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Preface

Special issue: Modeling the biological, epidemiological, immunological, molecular, virological aspects of COVID-19

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An outbreak of atypical pneumonia caused by a novel coronavirus was first identified in Wuhan, China in December 2019. The causative agent was initially called 2019 novel coronavirus (2019-nCoV), later renamed as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and the formal name for the associated disease given by the World Health Organization (WHO) is Coronavirus Disease 2019 (COVID-19). The virus swiftly spread to all areas of China and other countries. The WHO declared the coronavirus outbreak a public health emergency of international concern (PHEIC) on January 30, 2020. Mathematical models play an increasingly important role in forecasting transmission potential, optimizing control strategies, understanding the progression of infections within hosts, managing vaccine distribution and so on. These contributions have been recognized by many public health agencies like the WHO and the U.S. CDC.

To serve the needs of the fight against the COVID-19 pandemic, it is critical to accelerate the publication of modeling studies on COVID-19. With the support of Mathematical Biosciences and Engineering (MBE), we initiated a special issue entitled ”Modeling the Biological, Epidemiological, Immunological, Molecular, Virological Aspects of COVID-19” on January 31, 2020. By the deadline of September 1, 2020, a total of 118 formal submissions from researchers across 40 countries around the world had been received, among which 38 papers were finally accepted for publication after peer review. Among the accepted contributions, the average times from submission to acceptance, and from acceptance to publication are 43 days and 9 days, respectively. The special issue covers a wide range of topics using different modeling approaches and different data sources.

The works of Zhou et al. (doi: 10.3934/mbe.2020147), Yang and Wang (10.3934/mbe.2020148), Chang et al. (10.3934/mbe.2020178), Feng et al. (10.3934/mbe.2020204), Aldila et al. (10.3934/mbe.2020335), Wang (10.3934/mbe.2020380), and Johnston and Pell (10.3934/mbe.2020401) investigate the role of behavior change or social distancing driven by media coverage or governmental action in curtailing the spread of COVID-19. The information propagation about COVID-19 in Chinese social media during the early phase of the epidemic is modeled and analyzed by Yin et al. (10.3934/mbe.2020146). Some studies focus on evaluating the impact of non-pharmaceutical interventions such as quarantine, isolation, personal hygiene, travel restriction and city lockdown on curbing the disease spread (Dai et al., 10.3934/mbe.2020152; Tian et al., 10.3934/mbe.2020158; Saldaña et al., 10.3934/mbe.2020231; Bugalia et al., 10.3934/mbe.2020318; Yousif and Ali, 10.3934/mbe.2020412; Srivastav et al., 10.3934/mbe.2021010). Some concentrate on assessing the importance of the timing to relax or lift mobility restrictions (Santana-Cibrian et al., 10.3934/mbe.2020330; Iboi et al., 10.3934/mbe.2020369). Some authors estimate key epidemiological parameters including basic reproduction number and effective reproduction number, peak time and peak size, final size, serial interval (Liu et al., 10.3934/mbe.2020172; Wang et al., 10.3934/mbe.2020173; Zhao, 10.3934/mbe.2020198; Feng et al., 10.3934/mbe.2020205). Besides human-to-human transmission, Yang and Wang (10.3934/mbe.2020148), Rong et al. (10.3934/mbe.2020149), Saldaña et al. (10.3934/mbe.2020231), and Zhong and Wang (10.3934/mbe.2020357) also take environment-to-human transmission into consideration. Some address the effect of delay in diagnosis (Rong et al., 10.3934/mbe.2020149), lack of medical resources (Wang et al., 10.3934/mbe.2020165), difference in interventions (Xia et al., 10.3934/mbe.2020274), incoming travelers (Deeb and Jalloul, 10.3934/mbe.2020302), super-spreading events (Santana-Cibrian et al., 10.3934/mbe.2020330), nosocomial infections (Martos et al., 10.3934/mbe.2020410), transient behavior after mass vaccination (Akhavan Kharazian and Magpantay, 10.3934/mbe.2021019). Two models are proposed to describe SARS-CoV-2 dynamics in infected hosts (Li et al., 10.3934/mbe.2020159; Hattaf and Yousfi, 10.3934/mbe.2020288).

Most studies are based on deterministic ordinary differential equation type models whereas partial differential equation models (Zhu and Zhu, 10.3934/mbe.2020174; Wang and Yamamoto, 10.3934/mbe.2020266), complex network model (Yang et al., 10.3934/mbe.2020248), stochastic models (He et al., 10.3934/mbe.2020153; Olabode et al., 10.3934/mbe.2021050), discrete models (He et al., 10.3934/mbe.2020153, Li et al., 10.3934/mbe.2020208), individual-based model (Martos et al., 10.3934/mbe.2020410), and statistical models (Zhao, 10.3934/mbe.2020198; Nie et al., 10.3934/mbe.2020265; Xia et al., 10.3934/mbe.2020274; Chowdhury et al., 10.3934/mbe.2020323) are developed and analyzed as well. Early studies mainly deal with COVID-19 case data from China, and later studies fit models to data from various countries and regions including the United Kingdom (Feng et al., 10.3934/mbe.2020204), South Korea (Feng et al., 10.3934/mbe.2020205; Xia et al., 10.3934/mbe.2020274), Mexico (Saldaña et al., 10.3934/mbe.2020231; Santana-Cibrian et al., 10.3934/mbe.2020330), the United States (Wang and Yamamoto, 10.3934/mbe.2020266), Lebanon (Deeb and Jalloul, 10.3934/mbe.2020302), India (Bugalia et al., 10.3934/mbe.2020318; Srivastav et al., 10.3934/mbe.2021010), Indonesia (Aldila et al., 10.3934/mbe.2020335), Nigeria (Iboi et al., 10.3934/mbe.2020369), Canada (Wang, 10.3934/mbe.2020380), Saudi Arabia (Yousif and Ali, 10.3934/mbe.2020412) and so on. Mobile terminal positioning data (Nie et al., 10.3934/mbe.2020265) and Google community mobility data (Wang and Yamamoto, 10.3934/mbe.2020266) have also been used. In addition, Costris-Vas et al. (10.3934/mbe.2020383) write a survey paper on evaluating the accuracy of various models from recent pandemics.

With the broad spectrum of topics, we believe that these 38 peer-reviewed papers could represent a significant contribution of mathematical modeling in the fight against COVID-19. In fact, they have already received considerable attention in the field. For example, the paper by Yang and Wang (10.3934/mbe.2020148) is ranked the first most read paper in MBE with 2765 article views, 4465 PDF downloads and 54 citations. We hope the readers of this special issue will find helpful information for their own research and decision-making. So far, the ongoing COVID-19 pandemic has resulted in more than 85.62 million cases including 1.85 million deaths (data source: https://coronavirus.jhu.edu/map.html). With the joint efforts of health-care workers, vaccine developers, epidemiologists, modelers, the public and others, we look forward to returning to normal life in the near future.

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