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A STUDY ON SEIQR MATHEMATICAL MODEL WITH VACCINATION AND PREVENTIVE CONTROL EFFORTS

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Abstract

We present the dynamics of a SEIQR mathematical model with vaccination and preventive control measure in the susceptible class. The basic reproduction number of the model dynamics is obtained by using the next generation matrix method. The disease free equilibrium point of the model is found to be locally asymptotically stable if $R_0 \mid_{\omega=0} < 1$ and a unique endemic equilibrium point exist if $R_0 \mid_{\omega=0} > 1$. The disease free equilibrium point of the model is found to be globally asymptotically stable if $R_0 \mid_{\omega=0} \leq 1$ by using a suitable Lyapunov function. The contribution of the model parameters on the basic reproduction number is also determined through sensitivity analysis.

Keywords: Endemic equilibrium; Sensitivity Analysis; Lyapunov Function, Basic Reproduction Number, Stability.
MSC2010: 92B05.

1 Introduction

Mathematical models give an insight into the dynamics of a disease in a population and the factors responsible for the spread of the disease with the help of mathematical equations to emulate real life situations. The SIR (Susceptible, Infected, Recovered) mathematical model is the building block of most epidemic model. It was first introduced in 1927 by Kermack and Mckendrick. The fundamental parameters in the SIR model are the contact rate and recovery rate. However, the SIR model is not sufficient to effectively capture the dynamics of most diseases and that is why it has been extended to involve other compartments like exposed compartment, isolated compartment, quarantined compartment etc for effective analysis [1, 2]. Cao and Zhou formulated a stochastic SIRQ mathematical model with quarantined adjusted incidence by examining the qualitative behaviours [3]. Yan and Zou used a SEQIJR mathematical model to model SARS by finding the

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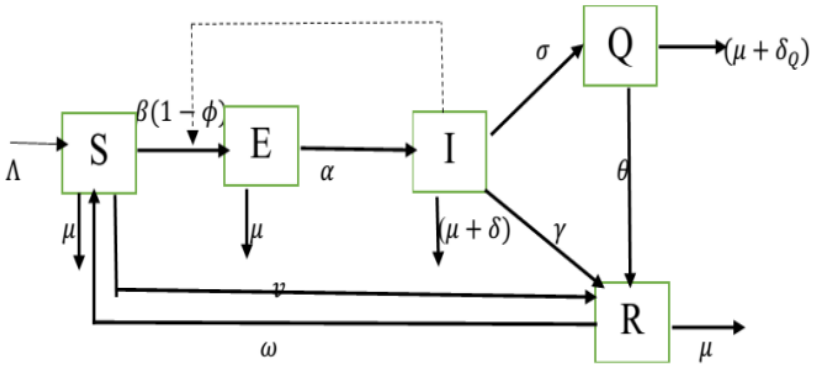

Fig.1. Flow chat of the model

optimal control strategies to manage the disease [4]. Quarantine/Isolation model can be used to model novel diseases like COVID-19 as seen in [5–8].
SEIQR models also have applications in information technology. Mishra and Ja [9] used the SEIQRS mathematical model to study the transmission of malicious objects in a computer network. Zheng et al. [10] used a modified SEIQR model to study the effects of different quarantined rates on worm propagation in mobile internet. It was established that a quarantined strategy that reduces viruses spread will be of advantage to manufacturers to isolate equipment more effectively and reduce economic losses.
In this research work, we use an expanded SEIQR mathematical model with vaccination and preventive effects captured in the model to analyze disease dynamics in a population and the impact of key parameters on the basic reproduction number.

2 Model Formulation

The population is divided into five compartments: S represents the susceptible compartment; E represents the exposed compartment; I represents the infectious compartment; Q represents the quarantined compartment and R represents the recovered compartment. The susceptible population is increased by recruitment at rate Λ and loss of immunity from the recovered class at rate ω. It is reduced as a result of interaction with infectious population and vaccination at rate β and v respectively which leads to an increase in the exposed and recovered population respectively. We use ϕ denote the fraction of the population who make preventive efforts to prevent contact with infectious people. The exposed population is reduced by migration to infectious class after a complete incubation of the disease at rate α. The infectious population is reduced by effective treatment at rate γ, progression to quarantine at rate σ and disease induced death at rate δ. The quarantined class is is reduced by effective treatment at rate θ and disease induced death at rate δ_Q. The recovered population is increased by effective treatment from the infectious class and quarantined class. Every compartment is reduced by natural death at rate μ. The model is thus described by the following systems of differential equations given below.

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$$\frac{dS}{dt} = \Lambda - \beta(1-\phi)SI - (\mu+v)S + \omega R \tag{2.1}$$
$$\frac{dE}{dt} = \beta(1-\phi)SI - (\alpha+\mu)E \tag{2.2}$$
$$\frac{dI}{dt} = \alpha E - (\sigma+\mu+\delta+\gamma)I \tag{2.3}$$
$$\frac{dQ}{dt} = \sigma I - (\theta+\delta_Q+\mu)Q \tag{2.4}$$
$$\frac{dR}{dt} = \gamma I + \theta Q + vS - (\mu+\omega)R \tag{2.5}$$

The parameters used in the model $(2.1)-(2.5)$ are described in Table 1.

Table 1. The description of the parameters of model.

Definition	Symbols
Recruitment term of the susceptible humans	Λ
Transmission rate contact rate	β
Natural death rate	μ
Progression rate from infectious stage to quarantined stage	σ
Progression rate from exposed stage to infectious stage	α
Disease induced death rate at infectious stage	δ
Disease induced death rate at quarantined stage	δ_Q
Effective treatment rate from infectious stage	γ
Effective treatment rate from quarantined stage	γ
Vaccination rate	v
Loss of immunity rate	ω

3 Results and discussions

3.1 Positivity of solutions

Theorem 1: (Positivity of solutions). Let $\mathcal{R}$ defined by $\{S(t), E(t), I(t), Q(t), R(t) \in \mathbb{R}^5_+\}$ with initial conditions $S(0) \geq 0, E(0) \geq 0, I0) \geq 0, Q(0) \geq 0, R(0) \geq 0$ then the solution of $S(t), E(t), I(t), Q(t), R(t)$ for system $(2.1)-(2.5)$ are positive for $t \geq 0$.

Proof: Equation (2.1) can be reduced to

$$\frac{dS}{dt} \geq \Lambda - (\mu+v)S \tag{3.1}$$

Solving (3.1) gives

$$S(t) \geq \frac{\Lambda}{(\mu+v)} + \left(S(0) - \frac{\Lambda}{(\mu+v)}\right)e^{-(\mu+v)t} \geq 0$$

Similar procedure establishes the positivity of the solution of $E(t), I(t), Q(t), R(t)$.

3.2 Invariant region

Theorem 2: (Invariant region). The feasible region $\mathcal{R}$ defined by $\{S(t), E(t), I(t), Q(t), R(t) \in \mathbb{R}^5_+ : N(0) \leq N(t) \leq \frac{\Lambda}{\mu}\}$ with initial conditions $S(0) \geq 0, E(0) \geq 0, I0) \geq 0, Q(0) \geq 0, R(0) \geq 0$ is positive invariant for system $(2.1)-(2.5)$.

Proof: $N(t) = S(t) + E(t) + I(t) + Q(R) + R(t)$ represents the total human population.

$$\frac{dN}{dt} = \Lambda - \mu N - \delta I - \delta_Q Q \tag{3.2}$$

$$\frac{dN}{dt} \leq \Lambda - \mu N \tag{3.3}$$

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Solving (3.3) gives

$$0 \leq 0N(t) \leq \left(N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1 - e^{-\mu t}) \right)$$

As $t \to \infty$,

$$N(0) \leq N(t) \leq \frac{\Lambda}{\mu} \tag{3.4}$$

The region where the model makes epidemiological sense is established and it is positively invariant and globally attracting in $\mathbb{R}^5_+$ with respect to the system under consideration.

3.3 Disease-free equilibrium point

The disease-free equilibrium point of system is obtained by setting equations $(2.1) - (2.5)$ to zero with the condition that there is no infection in the population. It exists at the point

$$\pi_0 = \left(\frac{\Lambda(\mu + \omega)}{(\mu + v)(\mu + \omega) - v\omega}, 0, 0, 0, \frac{\Lambda v}{(\mu + \omega)(\mu + v) - v\omega} \right) \tag{3.5}$$

3.4 Basic reproduction number

The next generation matrix approach by Driessche and Watmough [11] is applied to evaluate the basic reproduction number. The nonlinear terms with the new infection $\mathcal{F}$ and the outflow term $\mathcal{V}$ are given by

$$\mathcal{F} = \begin{pmatrix} \beta(1-\phi)SI \\ 0 \end{pmatrix}$$

$$\mathcal{V} = \begin{pmatrix} (\alpha + \mu)E \\ -\alpha E + (\sigma + \mu + \delta + \gamma)I \end{pmatrix}$$

The partial derivative of $\mathcal{F}$ and $\mathcal{V}$ with respect to E and I at the disease free equilibrium point gives

$$\mathbf{F} = \begin{pmatrix} 0 & \frac{\beta(1-\phi)\Lambda(\mu+\omega)}{(\mu+v)(\mu+\omega)-v\omega} \\ 0 & 0 \end{pmatrix}$$

$$\mathbf{V} = \begin{pmatrix} (\alpha + \mu) & 0 \\ -\alpha & (\sigma + \mu + \delta + \gamma) \end{pmatrix}$$

$$R_0 = \rho(\mathbf{F}\mathbf{V}^{-1}) = \frac{\mathbf{\Lambda}\alpha\beta(\mathbf{1} - \phi)(\mu + \omega)}{(\alpha + \mu)(\sigma + \mu + \delta + \gamma)[(\mu + \mathbf{v})(\mu + \omega) - \mathbf{v}\omega]}$$

When $\omega = 0$, the basic reproduction number becomes

$$R_0 \mid_{\omega=0} = \frac{\Lambda\alpha\beta(1 - \phi)}{(\alpha + \mu)(\sigma + \mu + \delta + \gamma)(\mu + v)}$$

3.5 Local stability of disease free equilibrium

Theorem 3: (Local stability of disease free equilibrium). The disease-free equilibrium for the system $(2.1) - (2.5)$ is locally asymptotically stable if $R_0 \mid_{\omega=0} < 1$ and unstable otherwise.

Proof: We shall consider the case when $\omega = 0$. The Jacobian matrix evaluated at the disease-free equilibrium is given by

$$J(\pi_0) = \begin{pmatrix} -(\mu + v) & 0 & -\frac{\beta(1-\phi)\Lambda}{(\mu+v)} & 0 & 0 \\ 0 & -(\alpha + \mu) & \frac{\beta(1-\phi)\Lambda}{(\mu+v)} & 0 & 0 \\ 0 & \alpha & -(\sigma + \mu + \delta + \gamma) & 0 & 0 \\ 0 & 0 & \alpha & -(\theta + \delta_Q + \mu) & 0 \\ 0 & 0 & \gamma & \theta & -\mu \end{pmatrix}$$

Some of the roots of the characteristic equation are are $-\mu$, $-(\mu + v)$ and $-(\theta + \delta_Q + \mu)$. The others roots can be obtained from the sub matrix given below.

$$\begin{pmatrix} -(\alpha + \mu) & \frac{\beta(1-\phi)\Lambda}{(\mu+v)} \\ \alpha & -(\sigma + \mu + \delta + \gamma) \end{pmatrix}$$

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The characteristic equation has negative root if the trace is negative and the determinant is positive.
Trace $J(\pi_0) = -(\alpha+\mu) - (\sigma+\mu+\delta+\gamma) < 0$
Determinant of $J(\pi_0) = (\alpha+\mu)(\sigma+\mu+\delta+\gamma)(1 - R_0\mid_{\omega=0})$. It is positive if $R_0 < 1$.
Hence, the disease-free equilibrium for the system $(2.1)-(2.5)$ is locally asymptotically stable if $R_0\mid_{\omega=0} < 1$ and unstable otherwise.

3.6 Existence of endemic equilibrium

Theorem 4: (Existence of endemic equilibrium). The model $(2.1)-(2.5)$ has an endemic equilibrium when $R_0\mid_{\omega=0} > 1$.

Proof: Let $E^*_{end} = (S^*, E^*, 1^*, Q^*, R^*)$ be a non trivial equilibrium of the model $(2.1)-(2.5)$. The model $(2.1)-(2.5)$ at steady state becomes

$$\begin{aligned}
S^* &= \frac{\Lambda}{(\mu+v)R_0\mid_{\omega=0})} \\
E^* &= \frac{\Lambda(R_0\mid_{\omega=0} -1)}{(\mu+v)R_0\mid_{\omega=0})} \\
I^* &= \frac{(\mu+v)(R_0\mid_{\omega=0} -1)}{\beta\beta(1-\phi)} \\
Q^* &= \frac{\sigma(\mu+v)(R_0\mid_{\omega=0} -1)}{\beta(1-\phi)(\theta+\delta_Q+\mu)} \\
R^* &= \frac{1}{\mu}\left[\left(\frac{\theta\sigma}{(\theta+\delta_Q+\mu)}+\gamma\right)\left(\frac{(\mu+v)(R_0\mid_{\omega=0} -1)}{\beta(1-\phi)}\right) + \frac{\Lambda v}{(\mu+v)R_0\mid_{\omega=0})}\right]
\end{aligned}$$

3.7 Global stability

Theorem 5: (Global stability of disease free equilibrium).The disease free equilibrium point of the model $(2.1)-(2.5)$ is globally asymptotically stable if $R_0\mid_{\omega=0} \leq 1$.

Proof: Consider the following linear Lyapunov function:

$$V = \alpha E + (\alpha+\mu)I$$
$$\dot{V} = \alpha[\beta(1-\phi)SI - (\alpha+\mu)E] + (\alpha+\mu)[\alpha E - (\sigma+\mu+\delta+\gamma)I]$$

Simplifying gives

$$\dot{V} \leq (\alpha+\mu)(\sigma+\mu+\delta+\gamma)[R_0\mid_{\omega=0} -1]I$$

It shows that $\dot{V} \leq 0$ if $R_0 < 1$ with equality if $R_0\mid_{\omega=0} = 1$ or $I = 0$. This shows that the largest invariant set in $\{S(t), E(t), I(t), Q(t), R(t) \in \mathbb{R}^5_+\}$ is the singleton π_0. Therefore, by the Lasalle invariance principle [12], every solution to system $(2.1)-(2.5)$ with initial conditions in $\mathbb{R}^5_+$ approaches π_0 as $t \to \infty$

3.8 Sensitivity analysis

The normalised forward sensitivity index of a variable x that depends on a parameter, P is defined as:

$$\Upsilon^P_x = \frac{\partial P}{\partial x} \times \frac{x}{P}$$

Positive sensitivity index shows a direct proportionality with respect to the basic reproduction number while negative index implies inverse proportionality. Sensitivity index of the basic reproduction number with respect to the model parameters are computed below.

Table 2. Sensitivity Index.

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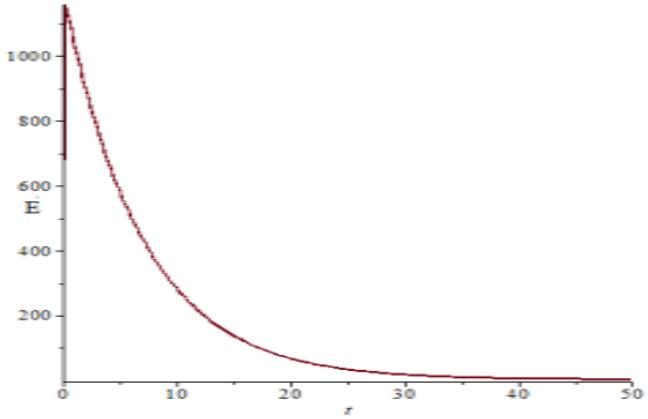

Fig.2. Exposed population trajectory

Parameter	$\Upsilon^{R_{0\|_{\omega=0}}}_{parameter}$
β	1
Λ	1
α	$\frac{\mu}{(\alpha+\mu)}$
v	$\frac{-v}{(\mu+v)}$
δ	$\frac{-\delta}{(\sigma+\mu+\delta+\gamma)}$
γ	$\frac{-\gamma}{(\sigma+\mu+\delta+\gamma)}$
σ	$\frac{-\sigma}{(\sigma+\mu+\delta+\gamma)}$
μ	$\frac{-\mu[\mu+v)(\alpha+\mu)+(\sigma+\mu+\delta+\gamma)(\alpha+2\mu+v)]}{(\mu+v)(\alpha+\mu)(\sigma+\mu+\delta+\gamma)}$

The greater the magnitude of the sensitivity index, the more sensitive $R_0\ |_{\omega=0}$ is with respect to that parameter. From the sensitivity analysis, vaccination will play the biggest role in reducing the basic reproduction number.

4 Numerical simulation

Numerical simulation is carried out using Maple software to show the trajectories of the population in exposed infected, quarantined and recovered class subject to the given initial values. The following values are used to establish theoretical results. $S(0) = 1000, E(0) = 200, I(0) = 100, Q(0) = 0, R(0) = 0, \beta = 0.864, \mu = 0.002, \sigma = 0.015, \beta = 0.1429, \delta = 0.0018, \gamma = 0.0667, v = 0.01, \omega = 0.002, \delta_Q = 0.001$. The trajectories of the compartmental dynamics are shown below.
The simulations show that there is a sharp increase in the exposed class and infected class at the early stages before a consistent decrease as more people move from the susceptible class due to more contact with the infected population. The quarantined class experience a steady increase until it reaches its peak before a steady decline to a particular level. The recovered class experience a steady gradual increase before reaching a saturation point as more people move from exposed and infected class.

5 Declaration of interest

The authors declares no competing interest of any form.

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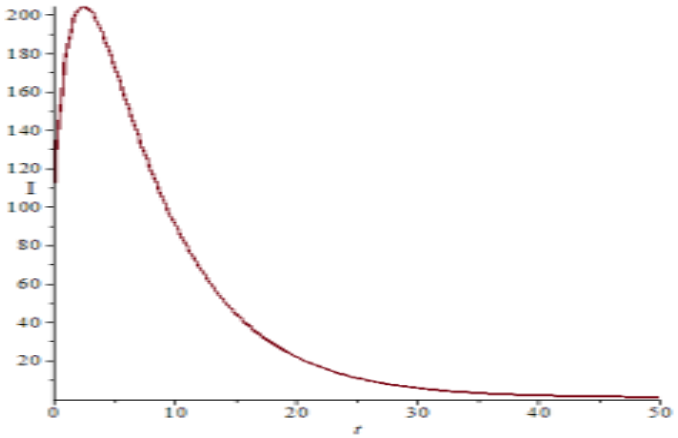

Fig.3. Infected population trajectory

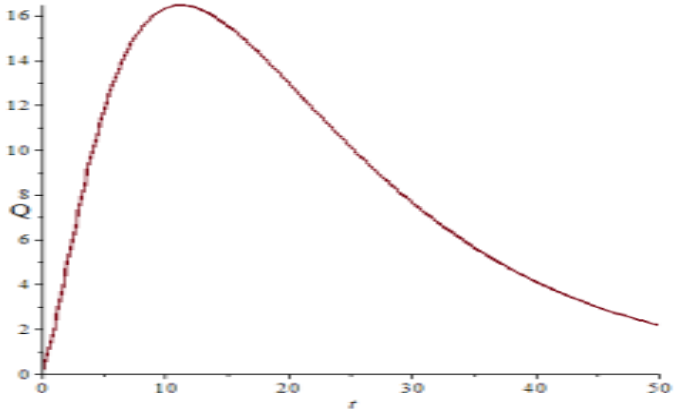

Fig.4. Quarantined population trajectory

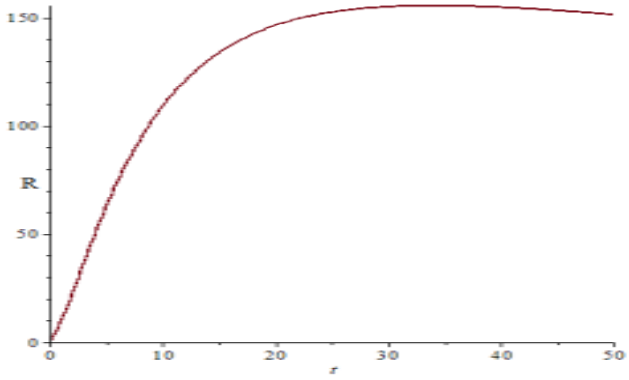

Fig.5. Recovered population trajectory

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7 Conclusion

In this paper, we analyzed a SEIQR mathematical model with vaccination and preventive efforts. The conditions for the local and global stability of the disease free equilibrium point are established. An endemic equilibrium point exists if $R_0 \mid_{\omega=0} > 1$. The impact of the model parameters on the basic reproduction number were also determined through sensitive analysis. Vaccination and scaling up treatment efficacy will go a long way to reducing the basic reproduction number.

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