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PATTERNS OF PANDEMIC IN A TWO STAGES SIRS MODEL WITH A PUBLIC HEALTH PROGRAM

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Abstract: The aim of this paper is to study the impact of introducing a vaccine on the dynamic of an infection in a SIRS model where primary and secondary infected are different. We investigate whether a public health program based on vaccinating a proportion of population can leads to control of the disease. This goal is reached by introducing and computing the basic reproduction number, $R_0(p)$, and showing the relation between $R_0(p)$ and the existence, stability and bifurcation of equilibriums. Also we obtain a threshold for vaccination coverage such that vaccination program eliminates the infection.

AMS Subject Classification: 92D25, 92D30
Key Words: basic reproduction number, two stages SIRS model, Vaccination program, infectious disease

1. Introduction

The health and socioeconomic risk posed by severe and sudden epidemics of infectious diseases like SARS, Avian Flu, West Nile Virus or bio-terrorist attacks are compelling modern societies to design and complete more effective control and preparedness programs. The ultimate intention of such studies is to provide a body of evidence that decision makers and institutions can used

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in designing policy recommendations and interventions. The first model of an epidemic was suggested by Bernoulli in 1760. He used this model to explain the effects and advantages of vaccination in order to prevent an epidemic. Simple mathematical models for studying the transmission dynamics belong to the class of compartmental models, and are governed by mass-action laws [3, 4, 7]. The rate of spread of infection is assumed to be proportional to the density of susceptible people and the density of infected people (strong homogenous mixing). Simpler models, based on 'weak homogenous mixing' (rate of infections proportional to the density of susceptible) are explored in [1, 2]. One quantity stands out in these models, the ratio of the rate of infection to the rate of recovery, denoted by R_0, called the basic reproduction number. It is the average number of new cases produced when one infected individuals is introduced into a completely susceptible community. A basic result in modern epidemiology is the existence of a threshold value for the basic reproduction number such that if R_0 is below the threshold, an epidemic outbreak does not follow the introduction of an infected individual in the community [6, 7, 8, 9]. The basic reproduction number is a very important quantity in epidemiology and plays a vital role, there is hardly a paper on epidemiology where R_0 does not play a role. Recently in [5, 6] a new approach for computing R_0 is presented that we explain it here by an example, consider the following SEI model with a latent category

$$\begin{aligned}
\frac{d}{dt}S &= \mu N - \mu S - \beta\frac{SI}{N},\\
\frac{d}{dt}E &= \beta\frac{SI}{N} - (\mu+\nu)E,\\
\frac{d}{dt}I &= \nu E - \mu I,
\end{aligned}$$

where S, E, I and N denote the size of susceptible, latently infected, infected and total population respectively,the Greek letters are the infection parameters, that we will explain them in our model. The second and third equations are called the infection subsystem. The infection-free equilibrium is $E = I = 0$, $S = N$ by replacing S with N in the infection subsystem the following system is obtained and called the linearized infection subsystem

$$\begin{aligned}
\frac{d}{dt}E &= \beta I - (\nu+\mu)E,\\
\frac{d}{dt}I &= \nu E - \mu I.
\end{aligned}$$

The linearized infection subsystem is written in the form $\frac{d}{dt}X = (T + \Sigma)X$ where $X = (E, I)^T$, and T, Σ are 2×2 matrices where T is computed in this case: By showing the infection states E, I respectively by 1, 2 and supposing that an infected individual of type j introduced to a infection-free community, the rate at which this individual produce infected individuals of type i, is the entry T_{ij}. So $T_{ij} = 0$ when no new cases produced by an individual in infected state j can be in infected state i immediately after infection. Regarding the linearized infection subsystem and T, Σ can be obtained. In this example

$$T = \begin{pmatrix} 0 & \beta \\ 0 & 0 \end{pmatrix}, \quad \Sigma = \begin{pmatrix} -(\mu + \nu) & 0 \\ \nu & -\mu \end{pmatrix}.$$

Then the next-generation matrix with large domain, K_L, is introduced with $K_L = -T\Sigma^{-1}$and the basic reproduction number, R_0, is the dominant eigenvalue of K_L, in this example $R_0 = \beta\nu/(\mu(\mu+\nu))$. In [10] the authors considered an infectious disease with this assumption: The individuals that being infected for the first time and the individuals which having experienced the infection at least once before are different in the recovery rate and infectivity, to control the infection they considered a vaccination program such that a constant percent of newborns are vaccinated, the authors formulated this situation in a model and analyzed the model to find the conditions of community in the future and also to understand the success of program. Their analysis was including: the computation of reproduction number and the relation between it and cases such as stability of equilibriums and the elimination of infection, determining a minimum for percent of vaccinated individuals in a successful program. In this paper we concentrate on a more general vaccination program which involves [10] as an special case, let us give a brief outline of the paper, we have a community with constant population size and an infectious disease in community also we suppose there are differences between infected individuals who being infected for the first time (primary infected) and who having experienced the infection at least once before (secondary infected). These differences include the infectivity, susceptibility and the rate of recovery. The infection is not fatal and the acquired immunity disappears as time goes on. Also there is no vertical transmission namely newborns are primary susceptible (individuals who have never experienced the infection) and the incidence rate is linear in fact proportional to the density of infected and susceptible individuals, to control the infection, we want to start a vaccination program such that a constant percent, p, of primary susceptible are vaccinated, note that if we restrict our vaccination program to newborns then we are in case [10]. We encounter to the following basic questions:

1 What is the necessary conditions to start the program?

2 What is the minimum percent of population for vaccination in a successful program?

3 How much we can increase the vaccination coverage? In the other word, whether increasing the vaccination coverage can leads to undesirable result?

4 When we can be assured that the infection removes?

5 When a pandemic may happens?

The goal of this paper is to answer to the these questions, in what follows we try to do so by the help of the key notion of reproductive number.

2. Formulation of the Model and the Basic Reproduction Number

Consider a community in which there is difference between individuals being infected for the first time (primary infected) and individuals having experienced the infection at least once before (secondary infected). Hence the total population is subdivided into: individuals who have never experienced the infection(primary susceptible, whose population is S_1), primarily infected individuals (whose population is I_1), recovered individuals (whose population is R), individuals who have lost their acquired immunity (secondary susceptible, whose population is S_2), secondary infected individuals (whose population is I_2) and vaccinated individuals (whose population is V). Individuals are assumed to be born, with rate μ, as S_1. Individuals in S_1 die with rate μ and get infected with primary rate of infection $\lambda(t) = k(I_1 + rI_2)$, where k is the transmission rate of I_1 and r is the relative infectivity of I_2 with respect to I_1 and also they get vaccinated with rate p. Individuals in I_1 die with rate μ and recover with rate α. Individuals in R die with rate μ and lose their immunity with rate σ, to become S_2. Individuals in S_2 die with rate μ and get infected with secondary rate of infection $g\lambda(t)$, where g represents the relative susceptibility of S_2 with respect to S_1. Individuals in I_2 die with rate μ and recover with rate $q\alpha$ and finally individuals in V die with rate μ and lose their immunity and become S_2 with rate $b\sigma$. The parameter b represents the relative loss of immunity of V with respect to R. If $b = 0$, then the vaccine conveys life long protection, while a value of $b = 1$ means that the vaccine induced immunity lasts as long as natural immunity. All parameters r, b, g and q are dimensionless. If $r > 1$, then I_2 have higher transmissibility than I_1 and vice versa. However, If $q > 1$,

then the infectious period of I_2 is shorter than that of I_1 and vice versa. Finally, a value of $g < 1$ means that S_2 have reduced susceptibility. We show the total population by N and the proportion of subpopulation i.e. $I_1(t/\mu_0)/N$, $I_2(t/\mu_0)/N$, $S_1(t/\mu_0)/N$, $R(t/\mu_0)/N$, $V(t/\mu_0)/N$ and $S_2(t/\mu_0)/N$ (where μ_0 is a quantity with dimension "*time*" and value "1") again by I_1, I_2, S_1, R, V and S_2 then we have the following dimension less system

$$\begin{aligned}
\frac{d}{dt}I_1 &= \lambda(t)S_1 - (\alpha+\mu)I_1,\\
\frac{d}{dt}I_2 &= g\lambda(t)S_2 - (\mu+q\alpha)I_2,\\
\frac{d}{dt}S_1 &= \mu - (\mu+p+\lambda(t))S_1,\\
\frac{d}{dt}R &= \alpha(I_1+qI_2) - (\sigma+\mu)R,\\
\frac{d}{dt}V &= pS_1 - (\mu+b\sigma)V,\\
\frac{d}{dt}S_2 &= \sigma(R+bV) - (g\lambda(t)+\mu)S_2,
\end{aligned} \tag{1}$$

where $\lambda(t) = \kappa(I_1 + rI_2)$ and $\kappa = Nk$. Clearly $I_1+I_2+S_1+R+V+S_2 = 1$ and all parameters as well as subpopulation proportions are nonnegative. System (1) is well posed in the sense that solutions exist and remain nonnegative for nonnegative initial conditions (see Figure 1).

In model (1), we assume that the size of population is constant and the infection is not fatal. If this model would be generalized to include fatality of infection and variable population size then the analysis would get much more complicated.

The basic reproduction number, denoted by R_0, is the average number of new cases produced by an infected case, during the infection period, when introduced into a population in which a proportion p of primary susceptible are vaccinated and which is free from the infection [8]. Model (1) has the infection-free equilibrium

$$\begin{aligned}
E_0 &= (I_1^0, I_2^0, S_1^0, R^0, V^0, S_2^0)\\
&= \left(0, 0, \frac{\mu}{(\mu+p)}, 0, \frac{p\mu}{(\mu+p)(\mu+b\sigma)}, \frac{bp\sigma}{(\mu+p)(\mu+b\sigma)}\right).
\end{aligned} \tag{2}$$

Mathematically, R_0 is the spectral radius of the next generation matrix. Based on the general approach in [6] and by following the method which we

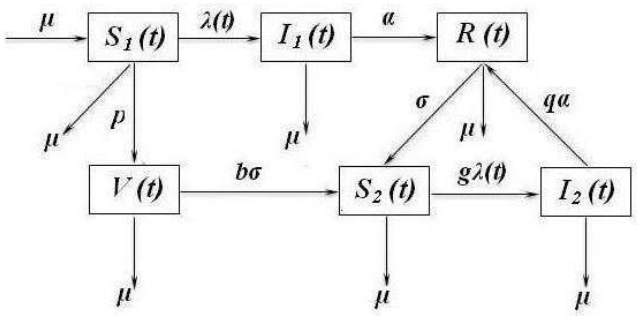

Figure 1: Compartmental model to show the transitions between model states

stated in Section 1 we have T and Σ as

$$T = \begin{pmatrix} \kappa S_1^0 & r\kappa S_1^0 \\ g\kappa S_2^0 & rg\kappa S_2^0 \end{pmatrix}, \quad \Sigma = \begin{pmatrix} -(\alpha+\mu) & 0 \\ 0 & -(q\alpha+\mu) \end{pmatrix}.$$

Hence the next generation matrix with large domain K_L is two dimensional and is given by

$$\begin{aligned} K_L = -T\Sigma^{-1} &= \begin{pmatrix} \kappa S_1^0 & r\kappa S_1^0 \\ g\kappa S_2^0 & rg\kappa S_2^0 \end{pmatrix} \begin{pmatrix} 1/(\alpha+\mu) & 0 \\ 0 & 1/(q\alpha+\mu) \end{pmatrix} \\ &= \begin{pmatrix} \kappa S_1^0/(\alpha+\mu) & r\kappa S_1^0/(q\alpha+\mu) \\ g\kappa S_1^0/(\alpha+\mu) & rg\kappa S_1^0/(q\alpha+\mu) \end{pmatrix}, \end{aligned}$$

and R_0 is given by

$$R_0 = \rho(K) = \frac{\kappa S_1^0}{\alpha+\mu} + rg\frac{\kappa S_2^0}{q\alpha+\mu}.$$

The number R_0 is a function of the vaccination coverage p, and we have

$$R_0(p) = \frac{\kappa\mu}{(\mu+p)(\mu+\alpha)} + \frac{rg\kappa bp\sigma}{(\mu+p)(\mu+b\sigma)(\mu+q\alpha)}. \tag{3}$$

In what follows the whole of our result are concerned to $R_0(p)$. In Section 2 we investigate the relation between $R_0(p)$ and existence and stability of equilibriums and in Section 3 by using the results of Section 2, firstly we obtain

necessary condition to start the vaccination program and obtain p_0 such that $R_0(p_0) = 1$ and show that p_0 is the minimum of p for success of program, and finally we show that in p_0 our system has a backward bifurcation. We summarize the main results with regard to answer to the sketched questions in Section 1 in the following main theorem.

Theorem 1. *(Main Theorem). Consider the two stages SIRS models (1) then we have:*

(a) The necessary condition to start the vaccination program is: $R_0(1) < 1 < R_0(0)$.

(b) For vaccination coverage p *we must have* $p_0 < p \leq 1$*, in other word we must at least vaccine* p_0 *percent of* S_1 *and at most we can extend the vaccination program to the whole of* S_1 *also in case* $p < p_0$ *a pandemic may happen.*

(c) $p > p_0$ *and the condition* (7) *together imply the global stability of infection-free equilibrium which practically means that the infection removes.*

(d) At p_0 *system (1) has a backward bifurcation, if* $p < p_0$ *then the system has two equilibriums and if* $p > p_0$ *the the system has one equilibrium.*

3. Equilibriums, Existence and Stability

In this section we show, how $R_0(p)$ and stability of E_0 are related and also the relation between $R_0(p)$ and the existence of the endemic equilibrium point, E_1, is investigated.

For stability of E_0 since the size of population is constant we can reduce (1) to a less dimensional model by writing one variable on the bass of the others for example writing V according to the others leads to the following model

$$\begin{aligned}
\frac{d}{dt}I_1 &= \lambda(t)S_1 - (\alpha+\mu)I_1,\\
\frac{d}{dt}I_2 &= g\lambda(t)S_2 - (\mu+q\alpha)I_2,\\
\frac{d}{dt}S_1 &= \mu - (\mu+p+\lambda(t))S_1,\\
\frac{d}{dt}R &= \alpha(I_1+qI_2) - (\sigma+\mu)R,\\
\frac{d}{dt}S_2 &= \sigma(R+b(1-I_1-I_2-S_1-R-S_2)) - (g\lambda(t)+\mu)S_2,
\end{aligned} \tag{4}$$

thus we study (4) in the following feasible region

$$\Omega = \{(I_1, I_2, S_1, R, S_2) : I_1, I_2, S_1, R, S_2 \geq 0, I_1 + I_2 + S_1 + R + S_2 \leq 1\}.$$

The linear part of (4) at $F_0 = (0, 0, \mu/(\mu + p), 0, bp\sigma/(\mu + p)(\mu + b\sigma))$ is as follows

$$\begin{pmatrix} -(\alpha+\mu)+\frac{\kappa\mu}{p+\mu} & \frac{\kappa r\mu}{p+\mu} & 0 & 0 & 0 \\ \frac{bg\kappa p\sigma}{(p+\mu)(\mu+b\sigma)} & -(q\alpha+\mu)+\frac{bg\kappa pr\sigma}{(p+\mu)(\mu+b\sigma)} & 0 & 0 & 0 \\ -\frac{\kappa\mu}{p+\mu} & -\frac{\kappa r\mu}{p+\mu} & -(p+\mu) & 0 & 0 \\ \alpha & q\alpha & 0 & -(\mu+\sigma) & 0 \\ -b\sigma-\frac{bg\kappa p\sigma}{(p+\mu)(\mu+b\sigma)} & -b\sigma-\frac{bg\kappa pr\sigma}{(p+\mu)(\mu+b\sigma)} & -b\sigma & (1-b)\sigma & -(\mu+b\sigma) \end{pmatrix}.$$

By calculation the eigenvalues are $r_1 = -(p + \mu) < 0$, $r_2 = -(\mu + \sigma) < 0$, $r_3 = -(\mu + b\sigma) < 0$ and r_4, r_5, which are the roots of the following equation

$$Ar^2 + Br + C = 0,$$

$$\begin{aligned} A &= p\mu + \mu^2 + bp\sigma + b\mu\sigma. \\ B &= p\alpha\mu + pq\alpha\mu - \kappa\mu^2 + 2p\mu^2 + \alpha\mu^2 + q\alpha\mu^2 + 2\mu^3 - bg\kappa pr\sigma \\ &+ bp\alpha\sigma + bpq\alpha\sigma - b\kappa\mu\sigma + 2bp\mu\sigma + b\alpha\mu\sigma + bq\alpha\mu\sigma + 2b\mu^2\sigma. \\ C &= pq\alpha^2\mu + p\alpha\mu^2 - \kappa q\alpha\mu^2 + pq\alpha\mu^2 + q\alpha^2\mu^2 - \kappa\mu^3 + p\mu^3 + \alpha\mu^3 \\ &+ q\alpha\mu^3 + \mu^4 - bg\kappa pr\alpha\sigma + bpq\alpha^2\sigma - bg\kappa pr\mu\sigma + bp\alpha\mu\sigma - b\kappa q\alpha\mu\sigma \\ &+ bpq\alpha\mu\sigma + bq\alpha^2\mu\sigma - b\kappa\mu^2\sigma + bp\mu^2\sigma + b\alpha\mu^2\sigma + bq\alpha\mu^2\sigma + b\mu^3\sigma. \end{aligned}$$

Since A is positive, if B and C are positive then the real parts of both of r_4 and r_5 are negative and if C is negative then the real part of r_4 or the real part of r_5 is positive. The positivity of B and C are respectively equivalent to the following conditions

$$R_0(p) - 1 < \frac{\mu^2(q\alpha+\mu)^2 + b\sigma(gpr(\alpha+\mu)^2 + \mu(q\alpha+\mu)^2)}{(\alpha+\mu)(q\alpha+\mu)(\mu^2+b\sigma(gpr+\mu))} \Leftrightarrow B > 0$$
$$R_0(p) - 1 < 0 \Leftrightarrow C > 0. \qquad (5)$$

So the local stability of E_0 is determined by the following proposition.

Proposition 3.1. *The infection-free equilibrium E_0 exists for all parameter values. It is locally stable if and only if $R_0(p) < 1$.*

Obviously $(S_1 - S_2)$ plane is an invariant manifold for (4). By projecting (4) on the $(S_1 - S_2)$ plane, we have the following system

$$\frac{d}{dt}S_1 = -(\mu + p)S_1 + \mu$$

$$\frac{d}{dt}S_2 = -(\sigma b)S_1 - (\sigma b + \mu)S_2 + \sigma b. \tag{6}$$

The system(6) is linear and has only one equilibrium, (S_1^0, S_2^0), also the eigenvalues at (S_1^0, S_2^0) are $r_1 = -(\mu + p) < 0$, $r_2 = -(b\sigma + \mu) < 0$, so (S_1^0, S_2^0) is stable and every solution of (6) converges to it. In other word every solution of (4) that contained entirely in $(S_1 - S_2)$ plane converges to F_0. If we can obtain conditions under which every solutions of (4) approaches enough $(S_1 - S_2)$ plane by the continuity with respect to the initial values we conclude that every solution of (4) converges to F_0, therefore F_0 is globally stable. We suppose

$$\mu > \kappa(1 + g)\max(1, r) \tag{7}$$

then we have

$$\frac{d(I_1 + I_2 + R)}{dt} < (\kappa(1 + g) - \mu)I_1 + (\kappa r(1 + g) - \mu)I_2 < 0$$

So if $\beta(t) = (I_1(t), I_2(t), S_1(t), R(t), S_2(t))$ is an arbitrary solution of (4), then $I_1(t) + I_2(t) + R(t)$ converges to zero, as $t \to \infty$, therefore $\beta(t)$ approaches $(S_1 - S_2)$ plane. Hence the global stability of E_0 is determined by the following proposition.

Proposition 3.2. *If $R_0(p) < 1$ and (7) is satisfied then the infection-free equilibrium is globally stable. So part (c) of main theorem is satisfied.*

Conjecture 3.3. we guess $R_0(p) < 1$ alone is sufficient for global stability of E_0 but we can't present sufficient mathematical reasons, numerical simulation confirm the guess (see section 5).

To find the other equilibrium(s), we set the derivatives in the left-hand side of (1) equal to zero which results in the following system of algebraic equations

$$\begin{aligned}
0 &= \lambda S_1 - (\alpha + \mu)I_1, \\
0 &= g\lambda S_2 - (\mu + q\alpha)I_2, \\
0 &= \mu - (\mu + p + \lambda)S_1, \\
0 &= \alpha(I_1 + qI_2) - (\sigma + \mu)R, \\
0 &= pS_1 - (\mu + b\sigma)V, \\
0 &= \sigma(R + bV) - (g\lambda + \mu)S_2.
\end{aligned}$$

The endemic equilibrium, $E_1 = (I_1^1, I_2^1, S_1^1, R^1, V^1, S_2^1)$, is obtained by assuming that $I_1 \neq 0$ and $I_2 \neq 0$ which implies that $\lambda \neq 0$. We look for an equation in

terms of λ, and the other model parameters, which can be used to determine the equilibrium(s). By calculation we have

$$
\begin{aligned}
I_1 =& \frac{\lambda\mu}{(\alpha+\mu)(p+\lambda+\mu)},\\
I_2 =& \frac{g\lambda(bp\alpha\mu\sigma+\alpha\lambda\mu\sigma+bp\mu^2\sigma+bp\alpha\sigma^2+b\alpha\lambda\sigma^2+bp\mu\sigma^2)}{(\alpha+\mu)(p+\lambda+\mu)(\mu+b\sigma)(gq\alpha\lambda+q\alpha\mu+g\lambda\mu+\mu^2+q\alpha\sigma+g\lambda\sigma+\mu\sigma)},\\
S_1 =& \frac{\mu}{p+\lambda+\mu},\\
R =& \frac{gq\alpha^2\lambda^2\mu+q\alpha^2\lambda\mu^2+g\alpha\lambda^2\mu^2+\alpha\lambda\mu^3+bgpq\alpha^2\lambda\sigma}{(\alpha+\mu)(p+\lambda+\mu)(\mu+b\sigma)(gq\alpha\lambda+q\alpha\mu+g\lambda\mu+\mu^2+q\alpha\sigma+g\lambda\sigma+\mu\sigma)},\\
&+\frac{bgq\alpha^2\lambda^2\sigma+bgpq\alpha\lambda\mu\sigma+bq\alpha^2\lambda\mu\sigma+bg\alpha\lambda^2\mu\sigma+b\alpha\lambda\mu^2\sigma}{(\alpha+\mu)(p+\lambda+\mu)(\mu+b\sigma)(gq\alpha\lambda+q\alpha\mu+g\lambda\mu+\mu^2+q\alpha\sigma+g\lambda\sigma+\mu\sigma)},\\
V =& \frac{p\mu}{(p+\lambda+\mu)(\mu+b\sigma)},\\
S_2 =& \frac{\mu(bp\sigma(\alpha+\mu)(q\alpha+\mu)(\mu+\sigma)+\alpha\sigma\lambda(q\alpha+\mu)(\mu+b\sigma))}{(p+\lambda+\mu)(\mu+b\sigma)((\alpha+\mu)(q\alpha+\mu)(g\lambda+\mu)(\mu+\sigma)-gq\sigma\alpha\lambda(\alpha+\mu))}.
\end{aligned}
$$

The first and second equations and $\lambda(t)=\kappa(I_1+rI_2)$ imply an equation for λ as follows

$$A\lambda^2+B\lambda+C=0,$$

$$
\begin{aligned}
A &= g(\alpha+\mu)(q\alpha+\mu+\sigma)(\mu+b\sigma),\\
B &= (\mu+b\sigma)(-gr\alpha\kappa\sigma-g\kappa\mu(q\alpha+\mu+\sigma)+(\alpha+\mu)((q\alpha+\mu)(\mu+\sigma)\\
&+ g(p+\mu)(q\alpha+\mu+\sigma))),\\
C &= (\mu+\sigma)(-bgpr\kappa(\alpha+\mu)\sigma-\kappa\mu(q\alpha+\mu)(\mu+b\sigma)+(p+\mu)(\alpha+\mu)\\
&\times (q\alpha+\mu)(\mu+b\sigma)).
\end{aligned}
$$

By calculation we have, $B^2-4AC\geq 0$, is equal to the following:

$$
\begin{aligned}
1-R_0(p) \leq\ & ((\mu+b\sigma)(gr\alpha\kappa\sigma+g\kappa\mu(q\alpha+\mu+\sigma)-(\alpha+\mu)((q\alpha+\mu)\\
&\times (\mu+\sigma)+g(p+\mu)(q\alpha+\mu+\sigma)))^2)/(4g(\alpha+\mu)(\mu+\sigma)\\
&\times (q\alpha+\mu+\sigma)(p+\mu)(\alpha+\mu)(q\alpha+\mu)(\mu+b\sigma)).
\end{aligned}
$$

Hence we have the following proposition

Proposition 3.4. *$R_0(p)>1$ if and only if there exist one endemic equilibrium point, E_1, also by calculation E_1 has at least two negative eigenvalues $r_1=-(\mu+\sigma)$ and $r_2=-(\mu+b\sigma)$which implies that dimension of its stable manifold is at least* 2.

Remark 3.5. By proposition (3.1) if $R_0(p) > 1$ then, E_0 is unstable hence the maximum dimension of its stable manifold is 4, since every four dimensional submanifold of $\mathbb{R}^5$ has lebesgue measure zero, almost every solution of (4) in a neighborhood of E_0 does not belong to stable manifold of E_0 in other word almost every solution of (4) in a neighborhood of E_o repelled from a neighborhood of E_0 so we conclude, if $R_0(p) > 1$ then introducing even few infected individuals into a infection-free community might bring it into a pandemic.

4. Vaccination Coverage Threshold and Bifurcation

In this section we try to find a threshold for p, such that if few infected individual is introduced to a completely susceptible community, a pandemic does not happen, by (3) we have

$$\frac{\partial}{\partial p}R_0(p) = \frac{1}{(\mu+p)^2}\left(\frac{rg\kappa b\sigma\mu}{(\mu+b\sigma)(\mu+q\alpha)} - \frac{\kappa\mu}{(\mu+\alpha)}\right). \tag{8}$$

If we assume that $R_0(0) < 1$ then, no vaccination program is needed and if we assume that $R_0(1) > 1$ then, any vaccination coverage is indeterminate so with the following condition caring out the vaccination program is significant

$$R_0(1) < 1 < R_0(0). \tag{9}$$

In other word (9) is necessary for vaccination program, therefore if we start to vaccinating, (9) must be satisfied. In general, we expect that vaccination lowers the reproduction number. Clearly $R_0(p)$ has a negative slope if and only if

$$\frac{\partial}{\partial p}R_0(p) < 0.$$

By (8) we conclude that the sign of $\frac{\partial}{\partial p}R_0(p)$ is independent of p and by (9) it is negative therefore increasing the vaccination coverage can not be a source of infection as we expected.

based on the information only on $R_0(p)$, the necessary condition for successful elimination of infection by sufficient vaccination coverage is

$$R_0(p) < 1$$

Then we must have

$$\frac{\kappa\mu}{(\mu+p)(\mu+\alpha)}+\frac{rg\kappa bp\sigma}{(\mu+p)(\mu+b\sigma)(\mu+q\alpha)}<1,$$

or equivalently

$$p>\frac{\mu(\kappa-\alpha-\mu)(q\alpha+\mu)(\mu+b\sigma)}{(\alpha+\mu)(-bg\kappa r\sigma+(q\alpha+\mu)(\mu+b\sigma))}.$$

Hence a threshold for vaccination coverage is obtained as follows:

$$p_0=\frac{\mu(\kappa-\alpha-\mu)(q\alpha+\mu)(\mu+b\sigma)}{(\alpha+\mu)(-bg\kappa r\sigma+(q\alpha+\mu)(\mu+b\sigma))}. \tag{10}$$

To avoiding a pandemic when few infected individual introduced into the population, p must be greater than p_0.

Proposition 4.1. *The condition* (9) *is necessary for caring out vaccination program and to avoiding a pandemic when few infected individuals introduced into a completely susceptible community we must have* $p > p_0$, *also* $R_0(p)$ *is monotonically decreasing with the increase of the* p *namely increasing the vaccination coverage leads to better control. This proposition and Remark* (3.5) *satisfy parts (a) and (b) of main theorem.*

Remark 4.2. By proposition (4.1) and (3.4) it is obvious that the system (1) has a backward bifurcation at $p = p_0$ because if $p > p_0$ then the model has only one equilibrium E_0 and if $p < p_0$ then it has two equilibrium E_0, E_1. Thus part (d) of main theorem is satisfied.

5. Numerical Simulation

In this section we show the validity of conjecture (3.3) by numerical computation. Let us return to (4) and correspond numerical values to the parameters, if we suppose $\kappa = 0.5$, $r = 0.9$, $\alpha = 0.2$, $\mu = 0.2$, $g = 0.5$, $q = 1.1$, $\sigma = 0.25$, $b = 1.5$, then we have $R_0(0) = 1.25 > 1$ and $R_0(1) = 0.0503138 < 1$ then the necessary conditions for vaccination are satisfied also $p_0 = 0.216107$ then we must choose p greater than p_0, we set $p = 0.22$ so we have $R_0(p) = 0.778246$ and the following system

$$\frac{d}{dt}I_1 \;=\; -0.4I_1+0.5I_1S_1+0.45I_2S_1,$$

$$\begin{aligned}
\frac{d}{dt}I_2 &= -0.42I_2 + 0.25I_1S_2 + 0.225I_2S_2, \\
\frac{d}{dt}S_1 &= -0.42S_1 - 0.5I_1S_1 - 0.045I_2S_1 + 0.2, \\
\frac{d}{dt}R &= 0.2I_1 + 0.22I_2 - 0.45R, \\
\frac{d}{dt}S_2 &= -0.375I_1 - 0.375I_2 - 0.125R - 0.375S_1 \\
&- 0.575S_2 - 0.25I_1S_2 - 0.225I_2S_2 + 0.375,
\end{aligned} \tag{11}$$

and the condition (7) is not valid, according to proposition (3.1) and (3.4) this system must has only one equilibrium, E_0, (the infection-free equilibrium). By calculation, uniqueness of equilibriums is confirmed and the only equilibrium is $(0, 0, 0.47619, 0, 0.341615)$. For its global stability we compute a number of solutions of (11) with the following initial values

$$\begin{aligned}
(I_1(0), I_2(0), S_1(0), R(0), S_2(0)) &= (0.4, 0, 0.1, 0, 0.5), \\
(I_1(0), I_2(0), S_1(0), R(0), S_2(0)) &= (0, 0.1, 0.2, 0.1, 0.6), \\
(I_1(0), I_2(0), S_1(0), R(0), S_2(0)) &= (0.3, 0.4, 0, 0.2, 0.1), \\
(I_1(0), I_2(0), S_1(0), R(0), S_2(0)) &= (0.1, 0.2, 0.3, 0.3, 0), \\
(I_1(0), I_2(0), S_1(0), R(0), S_2(0)) &= (0.15, 0.18, 0.32, 0.28, 0.12).
\end{aligned}$$

For these solutions the graph of each component is plotted in a figure below

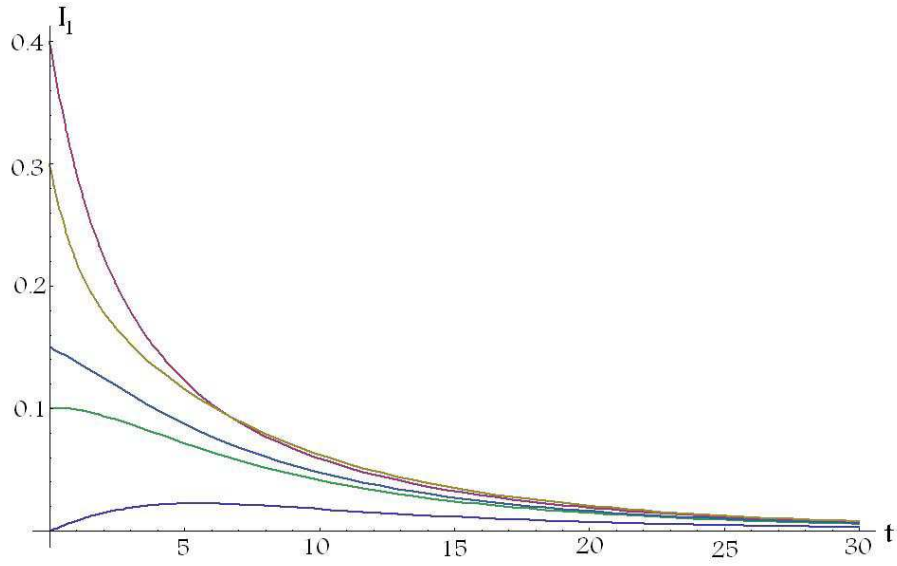

Figure 2. $\lim I_1(t)_{t\to\infty} = 0$

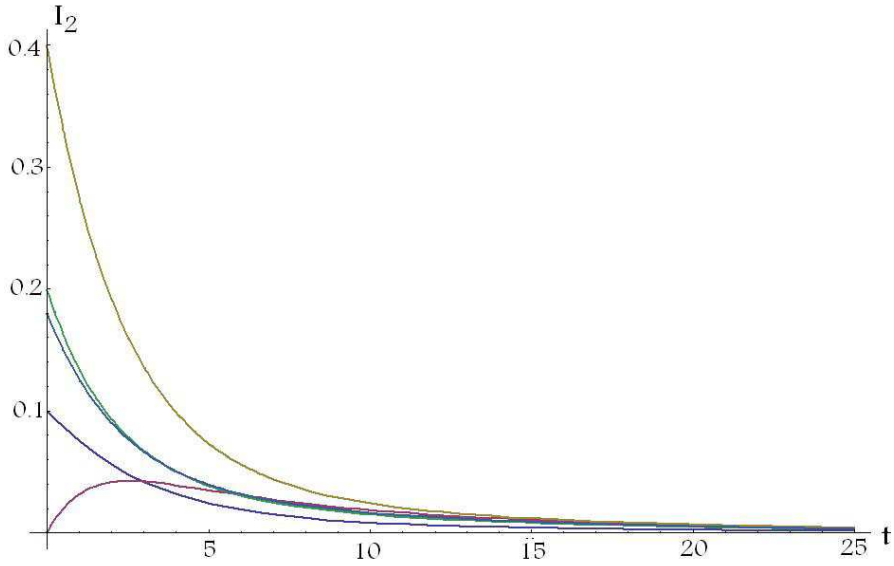

Figure 3. $\lim I_2(t)_{t\to\infty} = 0$

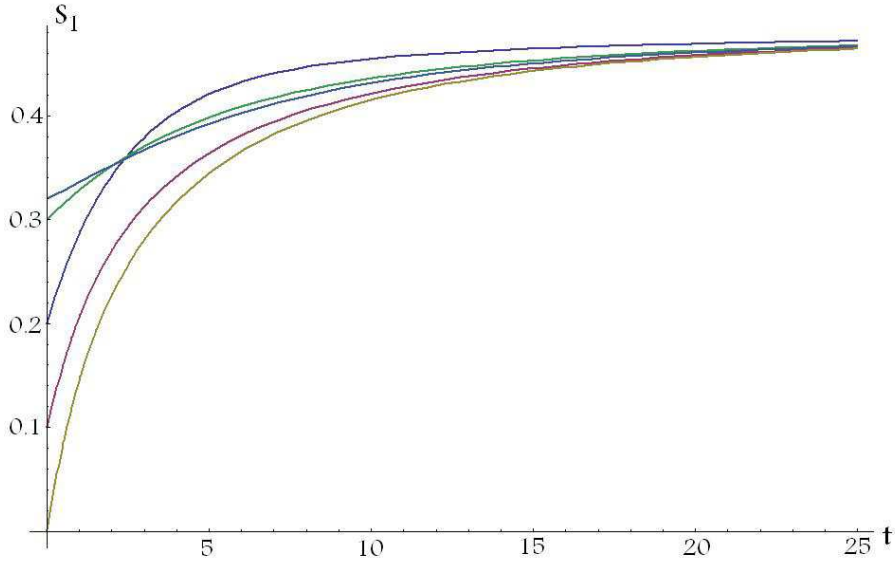

Figure 4. $\lim S_1(t)_{t\to\infty} = 0.47619$

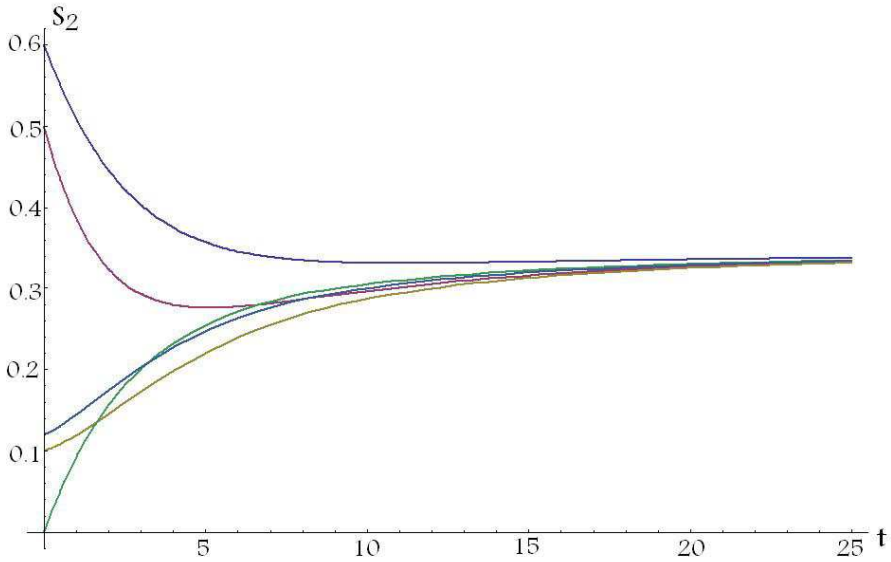

Figure 5. $\lim S_2(t)_{t\to\infty} = 0.341615$

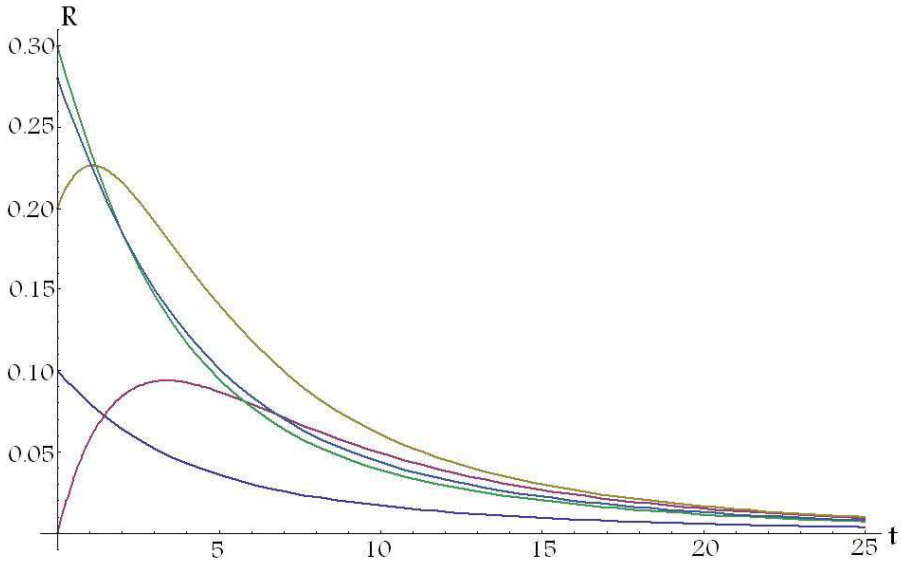

Figure 6. $\lim R(t)_{t\to\infty} = 0$

As figures show in general every solution converges to the infection-free equilibrium and this confirm our guess.

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