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Nonlinear robust adaptive sliding mode control of influenza epidemic in the presence of uncertainty

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ABSTRACT

In this paper, a nonlinear robust adaptive sliding mode control strategy is presented for the influenza epidemics in the presence of model uncertainties. The nonlinear epidemiological model of influenza with five state variables (the numbers of susceptible, exposed, infected, asymptomatic and recovered individuals) and two control inputs (vaccination and antiviral treatment) is considered. The objective of the proposed controller is decreasing the number of susceptible and infected humans to zero by tracking the desired scenarios. As a result of this decreasing, the number of exposed and asymptomatic individuals is also decreased and converged to the zero. Accordingly, it is shown that the number of recovered humans is increased to its maximum steady state value. The stability and tracking convergence of the control system are proved via the Lyapunov stability theorem. For the first time, a robust controller is designed and investigated for the uncertain process of influenza treatment in a population. Through a comprehensive evaluation, the effects of treatment period and the uncertainty amount on the performance of the controlled system are studied. According to the results, the nonlinear sliding mode controller guarantees the robust performance against a wide range of parametric uncertainties. Moreover, it is shown that much less rates of vaccination and antiviral treatment are required as the treatment interval is increased.

1. Introduction

An outbreak of Pandemic Influenza A (H1N1) was announced by the World Health Organization (WHO) on April 24, 2009 and its warning became more serious on June 11, 2009 [1,2]. Accordingly, the WHO received 18449 fatal patients from April 2009 to August 2010; which was reported from 214 countries all over the world [3]. Different health programs have been executed in order to prevent spread of Influenza. To implement various control strategies and assess their advantages/disadvantages and also the cost of implementation, predicting a reliable dynamic of epidemic is vital.

Dynamics of the epidemic are often described by mathematical models. These models are useful in evaluation of the related theories. Also, they can be used in comparing, planning, implementing and evaluating different detection, prevention, therapy and control programs [4]. For this purpose, some mathematical models have been developed for different diseases [5–10]. Colizza et al. [5] have developed a global stochastic model for the world-wide spread of pandemic influenza by considering the complete database of International Air Transport Association (IATA) [11]. Ferguson et al. [6] have developed a simulation-based model to investigate the effects of antiviral drugs and reducing contact rates for influenza disease in Southeast Asia. Also, Longini et al. [7] developed a stochastic model to evaluate the effectiveness of targeted antiviral prophylaxis and compared it with vaccination strategies. Similarly, the effect of antiviral drug based on stochastic simulation has been presented by Gani et al. [8].

In the field of deterministic models, Hethcote [4] have recommended the epidemiological models using a building block approach. Brauer [12] has made a deterministic model by dividing the population into susceptible, infected and removed compartments. Brauer [13] has also suggested other compartments such as asymptomatic, quarantined and isolated individuals. Arino et al. [14] have presented a deterministic compartmental model with five state variables for the influenza epidemic, and compared the results of their model with the previous stochastic ones.

Optimal control method is one of the control strategies that have been widely used for the different models of diseases. For example, Felippe de Souza et al. [15] have proposed an optimal control method for an HIV infection dynamics. Their cost function has been assigned such that the accumulated side effects of drugs and

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viral loads are minimized [15]. Also, Ledzewicz et al. [16] have presented an optimal control strategy for HIV infection and anti-viral treatment of AIDS. In their optimality criterion [16], the number of uninfected $CD4^+T$ cells is maximized; while, at the same time the drug dosage is minimized. Blayneh et al. [17] have used the optimal control theory for two deterministic models of malaria disease (as a vector-borne disease) and minimized the costs of contact prevention and treatment. They also considered the number of latent and infected groups in their cost function [17]. Recently, Lee et al. [18] have augmented the previous deterministic model of influenza epidemic [14] by adding three control inputs and implemented an optimal control strategy on this model (containing five state variables). They [18] used the vaccination, antiviral treatment and social distancing as the control inputs and showed that an optimal solution exists which minimizes the incidence and intervention costs. Some other advanced strategies were suggested in [19–23] for the optimization of the influenza vaccine allocation. Moreover, there are some works on the optimal control of HIV, cancer and tuberculosis diseases such as [24–27].

The epidemics of a disease depends on a lot of factors such as seasonal effects, structure of population and delays in vaccine production [18]. Thus, identifying the dynamics of epidemics may be complicated and the corresponding mathematical models cannot be easily obtained. In all of the above mentioned studies, the dynamics of epidemics must be fully identified and known. However, similar to other dynamic systems, the dynamics of epidemics are potentially accompanied with various sources of uncertainty and inaccuracy. The extracted mathematical models of epidemics may be vulnerable to the uncertainties in practice. Consequently, these uncertainties should be taken into account in the control of a disease epidemic. However, in the previous optimal control methods (such as [18] for influenza epidemics), the mathematical models of the process have been considered to be fully known and exact. As a result, the previous studies on the optimal control of different diseases may not lead to a desired performance in the presence of uncertainties.

To deal with the above deficiencies and achieve the robust performance in the presence of model uncertainties, robust and/or adaptive control methods are usually employed. Moradi et al. [27] have used an H_∞-robust controller for the drug delivery in the cancer chemotherapy process. Although this method had an acceptable performance for the uncertain plants, its conceptual design was rather complex. Moreover, in some previous optimal controllers [15–17,24–26] and the robust one [27], nonlinear dynamic model of the system should be linearized around some operating points. Thus, the controller has desired performance only around the operating points. For this purpose, Ibeas et al. [28] have suggested a robust controller for a specific SEIR epidemic model of diseases in a population with four state variables and one control input (vaccination). Recently, Moradi et al. [29] and Babaie et al. [30] have developed two adaptive control methods to adapt the drug dosage and the tumor volume in cancer chemotherapy inside the human body. However, the lack of a robust and/or adaptive control method for the influenza epidemic (with considering its last mathematical modeling) [18] is observed in the literature.

Accordingly, in this study and for the first time, a nonlinear robust adaptive sliding mode control strategy is developed to control the influenza epidemic. The objective of this control strategy is decreasing the number of individuals in susceptible and infected compartments of a population dealing with the influenza, in the presence of model uncertainties. For this purpose, two applicable control inputs (the rates of vaccination and antiviral treatment) are used for tracking the descending desired values for these compartments' population. The stability of the closed-loop control system and tracking convergence of the objective compartments' populations are proved using the Lyapunov stability theorem.

Unlike the previous linear controllers [15–17,24–27] that require the linearization of the process around the operating points, the proposed nonlinear sliding mode controller does not demand the linearization. As a result, the performance of the proposed controller is independent from the operating points or areas during the process. Moreover, unlike the previous optimal controllers [15–17,24–26] presented for different diseases, inclusion of the uncertainties in the nonlinear dynamics of the influenza epidemiological model are also considered in the structure of the proposed robust controller. The adaptation laws for updating the robust gains of the controller are defined to provide stability in the presence of dynamic uncertainties with unknown bounds.

2. Nonlinear epidemiological model of influenza

In this work, the nonlinear epidemiological model of influenza is adopted from [18]. This SEIAR model [18] is extracted from an initial SEIR model with five state variables (compartments) that have been proposed in [14]. Lee et al. [18] have augmented the previous influenza epidemic model [14] by adding three control inputs that are the vaccination, antiviral treatment and social distancing. In order to make the control inputs more practical and applicable in a real population, the third input (social distancing) is eliminated in this paper. In other words, it is hard to control the quarantine of the people or prevent them from their necessary travels as much as needed. Therefore, the nonlinear SEIAR epidemiological model of influenza with two control inputs (the rates of vaccination and antiviral treatment) and five variables (compartments) is described as:

$$\dot{S} = -\beta S\Lambda - \nu(t)S \tag{2.1}$$

$$\dot{E} = \beta S\Lambda - \kappa E \tag{2.2}$$

$$\dot{I} = p\kappa E - \alpha I - \tau(t)I \tag{2.3}$$

$$\dot{A} = (1-p)\kappa E - \eta A \tag{2.4}$$

$$\dot{R} = f\alpha I + \tau(t)I + \eta A + \nu(t)S \tag{2.5}$$

where $\Lambda = \varepsilon E + (1-q)I + \delta A$. Therefore, this system has five state variables S, E, I, A and R with positive values and initial conditions $S(0)=S_0$, $E(0)=E_0$, $I(0)=I_0$, $A(0)=A_0$ and $R(0)=R_0$. These positive state variables S, E, I, A and R are the Susceptible, Exposed, (symptomatic) Infected, Asymptomatic and Recovered compartments, respectively. In this SEIAR epidemiological model, S denotes the number of individuals that are susceptible and not yet infected with influenza, E represents the number of people exposed to influenza (infected but not yet infectious), I denotes the population of infected humans having infectious influenza symptoms, A represents the number of influenza carriers without any noticeable symptoms, and R is the number of recovered people from influenza. According to Eqs. (2.1)–(2.5), following statements can be mentioned: The exposed individuals (E) are infected with a rate of κ and they are divided into two groups: infected (I) and asymptomatic (A). The fraction p of infected humans will go to infected compartment and others (the fraction $1-p$ of infected humans) will proceed to asymptomatic group. The asymptomatic individuals (A) will go to recovered compartment (R) by the rate of η. Also, the infected humans leave their compartment at the rate of α, and a fraction f of these leaving persons will be recovered. Note that all parameters of the presented epidemiological model (2.1)–(2.5) including β, κ, p, α, η and f are positive constants. More details about this dynamic model are addressed in [18,14]. A conceptual flow diagram for visualization of the SEIAR influenza dynamics (2.1)–(2.5) is shown in Fig. 1.

In the above equations, $0 \le \nu(t) \le 1$ and $0 \le \tau(t) \le 1$ are two normalized control inputs of the system used to achieve the desired