$$

The initial values of the classes are:
{S(0), E(0), I(0), R(0) }= {9990, 9, 1, 0}.

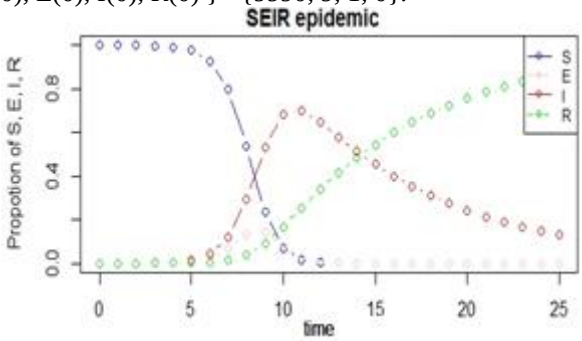

Figure 7: reducing the rate at which the infectious individuals move to the recovery class. That is from 0.2 to 0.125 hence SEIR curves with λ=μ= 0.03, α=0.2, β=2, ḋ=0.125, and R_0 =1 6 with

$$(s^*, e^*, i^*, r^*) = (9.13909e^{-06}, 1.26814e^{-06}, 0.13015, 0.869847)$$

The initial values of the classes are:
{S(0), E(0), I(0), R(0) }= {9990, 9, 1, 0}.

Comparing both figures (6 and 7) to the base figure (1), it is observed that increasing or decreasing the value of the recovery rate "ḋ" has a significant impact on the output of the model. This impact is shown both in the population size of the infectious class and the value of the basic reproduction number R_0 (6 and 16 respectively). When the recovery rate was increased the proportion of the infectious class reduced (compare figure 6 to figure 1) and when decreased it was the proportion of the infectious class increased (compare figure 7 to figure 1).

4. Conclusion

From this study it can be concluded that both the infection rate "α" and the recovery rate "ḋ" have the most significant effect on the output of the SEIR compartment epidemic model whiles the rate at which the individual move from the latent class to the infectious class do not have that much effect on the output of the model. This is evidence by both the value of the basic reproduction number and the proportions of the classes at the endemic equilibrium point when 25 years was considered as the time frame.

References

[1] Tom Britton, Desire Ouedraogo, SEIRS epidemics with disease fatalities in growing populations, *Mathematical Biosciences* (2017), doi: 10.1016/j.mbs.2017.11.006

[2] Greenhalgh, D. (1990): An epidemic model with a density-dependent death rate. IMA J. Math. Appl. Med. Biol. 7, pp 1-26.
[3] Castillo – Chavez and Feng (1998): Mathematical models for the disease dynamics of tuberculosis. Biometrics Unit Cornell University Ithaca, NY 14853, U.S.A.
[4] Castillo-Chavez, C., and Feng, Z. 1998. Global stability of an age- structure model for TB and its applications to optimal vaccination strategies, Math. Biosci. 151, 135_154.
[5] Dietz, K. 1979. Epidemiologic interference of virus populations, J. Math. Biol. 8, 291_300.
[6] Dietz, K., and Schenzle, D. 1985. Proportionate mixing models for age-dependent infection transmission, J. Math. Biol. 22, 117_120.
[7] Hethcote, H. W. 1976. Qualitative analysis for communicable disease models, Math. Biosci. 28, 335_356.
[8] Hethcote, H. W., Stech, H. W., and Van Den Driessche, P. 1981. Peri- odicity and stability in epidemic models: A survey, in ``Differential Equations and Applications in Ecology, Epidemics and Population Problems" (S. Busenberg and K. L. Cooke, Eds.), pp. 65_82, Academic Press, New York.
[9] Anderson, R. M., and May, R. M. 1982. ``Population Biology of Infectious Diseases," Springer-Verlag, Berlin_Heidelberg_New York.
[10] Anderson, R. M. 1982. ``Population Dynamics of Infectious Diseases,"Chapman 6 Hall, London_New York.
[11] Roy M. Anderson and Robert M. Mary.Infectious Disease of Humans. Oxford University Press, Oxford, 1991.
[12] Odo Diekmann and J.A.P.Heesterbeek. Mathematical epidemiology of infectious disease. Wiley series in mathematical and computation biology. John wiley and son,west Sussex, England, 2000.

Author Profile

Prince Osei Affi holds BSc. Mathematical Science (Option: Statistics), Diploma in Education and MPhil. Statistics.