The 1st International and 3rd National Conference on Biomathematics
19-21 January 2022, Damghan University, Iran.

Damghan university

A stochastic model for spread of Covid-19 based on the impact of different safety protocols

Afshin Babaei*, Seddigheh Banihashemi

Department of Applied Mathematics, University of Mazandaran, Babolsar, Iran

babaei@umz.ac.ir

Abstract— In this work, a stochastic mathematical model for the transmission of Coronavirus disease is investigated to study the effect of different safety protocols, for instance, social-distancing, mask use and quarantine on the spread of this virus. For this purpose, the details of the proposed deterministic COVID-19 model and its stochastic version are described. Finally, numerical solutions are determined by using a collocation approach to illustrate the impact of different parameters on the dynamics of the disease.

Keywords—Stochastic model, COVID-19, Reproduction number, Numerical simulation, Collocation method

I. Introduction

In recent two years, a group of viruses, called Coronavirus, has caused many issues for human beings all over the world. Hence, many mathematical and biological studies are presented to investigate the dynamics of COVID-19 and the results have been published as scientific papers. For examples [1, 2, 3, 4] are some works in the field of mathematical modeling and numerical simulations for this disease.

In this paper, we focus on the following stochastic COVID-19 model

(1)
$$
\begin{cases}
\mathrm{dS} = \left(\Lambda - (\lambda + \mu)\mathrm{S} \right)\mathrm{d}t - \frac{\sigma_1}{\beta}\lambda\mathrm{S}\ \mathrm{d}B_1(t), \\
\mathrm{dE} = \left(\lambda\mathrm{S} - (c + \mu)\mathrm{E} \right)\mathrm{d}t + \frac{\sigma_1}{\beta}\lambda\mathrm{S}\ \mathrm{d}B_1(t), \\
\mathrm{dI} = \left(c\rho(1-q)\mathrm{E} + \varphi\bar{\rho}\,\mathrm{Q} + \alpha_\mathrm{I}\mathrm{A} - (\gamma_\mathrm{I} + \delta_\mathrm{I} + \mu_\mathrm{I} + \mu)\mathrm{I} \right)\mathrm{d}t + \sigma_2\mathrm{A}\ \mathrm{d}B_2(t), \\
\mathrm{dA} = \left(c(1-\rho)(1-q)\mathrm{E} + \alpha_\mathrm{A}\mathrm{Q} - (\alpha_\mathrm{I} + \gamma_\mathrm{A} + \mu)\mathrm{A} \right)\mathrm{d}t - \sigma_2\mathrm{A}\ \mathrm{d}B_2(t), \\
\mathrm{dQ} = \left(cq\mathrm{E} - (\alpha_\mathrm{A} + \varphi\bar{\rho} + \mu)\mathrm{Q} \right)\mathrm{d}t, \\
\mathrm{dH} = \left(\delta_\mathrm{I}\mathrm{I} - (\gamma_\mathrm{H} + \mu_\mathrm{I} + \mu)\mathrm{H} \right)\mathrm{d}t - \sigma_3\mathrm{H}\ \mathrm{d}B_3(t), \\
\mathrm{dR} = \left(\gamma_\mathrm{I}\mathrm{I} + \gamma_\mathrm{A}\mathrm{A} + \gamma_\mathrm{H}\mathrm{H} - \mu\mathrm{R} \right)\mathrm{d}t + \sigma_3\mathrm{H}\ \mathrm{d}B_3(t).
\end{cases}
$$

In this model, S, E, I, A, Q and H represent the following categories, individuals susceptible or exposed to the virus and never infected before, the individuals that have been newly-infected but that are still not sick and cannot transmit infection, the infectious individuals with symptoms, the infectious individuals, that are not yet symptomatic, the infectious individuals that are with slight symptoms and hence at home quarantine, the infectious individuals that are hospitalized and the recovered individuals from the disease, respectively. It is necessary to mention that we have

$$
\mathrm{N}(t) = \mathrm{S}(t) + \mathrm{E}(t) + \mathrm{I}(t) + \mathrm{A}(t) + \mathrm{Q}(t) + \mathrm{H}(t) + \mathrm{R}(t).
$$

The force of infection, λ, is defined by

$$
\lambda = \beta(1 - \varepsilon_m c_m)\frac{\mathrm{I} + \theta\mathrm{A}}{\mathrm{N} - \theta_q(\mathrm{Q} + \mathrm{H})},
$$

where β is the effective contact rate, c_m is the proportion of people who use masks, ε_m represents the effect of using mask to prevent catching the infection by susceptible individuals, θ shows the transmission rate and $0 \leq \theta_q \leq 1$ is the efficacy of quarantine and hospitalization admission in preventing virus transmission. Moreover, c shows the contact rate, q represents the rate of quarantine for exposed persons. Λ is the birth rate. δ_I displays the transition rate from the symptomatic infected category to the quarantined infected category. γ_I and γ_A are the recovery rates of symptomatic infected persons and asymptomatic infected persons, respectively. γ_H is the recovery rate of individuals in the class H. Also, α_A and α_I show the movement rate from the class Q to the class A and the transition rate from A to the class I. ρ and μ_I represent the symptoms rate among infected individuals and the mortality rate due to Coronavirus. φ, $\bar{\rho}$ and μ represent the proportion of infected individuals with symptoms in quarantine, the movement rate from the category Q to I and the natural death rate, respectively.

In this stochastic model $B_i(t)$, $i = 1, 2, 3$ are standard Brownian motions [5] and σ_i, $i = 1, 2, 3$ are the intensities of environmental oscillations that $\sigma_i^2 > 0$.

II. Analysis of the model

In the model (1), when $\sigma_i = 0$, $i = 1, 2, 3$, then the deterministic COVID-19 model is obtained. In this case, the disease free equilibrium point can be determined as

$$
E^0 = (\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0)^\mathrm{T}.
$$

To survey the transmissibility of the disease, we need to get the basic reproduction number R_0. For the deterministic COVID-19 model, this number can be specified as

$$(2) \qquad R_0 = \frac{\varpi c}{\gamma \eta \xi (c + \mu)} \left(\xi \bar{\varrho} + \eta \theta \tilde{\beta} + q \bar{\delta} \right),$$

where $\tilde{\theta} = (1 - \rho)(1 - q)$ and

$$\begin{aligned}
\gamma &= \alpha_{\mathrm{I}} + \gamma_{\mathrm{A}} + \mu, & \eta &= \delta_{\mathrm{I}} + \gamma_{\mathrm{I}} + \mu_{\mathrm{I}} + \mu, & \xi &= \varphi \bar{\rho} + \alpha_{\mathrm{A}} + \mu, \\
\bar{\varrho} &= \gamma \rho (1 - q) + \tilde{\theta} \alpha_{\mathrm{I}}, & \tilde{\beta} &= \xi \tilde{\theta} + q \alpha_{\mathrm{A}}, & \bar{\delta} &= \alpha_{\mathrm{A}} \alpha_{\mathrm{I}} + \gamma \varphi \bar{\rho}.
\end{aligned}$$

Also, the endemic equilibrium $E_* = \left(\mathrm{S}^*, \mathrm{E}^*, \mathrm{I}^*, \mathrm{A}^*, \mathrm{Q}^*, \mathrm{H}^*, \mathrm{R}^* \right)^{\mathrm{T}}$ is determined by

$$\begin{aligned}
\mathrm{S}^* &= \Psi_{\mathrm{S}} \mathrm{E}^*, & \mathrm{I}^* &= \Psi_{\mathrm{I}} \mathrm{E}^*, \\
\mathrm{Q}^* &= \Psi_{\mathrm{Q}} \mathrm{E}^*, & \mathrm{H}^* &= \Psi_{\mathrm{H}} \mathrm{E}^*, \\
\mathrm{A}^* &= \Psi_{\mathrm{A}} \mathrm{E}^*, & \mathrm{R}^* &= \Psi_{\mathrm{R}} \mathrm{E}^*,
\end{aligned}$$

where

$$\mathrm{E}^* = \frac{\Lambda (\Lambda R_0 - \mu)}{(c + \mu)(\Lambda R_0 - \mu) + (1 - \theta_q)(\Psi_{\mathrm{Q}} + \Psi_{\mathrm{H}}) + \Psi_{\mathrm{I}} + \Psi_{\mathrm{R}} + \mu^2 + 1},$$

and

$$\begin{aligned}
\Psi_{\mathrm{S}} &= \frac{c + \mu}{\lambda}, & \Psi_{\mathrm{Q}} &= \frac{cq}{\xi}, \\
\Psi_{\mathrm{A}} &= \frac{c}{\xi \gamma} (\dot{\alpha} \xi + \alpha_{\mathrm{A}} q), & \Psi_{\mathrm{I}} &= \frac{c}{\eta \xi \gamma} \left(\dot{\theta} \xi \gamma + \varphi \bar{\rho} q \gamma + \alpha_{\mathrm{I}} \xi \dot{\alpha} + \alpha_{\mathrm{A}} \alpha_{\mathrm{I}} q \right), \\
\Psi_{\mathrm{H}} &= \frac{\delta_{\mathrm{I}}}{\omega} \Psi_{\mathrm{I}}, & \Psi_{\mathrm{R}} &= \frac{1}{\mu} \left(\gamma_{\mathrm{A}} \Psi_{\mathrm{A}} + \left(\gamma_{\mathrm{I}} + \frac{\gamma_{\mathrm{H}} \delta_{\mathrm{I}}}{\dot{\zeta}} \right) \Psi_{\mathrm{I}} \right).
\end{aligned}$$

III. Numerical Simulations

In this section, some numerical results are provided to show the behaviors of different disease classes in the proposed COVID-19 model. The numerical solution of this system is obtained using a stepwise collocation approach based on the Legendre polynomials [6].
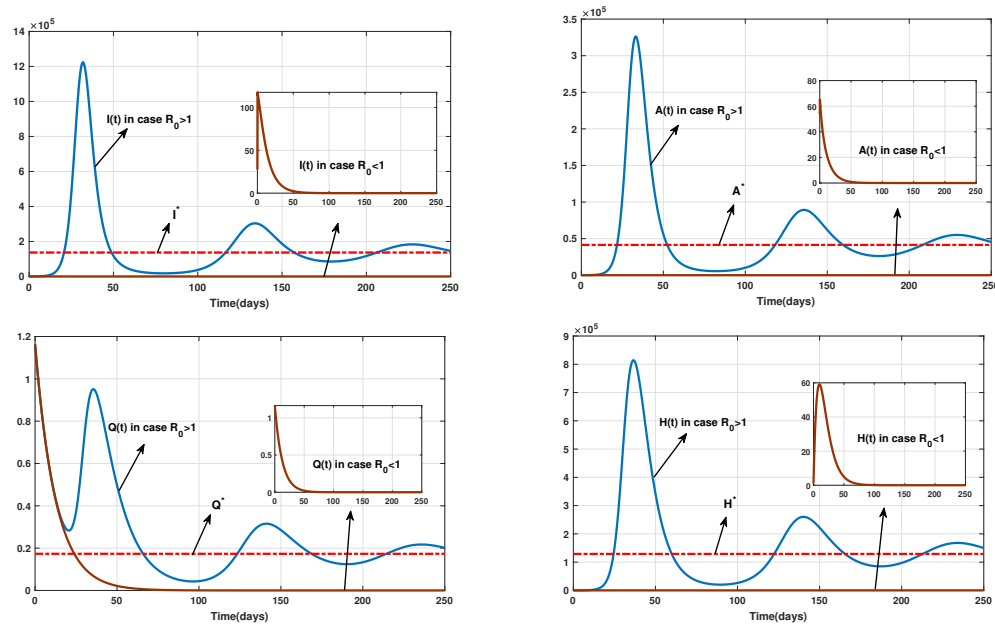
All the employed values of the parameters are described in Table I. Also, the initial conditions are considered as:

$$\mathrm{S}(0) = 11081739, \quad \mathrm{E}(0) = 106.2642, \quad \mathrm{I}(0) = 27.676, \quad \mathrm{A}(0) = 53.839,$$
$$\mathrm{Q}(0) = 1.1642, \quad \mathrm{H}(0) = 1, \quad \mathrm{R}(0) = 2.$$

Figures 1 shows the endemic equilibrium E_* and the trajectories of the solution for the cases $R_0 = 0.7730 < 1$ with $\beta = 0.36$ and for the cases $R_0 = 1.8569 > 1$ with $\beta = 0.8648$, when $\sigma_1 = \sigma_2 = \sigma_3 = 0$. Figure 2 displays the reproduction number R_0 for several values of $\beta \in [0, 1]$ (up) and $c_m \in [0, 1]$ (down) with $\sigma_1 = \sigma_2 = \sigma_3 = 0$. Figures 3 shows the trajectories of I(t), Q(t) for the stochastic model with $\sigma_1 = 0.2$, $\sigma_2 = 0.15$, $\sigma_3 = 0.22$ and different values of q. Also, Figure 4 shows the trajectories of I(t), Q(t) for the stochastic model (left) with $\sigma_1 = 0.15$, $\sigma_2 = 0.24$, $\sigma_3 = 0.36$ with different values of c_m. Figure 5 displays the trajectories of I(t), A(t), Q(t) and H(t) for the stochastic model with $\sigma_1 = 0.3$, $\sigma_2 = 0.2$, $\sigma_3 = 0.15$ and different values of β.

Table I. The parameter values in the stochastic COVID-19 model (1).

| Parameter	Value	Parameter	Value	Parameter	Value
Λ	$\mu \times N(0)$	γ_H	0.11624	α_I	0.078
β	0.8648	α_A	0.059	ρ	0.86834
c	14.781	c_m	0.0546	μ_I	0.01
θ	0.5944	ε_m	0.5	θ_q	1
q	1.8887×10^{-7}	φ	0.05	$\bar{\rho}$	0.1259
δ_I	0.13266	γ_I	0.33029	μ	$\frac{1}{69.5}$
γ_A	0.13978				

Fig. 1. The trajectories of the solution for the cases $R_0 < 1$ and $R_0 > 1$, when $\sigma_1 = \sigma_2 = \sigma_3 = 0$.
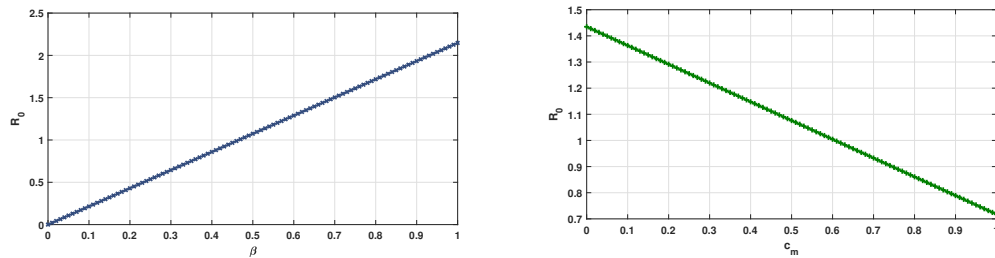
Fig. 2. Reproduction number R_0 for several values of $\beta \in [0, 1]$ (up) and $c_m \in [0, 1]$ (down).

References

[1] M. Ali, S.T.H. Shah, M. Imran, A. Khan, "The role of asymptomatic class, quarantine and isolation in the transmission of COVID-19," Journal of Biological Dynamics, vol. 14, pp. 389–408, 2020.
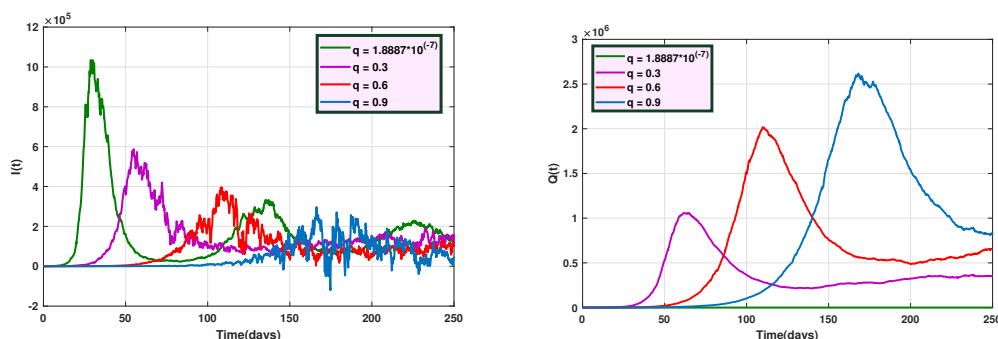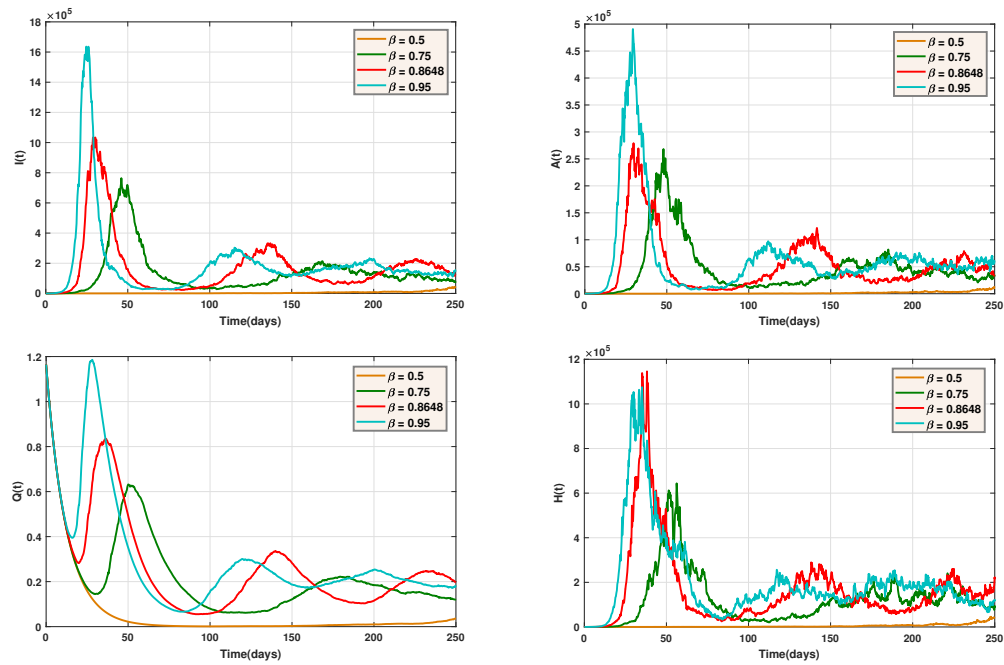
Fig. 3. Graphs of trajectories of I(t) and Q(t) for the stochastic model with different values of q.
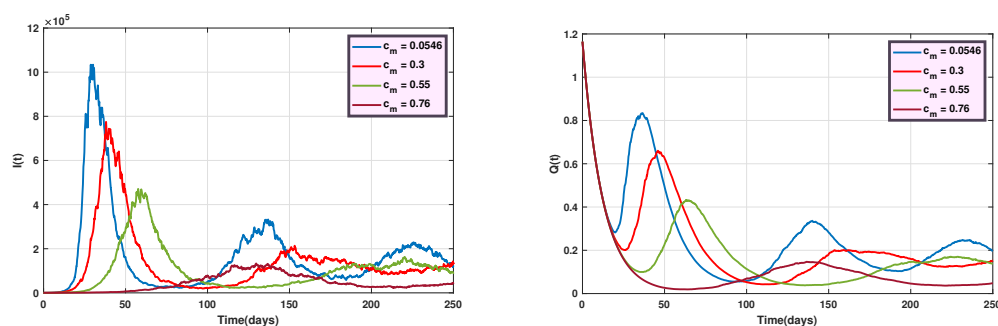
Fig. 4. The trajectories of I(t), Q(t) for the stochastic model with different values of c_m.

[2] A. Babaei, M. Ahmadi, H. Jafari, A. Liya, , "A mathematical model to examine the effect of quarantine on the spread of coronavirus," Chaos, Solitons and Fractals, vol. 142, 110418, 2021.

[3] S.E. Eikenberry, M. Mancuso, E. Iboi, T. Phan, K. Eikenberry, Y. Kuang, E. Kostelich, A.B. Gumel, "To mask or not to mask: Modeling the potential for face mask use by the general public to curtail the COVID-19 pandemic", Infectious Disease Modelling, vol. 5, pp. 293–308, 2020.

[4] F. Ndairou, I. Area, J.J. Nieto, D.F.M. Torres, "Mathematical modeling of COVID-19 transmission dynamics with a case study of Wuhan", Chaos, Solitons, and Fractals, vol. 135, 109846, 2020.

[5] O. Ovidiu, An Informal Introduction to Stochastic Calculus with Applications, World Scientific, Singapore, 2015.

[6] L. He, S. Banihashemi, H. Jafari, A. Babaei, "Numerical treatment of a fractional order system of nonlinear stochastic delay differential equations using a computational scheme", Chaos, Solitons and Fractals, vol. 149, 111018, 2021.

Fig. 5. The trajectories of I(t), A(t), Q(t) and H(t) for the stochastic model with different values of β.