

Optimal and Stability Analysis of the Co-infections Disease Mathematical Model

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Abstract A co-infection of a human or a pig with human influenza or COVID-19 strains and H5N1 strain may result in a pandemic strain, causing a widespread deadly pandemic. In this paper, we consider a new class of co-infections disease epidemic models for a rapid and slow virus. We study the transmission threshold by analyzing the basic reproduction number. The equilibrium points for the model are derived, and their local stability is analyzed with suitable assumptions on the model parameters. Understanding the model parameters is one of the prime subjects in this research work. Therefore, the sensitivity of essential parameters is investigated. Moreover, the optimal control problem for the proposed model is considered, and first-order optimality conditions are derived. Finally, numerical simulations indicate the effects of the model's basic reproduction number and control variables.

Keywords Co-infections model, stability analysis, basic reproduction number, optimal control

MSC(2010) 34D05, 34D20, 49J15, 92C60.

1. Introduction

Time evolution and the rapid spread of deadly viruses threaten human life and global economic growth. Therefore, understanding virus transmission is excellent attention to take precautions to control the disease. Recently, human beings suffers a lot from similar virus transmissions. The spread of the virus around the globe agitates its living organisms. For example, COVID-19 ruled out human life for a year, both health and wealth-wise. The spread of COVID-19 has been modeled and discussed by many researchers in their recent articles, for example, see [1, 10, 19, 20] and also the references therein. In particular, a patient with other health ailments (e.g., asthma, chronic obstructive pulmonary disease (COPD), pulmonary fibrosis, pneumonia, lung cancer, diabetes of type 1, human immunodeficiency virus (HIV), etc.,) suffered a lot in this COVID-19 outbreak.

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On the other hand, some virus for example asthma, chronic obstructive pulmonary disease (COPD), pulmonary fibrosis, pneumonia, lung cancer, diabetes of type 1 and HIV are virus that damages the cells in your immune system and weakens your ability to fight everyday infections and diseases. Some of the virus are not fully curable, but we can make patients lead their daily lives without any troubles. However, for more detail, we refer the interested readers to [2–4, 9] and the references therein. A mathematical model studies the transmission of two or more diseases called a co-infection model. Therefore, a good understanding of both the virus transmission and outbreak is important to investigate. Hence, we propose a co-infection diseases mathematical model in this work. For more references of co-infection diseases mathematical model, we refer the readers to [7, 11, 12, 14] and the references therein.

Coinfection is the process of infection of a single host with two or more pathogen variants (strains) or with two or more distinct pathogen species. Coinfection with multiple pathogen strains is particularly common in HIV, but it occurs in many other diseases. Coinfection with multiple pathogen species is also thought to be a very common occurrence. Particularly widely distributed combinations are HIV and tuberculosis, HIV and hepatitis, HIV and malaria, and others. Coinfection is of significant importance because it may have negative effect both on the health of the coinfecting individuals as well as on the public health in general. For instance, a coinfection of a human or a pig with human influenza strain and H5N1 strain may result in a pandemic strain, causing a widespread deadly pandemic. Among rapid virus such as COVID-19 or influenza affected patients, few of them are asymptomatic. Further, some are exposed to this virus patients are in quarantine. Those classes are also included in the following co-infection model. The population of the model includes twelve classes: S denotes the the susceptible individuals, E_1 and E_2 represent the exposed individuals of first (rapid virus) and Second (slow virus) respectively. I_1 for infected individuals of first virus, I_2 for infected individuals of second virus, and I_3 represents the individuals who are infected by both of the infections. The variable A denotes the individuals who are asymptomatic of first virus. Q denotes individuals who are in quarantine for first virus. R_1 denotes the individuals who are recovered from first virus. R_2 represents the individuals who are recovered from second virus, and R_3 represents the individuals who are recovered from both infections. Finally, D denotes individuals who died due to infection. Here the recovery of second virus individuals represents the individuals who can lead their life without any interception of the infections. To model coinfection, we need to introduce a new dependent variable, namely $I_3(t)$, the number of coinfecting individuals in the population. The model again is built on the basis of the competitive exclusion model (1.1), but with a coinfecting class I_3 . From the model flow diagram of the co-infections disease mathematical epidemic model Fig. 1, we derive the following system of nonlinear differential equations