

---

# Global Stability Analysis of the SEIR Deterministic Model in the Presence of Treatment at the Latent Period

Prince Osei Affi

Department of Mathematics and Statistics, University of Ghana, Legon, Ghana

**Email address:**

Pyrinefas1434@gmail.com, posei\_affi001@st.ug.edu.gh

**To cite this article:**

Prince Osei Affi. Global Stability Analysis of the SEIR Deterministic Model in the Presence of Treatment at the Latent Period. *Mathematics Letters*. Vol. 4, No. 4, 2018, pp. 67-73. doi: 10.11648/j.ml.20180404.12

**Received:** November 5, 2018; **Accepted:** November 19, 2018; **Published:** January 3, 2019

---

**Abstract:** In this paper, the objective was to find out the influence of introducing treatment at the latent period of disease (infectious) transmission as a result the global dynamics of the SEIR epidemic model with the introduction of treatment at the latent period is explored. The basic reproduction number is estimated. Whenever the basic reproduction number is not larger than unity ( $R_0 \leq 1$ ) then the disease – free equilibrium is globally stable and the disease dies out. But when the basic reproduction number is larger than unity ( $R_0 > 1$ ), then there exist the endemic equilibrium point which is stable and hence the disease will persist. This was demonstrated with a tuberculosis data obtained from Amansie west district health directorate in the Ashanti region of Ghana. In this instance the endemic equilibrium point was found to be stable. The sensitivity analysis also revealed that increasing the treatment rate introduced at the latent period will reduce the value of the basic reproduction number.

**Keywords:** Basic Reproduction Number, Disease – Free Equilibrium, Endemic Equilibrium Point

---

## 1. Introduction

The history of mathematical models in epidemiology has been in existence since the eighteen century [1]. There has been tremendous improvement in the development of the models since then. Below are some of the studies that made use of mathematical models in epidemiology: [2-5]. Several mathematical models have been developed, analysed and applied to many infectious diseases (tuberculosis, HIV, influenza malaria etc). Mathematical models have become significant tools in studying the transmission and control dynamics of infectious diseases.

Currently it has been observed that mathematical models play a major role in policy making. The most important results associated with mathematical epidemiological model is the behavior of the threshold called the basic reproduction number. This threshold represents the average number of secondary infections produced by one infectious individual [7]. If this threshold is less than one then the disease will die out but if greater than one then there will be an endemic that is the disease will persist [8,10]. The largely formulated mathematical epidemiology models are the compartment (deterministic) models where the population is divided into compartment with assumptions about the nature and time rate

of transfer from one compartment to another compartment.

SEIR model is presented in this paper. Some related studies were done on SEIR model [11-16]. Since treatment plays a major role in transmission dynamics of infectious disease [17-20]. There is the need to investigate into which period of the disease (infectious) transmission is appropriate to introduce treatment. This paper has explored the stability of the equilibria (disease – free and endemic) in the presence of treatment at the latent stage. That is investigating the steady state stability of the equilibria when treatment is introduced at the latent stage.

This study is organised as follows: in section 2, mathematical model is formulated and the corresponding basic reproduction number is estimated. In section 3, Equilibria points are studied. The stability of the Equilibria points are investigated in section 4, the model analysis and result is presented in section 5 and the final section which is the section 5 present the conclusion.

## 2. The Mathematical Model and the Basic Reproduction Number

The SEIR model is developed by dividing the host population into four classes that is: susceptible (S), exposed

(E), infectious (I) and recovery (R) (total population  $N = S + E + I + R$ ).

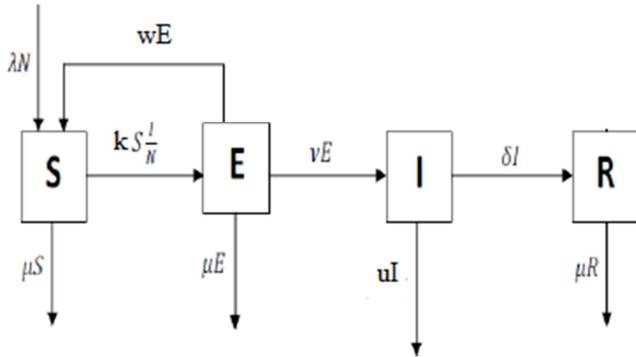


Figure 1. The flow chart of the SEIR deterministic model in the presence of treatment at the latent class.

2.1. Model Equations

Assuming that the epidemic is transmitted in a close system then the assumption of constant population size holds (birth rate equal to death rate that is  $\lambda = \mu$ ) see [6]. The above stated assumptions lead to the following ordinary differential equations to indicate the rate of change from one class to the other class. Below are the systems of the differential equations:

$$\begin{aligned} \frac{dE}{dt} &= \lambda N - \mu S - \frac{\kappa SI}{N} + \omega E \\ \frac{dE}{dt} &= \frac{\kappa SI}{N} + (\omega + \mu + v)E \\ \frac{dI}{dt} &= vE - (\mu + \delta)I \quad (1) \\ \frac{dR}{dt} &= \delta I - \mu R \end{aligned}$$

Rescaling the equation (1) by representing  $s = \frac{S}{N}, e = \frac{E}{N}, i = \frac{I}{N}$  and  $r = \frac{R}{N}$  where “s” is the proportion of susceptible population, “e” is exposed proportion of the population, “i” also the proportion of the infectious population and “r” the proportion of the recovery population gives the equation below:

$$\begin{aligned} \frac{ds}{dt} &= \lambda - \mu s - \kappa si + \omega e \\ \frac{de}{dt} &= \kappa si - (\omega + \mu + v)e \\ \frac{di}{dt} &= ve - (\mu + \delta)i \quad (2) \\ \frac{dr}{dt} &= \delta i - \mu r \end{aligned}$$

Where  $s + e + i + r = 1$

But since  $r = 1 - s - e - i$ , it is enough to study the system below as in Tom et al. 2017. [9]

$$\begin{aligned} \frac{ds}{dt} &= \lambda - \mu s - \kappa si + \omega e \\ \frac{de}{dt} &= \kappa si - (\omega + \mu + v)e \\ \frac{di}{dt} &= ve - (\mu + \delta)i \end{aligned} \quad (3)$$

2.2. Computation of the Basic Reproduction Number ( $R_0$ ) Using the Next Generation Matrix

Basic reproduction number is the average number of secondary infections produced by one infectious individual in a completely susceptible population at disease – free equilibrium [2-4].

Basic Reproduction number ( $R_0$ ) = (Rate of secondary infection) X (Duration of infection)

It is assumed that “S” is near disease – free equilibrium hence linearizing the equation (3) for the exposed and infectious results in the next generation matrix as used in [8].

$$A - F = \begin{pmatrix} 0 & \kappa \\ 0 & 0 \end{pmatrix} - \begin{pmatrix} (\omega + \mu + v) & 0 \\ -v & (\mu + \delta) \end{pmatrix}$$

A = matrix of infection and F = matrix of transition rate

$$A = \begin{pmatrix} 0 & \kappa \\ 0 & 0 \end{pmatrix} \text{ and } F = \begin{pmatrix} (\omega + \mu + v) & 0 \\ -v & (\mu + \delta) \end{pmatrix}$$

But since  $|F| = (\omega + \mu + v)(\mu + \delta)$  then

$$\begin{aligned} F^{-1} &= \frac{1}{(\omega + \mu + v)(\mu + \delta)} \begin{pmatrix} (\mu + \delta) & 0 \\ v & (\omega + \mu + v) \end{pmatrix} \\ &= \begin{pmatrix} \frac{1}{(\omega + \mu + v)} & 0 \\ \frac{v}{(\omega + \mu + v)(\mu + \delta)} & \frac{1}{(\mu + \delta)} \end{pmatrix} \end{aligned}$$

$$\begin{aligned} AF^{-1} &= \begin{pmatrix} 0 & \kappa \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\omega + \mu + v)} & 0 \\ \frac{v}{(\omega + \mu + v)(\mu + \delta)} & \frac{1}{(\mu + \delta)} \end{pmatrix} \\ &= \begin{pmatrix} \frac{\kappa v}{(\omega + \mu + v)(\mu + \delta)} & \kappa \\ 0 & 0 \end{pmatrix} \end{aligned}$$

Basic reproduction number is the spectral radius of  $AF^{-1}$  [8].

$$\text{Hence } R_0 = \frac{\kappa v}{(\omega + \mu + v)(\mu + \delta)}$$

3. The Equilibrium Point

Two equilibrium points are considered in this study: disease-free and endemic equilibrium points. To obtain these points the equation (3) are set to zero and the values of the proportions (s, e, and i) are solve for.

$$\begin{aligned} \frac{ds}{dt} = 0 &\Rightarrow \lambda - \mu s - \kappa si + \omega e = 0 \\ \frac{de}{dt} = 0 &\Rightarrow \kappa si - (\omega + \mu + \nu)e = 0 \\ \frac{di}{dt} = 0 &\Rightarrow \nu e - (\mu + \delta)i = 0 \end{aligned} \tag{4}$$

**3.1. Disease-free Equilibrium Point**

At this point it is assumed that there is no disease or infection in the system hence  $i = 0, e = 0$ . Putting  $i = 0$  and  $e = 0$  into equation (4) results in:

$$\begin{aligned} \lambda - \mu s - \kappa s(0) + \omega(0) &= 0 \\ \kappa s(0) - (\omega + \mu + \nu)(0) &= 0 \\ \nu(0) - (\mu + \delta)(0) &= 0 \end{aligned}$$

This simplifies to:

$$\begin{aligned} \lambda - \mu s &= 0 \\ \lambda = \mu s &\Rightarrow s = \frac{\lambda}{\mu} \end{aligned}$$

Therefore at the DFE  $(s, e, i) = \left(\frac{\lambda}{\mu}, 0, 0\right) = \{1, 0, 0\}$  since

$$\begin{aligned} \lambda - \mu s + \omega e - (\omega + \mu + \nu)e &= 0 \\ \lambda - \mu s + (-\mu - \nu)e &= 0 \\ (-\mu - \nu)e &= -\lambda + \mu s \end{aligned}$$

But since  $s = \frac{(\omega + \mu + \nu)(\mu + \delta)}{\kappa \nu}$  then

$$-(\mu + \nu)e = -(\lambda - \mu s) \Rightarrow -(\mu + \nu)e = -\left\{ \lambda - \mu \frac{(\omega + \mu + \nu)(\mu + \delta)}{\kappa \nu} \right\}$$

Dividing both sides by  $-(\mu + \nu)$  gives  $e^* = \frac{\lambda \kappa \nu - \mu(\omega + \mu + \nu)(\mu + \delta)}{\kappa \nu(\mu + \nu)}$

From  $i = \frac{\nu e}{\mu + \delta}$  and  $e^*$  above then  $i = \frac{\nu}{(\mu + \delta)} \left( \frac{\lambda \kappa \nu - \mu(\omega + \mu + \nu)(\mu + \delta)}{\kappa \nu(\mu + \nu)} \right) \nu \Rightarrow i^* = \frac{\lambda \kappa \nu - \mu(\omega + \mu + \nu)}{\kappa(\mu + \nu)}$  hence at the endemic equilibrium point we have:

$$(s^*, e^*, i^*) = \left\{ \frac{(\omega + \mu + \nu)(\mu + \delta)}{\kappa \nu}, \frac{\lambda \kappa \nu - \mu(\omega + \mu + \nu)(\mu + \delta)}{\kappa \nu(\mu + \nu)}, \frac{\lambda \kappa \nu - \mu(\omega + \mu + \nu)}{\kappa(\mu + \nu)} \right\}$$

**4. Stability of the Equilibrium Point**

To study the stability of the equilibrium points obtained above consider the linearization of the system of equation (4) about the disease-free equilibrium point by taking the Jacobian of them as in [6].

$$J(s, e, i) = \begin{pmatrix} -\mu - \kappa i & \omega & -\kappa s \\ \kappa i & -(\omega + \mu + \nu) & \kappa s \\ 0 & \nu & -(\mu + \delta) \end{pmatrix}$$

**4.1. Stability of the Disease – Free Equilibrium Point**

Theorem 3.1: The disease – free equilibrium point of the

the host population is constant ( $\lambda = \mu$ ).

**3.2. The Endemic Equilibrium Point**

This point indicates that the disease or the infection will persist in the system. The system of ordinary differential equations in (4) are solved for the values of  $s, e$  and  $i$ . But for easy identification let  $s = s^*, e = e^*$  and  $i = i^*$ . This modifies the equation (4) to:

$$\nu e - (\mu + \delta)i = 0 \Rightarrow i = \frac{\nu e}{\mu + \delta}$$

Also  $\kappa si - (\omega + \mu + \nu)e = 0 \Rightarrow s = \frac{(\omega + \mu + \nu)}{\kappa i}$ , substituting  $i$  into  $s$  give

$$\begin{aligned} s &= \frac{(\omega + \mu + \nu)e}{\kappa \left( \frac{\nu e}{\mu + \delta} \right)} = \frac{(\omega + \mu + \nu)(\mu + \delta)e}{\kappa \nu e} \Rightarrow s^* \\ &= \frac{(\omega + \mu + \nu)(\mu + \delta)}{\kappa \nu} \end{aligned}$$

From  $\kappa si - (\omega + \mu + \nu)e = 0 \Rightarrow \kappa si = (\omega + \mu + \nu)e$  putting this into  $\lambda - \mu s - \kappa si + \omega e = 0$  gives  $\lambda - \mu s - (\omega + \mu + \nu)e = 0$

system (4) is asymptotically stable if and only if  $R_0 \leq 1$  and unstable if  $R_0 > 1$ .

Proof:

At the DFE (disease – free equilibrium) the Jacobian matrix about the point was obtained  $(s, e, i) = (1, 0, 0)$ . This yields the

matrix:  $J(s, e, i) = \begin{pmatrix} -\mu & \omega & -\kappa \\ 0 & -(\omega + \mu + \nu) & \kappa \\ 0 & \nu & -(\mu + \delta) \end{pmatrix}$

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.

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

$$J(s, e, i)_{DFE} - I\lambda = \begin{pmatrix} -\mu & \omega & -\kappa \\ 0 & -(\omega + \mu + \nu) & \kappa \\ 0 & \nu & -(\mu + \delta) \end{pmatrix} - \begin{pmatrix} \lambda & 0 & 0 \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{pmatrix}$$

$$J(s, e, i)_{DFE} - I\lambda = \begin{pmatrix} -(\mu + \lambda) & \omega & -\kappa \\ 0 & -\{(\omega + \mu + \nu) + \lambda\} & \kappa \\ 0 & \nu & -\{(\mu + \delta) + \lambda\} \end{pmatrix}$$

The characteristics equation is obtain by finding the determinant of the above matrix and equate it to zero.

$$|J(s, e, i)_{DFE} - I\lambda| = \begin{vmatrix} -(\mu + \lambda) & \omega & -\kappa \\ 0 & -\{(\omega + \mu + \nu) + \lambda\} & \kappa \\ 0 & \nu & -\{(\mu + \delta) + \lambda\} \end{vmatrix}$$

$$= -(\mu + \lambda) \begin{vmatrix} -(\omega + \mu + \nu + \lambda) & \kappa \\ \nu & -(\mu + \delta + \lambda) \end{vmatrix} - 0 \begin{vmatrix} 0 & \kappa \\ 0 & -(\mu + \delta + \lambda) \end{vmatrix} - \kappa \begin{vmatrix} 0 & -(\omega + \mu + \nu + \lambda) \\ 0 & \nu \end{vmatrix}$$

$$= -(\mu + \lambda)[(\omega + \mu + \nu + \lambda)(\mu + \delta + \lambda) - \kappa\nu]$$

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

$-(\mu + \lambda)[(\omega + \mu + \nu + \lambda)(\mu + \delta + \lambda) - \kappa\nu] = 0$  Expanding the relation above results in:

$$-(\mu + \lambda)[\omega\mu + \omega\delta + \omega\lambda + \mu^2 + \mu\delta + \mu\lambda + \mu\nu + \nu\delta + \nu\lambda + \lambda\mu + \lambda\delta + \lambda^2 - \kappa\nu] = 0$$

Expanding the above equation again and grouping like terms gives:

$$\lambda^3 + (\omega + 3\mu + \nu + \delta)\lambda^2 + (2\mu\omega + \omega\delta + 3\mu^2 + 2\mu\delta + 2\nu\mu + \nu\delta - \kappa\nu)\lambda + (\mu^2\omega + \mu\omega\delta + \mu^2 + \mu^2\delta + \mu^2\nu + \mu\nu\delta - \mu\kappa\nu) = 0$$

Letting Y, Z be the coefficients of  $\lambda^2$ ,  $\lambda$  and A be the constant term then

$$Y = \omega + 3\mu + \nu + \delta$$

$$Z = 2\mu\omega + \omega\delta + 3\mu^2 + 2\mu\delta + 2\nu\mu + \nu\delta - \kappa\nu$$

$$A = \mu^2\omega + \mu\omega\delta + \mu^2 + \mu^2\delta + \mu^2\nu + \mu\nu\delta - \mu\kappa\nu$$

And the characteristic equation becomes:  $\lambda^3 + Y\lambda^2 + Z\lambda + A$

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.

#### 4.2. Stability of the Endemic Equilibrium Point

Theorem 3.2: The endemic equilibrium of system (4) is also asymptotically stable when  $R_0 > 1$  and unstable when  $R_0 \leq 1$ .

Proof:

At the endemic equilibrium it has been showed that:

$$s^* = \frac{(\mu + \nu)(\mu + \delta)}{\kappa\nu}, \quad e^* = \frac{\lambda\kappa\nu - \mu(\mu + \nu)(\mu + \delta)}{\kappa\nu(\mu + \nu)} \quad \text{and} \quad i^* = \frac{\lambda\kappa\nu - \mu(\mu + \nu)}{\kappa(\mu + \nu)}$$

hence the Jacobian matrix at the endemic equilibrium point is

$$J(s^*, e^*, i^*)_{EE} - \lambda I = \begin{pmatrix} -\mu - \kappa i^* & \omega & -\kappa s^* \\ \kappa i^* & -(\omega + \mu + \nu) & \kappa s^* \\ 0 & \nu & -(\mu + \delta) \end{pmatrix} - \begin{pmatrix} \lambda & 0 & 0 \\ 0 & \lambda & 0 \\ 0 & 0 & \lambda \end{pmatrix}$$

$$J(s^*, e^*, i^*)_{EE} = \begin{pmatrix} -\mu - \kappa i^* & \omega & -\kappa s^* \\ \kappa i^* & -(\omega + \mu + \nu) & \kappa s^* \\ 0 & \nu & -(\mu + \delta) \end{pmatrix}$$

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  $I = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$  and

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

$$J(s^*, e^*, i^*)EE - \lambda I = \begin{pmatrix} -(\mu + \kappa i^* + \lambda) & \omega & -\kappa s^* \\ \kappa i^* & -(\omega + \mu + \nu + \lambda) & \kappa s^* \\ 0 & \nu & -(\mu + \delta + \lambda) \end{pmatrix}$$

$$|J(s^*, e^*, i^*)EE - \lambda I| = \begin{vmatrix} -(\mu + \kappa i^* + \lambda) & \omega & -\kappa s^* \\ \kappa i^* & -(\omega + \mu + \nu + \lambda) & \kappa s^* \\ 0 & \nu & -(\mu + \delta + \lambda) \end{vmatrix}$$

$$= -(\mu + \kappa i^* + \lambda) \begin{vmatrix} -(\omega + \mu + \nu + \lambda) & \kappa s^* \\ \nu & -(\mu + \delta + \lambda) \end{vmatrix} - \omega \begin{vmatrix} \kappa i^* & \kappa s^* \\ 0 & -(\mu + \delta + \lambda) \end{vmatrix} - \kappa s^* \begin{vmatrix} \kappa i^* & -(\omega + \mu + \nu + \lambda) \\ 0 & \nu \end{vmatrix}$$

$$= -(\mu + \kappa i^* + \lambda)[(\omega + \mu + \nu + \lambda)(\mu + \delta + \lambda) - \nu \kappa s^*] + \omega[\kappa i^*(\mu + \delta + \lambda)] - \kappa s^* \nu \kappa i^*$$

Expanding the equation above and setting it to zero gives:

$$\lambda^3 + (3\mu + \kappa i^* + \omega + \nu + \delta)\lambda^2 + (2\mu^2 + 2\mu\nu + \mu\delta + 2\kappa i^*\mu + \kappa i^*\nu + \kappa i^*\delta + \omega\mu + \omega\delta + \nu\delta - \nu\kappa s^*)\lambda + \omega\mu^2 + \mu\omega\delta + \mu^2 + \nu\mu^2 + \mu\nu\delta - \mu\nu\kappa s^* + \kappa i^*\mu^2 + \kappa i^*\nu\mu + \kappa i^*\nu\delta = 0$$

Let Y, Z represents the coefficient of  $\lambda^2$  and  $\lambda$  respectively and A is the constant term in the polynomial above. Then  $Y = 3\mu + \kappa i^* + \omega + \nu + \delta$

$$Z = 2\mu^2 + 2\mu\nu + \mu\delta + 2\kappa i^*\mu + \kappa i^*\nu + \kappa i^*\delta + \omega\mu + \omega\delta + \nu\delta - \nu\kappa s^*$$

$$A = \omega\mu^2 + \mu\omega\delta + \mu^2 + \nu\mu^2 + \mu\nu\delta - \mu\nu\kappa s^* + \kappa i^*\mu^2 + \kappa i^*\nu\mu + \kappa i^*\nu\delta$$

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.

### 5. Model Analysis and Results

This section analysed the model and present the results. To analysed the model a tuberculosis data was obtained from Amansie west district health directorate in the Ashanti region of Ghana.

Table 1. Model parameter value.

Parameter Description	Symbol	Value	Source
Natural birth rate	$\lambda$	0.00875	[21]
Natural death rate	$\mu$	0.00875	[21]
Infection rate	$\kappa$	0.9853	[22]
Transmission rate from the exposed period to infectious period	$\nu$	0.1666	[23]
Treatment rate introduced at the latent period	$\omega$	0.035	[24]
Recovery rate	$\delta$	0.5	[23]

#### 5.1. Estimation of the Basic Reproduction Number

$$R_0 = \frac{\kappa\nu}{(\omega + \mu + \nu)(\mu + \delta)}$$

$$= \frac{(0.9853)(0.1666)}{(0.035 + 0.0085 + 0.1666)(0.0085 + 0.5)} = 1.6415$$

Since  $R_0 > 1 \Rightarrow 1.64 > 1$  then the prevalence of TB will result in an epidemic this was due to the fact that the infection rate was more than the treatment rate introduced at the latent period and the recovery rate.

#### 5.2. Estimation of the Equilibrium Point

At the disease-free equilibrium point the proportions  $(s, e, i) = [1, 0, 0]$  since  $(\lambda = \mu)$ .

But at the endemic equilibrium point taking the parameter estimate above into consideration and using

$(s^*, e^*, i^*) = \left\{ \frac{(\omega + \mu + \nu)(\mu + \delta)}{\kappa\nu}, \frac{\lambda\kappa\nu - \mu(\omega + \mu + \nu)(\mu + \delta)}{\kappa\nu(\mu + \nu)}, \frac{\lambda\kappa\nu - \mu(\omega + \mu + \nu)}{\kappa(\mu + \nu)} \right\}$  the following proportions of the susceptible, exposed and infectious population are obtain

$$(s^*, e^*, i^*) = \left\{ \begin{array}{l} \frac{(0.035 + 0.00853 + 0.1666)(0.00853 + 0.5)}{(0.9853)(0.1666)}, \\ \frac{(0.00853 \times 0.9853 \times 0.1666) - 0.00853(0.035 + 0.00853 + 0.1666)(0.00853 + 0.5)}{(0.9853 \times 0.1666)(0.00853 + 0.1666)}, \\ \frac{(0.00853 \times 0.9853 \times 0.1666) - 0.00853(0.035 + 0.00853 + 0.1666)}{0.9853(0.00853 + 0.1666)} \end{array} \right\}$$

$$(s^*, e^*, i^*) = (0.6092, 0.01699, 0.0028)$$

**5.3. Stability of the Equilibrium Point**

At the disease – free equilibrium point the characteristics equation has been derived above as  $\lambda^3 + Y\lambda^2 + Z\lambda + A$

Where

$$Y = 0.035 + 3(0.00853) + 0.1666 + 0.5 = 0.72719$$

$$Z = 2(0.00853 \times 0.035) + (0.035 \times 0.5) + 3(0.00853)^2 + 2(0.00853 \times 0.5) + 2(0.1666 \times 0.00853) + (0.1666 \times 0.5) - (0.9853 \times 0.1666) = -0.051462$$

$$A = (0.00853)^2 \cdot 0.035 + (0.00853 \times 0.035 \times 0.5) + (0.00853)^2 + (0.00853)^2 \cdot 0.5 + (0.00853)^2 \cdot 0.1666 + (0.00853 \times 0.1666 \times 0.5) - (0.00853 \times 0.9853 \times 0.1666) = -0.0004164$$

Hence the characteristics equation becomes  $\lambda^3 + 0.72719\lambda^2 - 0.051462\lambda - 0.0004164 = 0$ . From Routh-Hurwitz Stability criterion analysis since  $Z < 0$  and  $ZY - A < 0$  then the condition does not hold for the stability for the disease - free equilibrium point and hence the disease – free equilibrium is unstable leaving the endemic equilibrium point stable.

equilibrium and the endemic equilibrium. Disease – free equilibrium is globally stable when the basic reproduction number ( $R_0$ ) is not bigger than one ( $R_0 \leq 1$ ) that is the disease will die out but on the other hand disease – free equilibrium becomes unstable and the endemic equilibrium set in ( $R_0 > 1$ ) and hence the disease will persist. This was demonstrated with a tuberculosis data obtained from Amansie west district health directorate in the Ashanti region of Ghana. The sensitivity analysis also indicated that increasing the rate of treatment at the latent period will help reduce the basic reproduction number which will help the disease-free equilibrium point to be stable instead of the endemic equilibrium point like in the case of Amansie west district in the Ashanti region of Ghana.

**6. Sensitivity Analysis and Conclusion**

**6.1. Sensitivity Analysis**

This type of analysis deals with how the uncertainty in the output of a mathematical model (numerical or otherwise) can be apportioned to different sources of uncertainty in its input [25]. The analysis is also useful in understanding the relationship between the input and output variables. For the purpose of this paper analysis on how changes in the treatment rate introduced at latent period influence the endemicity (that is the threshold parameter  $R_0$ ). since  $R_0 = 1.64$  it implies on average each infectious individual transmit bacteria to 2 people. Hence in this study much concern will be on the changes that will make  $R_0 \leq 1$ .

$$R_0 = \frac{kv}{(\omega + \mu + v)(\mu + \delta)}$$

If  $\omega$  (the treatment rate introduced at the latent period) is double then:

$$R_{01} = \frac{kv}{(2\omega + \mu + v)(\mu + \delta)}$$

This will increase the denominator of the relation above and hence reduce the value of  $R_0$  (that is  $R_{01} < R_0$ ). Hence increasing the rate of treatment introduced at the latent period will help reduce the basic reproduction number  $R_0$ .

**6.2. Conclusion**

An SEIR epidemic model which incorporates treatment in the latent period has been formulated and analysed quantitatively. The model was developed based on the assumption of constant population size and infection rate. The model exhibit two equilibria: the disease-free

**Description of Parameters for the SEIR Model**

$\lambda$ : Natural birth rate,  $\mu$ : Natural death rate,  $\kappa$ : Infection rate,  $v$ : Transmission rate from the exposed period to infectious period,  $\omega$ : The treatment rate introduced at the latent (exposed) period,  $\delta$ : Recovery rate

**References**

- [1] D. Bernoulli, Reflexion sur les avantages de l'inoculation, Mercure de France (1760) 173. (Reprinted in L.P. Bouckaert, B.L. van der Waerden (Eds), Die Werke von Daniel Bernoulli, Bd. 2 Analysis und Wahrscheinlichkeitsrechnung, Birkhauser, Basel, 1982, p. 268).
- [2] R. M. Anderson and R. M. May (1991). Infectious diseases of humans. Oxford, UK: Oxford university press.
- [3] N. T. J. Bailey (1975). The mathematical theory of infectious diseases and its applications. London: Charles Griffin and company.
- [4] H. Hethcote (2000). The mathematics of infectious diseases. SIAM review, 42, 599-653.
- [5] J. M. Hyman and J. Li (1998). Modeling the effectiveness of isolation strategies in preventing STD epidemics. SIAM journal of applied mathematics, 58, 912.

- [6] S. Olaniyi, M. A. Lawal, and O. S. Obabiyi, "Stability and sensitivity analysis of a deterministic epidemiological model with pseudo-recovery," *IAENG International Journal of Applied Mathematics*, vol. 46, no.2, pp. 1–8, 2016.
- [7] O. Diekmann, J. A. Heesterbeek, and J. A. 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*, vol. 28, no. 4, pp. 365–382, 1990.
- [8] P. van den Driessche and J. Watmough (2002). Reproduction numbers and sub threshold Endemic equilibria for compartmental models of disease transmission. *Mathematical biosciences*, 180, 29-48.
- [9] Tom et al. SEIRS epidemics with disease fatalities in growing populations, *Mathematical Biosciences* (2017), doi: 10.1016/j.mbs.2017.11.006.
- [10] F. Brauer, P. van den Driessche and J. Wu (2008). *Mathematical epidemiology*, Springer.
- [11] X. Zhou and J. Cui (2011). Analysis of stability and bifurcation for an SEIR epidemic model with saturated recovery rate. *Communications in nonlinear science and numerical simulation*, 16, 4438-4450.
- [12] Sarah A. Al – Sheikh (2012). Modeling and Analysis of an SEIR Epidemic Model with a Limited Resource for Treatment. *Global Journals Inc. (USA)*.
- [13] J. Zhang, J. Li, and Z. Ma (2006). Global dynamics of an SEIR epidemic model with immigration of different compartments. *Acta Mathematica Scientia*, 26, 551-567.
- [14] N. Yi, Q. Zhang, K. Mao, D. Yang, and Q. Li (2009). Analysis and control of an SEI epidemic system with nonlinear transmission rate. *Mathematical and computer modeling*, 50, 1498-1513.
- [15] C. Sun, Y. Hsieh (2010). Global analysis of an SEIR model with varying population size and vaccination. *Applied mathematical modeling*, 34, 2685-2697.
- [16] H. Shu, D. Fan, and J. Wei Global (2012). Stability of multi-group SEIR epidemic models with distributed delays and nonlinear transmission. *Nonlinear Analysis: Real World Applications*, 13, 1581-1592.
- [17] J. M. Hyman and J. Li (1998). Modeling the effectiveness of isolation strategies in preventing STD epidemics. *SIAM journal of applied mathematics*, 58, 912.
- [18] Z. Fang and H. R. Thieme (1995). Recurrent outbreak of childhood diseases revisited: The impact of solution. *Mathematical biosciences*, 128, 93.
- [19] L. Wu and Z. Feng (2000). Homoclinic bifurcation in an SIQR model for childhood diseases. *Journal of differential equations*, 168, 150.
- [20] J. Wang, S. Liu, B. Zheng and Y. Takeuchi (2012). Qualitative and bifurcation analysis using an SIR model with a saturated treatment function. *Mathematical and computer modeling*, 55, 710-722.
- [21] Index mundi, (2012). [http://www.indexmundi.com/ghana/death\\_rate.html](http://www.indexmundi.com/ghana/death_rate.html).
- [22] Wikipedia. [http://www.wikipedia.com/Transmission risks and rates](http://www.wikipedia.com/Transmission_risks_and_rates), 2018.
- [23] Jones, J. H., (2007). Notes on Reproductive Number.
- [24] Sarkodie Eric (2014). Modeling the spread of tuberculosis in central region using the susceptible-exposed-infected-susceptible (seis) mathematical model.
- [25] Saltelli, A., Ratto, M., Andres, T., Campolongo, F., Cariboni, J., Gatelli, D. Saisana, M., and Tarantola, S. (2008). *Global Sensitivity Analysis. The Primer*, John Wiley & Sons.