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Stability Analysis at DFE of an Epidemic Model in the Presence of a Preventive Vaccine

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Abstract: *Various kinds of deterministic models for the spread of infectious disease have been analyzed mathematically and applied to control the epidemic. A vaccine is a biological preparation that improves immunity to a particular disease. In this paper, a deterministic model for the dynamics of an infectious disease in the presence of a preventive vaccine and natural death rate is formulated. The model has various kinds of parameter. In this paper, we try to present a model for the transmission dynamics of an infectious disease In order to control the epidemic by changing the value of the parameters.*
AMS: *92C60, 92D30, 92B05, 92D25.*
Keywords: *Basic reproduction number, diseases free equilibrium, Infectious diseases, Stability analysis*.

I. Introduction:

The spread of communicable diseases is often described mathematically by compartmental models. In 1927, Kermack and McKendrick proposed, as a particular case of a more general model presented in their seminal work [1]. Many epidemiological models have a disease free equilibrium (DFE) at which the population remains in the absence of disease [2]. The classical SIR models are very important as conceptual models (similar to predator-prey and competing species models in ecology). The SIR epidemic modeling yields the useful concept of the threshold quantity which determines when an epidemic occurs and formulas for the peak infective fraction and the final susceptible fraction [3]. There are two major types of control strategies available to curtail the spread of infectious diseases: pharmaceutical interventions (drugs, vaccines) and non-pharmaceutical interventions (social distancing, quarantine). Vaccination, when it is available, is an effective preventive strategy. Arino et al. [4] introduced vaccination of susceptible individuals into an SIRS model and also considered vaccinating a fraction of newborns. Buonomo et al. [5] studied the traditional SIR model with 100% efficacious vaccine. Effective vaccines have been used successfully to control smallpox, polio and measles. In this paper, we try to present a model for the transmission dynamics of an infectious disease with a preventive vaccine. In order to control or eradicate the disease, we discus about various parameters used in this model except the natural death rater μ (which is not controlled by human).

II. Model formulation:

In our model, we have divided the population into three compartments (susceptible, vaccinated susceptible and infectious) depending on the epidemiological status of individuals. We denote the population of those who are susceptible as S, who are vaccinated susceptible as V and those who subsequently infected as I. The model transfer diagram indicating the possible transitions between these compartments is shown in Fig 1.

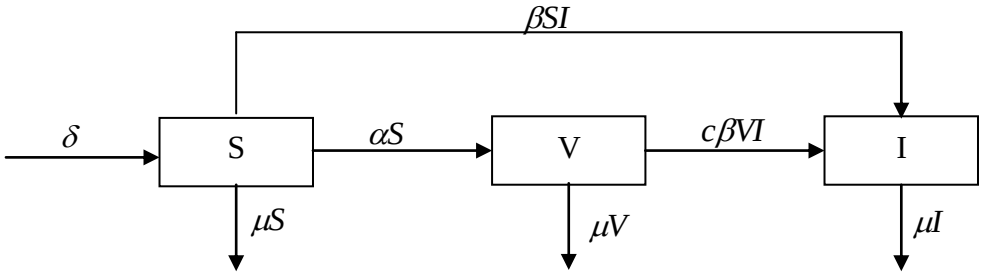

Fig 1: Model Structure.

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Populations enter the susceptible class at constant rate δ. Natural death rate is assumed to be μ. The population is assumed to undergo homogeneous mixing. We assume that each infective individual contacts an average number β with other individuals per unit time. Hence, the total number of contact by infective per unit time is βI. Susceptible individuals are vaccinated at the rate α. Since the vaccine only provides partial protection to the infection, vaccinated individuals may still become infected but at the lower infection rate $c\beta$ than fully susceptible individuals. Here $0<c<1$ and $1-c$ describes vaccine efficacy, i.e., probability of a vaccinated person to get immunity by the vaccine. When $c\to 0$, the vaccine is perfectly effective and when $c\to 1$, the vaccine has no effect at all on the immunity of vaccinated individuals. In this paper we consider all parameters are positive.

The differential equations of the model are given by:

$$\left.\begin{aligned}\frac{dS}{dt}&=\delta-\beta SI-\alpha S-\mu S\\ \frac{dV}{dt}&=\alpha S-\mu V-c\beta VI\\ \frac{dI}{dt}&=c\beta VI+\beta SI-\mu I\end{aligned}\right\} \quad (1)$$

III. Stability analysis of DFE:

The model has a disease-free equilibrium (DFE), obtained by setting the right hand sides of (1) to zero, given by

$$\delta-\beta SI-\alpha S-\mu S=0 \quad (2)$$

$$\alpha S-\mu V-c\beta VI=0 \quad (3)$$

$$c\beta VI+\beta SI-\mu I=0 \quad (4)$$

with $I=0$. This gives the DFE $p_0\left(S^*,V^*,I^*\right)=\left(\frac{\delta}{\mu+\alpha},\ \frac{\alpha\delta}{\mu(\mu+\alpha)},\ 0\right)$.

Now linearize the system (1) about the point p_0 we get

$$\left.\begin{aligned}\frac{dS}{dt}&=-(\alpha+\mu)S-\frac{\beta\delta}{\mu+\alpha}I\\ \frac{dV}{dt}&=\alpha S-\mu V-\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)}I\\ \frac{dI}{dt}&=\left(\frac{\beta\delta}{\mu+\alpha}+\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)}-\mu\right)I\end{aligned}\right\} \quad (5)$$

Which can be written in matrix form as

$$\frac{d}{dt}\begin{bmatrix}S\\V\\I\end{bmatrix}=\begin{bmatrix}-(\alpha+\mu) & 0 & -\frac{\beta\delta}{\mu+\alpha}\\ \alpha & -\mu & -\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)}\\ 0 & 0 & \frac{\beta\delta}{\mu+\alpha}+\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)}-\mu\end{bmatrix}\times\begin{bmatrix}S\\V\\I\end{bmatrix}$$

So the Jacobean matrix of the model (1) at the point p_0 is

$$J_{p_0}=\begin{bmatrix} -(\alpha+\mu) & 0 & -\frac{\beta\delta}{\mu+\alpha} \\ \alpha & -\mu & -\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)} \\ 0 & 0 & \frac{\beta\delta}{\mu+\alpha}+\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)}-\mu \end{bmatrix}$$

The eigenvalues of J_{p_0} are $\lambda_1=-(\mu+\alpha)$, $\lambda_2=-\mu$ and $\lambda_3=\frac{\beta\delta}{\mu+\alpha}+\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)}-\mu$. Since all parameters are positive then clearly $\lambda_1<0$ and $\lambda_2<0$. So the DFE $p_0=\left(\frac{\delta}{\mu+\alpha},\ \frac{\alpha\delta}{\mu(\mu+\alpha)},\ 0\right)$ is locally asymptotically stable if and only if $\lambda_3<0$.

IV. Basic reproductive number:

The basic reproduction number R_0 is "the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual" [6].

4.1. Lemma: The DFE p_0 is locally asymptotically stable if $R_0<1$ and unstable if $R_0>1$ [7]. i.e., if $R_0<1$, then the number of infectious populations is decreasing and there is no epidemic. Otherwise if $R_0>1$, then the number of infectious populations is increasing and there is an epidemic.

Since the DFE $p_0=\left(\frac{\delta}{\mu+\alpha},\ \frac{\alpha\delta}{\mu(\mu+\alpha)},\ 0\right)$ is locally asymptotically stable if and only if $\lambda_3<0$, i.e. $\frac{\beta\delta}{\mu+\alpha}+\frac{\alpha\beta\delta c}{\mu(\mu+\alpha)}<\mu$, i.e. $\frac{\beta\delta}{\mu(\mu+\alpha)}+\frac{\alpha\beta\delta c}{\mu^2(\mu+\alpha)}<1$. So by the above lemma $R_0=\frac{\beta\delta}{\mu(\mu+\alpha)}+\frac{\alpha\beta\delta c}{\mu^2(\mu+\alpha)}$

V. Controlling the epidemic:

Since for $R_0=\frac{\beta\delta}{\mu(\mu+\alpha)}+\frac{\alpha\beta\delta c}{\mu^2(\mu+\alpha)}<1$, there is no epidemic; we can take various steps to control the epidemic.

5.1. Step 1:

Suppose R_0 is a function of c. i.e., $R_0=R_0(c)=\frac{\beta\delta}{\mu(\mu+\alpha)}+\frac{\alpha\beta\delta c}{\mu^2(\mu+\alpha)}=M_1c+D_1$ where $M_1=\frac{\alpha\beta\delta}{\mu^2(\mu+\alpha)}>0$ and $D_1=\frac{\beta\delta}{\mu(\mu+\alpha)}$. Therefore $\frac{dR_0}{dc}=M_1>0$. i.e., $R_0(c)$ is increasing. So We can reduce the value of R_0 by decreasing the value of c. Moreover if $D_1<1$, there exists a bifurcation value $c_0=\frac{\mu^3+\mu^2\alpha-\beta\delta\mu}{\alpha\beta\delta}$ of c such that if $c<c_0$, then $R_0<1$ and if $c>c_0$, then $R_0>1$, i.e., if $c<c_0$, then P_0 is locally asymptotically stable and if $c>c_0$ then unstable. Therefore if all parameters except c are constant, then we can control the epidemic by decreasing the value of c (increasing the vaccine efficiency) so that $c<c_0$.

5.2. Step 2:

Suppose R_0 is a function of β, i.e., $R_0 = R_0(\beta) = \frac{\beta\delta}{\mu(\mu+\alpha)} + \frac{\alpha\beta\delta c}{\mu^2(\mu+\alpha)} = M_2\beta$

where $M_2 = \frac{\delta}{\mu(\mu+\alpha)} + \frac{\alpha\delta c}{\mu^2(\mu+\alpha)} > 0$. Therefore $\frac{dR_0}{d\beta} = M_2 > 0$, i.e., $R_0(\beta)$ is increasing. So We can reduce the value of R_0 by decreasing the value of β. Moreover there exists a bifurcation value $\beta_0 = \frac{\mu^2(\mu+\alpha)}{\delta\mu + \alpha\delta c}$ of β such that if $\beta < \beta_0$, then $R_0 < 1$ and if $\beta > \beta_0$, then $R_0 > 1$, i.e., if $\beta < \beta_0$, then P_0 is locally asymptotically stable and if $\beta > \beta_0$ then unstable. Therefore if all parameters except β are constant, then we can control the epidemic by decreasing the value of β (decreasing the contact rate with infected individual) so that $\beta < \beta_0$.

5.3. Step 3:

Similarly (as step 2) We can reduce the value of R_0 by decreasing the value of δ and we get a bifurcation value $\delta_0 = \frac{\mu^2(\mu+\alpha)}{\beta\mu + \alpha\beta c}$ of δ such that if $\delta < \delta_0$, then $R_0 < 1$ and if $\delta > \delta_0$, then $R_0 > 1$, i.e., if $\delta < \delta_0$, then P_0 is locally asymptotically stable and if $\delta > \delta_0$ then unstable. Therefore if all parameters except δ are constant, then we can control the epidemic by decreasing the value of δ so that $\delta < \delta_0$.

5.4. Step 4:

Suppose R_0 is a function of α. i.e., $R_0 = R_0(\alpha) = \frac{\beta\delta}{\mu(\mu+\alpha)} + \frac{\alpha\beta\delta c}{\mu^2(\mu+\alpha)}$. So $\frac{dR_0}{d\alpha} = \frac{\beta\delta(c-1)}{\mu^3 + 2\alpha\mu^2 + \alpha^2\mu} < 0$. i.e., $R_0(\alpha)$ is decreasing. We can reduce the value of R_0 by increasing the value of α. Moreover if $0 < \frac{\mu^3 - \beta\delta\mu}{\beta\delta c - \mu^2} < 1$, then $\alpha_0 = \frac{\mu^3 - \beta\delta\mu}{\beta\delta c - \mu^2}$ is a bifurcation value of α such that if $\alpha > \alpha_0$ then P_0 is locally asymptotically stable and if $\alpha < \alpha_0$ then the system is unstable. Therefore we can control the epidemic by increasing the value of α so that $\alpha > \alpha_0$.

VI. Numerical simulation:

In order to illustrate the various theoretical results, numerical experiments (using Matlab) were carried out to compute the solutions of linear system (5) using the parameter values as follows:

6.1. For step 1:

Table 1: Results for step-1.

	Example-1	Example-3
α (constant)	0.8	0.8
β (constant)	0.006	0.006
δ (constant)	0.008	0.008
c	0.1	0.3
μ (constant)	0.003	0.003
c_0	0.184453125	0.184453125
Relation between c and c_0	$c < c_0$	$c > c_0$
Comment	I is decreasing (Fig 2 (a))	I is increasing (Fig 2 (b))

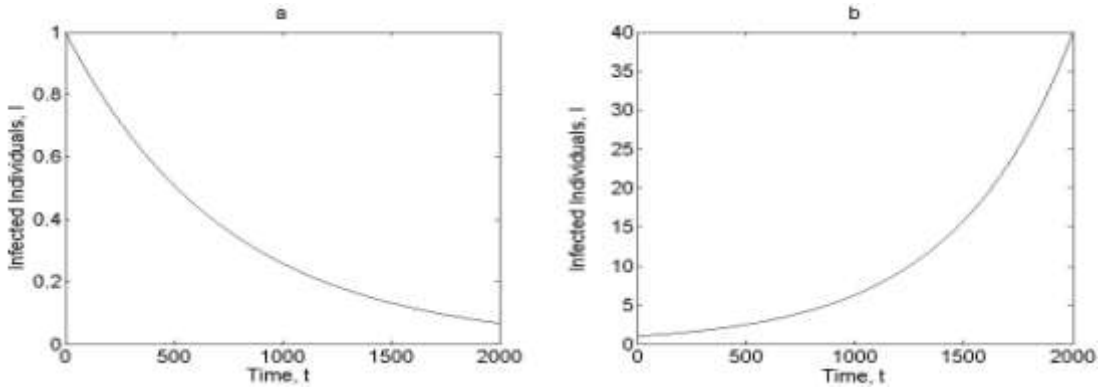

Fig 2: Graph of $I(t)$ for step-1.

6.2. For step 2:

Table 2: Results for step-2.

	Example-1	Example-3
α (constant)	0.8	0.8
β	0.003	0.007
δ (constant)	0.008	0.008
c (constant)	0.18	0.18
μ (constant)	0.003	0.003
β_0	0.006145408163265	0.006145408163265
Relation between β and β_0	$\beta < \beta_0$	$\beta > \beta_0$
Comment	I Is decreasing (Fig 3 (a))	I is increasing (Fig 3 (b))

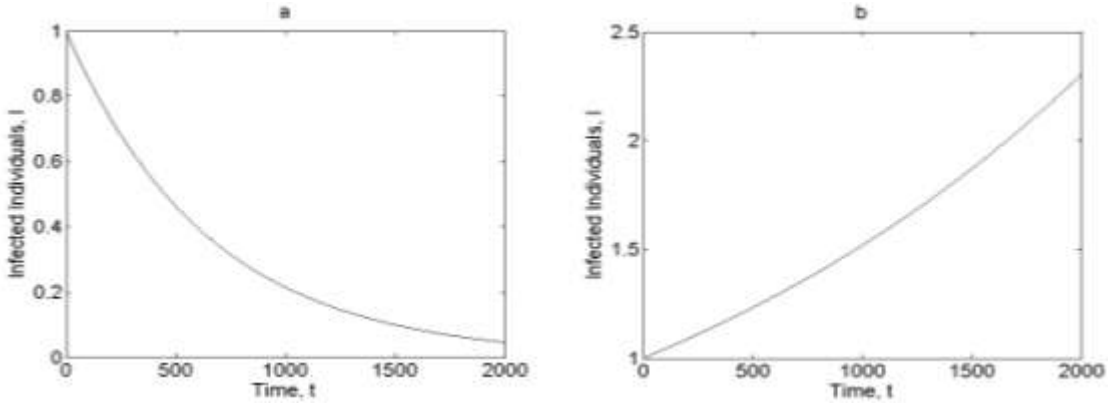

Fig 3: Graph of $I(t)$ for step-2.

6.3. For step 3:

Table 3: Results for step-3

	Example-1	Example-3
α (constant)	0.8	0.8
β (constant)	0.006	0.006
δ	0.004	0.009
c (constant)	0.18	0.18
μ (constant)	0.003	0.003
δ_0	0.00702332361516	0.00702332361516
Relation between δ and δ_0	$\delta < \delta_0$	$\delta > \delta_0$
Comment	I Is decreasing (Fig 4 (a))	I is increasing (Fig 4 (b))

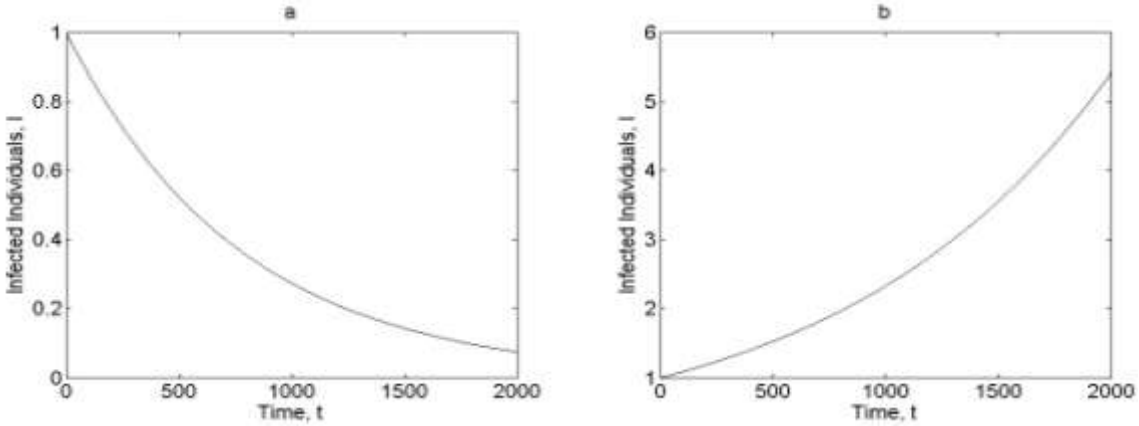

Fig 4: Graph of $I(t)$ for step-3.

6.4. For step 4:

Table 4: Results for step-4

	Example-1	Example-3
α	0.1	0.3
β (constant)	0.007	0.007
δ (constant)	0.008	0.008
c (constant)	0.003	0.003
μ (constant)	0.003	0.003
α_0	0.015964673913043	0.015964673913043
Relation between α and α_0	$\alpha < \alpha_0$	$\alpha > \alpha_0$
Comment	I Is increasing (Fig 5 (a))	I is decreasing (Fig 5 (b))

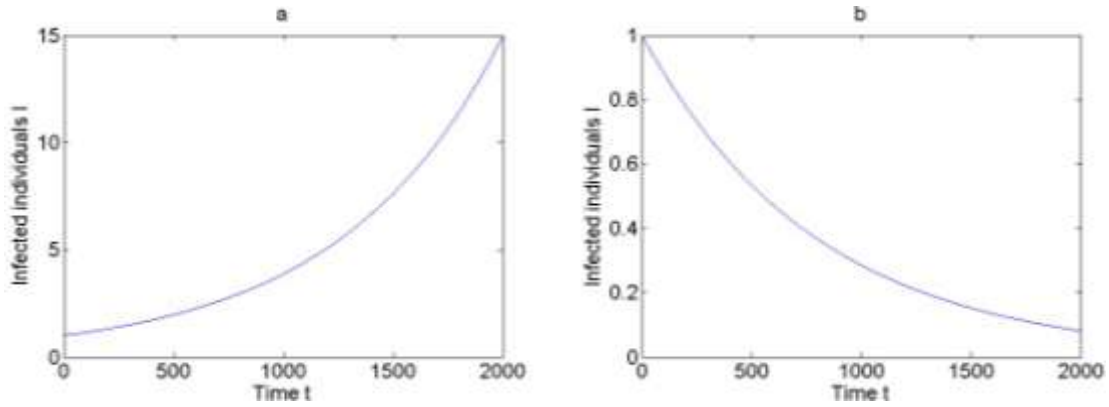

Fig 5: Graph of $I(t)$ for step-4.

VII. Discussion:

In the above simulations we consider the initial value of infected individual is 1, i.e., $I_0 = 1$. We see from the Table 1 that if all parameters except c are fixed there exist a bifurcation value c_0 . If $c < c_0$, then the number of infected individuals is is decreasing (Fig 2 (a)) as $t \to \infty$. On the other hand if $c > c_0$, then the number of infected individuals is increasing (Fig 2 (b)) as $t \to \infty$. Similarly from the Table 2 we see that if all parameters except β are fixed there exist a bifurcation value β_0 . If $\beta < \beta_0$, then the number of infected individuals is is decreasing (Fig 3 (a)) as $t \to \infty$. On the other hand if $\beta > \beta_0$, then the number of infected individuals is increasing (Fig 3 (b)) as $t \to \infty$. from the Table 3 there exist a bifurcation value δ_0 . If $\delta < \delta_0$, then the number of infected individuals is decreasing (Fig 4 (a)) as $t \to \infty$. On the other hand if $\delta > \delta_0$, then

the number of infected individuals is increasing (Fig 4 (b)) as $t \to \infty$. Finally from the Table 4 there exist a bifurcation value α_0. If $\alpha < \alpha_0$, then the number of infected individuals is increasing (Fig 5 (a)) as $t \to \infty$. On the other hand if $\alpha > \alpha_0$, then the number of infected individuals is decreasing (Fig 5 (b)) as $t \to \infty$.

VIII. Conclusion:

A new deterministic model is constructed and used to analyze the effect of a preventive vaccine on the transmission dynamics of an infectious disease. The model is thoroughly analyzed to investigate the stability at DFE. From the theoretical discussion and numerical simulations, we see that if the parameter value $c < c_0$ or $\beta < \beta_0$ or $\delta < \delta_0$ or $\alpha > \alpha_0$ then there is no epidemic. So, in the initial stage (when the number of infected individuals is not large), we shall control the epidemic successfully by controlling the parameters.

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