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STABILITY ANALYSIS OF A GENERALIZED SEIR EPIDEMIC MODEL WITH LIMITED RESOURCE FOR TREATMENT

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ABSTRACT

This paper addresses an SEIR epidemic model with limited resource for treatment and generalized it to study the dynamic behavior of the model. It is assumed that the treatment rate is proportional to the number of patients as long as this number is below a certain capacity and it becomes constant when that number of patients exceeds this capacity. Existences of disease-free and endemic equilibria for the model are investigated. In this paper stability for the system of differential equations for the generalized model has been studied and it is shown that this kind of treatment rate leads to the existence of multiple endemic equilibria where the basic reproduction number plays a big role in determining their stability.

KEYWORDS: SEIR Epidemic Model, Treatment Rate, Equilibrium, Stability Criteria, Basic Reproduction Number

AMS SUBJECT CLASSIFICATION: 34D23, 92B05, 92D30, 93D05

1. INTRODUCTION

Most of the models in mathematical epidemiology are compartmental models, with the population being divided into compartments with the assumptions about the nature and time rate of transfer from one compartment to another. In the paper [1] an SEIR epidemic model with a limited resource for treatment is investigated by the authors. They assumed that the treatment rate is proportional to the number of patients as long as this number is below a certain capacity and it becomes constant when that number of patients exceeds this capacity. Mathematical analysis is used to study the dynamic behavior of this model. Existence and stability of disease-free and endemic equilibria are investigated. They have shown that this kind of treatment rate leads to the existence of multiple endemic equilibria where the basic reproduction number plays a big role in determining their stability.

Mathematical models have been used extensively in research into the epidemiology of HIV/AIDS to help improve our understanding of the major contributing factors to the pandemic. Cai L. et. al. [2] discussed an HIV/AIDS epidemic model with treatment. The model allows for some infected individuals to move from the symptomatic phase to the asymptomatic phase by all sorts of treatment methods. Here first established the ODE treatment model with two infective stages. Mathematical analyses establish that the global dynamics of the spread of the HIV infectious disease are completely determined by the basic reproduction number $\Re_0$. If $\Re_0 \leq 1$, the disease-free equilibrium is globally stable, whereas the unique infected equilibrium is globally asymptotically stable if $\Re_0 > 1$. Then, they introduced a discrete time delay model to describe the effect of the time delay on the stability of the endemically infected equilibrium.

Authors proposed an epidemic model with non-monotonic incidence rate under a limited resource for treatment to

understand the effect of the capacity for treatment in [3]. They assumed that treatment rate is proportional to the number of infective when it is below the capacity and is constant when the number of infective is larger than the capacity. Existence and stability of the disease free and endemic equilibrium are investigated for both the cases. Some numerical simulations are given by them to illustrate the analytical result. Mathematical modeling for disease transmission in host population is of great practical value in predicting and controlling disease spread .An SEIR model with varying population size and vaccination strategy is investigated in [4] Three threshold parameters $\Re_0$; $\hat{\Re}_0$; $\bar{\Re}_0$ and $\tilde{\Re}_0$ are obtained to govern the disease eradication, which involve the total number of infective and their proportion in the population. Parameter conditions on the uniform persistence, the global stability of the disease – ‘‘free” equilibrium and the ‘‘endemic” equilibrium are derived. The global dynamics of model in population size are studied. In [5] Yi N . ET. al. Has been studied the dynamical behaviors of an SEIR epidemic system governed by differential and algebraic equations with seasonal forcing in transmission rate. The cases of only one varying parameter, two varying parameters and three varying parameters are considered to analyze the dynamical behaviors of the system. For the case of one varying parameter, the periodic, and chaotic and hyper chaotic dynamical behaviors are investigated via the bifurcation diagrams, Lyapunov exponent spectrum diagram and Poincare section. For the cases of two and three varying parameters, a Lyapunov diagram is applied. A tracking controller is designed to eliminate the hyperchaotic dynamical behavior of the system, such that the disease gradually disappears. Further Zhang J. ET. al. [6] studied an SEIR epidemic model with constant inflows of new susceptibles, exposeds, infectives, and recovereds. This model also incorporates a population size dependent contact rate and a disease-related death. As the infected fraction cannot be eliminated from the population, this kind of model has only the unique endemic equilibrium that is globally asymptotically stable. Under the special case where the new members of immigration are all susceptible, the model considered here shows a threshold phenomenon and a sharp threshold has been obtained. The paper is organized as follows: In section 2, a mathematical model is introduced and obtained the equilibria of the system, its existency and the basic reproduction number by next generation matrix method. In section 3, stability of equilibria is studied. Finally, some conclusions are drawn in section 4.

2. DERIVATION OF THE MODEL

Consider a population is divided into four epidemiological classes which are susceptible (S), exposed (latently infected) (E), infectious (I) and recovered (R). When there is an adequate contact of a susceptible with an infective, the susceptible becomes exposed and leaves the class S . Hence exposed individuals enter the class E . Now exposed becomes infected and leaves the class E . Hence infected individuals enter the class I of infectious people and have a full disease case of an infectious disease. Upon recovery they enter the class R as well as goes back through an immediate returning path δI to the exposed class.

The flow of individual depicted in the following transfer diagram (Figure 1):

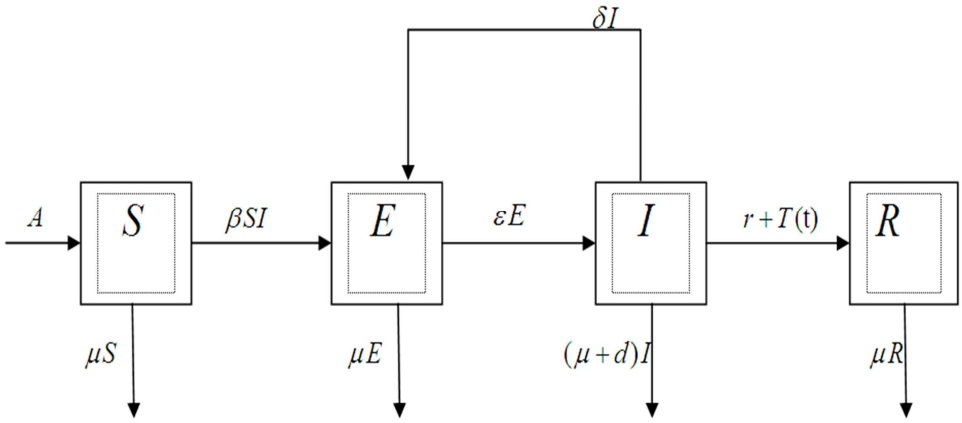

Figure 1: Transfer Diagram for Generalized SEIR Epidemic Model

The symbol are used here stand for

A = Recruitment rate,

β = infection rate,

μ = natural death rate,

ε = progression rate to symptoms development (the rate at which an Infected individual becomes infections perunit time),

δ = effective rate,

d = disease- related death,

r = removal rate (the rate at which an infectious individual recovers per unit time),

$T(t)$ = treatment rate function,

Where $A > 0,\ \beta > 0,\ \mu > 0,\ \varepsilon > 0,\ \delta \geq 0\ ,\ d > 0\ ,\ r > 0$

The differential equations corresponding to the transfer diagram are

$$\begin{aligned}
\frac{dS}{dt} &= A - \mu S - \beta SI \\
\frac{dE}{dt} &= \beta SI + \delta I - (\mu + \varepsilon)E \\
\frac{dI}{dt} &= \varepsilon E - (\mu + r + d + \delta)I - T(t) \\
\frac{dR}{dt} &= rI - \mu R + T(t)\ .
\end{aligned} \tag{1}$$

Now, the treatment function is defined by

$$T(t)=\begin{Bmatrix} cI; & 0\le I\le I_0 \\ \mathrm{k}; & I>I_0 \end{Bmatrix}$$

Where $k=c\,I_0$.This means that the treatment rate is proportional to the number of

Infected people as long as the number of infectives is less than or equal to a fixed value

I_0 But after that the treatment rate becomes constant.

The variable R does not appear in the first three equations of (1), so it is enough

To analyze the following reduced system

$$\begin{aligned} \frac{dS}{dt} &= A-\mu S-\beta SI \\ \frac{dE}{dt} &= \beta SI+\delta I-(\mu+\varepsilon)E \\ \frac{dI}{dt} &= \varepsilon E-(\mu+r+d+\delta)I-T(t). \end{aligned} \qquad (2)$$

It follows from system (2) that

$$\frac{ds}{dt}+\frac{dE}{dt}+\frac{dI}{dt}=A-\mu(S+E+I)-T(t)\le A-\mu(S+E+I)\ .$$

Then $\lim_{n\to\infty} Sup(\mathrm{S}+\mathrm{E}+\mathrm{I})\le\frac{A}{\mu}$.

So the feasible region for system (2) is

$$\Omega=\{(S,E,I):S+E+I\le\frac{A}{\mu},S>0,E\ge 0,I\ge 0\}.$$

The region Ω is positively invariant with respect to system (2).

Hence, system (2) is considered mathematically and epidemiologically well posed in Ω

2.1 Disease-Free Equilibrium and the Basic Reproduction Number

System (2) always has the disease-free equilibrium $X_0=(\frac{A}{\mu},0,0)$

Now, the basic reproduction number R_0 will be found by using the method of Next generation matrix.

Near the disease free equilibrium, $I<I_0$, so system (2) becomes

$$\frac{dS}{dt}=A-\mu S-\beta SI$$

$$\frac{dE}{dt} = \beta SI + \delta I - (\mu + \varepsilon) E \tag{3}$$

$$\frac{dI}{dt} = \varepsilon E - (\mu + r + d + \delta + c) I$$

Let $X = (E, I, S)^T$. System (3) can be written as

$$\frac{dX}{dt} = F(\mathrm{X}) - V(\mathrm{X})$$

Where

$$F(X) = \begin{pmatrix} \beta SI \\ 0 \\ 0 \end{pmatrix}, V(X) = \begin{pmatrix} -\delta I + (\mu + \varepsilon) E \\ -\varepsilon E + (\mu + r + d + c + \delta) I \\ -A + \beta SI + \mu S \end{pmatrix}$$

The Jacobian matrices of $F(X)$ and $V(X)$ at the disease free equilibrium X_0 are

Respectively,

$$DF(X_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}, DV(X_0) = \begin{pmatrix} V & 0 \\ J_1 & J_2 \end{pmatrix}$$

Where

$$F = \begin{pmatrix} 0 & \frac{\beta A}{\mu} \\ 0 & 0 \end{pmatrix} \text{ And } V = \begin{pmatrix} \mu + \varepsilon & -\delta \\ -\varepsilon & \mu + r + d + c + \delta \end{pmatrix}$$

$$FV^{-1} = \frac{1}{|V|} \begin{pmatrix} \varepsilon\beta A/\mu & \beta A(\mu + \varepsilon)/\mu \\ 0 & 0 \end{pmatrix} \text{ Is the next generation matrix of system (2)}$$

Where

$$|V| = \mu[(\mu + \varepsilon)(\mu + r + d + c)] + \mu^2\delta$$

Hence, the spectral radius of FV^{-1} which is denoted by basic reproduction number,is

$$R_0 = \rho(FV^{-1}) = \frac{\varepsilon\beta A}{\mu[(\mu + \varepsilon)(\mu + r + d + c)] + \mu^2\delta}$$

2.2 Endemic Equilibria

First of all, the disease – free equilibria $X_0 = (\frac{A}{\mu}, 0, 0)$ always exists when $I \le I_0$.

An endemic equilibria of system (2) satisfies

$$\begin{aligned} A - \mu S - \beta SI &= 0 \\ \beta SI + \delta I - (\mu + \varepsilon) E &= 0 \\ \varepsilon E - (\mu + r + d + \delta) I - T(t) &= 0 \ . \end{aligned} \quad (4)$$

When $0 < I \le I_0$, system (4) becomes

$$\begin{aligned} A - \mu S - \beta SI &= 0 \\ \beta SI + \delta I - (\mu + \varepsilon) E &= 0 \\ \varepsilon E - (\mu + r + d + c + \delta) I &= 0 \ . \end{aligned} \quad (5)$$

if $R_0 > 1$, system (5) admits a unique positive solution $X^* = (S^*, E^*, I^*)$ given by

$$S^* = \frac{A}{\mu R_0}, \quad E^* = \frac{\mu(\mu + r + d + c + \delta)}{\beta\varepsilon}[R_0 - 1] \ , \quad I^* = \frac{\mu}{\beta}[R_0 - 1] \ .$$

Thus, $I^* \le I_0$ if and only if $R_0 \le 1 + \beta I_0 / \mu \square P_0$.

So, X^* is an endemic equilibrium of system (2) if and only if $1 < R_0 \le P_0$.

Now, when $I > I_0$, system (4) becomes

$$\begin{aligned} A - \mu S - \beta SI &= 0 \\ \beta SI + \delta I - (\mu + \varepsilon) E &= 0 \\ \varepsilon E - (\mu + r + d + \delta) I - k &= 0 \ . \end{aligned} \quad (6)$$

In order to obtain positive solutions of system (6), we get from the first equation

Of (6) $S = \frac{A}{\mu + \beta I}$ and $E = \frac{\mu + r + d + \delta}{\varepsilon} I + \frac{k}{\varepsilon}$ respectively.

On substituting these values in second equation of system (6), we have

$$aI^2 + bI + c = 0 \quad (7)$$

Where

$$a = \beta[(\mu + \varepsilon)(\mu + r + d) + \mu\delta] > 0 \ ,$$

$$b=(\mu+\varepsilon)\left[\mu(\mu+r+d)+k\beta\right]-\varepsilon\beta A+\mu^2\delta$$

$$=\left[\mu(\mu+\varepsilon)(\mu+r+d+c)+\mu^2\delta\right]+(\mu+\varepsilon)(\beta k-\mu c)-R_0\left[\mu(\mu+\varepsilon)(\mu+r+d+c)+\mu^2\delta\right],$$

$$c=\mu k(\mu+\varepsilon)>0.$$

Let the discriminant of (7) be $\Delta=b^2-4ac$.

If $b\geq 0$, then (7) has no positive solution. Also if $\Delta<0$, then (7) has no real

Solution. Thus we see that if $b<0$ and $\Delta\geq 0$, then (7) has two positive solutions

I_1 and I_2 where

$$I_1=\frac{-b-\sqrt{\Delta}}{2\beta\left[(\mu+\varepsilon)(\mu+r+d)+\mu\delta\right]} \text{ and } I_2=\frac{-b+\sqrt{\Delta}}{2\beta\left[(\mu+\varepsilon)(\mu+r+d)+\mu\delta\right]}$$

And this is possible if

$$\mathrm{R}_0\geq 1+\frac{(\mu+\varepsilon)(\beta k-\mu c)}{\mu(\mu+\varepsilon)(\mu+r+d+c)+\mu^2\delta}+\frac{2\sqrt{\mu k(\mu+\varepsilon)\beta\left[(\mu+\varepsilon)(\mu+r+d)+\mu\delta\right]}}{\mu(\mu+\varepsilon)(\mu+r+d+c)+\mu^2\delta}\equiv P_1.$$

Then

$$S_1=\frac{A}{\mu+\beta I_1},\ S_2=\frac{A}{\mu+\beta I_2},\ E_1=E_2=\frac{\mu(\mu+r+d+c+\delta)}{\beta\varepsilon}\left[R_0-1\right]$$

Then

$X_i=(S_i,E_i,I_i)$, $i=1,2$ are endemic equilibria of system (2) if $I_i>I_0$

Thus, $I_1>I_0\Leftrightarrow\frac{-b-\sqrt{\Delta}}{2\beta\left[(\mu+\varepsilon)(\mu+r+d)+\mu\delta\right]}>I_0$ which implies that

$$R_0>1+\frac{(\mu+\varepsilon)(\beta k-\mu c)}{\mu(\mu+\varepsilon)(\mu+r+d+c)+\mu^2\delta}+\frac{2\beta\left[(\mu+\varepsilon)(\mu+r+d)+\mu\delta\right]I_0}{\mu(\mu+\varepsilon)(\mu+r+d+c)+\mu^2\delta}\equiv P_2$$

And $I_2<I_0\Leftrightarrow R_0<P_2$

Thus the endemic equilibria $X^*=(S^*,E^*,I^*)$ of system (2) exists if and only if $1<R_0\leq P_0$

And two more endemic equlibria $X_i=(S_i,E_i,I_i)$, $i=1,2$ of system (2) exist if and only if

$R_0>P_1$ and $R_0>P_2$.

3. STABILITY OF EQUILIBRIA

(A) .Local and Global Stability of Disease-Free Equilibrium X_0

Theorem 1: The disease-free equilibrium X_0 is locally asymptotically stable.

Proof: By analyzing the eigen values of the Jacobian matrices of system (2), we get results about the local stability of these equilibria .

The jacobian matrix evaluated at X_0 is

$$J(X_0)=\begin{pmatrix} -\mu & 0 & -\frac{\beta A}{\mu} \\ 0 & -(\mu+\varepsilon) & \delta \\ 0 & \varepsilon & -(\mu+r+d+c+\delta) \end{pmatrix}$$

Then its characteristic equation is

$$z^3+b_1 z^2+b_2 z+b_3=0$$

Where

$$b_1=(3\mu+\varepsilon+r+d+c+\delta)\ ,$$

$$b_2=\left[\mu(\mu+\varepsilon)+2\mu(\mu+r+d+c+\delta)+\varepsilon(\mu+r+d+c+\delta)\right]\ ,$$

$$b_3=\mu^2(\mu+r+d+c+\delta)+\varepsilon\mu(\mu+r+d+c)\ .$$

Clearly, $b_1>0$, $b_3>0$ and $b_1b_2-b_3>0$.

Therefore, by Routh-Hurwitz criteria, we conclude that the eigen values of $J(X_0)$

Are all negative. Thus, the disease-free equilibrium X_0 is locally asymptotically stable.

Theorem 2: If $R_0<1$, the disease-free equilibrium X_0 is locally asymptotically

Stable and the disease die out. But if $R_0>1$, then X_0 is unstable .

Proof: To investigate the global stability of X_0 , consider the Lyapunov function

$$L=\varepsilon E+(\mu+\varepsilon)I$$

Then $\frac{dL}{dt}=\varepsilon\frac{dE}{dt}+(\mu+\varepsilon)\frac{dI}{dt}$

$$\frac{dL}{dt}=[\varepsilon\beta\frac{A}{\mu}-(\mu+\varepsilon)(\mu+r+d+c)-\mu\delta]\mathrm{I}$$

$$\frac{dL}{dt}=\left[(\mu+\varepsilon)(\mu+r+d+c)+\mu\delta\right](R_0-1)I\le 0 \text{ if } R_0<1 .$$

Hence, the maximal compact invariant set in $\{(S,E,I)\in\Omega:\frac{dL}{dt}=0\}$ is the

Singleton $\{X_0\}$ Using Lasalle's invariance principle proved the theorem.

(B) .Local and Global Stability of Endemic Equilibrium X^*

Theorem 3: if $R_0>1$, then the endemic equilibrium X^* is locally asymptotically

Stable.

Proof: The jacobian matrix evaluated at X^* is

$$J(X^*)=\begin{pmatrix} -\mu R_0 & 0 & -\beta\frac{A}{\mu R_0} \\ \mu(R_0-1) & -(\mu+\varepsilon) & \delta \\ 0 & \varepsilon & -(\mu+r+d+c+\delta) \end{pmatrix}$$

Then its characteristic equation is

$$\lambda^3+a_1\lambda^2+a_2\lambda+a_3=0$$

Where

$$a_1=\left[\mu R_0+2\mu+\varepsilon+r+d+c+\delta\right] ,$$

$$a_2=\left[(\mu+\varepsilon+\mu R_0)(\mu+r+d+c)+\mu R_0(\mu+\varepsilon+\delta)+\mu\delta\right] ,$$

$$a_3=2\mu\left[(\mu+\varepsilon)(\mu+r+d+c)+\mu\delta\right]R_0-\mu\left[(\mu+\varepsilon)(\mu+r+d+c)+\mu\delta\right]$$ Clearly, $a_1>0$, $a_3>0$ if $R_0>1$ and $a_1a_2-a_3>0$.

Therefore, by Routh-Hurwitz criteria we conclude that the eigen values of $J(X^*)$ are all negative when $R_0>1$ Thus, if $R_0>1$, then the endemic equilibrium X^* is locally asymptotically stable.

Theorem 4: If $R_0>1$, the endemic equilibrium X^* is globally asymptotically stable.

Proof: Now we consider the following Lyapunov function

$$V=\left(S-S^*\ln\frac{S}{S^*}\right)+\left(E-E^*-E^*\ln\frac{E}{E^*}\right)+\frac{(\mu+\varepsilon)}{\varepsilon}\left(I-I^*-I^*\ln\frac{I}{I^*}\right).$$

Then $\frac{dV}{dt}=\left(1-\frac{S^*}{S}\right)\frac{dS}{dt}+\left(1-\frac{E^*}{E}\right)\frac{dE}{dt}+\frac{(\mu+\varepsilon)}{\varepsilon}\left(1-\frac{I^*}{I}\right)\frac{dI}{dt}$

$$\frac{dV}{dt}=\left(1-\frac{S^*}{S}\right)(A-\mu S-\beta SI)+\left(1-\frac{E^*}{E}\right)(\beta SI+\delta I-(\mu+\varepsilon)E)+\frac{(\mu+\varepsilon)}{\varepsilon}\left(1-\frac{I^*}{I}\right)[\varepsilon E-(\mu+r+d+\delta+c)I]$$

Substituting $A=\beta S^*I^*+\mu S^*$ we get

$$\frac{dV}{dt}=\left(1-\frac{S^*}{S}\right)(\beta S^*I^*+\mu S^*-\mu S-\beta SI)+\left(1-\frac{E^*}{E}\right)(\beta SI+\delta I-(\mu+\varepsilon)E)+\frac{(\mu+\varepsilon)}{\varepsilon}\left(1-\frac{I^*}{I}\right)[\varepsilon E-(\mu+r+d+\delta+c)I]$$

$$\frac{dV}{dt}=-\mu\frac{(S-S^*)^2}{S}+\beta S^*I^*-\beta S^*I^*\frac{S^*}{S}+\beta S^*I-\beta SI\frac{E^*}{E}+(\mu+\varepsilon)E^*-(\mu+\varepsilon)\,E\frac{I^*}{I}$$
$$-\frac{(\mu+\varepsilon)}{\varepsilon}(\mu+r+d+\delta+c)I+\frac{(\mu+\varepsilon)}{\varepsilon}(\mu+r+d+\delta+c)I^*+\delta I-\delta I\frac{E^*}{E}-(\mu+\varepsilon)E\frac{I^*}{I}$$

Using the values $\varepsilon E^*=(\mu+r+d+\delta+c)I^*$ and $\varepsilon E=(\mu+r+d+\delta+c)I$

$$\frac{dV}{dt}=-\mu\frac{(S-S^*)^2}{S}+(\mu+\varepsilon)E^*\left(3-\frac{S^*}{S}-\frac{SE^*I}{S^*EI^*}-\frac{EI^*}{E^*I}\right)+\delta I^*\left(\frac{S^*}{S}+\frac{SE^*I}{S^*EI^*}-2\right)\le 0$$

Therefore, $\frac{dV}{dt}=0$ holds only when $S=S^*$, $E=E^*$ and $I=I^*$.

(C) .<u>Local Stability of Endemic Equilibria</u> X_1 <u>and</u> X_2

For proof of the theorem 5 we use the following lemma

Lemma: Let M be a 3 x 3 real matrix. If $tr(M),\det(M),and\ \det(M^{[2]})$ are all

Negative, then all of the eigenvalues of M have negative real parts.

Theorem 5: The endemic equilibria X_i, $i=1,2$ are locally asymptotically stable if

$$\frac{S_i}{I_i}<1+\frac{2\mu+r+d+\delta}{\varepsilon}$$

Proof: By analyzing the Jacobian matrix at these equilibria we find that

$$J(X_1) = \begin{pmatrix} -\mu-\beta I_1 & 0 & -\beta S_1 \\ \beta I_1 & -(\mu+\varepsilon) & \delta \\ 0 & \varepsilon & -(\mu+r+d+\delta) \end{pmatrix}$$

$$J(X_1) = \begin{pmatrix} -\frac{A}{S_1} & 0 & -\beta S_1 \\ \beta I_1 & \frac{-\beta S_1 I_1 - \delta I_1}{E_1} & \delta \\ 0 & \varepsilon & \frac{k-\varepsilon E_1}{I_1} \end{pmatrix}$$

The second additive compound matrix of $J(X_1)$ is given by

$$J(X_1)^{[2]} = \begin{pmatrix} -\mu-\beta I_1-(\mu+\varepsilon) & \delta & \beta S_1 \\ \varepsilon & -\mu-\beta I_1-(\mu+r+d+\delta) & 0 \\ 0 & \beta I_1 & -(\mu+\varepsilon)-(\mu+r+d+\delta) \end{pmatrix}$$

$tr(J(X_1)) = \frac{-A}{S_1} - \frac{\beta S_1 I_1}{E_1} - \frac{\delta I_1}{E_1} + \frac{k}{I_1} - \frac{\varepsilon E_1}{I_1} < 0$ and

Similarly, $tr\left(J(X_2)\right) < 0$.

Now, $\det(J(X_1)) = -\frac{1}{E_1}\left[\beta\varepsilon A E_1 - \beta\varepsilon A - \frac{A\delta k}{S_1} + \beta^2 S_1 I_1 \varepsilon E_1\right] < 0$ and

$\det\left(J(X_2)\right) < 0$.

And

$$\det(J(X_1)^{[2]}) = (-\beta I_1 - 2\mu - \varepsilon)[(-\beta I_1 - 2\mu - r - d - \delta)(-2\mu - \varepsilon - r - d - \delta)]$$
$$-\varepsilon[\delta(-2\mu - \varepsilon - r - d - \delta) - \beta^2 S_1 I_1]$$

I.e. $\det(J(X_1)^{[2]}) < 0$ if $\beta^2 I_1^{\,2}\left[2\mu + r + d + \delta + \varepsilon\right] < \beta^2 S_1 I_1 \varepsilon$.

And similarly, $\det(J(X_2)^{[2]}) < 0$

Thus, by applying above lemma we can say that the endemic equilibria X_i , $i = 1, 2$ are locally asymptotically stable if $\frac{S_i}{I_i} < 1 + \frac{2\mu + r + d + \delta}{\varepsilon}$.

CONCLUSIONS

In this paper, I have generalized an SEIR epidemic model of Sarah A. Al-Sheikh [19]. In this model I have considered that the infected individuals enter to the recovered class by transmission rate $r+T(t)$ as well as return to the exposed class by transmission rate δI . I have found disease-free and endemic equilibria for the model and analyzed the stability criteria for the both equilibria and found that if $R_0<1$, there exists no positive equilibrium and the Disease-free equilibrium is global asymptotically stable and the disease dies out .But if $R_0>1$ the disease-free equilibrium becomes unstable and the disease persists. Then in this case the endemic equilibria is exists and global asymptotically stable and also discussed locally asymptotic stability criteria for two endemic equilibria X_1 and X_2 .In the paper, throughout the work if $\delta=0$, I found the results discussed by Al-Sheikh Sarah A. for the model [1] .

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