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# STABILITY ANALYSIS OF SEIR MODEL USING NON-NEWBORN VACCINATION AND COST EFFECTIVE TREATMENT

MUHAMMAD USMAN, NOOR BADSHAH*

Department of Basic Sciences and Islamiat, University of Engineering and Technology, Peshawar, Khyber Pakhtunkhawa, Pakistan



**Abstract.** This study focused on the modification and probation of a Susceptible-Exposed-Infected-Recovered (SEIR) model for non-newborn vaccination and cost effective treatment. The system of differential equations has been derived from SEIR model to creates a bond between susceptible S, infected I, exposed E and recovered E participants for understanding the spread out of contagious diseases. Further, the local stabilities of both disease free equilibrium points and endemic equilibrium points were found stable at epidemic conditions i.e. epidemic ($R_0 > 1$) and no epidemic ($R_0 \leq 1$). In addition, numerical simulation has been performed to investigate the proposed model at regular set of values of parameters. Moreover, our vaccination target is only non-newborn individuals to protect the population without effecting the economy of country.

**Keywords:** cost effective treatment; SEIR model; non-newborn vaccination; stability analysis.

**2010 AMS Subject Classification:** 93A30.

## 1. Introduction

The construction of new models and modification of models in the field of mathematical epidemiology gives attainable approach for better future of science and technology. Up to now various research have been made in the field of mathematics among them mathematical biology

*Corresponding author
E-mail address: noor2knoor@gmail.com
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has gained much of attraction because of its vast applications in the area of medicine [1]. The early developments in the field of mathematical biology have been carried out in 18th century [2]. Later, these studies flourished by many researchers to develop the most appropriate mathematical model to scrutinize biological diseases [2, 11]. In recent years, among all the infectious diseases like influenza, dengue, measles, Spanish flue, etc., dengue virus which also known as vector-borne contagious disease considered as the major threat for public health in Pakistan [3, 7]. Therefore, epidemic models such as: SI, SIS, SIR, SEIR and SEIRS are required to overcomes infectious problems of the whole world [6, 10]. However, these epidemic models are based on three aims. Firstly, to understand the spreading and transmission of contagious disease, structure of epidemic model and behaviour of concern parameters. Secondly, to calculate threshold quantity which is also known as basic reproductive number which predict either epidemic occur or not. And third aim is to construct a strategy for the control and eradication of contagious disease [20]. In addition, these mathematical models have been derived on the base of first order differential equations, which are helpful in analyzing the spread and control of contagious diseases [12, 15]. Usually, these mathematical models are the categorical models, which represents four compartments such as susceptible, exposed, infected and recovered, while each compartment represents a particular step of the epidemic. However, in these models the change rate from one class to another class is numerically presented with the help of derivatives [16]. Further, the system of ODE's (i.e. SIR, SEIR, SEIRS mathematical model etc.) is described by using classes of population and rate change derivatives as a function of time [4].

Herein, the SIR epidemiological model described the dynamics of infectious diseases with continue immunity and a qualitative discussion to analyze stability. More importantly, the disease-free equilibrium points of SIR model are found locally and globally asymptotically stable if the reproduction number $R_0 < 1$, while the endemic equilibrium points of SIR models are locally asymptotically stable when reproduction number is $R_0 > 1$. However, in order to eradicate disease successfully by using SIR model, the vaccination level should be larger because disease preventation rely on vaccination proportion as well as efficiency of the vaccine [19]. Moreover, the SEIRS model also depicts the infectious diseases among with different parameters such as unequal birth and death rates, vaccinations for newborns and non-newborns and temporary immunity with the help of vital features of SI, SIS and SIR models. However, in case of SEIRS the mathematical approach in determined the disease-free and endemic equilibrium points with local stability were analyzed according to its epidemic conditions i.e. non-epidemic $R_0 \leq 1$ and epidemic $R_0 > 1$) using the time-series and phase portraits of the susceptible S, exposed E, infected I, and recovered R individuals [16].

In our study we discussed four classes of proposed model i.e. S = susceptible, E = exposed, I = infected and R = recovered of with different parameters including birth rate, natural death rate, disease death rate, vaccine for non-newborn and treatment rate. In addition, the regular set of values will be used for these parameters in numerical simulation. Further, graphical study has been investigated based On the numerical values. Moreover, the treatment rate function is supposed which is directly proportional to number of infectious patients up to certain limit. Further more, the stability analysis has been carried out by use of multiple endemic equilibrium points. Also, experimental work has been made on the bases of these equilibrium points and local stability. Thus, this research work will be helpful for the future study in the field of mathematical biology.

## 2. SEIR MODEL AND ITS BASIC REPRODUCTIVE NUMBER

The proposed SEIR model with limited (non-newborn only) vaccination and cost effective treatment will provide the whole portrait of contagious diseases and its corresponding with ecology. Figure 1 shows the block diagram of modified SEIR model, which is constructed by dividing the whole population $\Pi$ in four epidemic categories (classes) those are Susceptible (S), Exposed (E), Infected (I) and Recovered (R) [4, 9].

The four categories S, E, I and R of the SEIR model are depict for detail in Table 1. For the proposed SEIR model, the model permits with different birth and death rates, vaccinations only for non-newborns (i.e children and adults) and cost effective treatment for individuals from susceptible category.

The Table 2 summarizes the details of different +ive parameters lodge in the SEIR model for each of the four categories.

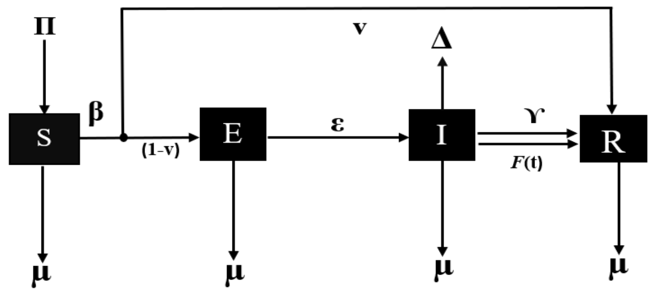



FIGURE 1. SEIR model with limited Vaccination and Cost effective treatment

TABLE 1. Categories

| Categories | Names | Units | Meanings |
|---|---|---|---|
| S | Susceptible specimens | No of Individuals | Individuals of susceptible to contagious who are limited vaccinated and are to be exposed |
| E | Exposed specimens | No of Individuals | Individuals of Exposed to contagious who contract the disease but not yet become infectious and not capable of transmit infection |
| I | Infected specimens | No of Individuals | Individuals of Infected specimen can pass the infection to other individuals of susceptible |
| R | Recovered specimens | No of Individuals | Individuals of Recovered from contagious disease who are treated from infection |

TABLE 2. Parameters

| Parameters | Names | Units | Meanings |
|---|---|---|---|
| $\prod$ | Birth rate | $\frac{\frac{\text{birth}}{\text{Person}}}{\text{day}}$ | Birth rate of (non-newborn) susceptible per year |
| $\mu$ | Natural Death rate | $\frac{\frac{\text{deaths}}{\text{Person}}}{\text{day}}$ | Natural death rate of recovered, exposed, infected and susceptible per year |
| $v$ | Vaccination non-newborn | Per day $(\frac{1}{day})$ | Rate of limited vaccination to susceptible |
| $\varepsilon$ | Transmission rate (Exposed to Infected) | per day | The rate at which individuals leave exposed category and enter into infected category |
| $\gamma$ | Transmission rate (Infected to Recovered) | per day | The rate at which individuals leave infected category and enter into recovered class |
| F(t) | Treatment Rate | per day | The rate at which the infected individual are treated |
| $\Delta$ | Disease Death Rate | $\frac{\frac{\text{deaths}}{\text{Person}}}{\text{day}}$ | Disease death rate of infected inviduals |

Arithmetically, the SEIR model is explicit as a system of ordinary differential equations given by [16, 17]:

$$
\begin{aligned}
S' &= \frac{dS}{dt} = \Pi - \beta SI - \mu S, \\
E' &= \frac{dE}{dt} = \beta SI - \mu E - \varepsilon E + (1-v)E, \\
I' &= \frac{dI}{dt} = \varepsilon E - \mu I - \Delta I - \gamma I - F(t), \\
R' &= \frac{dR}{dt} = \beta v + \gamma I + F(t) - \mu R.
\end{aligned} \tag{1}
$$

In this research, the treatment function is defined as

$$
F(t) = \begin{cases} kI & if \ 0 < I \leq I_0 \\ 0 & if \ I = 0 \\ c & if \ I > I_0 \end{cases}
$$

where $c = kI_0$ this tells that $F(t) \propto$ I as well as the number of infectious individuals are less or equal to a static value $I_0$ but later on treatment rate turn into constant. This research has main concern with cost effective treatment, in which medication and bedding in hospitals may or may not be sufficient.

The reduce system of (1) is enough to analyze because in first three equations of system (1) $R$ is not use

$$
\begin{aligned}
S' &= \frac{dS}{dt} = \Pi - \beta SI - \mu S, \\
E' &= \frac{dE}{dt} = \beta SI - \mu E - \varepsilon E + (1-v)E, \\
I' &= \frac{dI}{dt} = \varepsilon E - \mu I - \Delta I - \gamma I - F(t).
\end{aligned} \tag{2}
$$

From system (2)

$$
S' + E' + I' = \ \leq \Pi - \mu(S + E + I) \tag{3}
$$

Supposing we get

$$\overline{\Sigma} \leq \frac{\Pi}{\mu} \tag{4}$$

Thus we have $\lim_{n\to\infty} \sup(S+I+R) \leq \dfrac{\Pi}{\mu}$ so the possible and reasonable region for the set of equations of system (1) is

$$\Lambda = \{(S,E,I) : S+E+I \leq \frac{\Pi}{\mu}, S>0, E\geq 0, I\geq 0\}. \tag{5}$$

Therefore the system (2) is well posed by arithmetically and endemically in $\Lambda$ because the region $\Lambda$ is positively invariant w.r.t system (2).

For finding $R_0$ (i.e Basic Reproductive Number), the most reliable method is next generation method (N.G.M) [8, 18].

System (2) always gives Disease free equilibrium points i.e $X^0_{dfe} = (S^0, E^0, I^0) = (\dfrac{\Pi}{\mu}, 0, 0)$. Moreover for these disease free equilibrium points $I < I_0$, therefore the system(2) turns to

$$\begin{aligned} S' = \quad & \frac{dS}{dt} = \Pi - \beta SI - \mu S, \\ E' = \quad & \frac{dE}{dt} = \beta SI - (\mu + \varepsilon - (1-v))E, \\ I' = \quad & \frac{dI}{dt} = \varepsilon E - (\mu + \Delta + \gamma + k)I. \end{aligned} \tag{6}$$

Then system(6) may be written as

$$\frac{dY}{dt} = \digamma(Y) - \Upsilon(Y), \tag{7}$$

$$\frac{dY}{dt} = \begin{bmatrix} \beta SI \\ 0 \end{bmatrix} - \begin{bmatrix} (\mu+\varepsilon)E - (1-v)E \\ -\varepsilon E + \mu I + \Delta I + \gamma I + kI \end{bmatrix}.$$

The Jacobian matrices of transmission matrix $\digamma(Y)$ and transition matrix $\Upsilon(Y)$ at disease free equilibrium points $X_0^*$ are, respectively [5, 18]

$$D\digamma(X_0^*) = \begin{bmatrix} F & 0 \\ 0 & 0 \end{bmatrix}, \quad D\Upsilon(X_0^*) = \begin{bmatrix} V & 0 \\ J_1 & J_2 \end{bmatrix}$$

where

$$F = \begin{bmatrix} 0 & \beta\frac{\Pi}{\mu} \\ 0 & 0 \end{bmatrix}$$

and

$$V = \begin{bmatrix} \mu + \varepsilon - (1-v) & 0 \\ -\varepsilon & \mu + \gamma + \Delta + k \end{bmatrix}.$$

To remove confusion we suppose $\Omega = FV^{-1}$ and the N.G.M of system (2) is

$$\Omega = FV^{-1} = \begin{bmatrix} \frac{\varepsilon\beta\Pi}{\mu(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)} & \frac{\beta\Pi}{\mu(\mu+\gamma+\Delta+k)} \\ 0 & 0 \end{bmatrix}.$$

Now we will find the spectral radius of N.G.M [14] that is defined as $\rho(\Omega) = max\{eigen\ value\ of\ \Omega\}$

$$\Rightarrow \begin{vmatrix} \frac{\varepsilon\beta\Pi}{\mu(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)} - \lambda & \frac{\beta\Pi}{\mu(\mu+\gamma+\Delta+k)} \\ 0 & -\lambda \end{vmatrix} = 0.$$

Hence the basic reproductive number $R_0$ of system (2) is given by

$$R_0 = \frac{\varepsilon\beta\Pi}{\mu(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)} > 0 \tag{8}$$

## 3. Equilibrium Points of SEIR Model

Here we will find and discuss equilibrium points of our proposed model. First we known that, the disease free equilibrium points of system (2) $X^0_{dfe} = (S^0, E^0, I^0) = (\frac{\Pi}{\mu}, 0, 0)$ always exits when $I \leq I_0$ [16, 13]. Now we will find the endemic equilibrium points of system (2) which satisfies

$$\begin{aligned} \Pi - \beta SI - \mu S &= 0, \\ \beta SI - (\mu + \varepsilon - (1-v))E &= 0, \\ \varepsilon E - (\mu + \Delta + \gamma)I - F(t) &= 0. \end{aligned} \tag{9}$$

For above system, if $0 < I \leq I_0$, then $F(t) = kI$ and if $I > I_0$, then $F(t) = c$, Moreover If $R_0 > 1$, system (8) confess a unique positive result i.e $X^*_{ee} = (S^*, E^*, I^*)$ given by

$$\begin{aligned} \Pi - \beta S^* I^* - \mu S^* &= 0, \\ \beta S^* I^* - (\mu + \varepsilon - (1 - v))E^* &= 0, \\ \varepsilon E^* - (\mu + \Delta + \gamma + k)I^* &= 0. \end{aligned} \tag{10}$$

From system (10)

$$S^* = \frac{\Pi}{\beta I^* + \mu} = \frac{\Pi}{\mu(1 + \frac{\beta I^*}{\mu})} \tag{11}$$

in system (10)

$$E^* = \frac{(\mu + \Delta + \gamma + k)I^*}{\varepsilon} \tag{12}$$

From third equation of system (10)

$$I^* = \frac{\varepsilon E^*}{\mu + \Delta + \gamma + k}. \tag{13}$$

Put the value of $I^*$ in equation (12) we get

$$E^* = \frac{\beta \Pi \varepsilon - \mu(\mu + \Delta + \gamma + k)(\mu + \varepsilon - (1 - v))}{\beta \varepsilon(\mu + \varepsilon - (1 - v))}. \tag{14}$$

Put the value of $E^*$ from system (14) in equation (13) we get

$$I^* = \frac{\beta \Pi \varepsilon - \mu(\mu + \Delta + \gamma + k)(\mu + \varepsilon - (1 - v))}{\beta(\mu + \varepsilon - (1 - v))(\mu + \Delta + \gamma + k)}. \tag{15}$$

Putting the value of $I^*$ in equation (11) we get the value of $S^*$ i.e.

$$S^* = \frac{\Pi}{\mu R_0}. \tag{16}$$

We know that from equation (11) $S^* = \frac{\Pi}{\beta I^* + \mu}$ putting this value in equation (16) we get

$$I^* = \frac{\mu(R_0 - 1)}{\beta}. \tag{17}$$

Putting the value of $I^*$ in equation (13) we get

$$E^* = \frac{\mu(\mu + \Delta + \gamma + k)(R_0 - 1)}{\beta \varepsilon}. \tag{18}$$

Hence from equation (17) $R_0 \leq 1 + \frac{\beta I_0}{\mu} \cong Q_0$ iff $I^* \leq I_0$. Therefore $X^*_{ee} = (S^*, E^*, I^*)$ are endemic equilibrium points of system (2) iff $1 < R_0 \leq Q_0$. In system (9) when $I > I_0$, to get the positive solution of system (2), we solve S and E from first and third equation of system (9) respectively and substitute the value of S and E in second equation of system (9). We have $S = \frac{\Pi}{\mu+\beta I}$ and $E = \frac{(\mu+\gamma+\Delta)I+c}{\varepsilon}$ after substitution in second equation of system (9) we get

$$\begin{aligned}
&(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta)\beta I^2\\
&+[(\mu+\varepsilon-(1-v))((\mu+\gamma+\Delta)\mu+c\beta)-\beta\Pi\varepsilon]I\\
&+c(\mu+\varepsilon-(1-v))\mu=0
\end{aligned} \tag{19}$$

Suppose that

$$\begin{aligned}
(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta)\beta &= d,\\
(\mu+\varepsilon-(1-v))((\mu+\gamma+\Delta)\mu+c\beta)-\beta\Pi\varepsilon &= e,\\
(\mu+\varepsilon-(1-v))\mu &= f.
\end{aligned} \tag{20}$$

After putting the values in equation (19) we get

$$dI^2 + eI + f = 0. \tag{21}$$

The system (21) gives us discriminant i.e. $\overline{D} = e^2 - 4df$ with two positive real roots $e < 0$ and $\overline{D} \geq 0$.

As we know form equation (8)

$$\varepsilon\beta\Pi = [\mu(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)]R_0 \tag{22}$$

so

$$e = (\mu+\varepsilon-(1-v))[(\mu+\gamma+\Delta)\mu+c\beta-\mu(\mu+\gamma+\Delta+k)R_0]. \tag{23}$$

Putting the values of d, e and f in the equation of discriminant $\overline{D}$. We get

$$\begin{aligned}
\overline{D} =&[(\mu+\varepsilon-(1-v))((\mu+\gamma+\Delta)\mu+c\beta-\mu(\mu+\gamma+\Delta+k)R_0)]^2\\
&-4[(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta)\beta][c(\mu+\varepsilon-(1-v))\mu].
\end{aligned} \tag{24}$$

For positive real root $\overline{D} \geq 0$ we have

$$[((\mu+\gamma+\Delta)\mu+c\beta-\mu(\mu+\gamma+\Delta+k)R_0)] \geq 2\sqrt{(\mu+\gamma+\Delta)c\beta\mu}. \tag{25}$$

After simplification of above equation and for $e<0$ the $R_0$ is equivalent to

$$R_0 \geq 1+\frac{c\beta-\mu k}{\mu(\mu+\gamma+\Delta+k)}. \tag{26}$$

Therefore for equation(21) has two positive roots $I_{*1}$ and $I_{*2}$.

when $R_0 \geq Q_1$ where

$$I_{*1}=\frac{-e-\sqrt{\overline{D}}}{2d} \quad \text{and} \quad I_{*2}=\frac{-e+\sqrt{\overline{D}}}{2d} \tag{27}$$

then set

$$S_{*1}=\frac{\Pi}{\mu+\beta I_{*1}} \quad \text{and} \quad S_{*2}=\frac{\Pi}{\mu+\beta I_{*2}} \tag{28}$$

and

$$E_{*1}=E_{*2}=\frac{\mu(\mu+\gamma+\Delta+k)}{\beta\varepsilon}(R_0-1) \tag{29}$$

then $X_{*i}=(S_{*i},E_{*i},I_{*i}), i=1,2$ are endemic equilibrium points of system (2) if $I_{*i}>I_0$. As we know

$$I_{*1}>I_0 \quad \text{iff } 2\beta(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta)I_0+e<-\sqrt{\overline{D}}. \tag{30}$$

In above equation right hand side is negative and greater than the value at left hand side so if negative value is greater therefore the left hand value is always less than zero i.e.

$$e+2\beta(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta)I_0<0. \tag{31}$$

It follows the definition of $e$ that is

$$\mu(\mu+\gamma+\Delta+k)R_0 > 2\beta I_0(\mu+\gamma+\Delta) +\mu(\mu+\gamma+\Delta)+c\beta. \tag{32}$$

Adding and subtracting $k\mu$ in above equation we get:

$$R_0 > 1 + \frac{2\beta I_0(\mu+\gamma+\Delta)}{\mu(\mu+\gamma+\Delta+k)} + \frac{c\beta - k\mu}{\mu(\mu+\gamma+\Delta+k)} \cong Q_2. \tag{33}$$

Similarly if

$$I_{*2} > I_0 \quad \text{iff} 2\beta(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta)I_0 + e < \sqrt{D}. \tag{34}$$

Then

$$R_0 < 1 + \frac{2\beta I_0(\mu+\gamma+\Delta)}{\mu(\mu+\gamma+\Delta+k)} + \frac{c\beta - k\mu}{\mu(\mu+\gamma+\Delta+k)} \cong Q_2. \tag{35}$$

By a comparable statement we get that $I_2 < I_0$ iff $R_0 > Q_2$ now we will sum up the above discussion as following:

$$\begin{aligned} &\text{Let} \quad Q_0 = 1 + \frac{\beta I_0}{\mu},\ Q_1 = 1 + \frac{c\beta - \mu k}{\mu(\mu+\gamma+\Delta+k)} + \frac{2\sqrt{(\mu+\gamma+\Delta)c\beta\mu}}{\mu(\mu+\gamma+\Delta+k)} \\ &\qquad \text{and } Q_2 = 1 + \frac{2\beta I_0(\mu+\gamma+\Delta)}{\mu(\mu+\gamma+\Delta+k)} + \frac{c\beta - k\mu}{\mu(\mu+\gamma+\Delta+k)}. \end{aligned} \tag{36}$$

1. Disease free equilibrium points i.e.$X^0_{dfe} = (S^0, E^0, I^0) = (\frac{\Pi}{\mu}, 0, 0)$ always exist in system (2).

2. There is existence of endemic equilibrium points i.e. $X^*_{ee} = (S^*, E^*, I^*)$ of system (2) iff $1 < R_0 \leq Q_0$.

3. There is existence of two more endemic equilibrium points i.e. $X_{*i} = (S_{*i}, E_{*i}, I_{*i}), i = 1, 2$ iff $R_0 > Q_1$ and $R_0 > Q_2$.

## 4. Local Stability of Equilibrium Points

In this section we analyze the eigenvalues of Jacobian matrices of system (2) and check the local stability of disease free equilibrium points and endemic equilibrium points [16]. The

Jacobian matrix is calculated from equilibrium points as:

$$\begin{bmatrix} \frac{dS}{dt} \\ \\ \frac{dE}{dt} \\ \\ \frac{dI}{dt} \\ \end{bmatrix} = \begin{bmatrix} \Pi - \beta SI - \mu S \\ \\ \beta SI - (\mu+\varepsilon)E + (1-v)E \\ \\ \varepsilon E - \mu I - \Delta I - \gamma I - kI \\ \end{bmatrix}.$$

Where Jacobian matrix w.r.t equilibrium points is

$$J(X^0_{dfe} or X^*_{ee}) = J(S,E,I) = \begin{bmatrix} \frac{\partial S}{\partial S} & \frac{\partial S}{\partial E} & \frac{\partial S}{\partial I} \\ \\ \frac{\partial E}{\partial S} & \frac{\partial E}{\partial E} & \frac{\partial E}{\partial I} \\ \\ \frac{\partial I}{\partial S} & \frac{\partial I}{\partial E} & \frac{\partial I}{\partial I} \end{bmatrix}$$

$$= \begin{bmatrix} -\mu & 0 & -\beta S \\ \\ 0 & -(\mu+\varepsilon-(1-v)) & 0 \\ \\ 0 & \varepsilon & -(\mu+\gamma+\Delta+k) \end{bmatrix}$$

by using the jacobian matrix we evaluate the eigenvalues from $|J(X^0_{dfe} or X^*_{ee}) - \lambda I| = 0$. then we check our system either it is stable or not. If all the eigenvalues are negative then system is stable otherwise if at least one eigenvalue is positive the system is unstable.

**4.1. Disease free equilibrium points $X^0_{dfe}$.** By using the Disease free equilibrium points i.e. $X^0_{dfe} = (S^0, E^0, I^0) = (\frac{\Pi}{\mu}, 0, 0)$ , for system (6) the jacobian matrix $J(X^0_{dfe})$ is given as:

$$J(X^0_{dfe}) = \begin{bmatrix} -\mu & 0 & -\beta\frac{\Pi}{\mu} \\ \\ 0 & -(\mu+\varepsilon-(1-v)) & 0 \\ \\ 0 & \varepsilon & -(\mu+\gamma+\Delta+k) \end{bmatrix}.$$

Now eigenvalues are found by using the characteristic equation which we discuss below:

(37) $$|J(X^0_{dfe} or X^*_{ee}) - \lambda I| = 0$$

$$\left|\begin{bmatrix} -\mu & 0 & \frac{\beta\pi}{\mu} \\ 0 & -(\mu+\varepsilon-(1-v)) & 0 \\ 0 & \varepsilon & -(\mu+\gamma+\Delta+k \end{bmatrix} - \lambda \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}\right| = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}$$

$$(-\mu-\lambda)[(-(\mu+\varepsilon-(1-v))-\lambda)(-(\mu+\gamma+\Delta+k)-\lambda)-0] = 0$$

(38)

$$\Rightarrow \lambda = -\mu,\ -(\mu+\varepsilon-(1-v)),\ -(\mu+\gamma+\Delta+k).$$

Similarly when $F(t) = 0$

(39) $$\Rightarrow \lambda = -\mu,\ -(\mu+\varepsilon-(1-v)),\ -(\mu+\gamma+\Delta).$$

All the eigenvalues are negative in above result, so the disease free equilibrium points are locally stable for system (2).

### 4.2. Endemic equilibrium points $X^*_{ee}$. As researcher knows

$$J(S,E,I) = \begin{bmatrix} -\mu-\beta I^* & 0 & -\beta S^* \\ \beta I^* & -(\mu+\varepsilon-(1-v)) & 0 \\ 0 & \varepsilon & -(\mu+\gamma+\Delta+k) \end{bmatrix}.$$

For system (4)

$$J(X^*_{ee}) = \begin{bmatrix} \mu R_0 & 0 & -\beta\frac{\Pi}{\mu R_0} \\ \mu(R_0-1) & -(\mu+\varepsilon-(1-v)) & 0 \\ 0 & \varepsilon & -(\mu+\gamma+\Delta+k) \end{bmatrix}$$

now by characteristic equation i.e. $|J(X_{ee}^*)-\lambda I|=0$ we have

$$\begin{vmatrix} \mu R_0-\lambda & 0 & -\beta\frac{\Pi}{\mu R_0} \\ \mu(R_0-1) & -(\mu+\varepsilon-(1-v))-\lambda & 0 \\ 0 & \varepsilon & -(\mu+\gamma+\Delta+k)-\lambda \end{vmatrix}=0$$

$$\begin{aligned} &\lambda^3+[\mu R_0+(\mu+\varepsilon-(1-v))+(\mu+\gamma+\Delta+k)]\lambda^2 \\ &+[\mu R_0[(\mu+\varepsilon-(1-v))+(\mu+\gamma+\Delta+k)]+(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)]\lambda \\ &+\mu R_0(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)+\frac{\beta\Pi\varepsilon(R_0-1)}{R_0}=0. \end{aligned} \tag{40}$$

For our requirement to check the local stability of endemic equilibrium points Routh-Hurwitz criteria is used [15, 16]. Suppose

$$\ell_0=1,\ \ell_1=[\mu R_0+(\mu+\varepsilon-(1-v))+(\mu+\gamma+\Delta+k)],$$

$$\ell_2=[\mu R_0[(\mu+\varepsilon-(1-v))+(\mu+\gamma+\Delta+k)]+(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)], \tag{41}$$

$$\ell_3=\mu R_0(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k)+\frac{\beta\Pi\varepsilon(R_0-1)}{R_0}.$$

Then equation (41) becomes

$$\ell_0\lambda^3+\ell_1\lambda^2+\ell_2\lambda+\ell_3=0. \tag{42}$$

It is clear that, $\ell_0>0,\ \ell_1>0,\ \ell_2>0,\ \ell_3>0$

$$\begin{aligned} \ell_1\ell_2-\ell_3=&[\mu R_0+(\mu+\varepsilon-(1-v))+(\mu+\gamma+\Delta+k)][\mu R_0[(\mu+\varepsilon-(1-v)) \\ &+(\mu+\gamma+\Delta+k)]-[\mu R_0(\mu+\varepsilon-(1-v))(\mu+\gamma+\Delta+k) \\ &+\frac{\beta\Pi\varepsilon(R_0-1)}{R_0}]>0. \end{aligned} \tag{43}$$

Above discussion satisfies the three conditions of Routh-Hurwitz criteria given below:

$$\ell_1 > 0, \tag{44}$$

$$\ell_3 > 0 \tag{45}$$

and

$$\ell_1\ell_2 - \ell_3 > 0. \tag{46}$$

Hence by Routh-Herwitz criteria, all the eigenvalues of $J(X_{ee}^*)$ are negative therefore endemic equilibrium points are locally stable for proposed model.

## 5. NUMERICAL SIMULATION

The proposed SEIR model with non-newborn vaccination and cost effective treatment was estimated in Matlab. Table 3 lists a regular set of mathematical values for parameters of proposed model for all the experiments of malaria.

TABLE 3. Mathematical values for parameters of proposed model

| Parameters | values | Parameters | values |
|---|---|---|---|
| $\prod$ | 0.0000520 | $\varepsilon$ | 0.33333 |
| $\mu$ | 0.0000202 | $\gamma$ | 0.14286 |
| $v$ | 0.70 | $\Delta$ | 0.000027 |
| $\beta$ | 0.20 (No epidemic) 5 (epidemic) | F(t) | 0.01 |

The value of $R_0$ depends upon above values of parameters and computed for SEIR model in Table 4. Moreover, we will get two values of $R_0$ because of two conditions i.e. epidemic and no epidemic.

TABLE 4. Mathematical values of $R_0$

| Parameters | values |
|---|---|
| $R_0$ | 0.8615 (No epidemic) 21.5370 (epidemic) |

**5.1. Experimental outcomes.** Numerical simulations is perform using the proposed SEIR model with non-newborn vaccination and cost effective treatment along with constants and mathematical values of parameters of our model in Table 3. So as to distinguish between the occurrence for the epidemic conditions of $R_0$ i.e. no epidemic ($R_0 \leq 1$) and epidemic ($R_0 > 1$) are analyze separately. The local stability of disease free equilibrium points and endemic equilibrium points for both cases i.e. no epidemic and epidemic are estimated with help of corresponding eigenvalues and jacobian matrix.

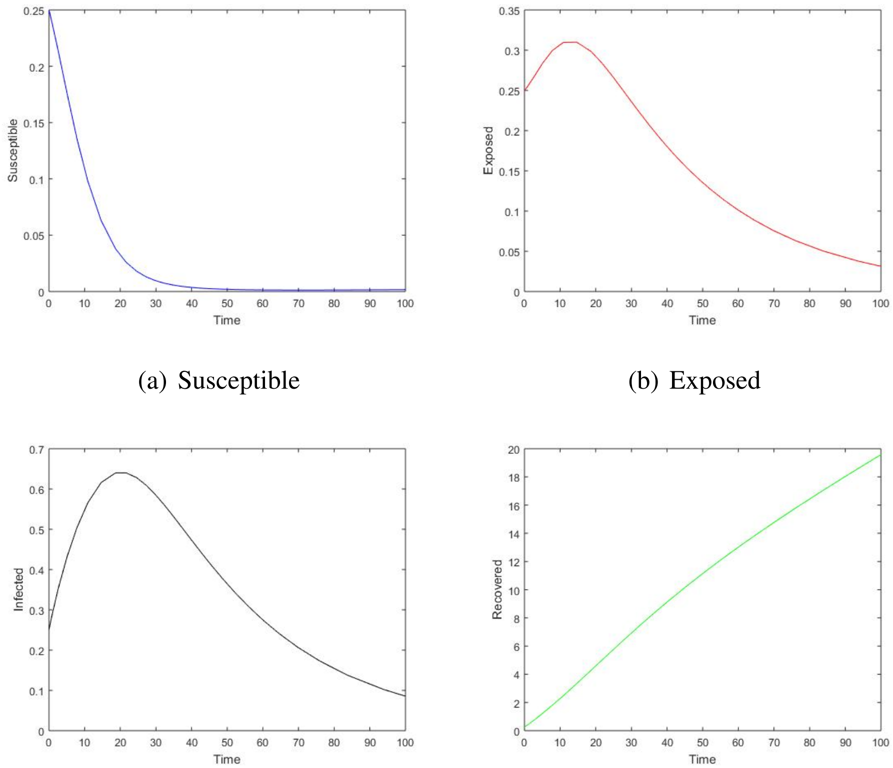
**5.1.1.** ***No epidemic***. The epidemic required condition $R_0$ is calculated as $R_0 = 0.8615$ implies no epidemic for the contagious disease because $R_0 \leq 1$. The value of $R_0$ depends upon the mathematical values of model parameters and constants with $\beta = \frac{1}{5}$ for our SEIR model. Here $\beta = \frac{1}{5}$ means that 0.2 susceptible participants becomes exposed because of infected participants and left the susceptible category and enter the exposed category per day. The disease free equilibrium points $X^0_{dfe}$ and endemic equilibrium points $X^*_{ee}$ and eigenvalues $\lambda_i$ of their jacobian matrices i.e. $J(X^0_{dfe})$ and $J(X^*_{ee})$ in company with local stabilities.

TABLE 5. Local stability $\beta = \frac{1}{5}(noEpidemic)$

| Points | S | E | I | $\lambda_1$ | $\lambda_2$ | $\lambda_3$ | Stability |
|---|---|---|---|---|---|---|---|
| DEF | 2.5743 | 0 | 0 | -0.0000202 | -0.5800000 | -0.14000000 | Stable |
| EE | 2.9822 | -0.000014416 | -0.000013991 | -0.580000 | -0.3400000 | -0.00001 | Stable |

Table 5 shows that the disease free equilibrium points i.e. $X^0_{def}$ are locally stable because all the eigenvalues i.e. $\lambda_1$ , $\lambda_2$ and $\lambda_3$ are negative with $\beta = \frac{1}{5}$. Where as the endemic equilibrium points i.e. $X^*_{ee}$ are also locally stable (because all eigenvalues are negative in it) with $\beta = \frac{1}{5}$. Figure 2 describes the two dimensional phase portraits of four categories with 0.25 initial conditions of S, E, I and R.

**5.1.2.** ***Epidemic***. The epidemic required condition $R_0$ is calculated as $R_0 = 21.5370$ implies epidemic for the contagious disease because $R_0 > 1$. The value of $R_0$ depends upon the mathematical values of model parameters and constants with $\beta = 5$ for our SEIR model. Here $\beta = 5$




(a) Susceptible (b) Exposed

(c) Infected (d) Recovered

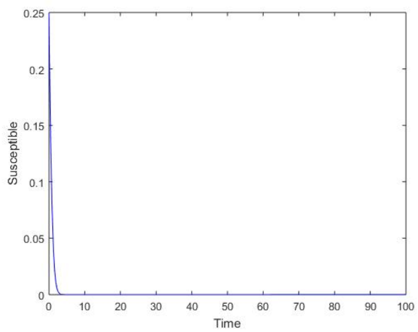
FIGURE 2. Two dimensional phase portraits of four categories of S, E, I and R ($\beta = 1/5(N0Epidemic)$).

means that 5 susceptible participants becomes exposed because of infected participants and left the susceptible category and enter the exposed category per day. Table 6 shows the disease free equilibrium points $X^0_{dfe}$ and endemic equilibrium points $X^*_{ee}$ and eigenvalues $\lambda_i$ of their jacobian matrices i.e. $J(X^0_{dfe})$ and $J(X^*_{ee})$ in company with local stabilities.

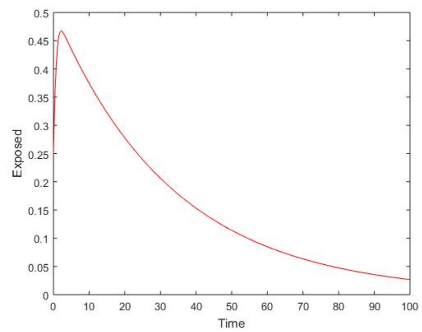
TABLE 6. Local stability $\beta = 5(Epidemic)$

| Points | S | E | I | $\lambda_1$ | $\lambda_2$ | $\lambda_3$ | Stability |
|---|---|---|---|---|---|---|---|
| DEF | 2.5743 | 0 | 0 | -0.0000202 | -0.5800000 | -0.1400000 | Stable |
| EE | 0.1195 | 0.0000829 | 0.00008548 | -0.5806000 | -0.3390000 | -0.0009000 | Stable |

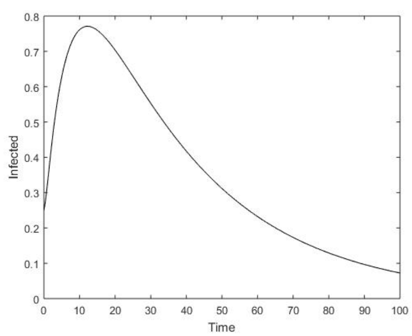
Table 6 shows that the disease free equilibrium points i.e. $X^0_{def}$ are locally stable because all the eigenvalues i.e. $\lambda_1$ , $\lambda_2$ and $\lambda_3$ are negative with $\beta = 5$. Where as the endemic equilibrium points i.e. $X^*_{ee}$ are also locally stable (because all three eigenvalues are negative in it. Moreover, if only one value is negative then it will locally unstable) with with $\beta = 5$. Figure 3 describes the two dimensional phase portraits of four categories with initial condition 0.25.



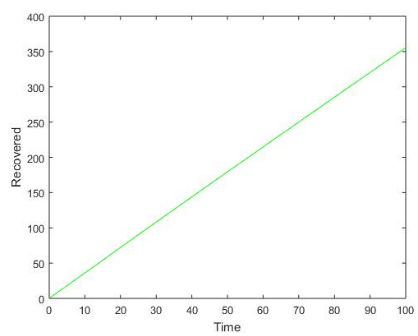

(a) Susceptible




(b) Exposed




(c) Infected




(d) Recovered

FIGURE 3. Two dimensional phase portraits of four categories of S, E, I and R ($\beta = 5(Epidemic)$).

## 6. CONCLUSION

In this research work, modified SEIR model based on non-newborn vaccination and cost effective treatment for mutual benefits is proposed. Herein, we generalize models of vaccination and treatment for large population. The main focus was to handle a problem when hospitals has lack of bedding and medication some time in war like conditions and in our rural areas and villages. Further, by using basic reproductive number $R_0$, the behaviour of our proposed model has been found. The Disease free equilibrium points $X^0_{dfe}$ and endemic equilibrium points $X^*_{ee}$

exists and model is locally stable. Moreover, the proposed model is epidemic when $R_0 \leq 1$ and endemic when $R_0 > 1$. For future, we may modified the model w.r.t to age limit structure, vital dynamics and isolations in climate behaviour to produce suitable epidemic models in the field of mathematical biology.

## CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

## REFERENCES


[1] S.M. Moghadas, A.B. Gumel, A mathematical study of a model for childhood diseases with non-permanent immunity, J. Comput. Appl. Math. 157 (2003), 347–363.

[2] J. Saramäki, K. Kaski, Modelling development of epidemics with dynamic small-world networks, J. Theor. Biol. 234 (2005), 413–421.

[3] N. Badshah, H. Shah, and M. Javid, Estimation of basic reproduction number for dengue fever in Lahore, Pakistan, Sains Malaysiana. 44 (2015), 1423-1430.

[4] S.A.A. Sheikh, Modeling and analysis of an seir epidemic model with a limited resource for treatment, Glob. J. Sci. Front. Res. Math. Decision Sci. 12 (2012), 56-66.

[5] Y. Bai, X. Mu, Global asymptotic stability of a generalized sirs epidemic model with transfer from infectious to susceptible, J. Appl. Anal. Comput. 8 (2018), 402-412.

[6] H.W. Hethcote, The mathematics of infectious diseases, SIAM Rev. 42 (2000), 599-653.

[7] S. Basu, G.H. Friedland, J. Medlock, J.R. Andrews, N.S. Shah, N.R. Gandhi, A. Moll, P. Moodley, A.W. Sturm, A.P. Galvani, Averting epidemics of extensively drug-resistant tuberculosis, Proc. Nat. Acad. Sci. 106 (2009), 7672–7677.

[8] O. Diekmann, J.A.P. Heesterbeek, M.G. Roberts, The construction of next-generation matrices for compartmental epidemic models, J. R. Soc. Interface. 7 (2009), 873-885.

[9] S. Elkhaiar, A. Kaddar, Stability analysis of an seir model with treatment, Res. Appl. Math. 1 (2017), 1-16.

[10] D.A. Focks, E. Daniels, D.G. Haile, J.E. Keesling, A simulation model of the epidemiology of urban dengue fever: literature analysis, model development, preliminary validation, and samples of simulation results, Amer. J. Trop. Med. Hygiene. 53 (1995), 489-506.

[11] H.W. Hethcote, The mathematics of infectious diseases, SIAM Rev. 42 (2000), 599-653.

[12] M.J. Keeling, P. Rohani, Modeling infectious diseases in humans and animals, Princeton University Press, Princeton, (2011).

[13] G. Li, W. Wang, Z. Jin, Global stability of an seir epidemic model with constant immigration, Chaos Solitons Fractals. 30 (2006), 1012-1019.

[14] M.G. Roberts, J.A.P. Heesterbeek, A new method for estimating the effort required to control an infectious disease, Proc. R. Soc. Lond. Ser. B: Biol. Sci. 270 (2003), 1359-1364.

[15] G.C. Smith, C.L. Cheeseman, A mathematical model for the control of diseases in wildlife populations: culling, vaccination and fertility control, Ecol. Model. 150 (2002), 45-53.

[16] M. Trawicki, Deterministic seirs epidemic model for modeling vital dynamics, vaccina- tions, and temporary immunity, Mathematics. 5 (2017), 7.

[17] V. Tweedle, R.J. Smith,A Mathematical Model of Bieber Fever: The most infectious disease of our time. In: Mushayabasa, S., Bhunu, C.P. (eds.) Understanding the Dynamics of Emerging and Re-Emerging Infectious Diseases using Mathematical Models, ch. 7, pp. 157–177. Transworld Research Network (2012).

[18] H.M. Yang, The basic reproduction number obtained from jacobian and next generation matrices-a case study of dengue transmission modelling, Biosystems. 126 (2014), 52-75.

[19] O.D. Makinde, On non-perturbative approach to transmission dynamics of infectious diseases with waning immunity, Int. J. Nonlinear Sci. Numer. Simul. 10 (2009), 451-458.

[20] W. Yang, C. Sun, J. Arino, Global analysis for a general epidemiological model with vaccination and varying population, J. Math. Anal. Appl. 372 (2010), 208-223.