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Editorial: Modeling of COVID-19 and other infectious diseases: Mathematical, statistical and biophysical analysis of spread patterns

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Editorial on the Research Topic

[Modeling of COVID-19 and other infectious diseases: Mathematical, statistical and biophysical analysis of spread patterns](#)

Viral pandemics and infectious diseases have always constituted an imminent threat to humanity. Throughout history, humanity has struggled with viral outbreaks and pandemics. Some of the most significant examples include the Spanish Flu in 1918-1919, which infected an estimated 500 million people worldwide and caused 50 million deaths. Efforts to control the spread of infectious diseases have led to the development of vaccines, antibiotics, and public health measures, but these diseases continue to pose a significant threat to global health and wellbeing. Scientific advancements in science, public health, medications, and vaccines are pivotal in the containment and even the elimination of many of those threats. However, these efforts can be challenged by factors such as limited resources, anti-vaccine sentiment, and difficulty in controlling the spread in communities with limited access to healthcare.

The coronavirus disease 2019 (COVID-19) continues as the main cause of hospitalization and death and as a main public health risk since the first case was registered in December 2019 in China. It was declared a global pandemic by the World Health Organization (WHO) on March 11, 2020. The recent emergence of variants creates a major cause of concern since they can lead to an epidemic rebound especially with the possibility of the emergence of vaccine resisting, deadlier or more transmissible future variants. The COVID-19 infection reached at least 680 million people globally and caused over 6.80 million deaths [1]. Mathematical models and simulations were used to describe the spread of infectious diseases by using mathematical equations to represent the spread of an infectious agent in a population. The models consider factors such as the infectiousness of the disease, the number of susceptible and infected individuals, and the rate at which people recover or die. The output of these models can provide important insights into the dynamics of disease spread, and can be used to predict the potential spread of an outbreak, inform public health policy, and evaluate the efficacy of interventions. Simulations of these models can also be used to visualize the spread of the disease over time, and to test the impact

of different control measures. Such studies include: Non-linear dynamics, non-equilibrium processes, and self-organization modeling of infectious diseases, statistical, spatiotemporal and big data analytics of COVID-19, applications from the social sciences, public health, economics, engineering in relation to COVID-19 pandemics, and modeling, simulations and forecasting of spread patterns, vaccine efficiency, treatment, behavioral aspects and public policies [2–10].

Another important field of study is that of vaccines, their efficacies and their implementation schemes. Studies on the efficacy of vaccines in the fight against infectious diseases like COVID-19 involve evaluating the effectiveness of the vaccine in reducing the incidence of the disease, severity of symptoms, and the transmission of the virus. These studies typically use randomized controlled trials (RCTs), where individuals are randomly assigned to receive either the vaccine or a placebo, and are followed over time to determine the incidence of the disease in each group. The efficacy of the vaccine is then determined by comparing the incidence of the disease in the vaccinated group to that of the unvaccinated group. It is important to note that vaccine efficacy can vary based on various factors such as the population being studied, the duration of follow-up, and the level of circulating virus in the population [11, 12]. Ongoing monitoring and analysis of vaccine efficacy is crucial to ensure the continued safety and effectiveness of vaccines as the pandemic continues to evolve.

This Research Topic includes articles that study spread patterns of infectious diseases using several mathematical, statistical, computational, and biophysical methods covering compartmental models, agent-based models (ABM), spatiotemporal analysis, data-driven analysis, artificial intelligence, and analytic methods. [Sherwani et al.](#) analyzed the seroprevalence of anti-S1-RBD antibodies in pre-pandemic and pandemic subjects from Saudi Arabia and found out that antibody levels increased in samples collected during the pandemic, even though these subjects were not clinically COVID-19 positive. [Zhao and Liu](#) reviewed the distribution characteristics of COVID-19 in America based on space-time scan statistic. Their empirical results reveal the relative risk of the first-level and the second-level clustering area of the epidemic across several states. The influence of co-morbidities during SARS-CoV-2 infection in the Indian Population was analyzed by [Matysek et al.](#). They found out that the highest correlation coefficient were age, random serum glucose, serum urea, gender and serum cholesterol, whereas the highest inverse correlation coefficient was assessed for alanine transaminase, red blood cells count and serum creatinine. [Wu et al.](#) worked on modeling the small scale outbreak of COVID-19, especially in China and proposed a new version of cellular automata with a time matrix, to simulate outbreaks.

The policy choices for Shanghai in response to challenges of Omicron were inspected by [Qian et al.](#) who showed that effective policies for Omicron include high level of testing capacity to identify and quarantine the infected cases, especially the asymptomatic cases in addition to immediate home-isolation and fast transfer to centralized quarantine location. [Harris](#) showed how controls on access alone through concentric regulatory zones, without restrictions on movement, were inadequate to halt an advancing COVID-19 outbreak in the highly populous area of South Brooklyn, New York. [Kim et al.](#) introduced a mathematical modeling approach to study the economic impact of COVID-19 interventions and their study asserts the importance of the rapidity of vaccine rollout to the cost effective control of the number of infections and deaths. [Yu et al.](#) employed machine learning models based on blood inflammatory cytokines to identify the hospitalized mortality of patients with COVID-19. Their study constructs predictive models to assess patients who may have poor prognoses early and accurately. [Liu et al.](#) modeled the effects of vaccination, nucleic acid testing, and face mask wearing interventions against COVID-19 in large sports events using an SEIR model and found out that the combined use of these measures could largely decrease the number of infections. Future possible studies in mathematical modeling of infectious diseases include the incorporation of spatial dynamics, social dynamics, genomic data, more accurate models of transmission, impact of vaccination and developing real-time models for outbreak responses.

Author contributions

OE prepared the draft of the manuscript. SK and KH revised and improved the manuscript. All authors contributed to the article and approved the submitted version.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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