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ON CONTRIBUTION OF DYNAMICAL SYSTEMS TO EPIDEMIOLOGY

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Abstract

The involvement of mathematical modeling in understanding the spreading of infectious diseases is briefly presented in this short review. The article addresses to different readers, from specialists familiar to the field of mathematical modeling to the larger public interested in these topics.

1 Introduction

The way an infectious disease (like Covid-19) spreads is a challenge both for science but also the large population. It is known from history that infectious diseases have caused much suffering to the humanity. From time to time and from place to place such pandemic plagues have appeared during the previous ages of the society. We can cite, at least, two very bad previous pandemic periods, with a very high number of death, the Black Plague and the Spanish flu. The first was one of the worst pandemic recorded in history, which stormed the humanity from 1346 to 1353 and has caused the death of 75–200 million people [1]. This number represented about one-third of the total world population at that time [2]. According to the World Health Organization, the Plague was created by the bacterium Yersinia pestis, which was spreading by fleas [3]. The second, and more recent, was the 1918 influenza pandemic, commonly known by the Spanish flu or as the Great Influenza epidemic. The estimated number of deaths was 17–50 million people [4] but due to the censors during World War I, this number could

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arrive to 100 million. We will never know the actual number of total death. It was an exceptionally deadly global influenza pandemic caused by the H1N1 influenza A virus.

Various methods to constraint the disease and save people have been proposed over the years and more medical solutions have been tested and developed in this regard. Perhaps, the best medical solution against the plague caused by this bacteria was the invention of antibiotics, which saved the lives of millions of people over the years.

2 Models of population dynamics in epidemiology

Along with the research aimed at finding medical solutions, a new theoretical framework of mathematical modeling of various characteristics related to a pandemic has started to develop. Perhaps, the works of Lotka [5] and Volterra [6] around the year 1925 were the pioneering works in this new domain. They have studied different types of interactions between groups of preys and predators in real-life phenomena related to ecology. Their models of population dynamics are known in the literature as *predator-prey* models or *Lotka-Volterra* models. The field evolved rapidly, both in terms of new models being proposed but also in terms of new domains where the models may have applications.

One of the new domains is epidemiology and, particularly, the transmission of infectious diseases, since the ways an infectious disease spreads in a population have many links with predator-prey models. A mathematical model which studies the interactions of three groups of individuals in a population affected by an infectious disease is the so-called SIR model [7], [8]. The three interacting groups are S-susceptible, I-infected and R-recovered. In other words, the SIR model considers the whole population to be studied as being formed by three different groups of individuals: the group S which contains individuals which may become infected, the group I of infected individuals and, finally, the group R of recovered individuals. Notice that, all individuals from one of the three groups have the same characteristics related to the disease. At any time t, these three groups interact one to another and some individuals may pass from one group to another group. These interactions depending on time t are modeled by mathematical equations (particularly, differential or difference equations) of Lotka-Volterra type. Then, such equations are studied using different mathematical tools, such as the theory of dynamical systems, to discover different properties of the equations, which, in turn, explain different ways of possible interactions of the three groups in the studied population. There are many published scientific articles on SIR models and their variants, such as the models

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SIS (Susceptible-Infected-Susceptible), SIRD (Susceptible-Infectious-Recovered-Deceased) [9], SIRV (Susceptible-Infectious-Recovered-Vaccinated) [10] and SEIR (Susceptible-Exposed-Infectious-Recovered) [11]. Such models received a special attention in the current pandemic caused by Covid-19. For example, a top Journal *Nonlinear Analysis: Real-World Applications* presents a list of most downloaded articles and, during May 2022, an article [12] on a variant of SIR models (the SAIRS epidemic model) was the first article in the list.

Another direction of research where mathematical models contribute in understanding the spreading of the culprits (microbes such as viruses, bacteria, parasites and fungi) in an infectious disease, is by modeling the interactions between microbes and different types of cells from immune system, such as neutrophils and lymphocytes. For example, in [13] are presented more such models to study interactions between host immunity and parasite spreading. A four-dimensional model based on differential equations studying interactions between an invading pathogen and the innate immune system is presented in [14], while a model for interactions between influenza A virus and local tissues such as respiratory tract, is reported in [15].

In conclusion, mathematical modeling and, in particular, tools and models from dynamical systems theory, represent a relevant domain which contributes to understanding the spreading of infectious diseases and other aspects in epidemiology.

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