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Existence and global behaviour of solutions of a nonlinear system modelling some epidemic diseases

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Abstract

In this study, we introduce a new mathematical model with a vaccination strategy in which different levels of susceptibility of individuals to an epidemic are considered. This model, which also takes into account the latent period, consists of a delay differential equation system. After showing the uniqueness of solution of the system, we present the equilibrium points of the model and the reproduction number $\mathcal{R}_0$ which is a vital threshold in spread of diseases. Then by using Lyapunov function and LaSalle Invariance Principle [21], we give some results about the global stabilities of the equilibrium points ofthe model according to $\mathcal{R}_0$.

Keywords: Global stability analysis, Lyapunov function, LaSalle invariance principle, Mathematical epidemiology, Vaccination strategy, Covid 19.

2010 MSC: 34D05, 34D08, 34D20, 92B05, 92D25, 92D30.

1. Introduction

Mathematics, as a basic science, is constantly developing to define and analyze problems in many fields within a discipline. In this context, nonlinear integral, differential and integro-differential equations are among the most effective tools used, [1–6].

On the other hand, mathematical modelling has an important role to take stock of problems and phenomenons in some areas. Medicine, biology and epidemiology are at the top of these areas, [8, 11, 15, 17]. Especially if it is needed to focus on epidemiology, we can unfortunately say that many infectious diseases have deeply affected to all creatures. Millions of people died of various infectious diseases so far in history. Influenza A (H1N1), which spread in more than 200 countries starting in the USA in 2009, caused at least 12469 deaths, [31]. After three years, MERS respiratory syndrome which is a viral disease, erupted in Saudi Arabia and resulted in that approximately %35 of the patients have died. Then, a new disease known as Ebola Virus Disease (EVD) was included in the literature by reporting a case believed

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to be infected by bats in West Africa in 2014. EVD, which continued its effect until 2016, resulted in death in about half of the 28616 people it was infected, [32].

In 2020, unfortunately, Covid-19 (Sars-Cov2), which turned into a pandemic, caused nearly 2 million deaths in the same year and still continues to spread rapidly around the world.

Applications of mathematical modeling in epidemiology have been started regularly in 1927 by Kermack and McKendrick [16] who pioneered understanding of spread and control of infectious diseases, and continue increasingly. They have used a system of ODE to describe spreading of infectious diseases in a population. In this system, known as the SIR epidemic model in literature, the population consists of non-intersecting three compartments. These compartments are as follows; susceptibles (S), infectious (I) and removed or recovered individuals (R). Then many authors studied mathematical epidemiology, [7, 9, 10, 14, 22–25].

Also, different compartmental epidemic models in which the latent period is also taken into account have been introduced by some authors, and many results about these epidemic models have been obtained, [13, 18, 26, 30].

The studies on stability analysis of all these models depend on the threshold $\mathcal{R}_0$ which is defined as the number of secondary cases generated by an infected individual in a population. In general, if $\mathcal{R}_0 < 1$ then invasion of individuals by the pathogen will not give rise to large outbreaks, and the disease gradually becomes extinct. Otherwise the disease continues to spread in the population. Routh-Hurwitz Criteria [28] and LaSalle's Invariance Principle [21] associated with Lyapunov functionals are commonly used to analyze stability of epidemic models.

On the other hand, especially in epidemics such as Covid-19 with high spreading rate and severe negative consequences, it is extremely important to have a successful vaccine. Moreover, the benefit from vaccination is directly related to an effective vaccination strategy.

Health conditions like lung or heart disease, diabetes or conditions that negatively affect the immune system are described as high risk factors to catching the epidemic diseases, [33]. It is defined the individuals in this context as high risk susceptible individuals in this paper.

In this study, a mathematical model, based on vaccination taking into account the division of susceptible individuals into two subclasses such as "high risk susceptibles" and "other susceptibles" has been created, and the effect of this strategy on the course of the epidemic is analyzed. Then global stabilities of the equilibrias of the model are studied. Finally a simulation of the course of disease according to the different vaccination rates in the population is presented.

Unlike the classical models, in the model presented in this paper, the effect of different susceptibility levels on the total protection rate of the population with vaccination is considered. Also, one of the original contributions of the model presented is that the protection provided by vaccination is taken into account in inverse proportion to the contagiousness rates for individuals with different susceptibility levels.

2. Description of the Model

We formulate an SVEIR epidemic model such that S, V, E, I and R represent the susceptible, vaccinated, exposed to the pathogen, infectious and removed classes, respectively. In the model, we firstly assume that the susceptible individuals consist of two separate subgroups: "high risk susceptibles" and "other susceptible individuals". Also, all new members of the population join to S with a fixed rate b in addition that d represents the natural death rate of all compartments.

On the other hand, β_1 and β_2 are the transmission rate from "high risk susceptibles" and "other susceptibles" to E, respectively such that $0 < \beta_2 \leqslant \beta_1 \leqslant 1$. We should immediately note that the β_1/β_2 value also represents the disadvantage of high risk susceptibles in terms of catching the disease compared to other susceptible individuals. Moreover, this is not only a disadvantage for high risk individuals, but also a disadvantage for the entire population as it can ease the spread of the epidemic.

We also assume that the compartment S consists of high risk susceptibles at rate k in addition that $\varepsilon_1$and ε_2 are the vaccination rates of high risk susceptibles and other susceptibles, respectively. Considering the fact that high risk susceptibles may be more likely to become infectious when they encounter the pathogen [27], it can be said that vaccination of these individuals will have a greater effect on reducing the spread of the epidemic than other susceptible individuals. The model essentially depends on this reality and we reflect this fact to the model via again β_1/β_2 coefficient, which is greater than or equal to 1. That is, the disadvantage of high risk individuals in terms of catching the disease compared to other susceptible individuals turns into an advantage in repression of the spreading via vaccination. This advantage is represented by β_1/β_2 coefficient, parallel to the situation in spreading.

Although one individual is vaccinated, he may be infected. So we assume β_3 is the transmission rate from V to E. Also γ and α show the recovery rates of infectious and vaccinated individuals, respectively. Finally, μ denotes the death rate due to the infection in the compartment I.

So, we present the model as follow

$$\begin{aligned}
\frac{dS}{dt} &= b-[k\beta_1+(1-k)\beta_2]\,S(t)\,I(t)-(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d)S(t),\\
\frac{dV}{dt} &= (k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2)S(t)-\beta_3 V(t)\,I(t)-(d+\alpha)\,V(t),\\
\frac{dE}{dt} &= [k\beta_1+(1-k)\beta_2]\,S(t)\,I(t)+\beta_3 V(t)\,I(t)-\widetilde{E}(t,\tau)-dE(t),\\
\frac{dI}{dt} &= \widetilde{E}(t,\tau)-(d+\mu+\gamma)\,I(t),\\
\frac{dR}{dt} &= \gamma I(t)+\alpha V(t)-dR(t),
\end{aligned} \tag{2.1}$$

where $S(t), V(t), \widetilde{E}(t,\tau), I(t)$ and $R(t)$ denote the size of the subclasses: susceptibles, vaccinated, exposed to the pathogen with exposure age τ, infectious and recovered individuals at time t, respectively. Naturally, these functions and all parameters are nonnegative.

We write $\widetilde{E}(t,\tau)$ to denote the size of exposed individuals who entered in the latent period with exposure age τ (i.e, time elapsed since exposure to the pathogen) at time t.

So, defining the latent period as s, we can say that the number of individuals who completed their latent period at time t is $\widetilde{E}(t,\tau)$. Also, taking into account that the natural death rate d the following description is meaningful,

$$\widetilde{E}(t,\tau)=\{[k\beta_1+(1-k)\beta_2]\,S(t-\tau)+\beta_3 V(t-\tau)\}\,I(t-\tau)e^{-d\tau}.$$

Indeed this result is obtained by the solution of following Cauchy problem

$$\begin{aligned}
\left(\frac{\partial}{\partial t}+\frac{\partial}{\partial \tau}\right)\widetilde{E}(t,\tau) &= -d\widetilde{E}(t,\tau),\\
\widetilde{E}(t,0) &= [k\beta_1+(1-k)\beta_2]\,S(t)\,I(t)+\beta_3 V(t)\,I(t).
\end{aligned}$$

Also $N(t)$ shows the total size of the population at time t such that $S(t)+V(t)+E(t)+I(t)+R(t)=N(t)$ for all $t\geqslant 0$. We should note that, since the functions E and R does not appear in the equations for dS/dt, dV/dt and dI/dt, it is enough to examine the behaviour of the system consisting of equations in (2.1) without dE/dt and dR/dt. Taking into account that exposed and recovered individuals don't effect directly to transmission of the disease, we also should note that this assumption is meaningful as epidemiologically and mathematically.

So we can rewrite the model as follow

$$\begin{cases} \frac{dS}{dt} = b - [k\beta_1 + (1-k)\beta_2]\, S(t)\, I(t) - (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d)S(t), \\ \frac{dV}{dt} = (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)S(t) - \beta_3 V(t)\, I(t) - (d+\alpha)\, V(t), \\ \qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad t \in [0,\infty) \\ \frac{dI}{dt} = [k\beta_1 + (1-k)\beta_2]\, S(t-\tau)I(t-\tau)e^{-d\tau} \\ \qquad\qquad + \beta_3 V(t-\tau)I(t-\tau)e^{-d\tau} - (d+\mu+\gamma)\, I(t), \\ S(t) = g_1(t), \\ V(t) = g_2(t), \qquad\qquad\qquad\qquad\qquad\qquad t \in [-\tau, 0] \\ I(t) = g_3(t), \end{cases} \tag{2.2}$$

where $g \in C\left([-\tau,0], \left[0, \frac{b}{d}\right]^3\right)$.

If we choose $x = (S, V, I)$ and $g = (g_1, g_2, g_3)$ then finding the solution of (2.2) is equvalent to solving the following equation

$$\begin{aligned} x'(t) &= f\left(x^t\right),\ t \geqslant 0 \\ x_0(t) &= g(t),\ -\tau \leqslant t \leqslant 0 \end{aligned} \tag{2.3}$$

here $f : \Omega \to \left[0, \frac{b}{d}\right]^3$. $x^s(\theta) = x(s+\theta)$ and $x \in C\left([-\tau,\infty), \left[0, \frac{b}{d}\right]^3\right)$ such that $\Omega \subset C\left([-\tau,0], \left[0, \frac{b}{d}\right]^3\right)$. Also f is described as

$$\begin{aligned} f_1(x) &= b - [k\beta_1 + (1-k)\beta_2]\, S(0)\, I(0) - (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d)S(0), \\ f_2(x) &= (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)S(0) - \beta_3 V(0)\, I(0) - (d+\alpha)\, V(0), \\ f_3(x) &= [k\beta_1 + (1-k)\beta_2]\, S(-\tau)I(-\tau)e^{-d\tau} + \beta_3 V(-\tau)I(-\tau)e^{-d\tau} \\ &\quad - (d+\mu+\gamma)\, I(0) \end{aligned}$$

with initial function $S(t) = g_1(t)$, $V(t) = g_2(t)$ and $I(t) = g_3(t)$ for $-\tau \leqslant t \leqslant 0$.

As known $C\left([-\tau,0], \mathbb{R}^3\right)$ is a Banach space of continuous functions, and $\|\cdot\|_C$ denotes the norm on $C([-\tau,0], \mathbb{R}^n)$ and is defined by

$$\|\zeta\|_C = \sup\{|\zeta_1(t)| + |\zeta_2(t)| + |\zeta_3(t)| : -\tau \leqslant t \leqslant 0\}.$$

On the other hand we can say that the equation (2.3) has a unique solution if f is Lipschitz continuous in every compact subset $M \subset \Omega$. Indeed this result depends on Schauder fixed point theorem [19].

2.1. Feasible region for the model and uniqueness of the solution

Let us recall that the definition of invariant and positively invariant set and determine positively invariant region for the model.

A set Γ is invariant with respect to

$$\frac{dN}{dt} = g(N)$$

if $N(0) \in \Gamma$ requires $N(t) \in \Gamma$ for all $t \in \mathbb{R}$. Especially if $N(0) \in \Gamma$ requires $N(t) \in \Gamma$ for $t \in [0,\infty)$ then it is said that Γ is positively invariant.

Lemma 2.1. *The set*

$$\Omega = \left\{ (S,V,I) \in C\left([-\tau,0],\mathbb{R}^3_+\right) : S(t) \leqslant \frac{b}{k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d}, \right.$$
$$\left. V(t) \leqslant \frac{b(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d\right)(d+\alpha)} \text{ and } S(t)+V(t)+I(t) \leqslant \frac{b}{d} \right\}$$

is positively invariant for the model (2.2).

Proof. We can write

$$\frac{dN}{dt} + dN(t) = b - \mu I \leqslant b \tag{2.4}$$

from using (2.2). If we focus on the solution of

$$\frac{dN}{dt} + dN(t) = b,$$

we have

$$\frac{d}{dt}\left(N(t)e^{dt}\right) = be^{dt}.$$

Taking into account

$$N(t) = \frac{b}{d} + ce^{-dt},$$

for $t = 0$, we obtain

$$c = N(0) - \frac{b}{d}.$$

Thus we have

$$N(t) = N(0)e^{-dt} + \frac{b}{d}\left(1 - e^{-dt}\right). \tag{2.5}$$

By the Standard Comparison Theorem [20], the maximal solution of equation (2.4) gets as (2.5). Hence

$$N(t) \leqslant N(0)e^{-dt} + \frac{b}{d}\left(1 - e^{-dt}\right)$$

for $t \in [0,\infty)$. Particularly, $N(t) \leqslant b/d$ for $t \geqslant 0$ if $N(0) \leqslant b/d$. Also if the above operations are only applied for the first two equations of the model (2.2) then it can be seen that $S(t) \leqslant \frac{b}{k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d}$ and $V(t) \leqslant \frac{b(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2)}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d\right)(d+\alpha)}$ for $t \in [0,\infty)$ if $S(0) \leqslant \frac{b}{k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d}$ and $V(0) \leqslant \frac{b(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2)}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d\right)(d+\alpha)}$.

Hence Ω is positively invariant for system (2.2). So, the region Ω attracts all solutions and it is enough to deal with the dynamics of (2.2) in Ω. Thus the model (2.2) can be considered in Ω, [18, 29]. □

Theorem 2.2. *Eqution (2.3) has a unique solution with initial function* $S(t) = g_1(t)$, $V(t) = g_2(t)$ *and* $I(t) = g_3(t)$ *for* $-\tau \leqslant t \leqslant 0$.

Proof. It sufficient to show that f given in (2.3) is Lipschitz continuous in every compact subset $M \subset \Omega$. Let $x, y \in M$, then we write from the description of f

$$\begin{aligned} & \|f(x) - f(y)\| \\ = \; & |f_1(x) - f_1(y)| + |f_2(x) - f_2(y)| + |f_3(x) - f_3(y)| \\ = \; & [k\beta_1 + (1-k)\beta_2]\,|x_1(0)\,x_3(0) - y_1(0)\,y_3(0)| \end{aligned}$$

$$
\begin{aligned}
&+\left[2\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2\right)+d\right]|x_1(0)-y_1(0)|\\
&+\beta_3|x_2(0)x_3(0)-y_2(0)y_3(0)|+(d+\alpha)|x_2(0)-y_2(0)|\\
&+[k\beta_1+(1-k)\beta_2]e^{-d\tau}|x_1(-\tau)x_3(-\tau)-y_1(-\tau)y_3(-\tau)|\\
&+\beta_3e^{-d\tau}|x_2(-\tau)x_3(-\tau)-y_2(-\tau)y_3(-\tau)|+(d+\mu+\gamma)|x_3(0)-y_3(0)|\\
\leqslant\ &[k\beta_1+(1-k)\beta_2](|x_3(0)|+|y_1(0)|)\|x-y\|_C+\left[2\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2\right)+d\right]\|x-y\|_C\\
&+\beta_3(|x_3(0)|+|y_2(0)|)\|x-y\|_C+(d+\alpha)\|x-y\|_C\\
&+[k\beta_1+(1-k)\beta_2]|(|x_3(-\tau)|+|y_1(-\tau)|)|e^{-d\tau}\|x-y\|_C\\
&+\beta_3(|x_3(-\tau)|+|y_2(-\tau)|)e^{-d\tau}\|x-y\|_C+(\gamma+d+\mu)\|x-y\|_C
\end{aligned}
\tag{2.6}
$$

Taking into account the facts $|x_i(\theta)|\leqslant\frac{b}{d}$ for $-\tau\leqslant\theta\leqslant 0$ then we conlude

$$
\begin{aligned}
\|f(x)-f(y)\| \leqslant\ &\left\{([k\beta_1+(1-k)\beta_2]+\beta_3)\frac{2b}{d}\left(1+e^{-d\tau}\right)\right.\\
&\left.+2\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2\right)+3d+\mu+\gamma+\alpha\right\}\|x-y\|_C.
\end{aligned}
$$

from (2.6). So if we take

$$
L\geqslant([k\beta_1+(1-k)\beta_2]+\beta_3)\frac{2b}{d}\left(1+e^{-d\tau}\right)+2\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2\right)+3d+\mu+\gamma+\alpha,
$$

the inequality

$$
\|f(x)-f(y)\|\leqslant L\|x-y\|_C
$$

hold in every compact subset $M\subset\Omega$. □

2.2. The Equilibrias and Reproduction Number of the Model

Now, let us find the disease-free equilibria for the model (2.2). Using $I_0=0$ in the system of algebraic equations

$$
\begin{aligned}
0 &= b-[k\beta_1+(1-k)\beta_2]S_0I_0-\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d\right)S_0\\
0 &= \left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2\right)S_0-\beta_3V_0I_0-(d+\alpha)V_0\\
0 &= [k\beta_1+(1-k)\beta_2]S_0I_0e^{-d\tau}+\beta_3V_0I_0e^{-d\tau}-(d+\mu+\gamma)I_0
\end{aligned}
$$

the disease-free equilibrium point is found as

$$
P_0=(S_0,V_0,I_0)=\left(\frac{b}{k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d},\frac{b\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2\right)}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d\right)(d+\alpha)},0\right).
$$

To get $\mathcal{R}_0$ we use the next generation matrix method, [12]. Let $X=(I,V,S)^T$, so we can write

$$
\frac{dX}{dt}=\mathcal{P}(X)-\mathcal{F}(X)
$$

from (2.2) such that

$$
\mathcal{P}(X)=\begin{bmatrix}[k\beta_1+(1-k)\beta_2]S(t-\tau)I(t-\tau)e^{-d\tau}+\beta_3V(t-\tau)I(t-\tau)e^{-d\tau}\\0\\0\end{bmatrix}
$$

and

$$\mathcal{F}(X) = \begin{bmatrix} (d+\mu+\gamma)\, I(t) \\ -(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)S(t) + \beta_3 V(t)\, I(t) + (d+\alpha)\, V(t) \\ -b + [k\beta_1 + (1-k)\beta_2]\, S(t)\, I(t) + (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d)S(t) \end{bmatrix}.$$

Differentiating $\mathcal{P}(X)$ and $\mathcal{F}(X)$ with respect to I, V, S and computing respectively them at the disease-free equilibrium $P_0 = (S_0, V_0, I_0)$, we get

$$P = d\mathcal{P}_{1x1}(P_0) = \left[e^{-d\tau} S_0[k\beta_1 + (1-k)\,\beta_2] + e^{-d\tau}\beta_3 V_0\right],$$
$$F = d\mathcal{F}_{1x1}(P_0) = [d+\mu+\gamma]$$

and

$$PF^{-1} = \frac{e^{-d\tau}\left(S_0[k\beta_1 + (1-k)\,\beta_2] + \beta_3 V_0\right)}{d+\mu+\gamma}.$$

Therefore, the basic reproduction number of the model (2.2) is found as

$$\begin{aligned} \mathcal{R}_0 &= \rho\left(PF^{-1}\right) = \frac{e^{-d\tau}\left(S_0[k\beta_1 + (1-k)\,\beta_2] + \beta_3 V_0\right)}{d+\mu+\gamma} \\ &= \frac{be^{-d\tau}\left\{[k\beta_1 + (1-k)\,\beta_2]\,(d+\alpha) + (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)\beta_3\right\}}{(d+\mu+\gamma)\left(d + k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2\right)(d+\alpha)}. \end{aligned}$$

To determine whether another equilibrium point of the system (2.2) exists or not, we must solve the following system of algebraic equations with $I_* \neq 0$.

$$\begin{aligned} 0 &= b - [k\beta_1 + (1-k)\,\beta_2]S_*I_* - (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d)S_* \\ 0 &= (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)S_* - \beta_3 V_* I_* - (d+\alpha)\, V_*, \\ 0 &= [k\beta_1 + (1-k)\beta_2]\, S_*I_*e^{-d\tau} + \beta_3 V_* I_* e^{-d\tau} - (d+\mu+\gamma)\, I_*. \end{aligned} \tag{2.7}$$

From the system (2.7), we can respectively obtain

$$\begin{aligned} S_* &= \frac{b}{k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d + [k\beta_1 + (1-k)\,\beta_2]I_*}, \\ V_* &= \frac{b(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d + [k\beta_1 + (1-k)\,\beta_2]I_*\right)(\beta_3 I_* + d + \alpha)} \end{aligned} \tag{2.8}$$

Taking into account (2.7) and (2.8), we obtain the equation

$$c_0 I_*^2 + c_1 I_* + c_2 = 0, \tag{2.9}$$

where

$$\begin{aligned} c_0 &= -[k\beta_1 + (1-k)\beta_2]\,\beta_3(d+\mu+\gamma), \\ c_1 &= be^{-d\tau}\beta_3\,[k\beta_1 + (1-k)\beta_2] \end{aligned}$$

$$
\begin{aligned}
& -(d+\mu+\gamma)\left\{[k\beta_1+(1-k)\beta_2](\alpha+d)+(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d)\beta_3\right\},\\
c_2 &= be^{-d\tau}\left[[k\beta_1+(1-k)\beta_2](\alpha+d)+(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2)\beta_3\right]\\
& -(\alpha+d)(d+k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2)(d+\mu+\gamma)\\
&= (\alpha+d)(d+k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2)(d+\mu+\gamma)(\mathcal{R}_0-1)
\end{aligned}
$$

Let $\mathcal{R}_0<1$. Then $c_2/c_0>0$.
On the other hand if we define

$$
M=\frac{be^{-d\tau}\beta_3[k\beta_1+(1-k)\beta_2]}{(d+\mu+\gamma)\left\{[k\beta_1+(1-k)\beta_2](d+\alpha)+(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d)\beta_3\right\}}
$$

then

$$
c_1=(d+\mu+\gamma)\left\{[k\beta_1+(1-k)\beta_2](d+\alpha)+(k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2+d)\beta_3\right\}(M-1).
$$

Also taking into account that

$$
\frac{\mathcal{R}_0}{M}>1,
$$

we can say that $M<\mathcal{R}_0$ and so $c_1/c_0>0$ for $\mathcal{R}_0<1$. Hence we conclude that all roots of equation (2.9) are negative, for $\mathcal{R}_0<1$.

When $\mathcal{R}_0>1$, $c_2/c_0<0$ and so equation (2.9) has only one positive root. This root is called as endemic equilibrium and we represent it with P_*.

Proposition 2.3. *Model (2.2) always has an equilibrium P_0. If $\mathcal{R}_0\leqslant 1$ then P_0 is the only equilibrium in Ω; if $\mathcal{R}_0>1$ then there are two equilibrias; P_0 and P_*.*

3. Stabilities of the Equilibrias

In this section, we deal with stabilities of the disease-free equilibrium point P_0 and the endemic equilibrium point P_* of the system (2.2).

Theorem 3.1. *P_0 is locally asymptotically stable if $R_0<1$, and unstable if $R_0>1$.*

Proof. The Jacobian matrix at P_0 of the system (2.2) is

$$
J(P_0)=\begin{bmatrix}
-k\frac{\beta_1}{\beta_2}\varepsilon_1-(1-k)\varepsilon_2-d & 0 & -[k\beta_1+(1-k)\beta_2]S_0\\
k\frac{\beta_1}{\beta_2}\varepsilon_1+(1-k)\varepsilon_2 & -d-\alpha & -\beta_3V_0\\
0 & 0 & e^{-d\tau}\{[k\beta_1+(1-k)\beta_2]S_0+\beta_3V_0\}-(d+\mu+\gamma)
\end{bmatrix}.
$$

Thus, the corresponding characteristic equation is described by

$$
\left(-k\frac{\beta_1}{\beta_2}\varepsilon_1-(1-k)\varepsilon_2-d-\lambda\right)(-d-\alpha-\lambda)[(d+\mu+\gamma)(\mathcal{R}_0-1)-\lambda]=0. \tag{3.1}
$$

It can be easily seen that the equation (3.1) always has negative eigenvalues $\lambda_1 = -k\frac{\beta_1}{\beta_2}\varepsilon_1 - (1-k)\varepsilon_2 - d$, $\lambda_2 = -d - \alpha$. Then, the other eigenvalue of characteristic equation (3.1) determined by

$$\lambda_3 = (d+\mu+\gamma)(\mathcal{R}_0 - 1). \tag{3.2}$$

If $\mathcal{R}_0 < 1$, then all roots of equation (3.1) are negative. On the other hand, if $\mathcal{R}_0 > 1$ then in this case, one of roots of the equation (3.1) has positive real parts. Therefore, if $\mathcal{R}_0 < 1$ then P_0 is locally asymptotically stable; if $\mathcal{R}_0 > 1$, is unstable. □

Theorem 3.2. P_0 *is globally asymptotically stable if* $\mathcal{R}_0 < 1$.

Proof. Let us define a nonnegative function:

$$L(t) = I(t) + e^{-d\tau}\left([k\beta_1 + (1-k)\beta_2]\int_{t-\tau}^{t} S(z)\,I(z)\,dz + \beta_3\int_{t-\tau}^{t} V(z)\,I(z)\,dz\right).$$

As can be seen $L(t) = 0$ if $I(t) = I_0$, $S(t) = S_0$, $V(t) = V_0$. Differentiating with respect to time yields and considering the facts $S(t) \leqslant \frac{b}{k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d}$ and $V(t) \leqslant \frac{b\left(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2\right)}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d\right)(d+\alpha)}$ then we obtain

$$\begin{aligned}
&\frac{dL}{dt}\\
&= I(t)\left[e^{-d\tau}\{S(t)[k\beta_1 + (1-k)\beta_2] + \beta_3 V(t)\} - (\gamma + d + \mu)\right]\\
&= I(t)(\gamma+d+\mu)\left[\frac{e^{-d\tau}\{S(t)[k\beta_1 + (1-k)\beta_2] + \beta_3 V(t)\}}{(\gamma+d+\mu)} - 1\right]\\
&\leqslant I(t)(\gamma+d+\mu)\left[\frac{e^{-d\tau}\left(b[k\beta_1 + (1-k)\beta_2] + \left(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d\right)\beta_3 V(t)\right)}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d\right)(\gamma+d+\mu)} - 1\right]\\
&\leqslant I(t)(\gamma+d+\mu)\left[\frac{e^{-d\tau} b\left\{[k\beta_1 + (1-k)\beta_2](d+\alpha) + \beta_3\left(\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2\right)\right\}}{\left(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d\right)(\gamma+d+\mu)(d+\alpha)} - 1\right]\\
&= I(t)(\gamma+d+\mu)(\mathcal{R}_0 - 1).
\end{aligned}$$

So we obtain

$$\frac{dL}{dt} \leqslant 0$$

for $\mathcal{R}_0 < 1$. If the fact $\frac{dL}{dt} = 0$ at the point P_0 is used, this shows that L is a Lyapunov function in Ω for (2.2). According to LaSalle's Invariance Principle the limit set of each solution is contained in the largest invariant subset of

$$\left\{(S, V, I) : \frac{dL}{dt} = 0\right\}.$$

Also the largest invariant subset consists only singleton P_0 for $\mathcal{R}_0 < 1$. Hence P_0 is globally asymptotically stable. □

Theorem 3.3. P_* *is globally asymptotically stable if* $\mathcal{R}_0 > 1$.

Proof. By taking into account $P_* = (S_*, V_*, I_*)$, we consider the following;

$$U(t) = U_1(t) + U_2(t)$$

such that

$$U_1(t) = S_* h\left(\frac{S(t-\tau)}{S_*}\right) + V_* h\left(\frac{V(t-\tau)}{V_*}\right) + e^{d\tau} I^* h\left(\frac{I(t)}{I_*}\right)$$

and

$$U_2(t) = [(k\beta_1 + (1-k)\beta_2) S_* I_* + \beta_3 V_* I_*] \int_{t-\tau}^{t} h\left(\frac{I(z)}{I_*}\right) dz$$

where

$$h(y) = y - 1 - \ln y.$$

On the other hand we should note that $h(y) \geqslant 0$ for all $y > 0$ and the function h achieves its global minimum at $y = 1$.

Let us obtain the derivatives of U_1 and U_2 respectively. We firstly can write

$$\begin{aligned}
&\frac{dU_1}{dt} \\
= &\left(b - [k\beta_1 + (1-k)\beta_2] S(t-\tau)I(t-\tau) - (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d)S(t-\tau)\right) \times \\
&\times \left(1 - \frac{S_*}{S(t-\tau)}\right) \\
&+ \left((k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)S(t-\tau) - \beta_3 V(t-\tau)I(t-\tau) - (d+\alpha) V(t-\tau)\right) \times \\
&\times \left(1 - \frac{V_*}{V(t-\tau)}\right) \\
&+ [(k\beta_1 + (1-k)\beta_2) S(t-\tau)I(t-\tau) + \beta_3 V(t-\tau)I(t-\tau)] \left(1 - \frac{I_*}{I(t)}\right) \\
&- e^{ds} (d+\mu+\gamma) I(t) \left(1 - \frac{I_*}{I(t)}\right)
\end{aligned} \tag{3.3}$$

and

$$\begin{aligned}
\frac{dU_2}{dt} = &[k\beta_1 + (1-k)\beta_2] S_* I_* \ln \frac{I(t-\tau)}{I(t)} + [k\beta_1 + (1-k)\beta_2] S_* I(t) \\
&- [k\beta_1 + (1-k)\beta_2] S_* I(t-\tau) + \beta_3 V_* I_* \ln \frac{I(t-\tau)}{I(t)} \\
&+ \beta_3 V_* I(t) - \beta_3 V_* I(t-\tau).
\end{aligned} \tag{3.4}$$

If we use the following facts obtained from (2.7) in (3.3)

$$b = (k\beta_1 + (1-k)\beta_2) S_* I_* + (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2 + d)S_*,$$

$$(d+\alpha) V^* = (k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)S_* - \beta_3 V_* I_*,$$

$$e^{d\tau} (d+\mu+\gamma) = (k\beta_1 + (1-k)\beta_2) S_* + \beta_3 V_*,$$

$$(k\frac{\beta_1}{\beta_2}\varepsilon_1 + (1-k)\varepsilon_2)S_* = \beta_3 V_* I_* + (d+\alpha) V_*$$

then we can write

$$\begin{aligned}
\frac{dU}{dt} &= dS_*\left(2-\frac{S(t-\tau)}{S_*}-\frac{S_*}{S(t-\tau)}\right)\\
&+((k\beta_1+(1-k)\beta_2)\,S_*I_*)\left(1-\frac{S_*}{S(t-\tau)}+\ln\frac{S_*}{S(t-\tau)}\right)\\
&+(k\beta_1+(1-k)\beta_2)\,S_*I_*\left(1-\frac{S(t-\tau)I(t-\tau)}{S_*I(t)}+\ln\frac{S(t-\tau)I(t-\tau)}{S_*I(t)}\right)\\
&+(d+a)V^*\left(3-\frac{S_*}{S(t-\tau)}-\frac{V(t-\tau)}{V_*}-\frac{S(t-\tau)V_*}{S_*V(t-\tau)}\right)\\
&+\beta_3V^*I^*\left(1-\frac{S_*}{S(t-\tau)}+\ln\frac{S_*}{S(t-\tau)}\right)\\
&+\beta_3V^*I^*\left(1-\frac{S(t-\tau)V_*}{S_*V(t-\tau)}+\ln\frac{S(t-\tau)V_*}{S_*V(t-\tau)}\right)\\
&+\beta_3V^*I^*\left(1-\frac{V(t-\tau)I(t-\tau)}{V_*I(t)}+\ln\frac{V(t-\tau)I(t-\tau)}{V_*I(t)}\right).
\end{aligned}$$

from (3.3) and (3.4).

Finaly taking into account that

$$\begin{aligned}
\left(2-\frac{S(t-\tau)}{S_*}-\frac{S_*}{S(t-\tau)}\right) &\leqslant 0\\
\left(3-\frac{S_*}{S(t-\tau)}-\frac{V(t-\tau)}{V_*}-\frac{S(t-\tau)V_*}{S_*V(t-\tau)}\right) &\leqslant 0
\end{aligned}$$

and

$$1-x+\ln x\leqslant 0$$

we can say that

$$\frac{dU}{dt}\leqslant 0.$$

Finally if the fact $dU/dt=0$ at the point P_* is used then it is conclude that U is a Lyapunov function on Ω for (2.2).

In other respects, let us explore the largest invariant subset of

$$\left\{(S,V,I):\frac{dU}{dt}=0\right\}. \tag{3.5}$$

The following equalities must be satisfied in order to have $dU/dt=0$,

$$\begin{aligned}
\left(1-\frac{S_*}{S(t-\tau)}+\ln\frac{S_*}{S(t-\tau)}\right) &= 0\\
\left(1-\frac{S(t-\tau)V_*}{S_*V(t-\tau)}+\ln\frac{S(t-\tau)V_*}{S_*V(t-\tau)}\right) &= 0\\
\left(1-\frac{V(t-\tau)I(t-\tau)}{V_*I(t)}+\ln\frac{V(t-\tau)I(t-\tau)}{V_*I(t)}\right) &= 0
\end{aligned} \tag{3.6}$$

So we get $S(t)=S_*$, $V(t)=V_*$ and $I(t)=I_*$ from (3.6).

Hence the largest invariant subset of (3.5) consists only P_*. By the LaSalle's principle [21], we infer that solutions of (2.2) tends to the endemic equilibrium P_*. More clearly, $S(t)\to S_*$, $V(t)\to V_*$ and $I(t)\to I_*$ as $t\to\infty$. This shows that P_* is globally asymptotically stable on Ω. □

Example 3.4. Let we consider a population with the followings,

$$b = 4000,\ \beta_1 = 1.6 \times 10^{-8}; \beta_2 = 0.8 \times 10^{-8},\ \beta_3 = 1 \times 10^{-13},$$

$$k = 0.4,\ d = 0.000015,\ \mu = 0.015,$$

$$\alpha = 0.5,\ \gamma = 0.15,\ s = 14.$$

Where we assume $S(0) = 69\,997\,900$, $I(0) = 100$, $R(0) = 0$, $V(0) = E(0) = 1000$.

Then the simulation of the course of disease according to the different vaccination rates in the population is obtained as the following figures. The figures are gotten using the Wolfram Mathematica 12.1 with NDSolve code.

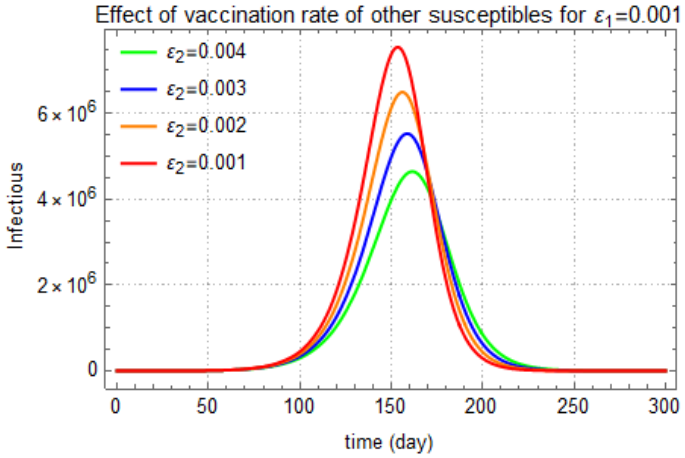

Figure 1: Effect of vaccination of susceptibles who has not high risk.

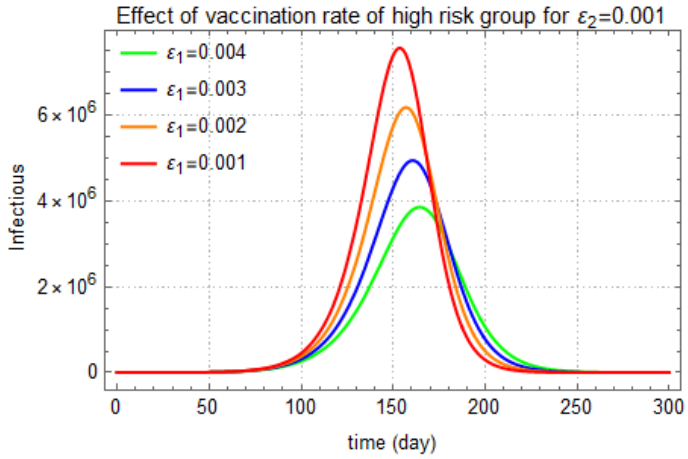

Figure 2: Effect of vaccination of high risk susceptibles.

Conclusion

In this study, a mathematical model, based on vaccination taking into account different levels of susceptibility of individuals to an epidemic is created, and the effect of this strategy on the course of the epidemic is analyzed. Then global stabilities of the equilibrias of the model are studied. Also a simulation of the course of the disease according to the different vaccination rates in the population is presented.

Unlike the classical models, in the model presented in this paper, the effect of different susceptibility levels on the total protection rate of the population with vaccination is considered. Also, one of the original contributions of the model presented is that the protection provided by vaccination is taken into account in inverse proportion to the contagiousness rates for individuals with different susceptibility levels.

As can be seen in the figures above, changing of vaccination rate of the high risk group is more effective than the other susceptibles. For example, when the vaccination rate of other susceptible individuals (ε_2) is increased from 0.001 to 0.004 by keeping the vaccination rate of high risk individuals is constant then the maximum number of infectious from over 7 million decreases to about 5 million.

On the other hand, when the vaccination rate of high risk susceptible individuals (ε_1) is increased from 0.001 to 0.004 by keeping the vaccination rate of other susceptible individuals is constant, the maximum number of infectious decreases below 4 million.

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