Biomedical Signal Processing and Control 40 (2018) 83–90

Contents lists available at ScienceDirect

Biomedical Signal Processing and Control

journal homepage: www.elsevier.com/locate/bspc

Reducing vaccination level to eradicate a disease by means of a mixed control with isolation

Erivelton G. Nepomuceno [a,*], Ricardo H.C. Takahashi [b], Luis A. Aguirre [c]

[a] Control and Modelling Group (GCOM), Department of Electrical Engineering, Federal University of São João del-Rei, São João del-Rei, MG 36307-352, Brazil
[b] Department of Mathematics, Federal University of Minas Gerais, Belo Horizonte, MG 31270-901, Brazil
[c] Department of Electronic Engineering, School of Engineering, Federal University of Minas Gerais, Belo Horizonte, MG 31270-901, Brazil

ARTICLE INFO

Article history:
Received 20 February 2017
Received in revised form 27 July 2017
Accepted 3 September 2017

Keywords:
Biological systems
SIR Model
Vaccination
Isolation
Epidemiology
Mixed control
Disease dynamics

ABSTRACT

The present study has investigated mixed control strategy to reduce the required level of vaccination to eradicate a disease. It is well known that despite the advances on the development of new vaccines and control strategies to eradicate diseases, many diseases such as measles, tuberculosis and flu are still persistent. Any effort made to bring some light in this issue should be considered and developed. Here, we present a dynamic analysis of the SIR model to develop a simple but efficient strategy of control based on the simultaneously application of vaccination and isolation. We show how to significantly decrease the required level of vaccination to eradicate a disease. We have also found that a growth in population decreases the effects of isolation in the required time to eradicate a disease. Finally, we noticed that the effect of isolation for both fixed size population or variable population is more significant for lower levels of vaccination, which is particularly interesting in real life situations, where the high levels of vaccination are not undertaken. Numerical simulations are provided to show the effectiveness of the proposed technique.

1. Introduction

Infectious diseases are one of the most important causes of morbidity and mortality in the world. Nevertheless, policies aimed at limiting their occurrence has been limited, particularly in developing countries [14]. One of the difficulties to achieve this task is the developing of effective vaccines. Even when there is a discovery of an effective vaccine the battle has not finished, as virus and bacteria evolve very fast, a phenomenon called drug resistance may occur. A recent and challenger example is the appearance of a drug-resistant Tuberculosis in China [20,39]. According to [39], 5.7% of the cases had multidrug-resistant Tuberculosis.

This situation becomes particularly severe when the number of eradicated diseases is analysed. Unfortunately, this number is still very little and although there is great reasons to celebrate the global eradication of smallpox, the same results are not yet achieved to many other diseases, such as measles, tuberculosis, and different types of influenza [13,14]. Among the main reasons that explain this failure, an efficient control strategy of the vaccines is certainly one of them. The scientific community is aware of that and a myriad of papers on such issue is easily identified, such as [4,17,26,34,35].

One of the important scientific activities to help in eradicating diseases is the mathematical epidemiology. The author of [10] states in a concise way the reason of such studies: "The main reasons for studying mathematical models of disease spread is the hope that improved understanding of the transmission mechanism may lead to more effective control strategies". An example of such approach can be seen in [31], where mathematical analysis and numerical simulation are used to show the importance of CTL immune responses in eradication of the hepatitis B.

Among many mathematical strategies of modelling, the compartmental models [4,17], in general called SIR models, are usually considered one of the most important [8,9]. Although, it seems quite simple, the SIR model has been investigated in many aspects, such as nonlinear analysis of wave travelling of dispersal SIR epidemic model [36], variable population [1,37], on discrete time approach [3], HIV on micro-level population [11] and optimal control [2,6,12,15,16,41] to cite a few examples.

There are many works applying control theory on SIR and other compartmental models [2,5,15,25,27–29,37,41]. As pointed earlier, one of the most important goals of vaccinations campaigns is the eradication of the disease. There are many diseases that remain endemic and one of the reasons is that the levels of required vac-

* Corresponding author.
E-mail addresses: nepomuceno@ufsj.edu.br (E.G. Nepomuceno), aguirre@cpdee.ufmg.br (L.A. Aguirre).

http://dx.doi.org/10.1016/j.bspc.2017.09.004
1746-8094/

cines are sometimes very high. According to [14], only when the public coverage is above 93% in the measles case, does eradication occur. Although, a great effort has been done on strategies, particularly using optimal control [25,41], less attention has been observed in a mixed control to reduce the required level of vaccination to eradicate the disease. Mixed control is not a new method [7] it is currently using in many application situation, such as [23,40]. The authors of [19] use vaccination and isolation with the aim of reducing cost by means of an optimal control [16]. Another interesting paper is developed in [21], where the authors formulate by means of an optimal control a strategy to reduce the number of infected chronic hepatitis B individuals by means of isolation and vaccination. Similar works have been reported in [22] and [15], but focused in the outbreaks of hand, foot, and mouth disease in Taiwan and predicting and evaluating the epidemic rend of Ebola virus disease in West Africa, respectively. There also stochastic analysis of mixed control, particularly interesting for small populations, in the following works [24,30]. From a complex system perspective, an interesting work that applies mixed control can be seen in [38], where the authors deal with human contact networks that may change topologically from time to time.

This paper aims at contributing to present a procedure to calculate a threshold level of vaccination and isolation when these two control actions are present simultaneously. The theoretical investigation of epidemiological models with vaccination and isolation seems to be in its infancy, and is a thrilling area of future research [33]. The authors in [33] gives a detailed description of global analysis in SIRS epidemic model. Here, we further investigated this issue and show a possibility to use isolation, not only as replacing strategy, but as a way to decrease a level of vaccination required to eradicate a disease, as well as an effective way to reduce the settling time, that is, the time to reach the eradication. We also reported that the impact of isolation for each fixed size or variable population is extra sizeable for decrease ranges of vaccination, different from the numerical solutions found in [33], where the population is found fixed. In other words, situations that it feasible to have an expressive or maybe overall insurance of vaccination, the isolation is not so essential. However, for conditions, which may be effortlessly discovered in actual life, where the excessive levels of vaccination are not undertaken, a mixed control provides considerable help. We also describe in detail the difference of dynamical behaviour between vaccination and isolation.

A previous version of this work has been presented in [27].

2. The SIR model

Let the SIR model [17,27,28] be described as:

$$\begin{aligned} \mathrm{d}S/\mathrm{d}t &= \mu N(1-p) - \mu S - \beta IS/N, \\ \mathrm{d}I/\mathrm{d}t &= \beta IS/N - \gamma I - \mu I, \\ \mathrm{d}R/\mathrm{d}t &= \gamma I - \mu R + p\mu N, \end{aligned} \tag{1}$$

where S, I and R are susceptible, infected and recovered individuals, respectively; p is a vaccination rate, N is the size of population, β is the transmission rate, μ is birth rate. We assume that population size is constant and $S(t)+I(t)+R(t)=N$. Following [15], the constant population size assumption is usual and is based on the hypothesis that the time scale of epidemic process is significantly faster than that of demographic rates. This strategy has been applied, for instance, in [15,18,33] and also reported in [17], where the author suggest its validity for some size population range and according to specific diseases. Finally, γ is recover rate. All the parameters of Eq. (1) are described in Table 1. The formulation of incidence in Eq. (1) is called standard incidence [17] and avoids the linear increasing of contact rate due to the size of population N.

Table 1
Variables and parameters of the SIR model.

Variable	Description	Unity
N	Size of population	individuals
S	Number of susceptible individuals	individuals
I	Number of infected individuals	individuals
R	Number of recovered individuals	individuals
μ	Birth rate	time^{-1}
p	Vaccination rate	time^{-1}
β	Average number of adequate contacts for transmission	(individual $\times$ time)$^{-1}$
γ	Recover rate	time^{-1}

Eq. (1) may be simplified when it is divided by N and excluding R, since $R=N-S-I$. Thus, we have

$$\begin{aligned} \mathrm{d}s/\mathrm{d}t &= \mu(1-p) - \mu s - \beta is, \\ \mathrm{d}i/\mathrm{d}t &= \beta is - \gamma i - \mu i. \end{aligned} \tag{2}$$

When $p=0$, (2) is the classic SIR model [17].

3. Stability analysis according to β

The stability of fixed points of the SIR model is analysed in function of β. The fixed points are given by

$$\begin{aligned} \mathrm{d}s/\mathrm{d}t &= f(s,i) = 0 \,\text{and} \\ \mathrm{d}i/\mathrm{d}t &= g(s,i) = 0, \end{aligned} \tag{3}$$

which results in:

$$P_1 = (s_1, i_1) = (1, 0) \,\text{and} \tag{4}$$

$$P_2 = (s_2, i_2) = \left(\frac{\gamma+\mu}{\beta}, \frac{\mu}{\gamma+\mu} - \frac{\mu}{\beta} \right). \tag{5}$$

The Jacobian matrix is given by

$$J = \frac{\partial(f,g)}{\partial(s,i)} = \begin{bmatrix} \dfrac{\partial f}{\partial s} & \dfrac{\partial f}{\partial i} \\ \dfrac{\partial g}{\partial s} & \dfrac{\partial g}{\partial i} \end{bmatrix} \tag{6}$$

$$= \begin{bmatrix} -\mu - \beta i & -\beta s \\ \beta i & \beta s - (\gamma+\mu) \end{bmatrix}.$$

Evaluating the Jacobian matrix on P_1 and P_2 we have:

$$J_{P_1} = \begin{bmatrix} -\mu & -\beta \\ 0 & \beta - (\gamma+\mu) \end{bmatrix} \text{ and} \tag{7}$$

$$J_{P_2} = \begin{bmatrix} -\dfrac{\mu\beta}{\gamma+\mu} & -(\gamma+\mu) \\ -\dfrac{\mu\beta}{\gamma+\mu} - \mu & 0 \end{bmatrix}. \tag{8}$$

The eigenvalues associated to P_1 and P_2 are the roots of

$$\rho_1^2 - T_1\rho_1 + \Delta_1 = 0 \,\text{and} \tag{9}$$

$$\rho_2^2 - T_2\rho_2 + \Delta_2 = 0, \tag{10}$$

where $T_{1,2}$ and $\Delta_{1,2}$ are the trace and determinant of matrix $J_{P_{1,2}}$:

$$T_1 = \beta - \gamma - 2\mu \tag{11}$$

$$\Delta_1 = -\mu\beta + \mu(\gamma+\mu) \tag{12}$$

$$T_2 = -\frac{\beta\mu}{\gamma+\mu} \tag{13}$$

$$\Delta_2 = \beta\mu - \mu(\gamma+\mu). \tag{14}$$