Research Article GU J Sci 36(3): 1302-1309 (2023) DOI:10.35378/gujs.1096827

Gazi University

Journal of Science

http://dergipark.gov.tr/gujs

A Novel Mathematical Model of the Dynamics of COVID-19

Elif DEMIRCI*

Ankara University, Faculty of Science, Department of Mathematics, Tandogan, 06100, Ankara, Turkiye

Highlights

- A novel mathematical model for COVID-19 is introduced.
- Stability analysis of the disease-free equilibrium point is analyzed.
- Basic reproduction number is evaluated for the given model.

Article Info

Received: 01 Apr 2022
Accepted: 21 July 2022

Keywords

Epidemic model
Basic reproduction number
Stability

Abstract

The severity of the COVID-19 pandemic requires a better understanding of the spread of SARS-COV2. As of December 2019, several mathematical models have been developed to explain how SARS-COV2 spreads within populations, and proposed models have evolved as more is learned about the dynamics of the outbreak. In this study, we propose a new mathematical model that includes demographic characteristics of the population. Social isolation and vaccination are also taken into account in the model. Besides transmission arising from intercourse with undiagnosed infected persons, we also consider transmission by contact with the exposed group. In this study, after the model is established, the basic reproduction number is calculated and local stability analysis of disease-free equilibrium is given. Finally, we give numerical simulations for the proposed model.

1. INTRODUCTION

Mathematical models are effective tools to explain the spreading dynamics of epidemics ([1]). Epidemic models are mathematical formulations that are proposed to explain the spread of diseases in populations, which differ depending on the nature of the considered disease. An epidemic model, which usually consists of a system of difference or differential equations (ordinary or partial) and initial conditions, provide predictions about how the disease will spread in the future, and also guide the steps to be taken to control the epidemic.

Many mathematical models have been discussed to explain the spread of SARS-COV2, which has affected the whole world as of December 2019 ([2]- [8]). The model given by Nistal et al. is a system of difference equations ([2]). Cakir and Savas ([4]) modeled the time-dependent variation of the number of infectious individuals with the help of a single differential equation. In other proposed models, the population is divided into compartments and the transitions between these compartments are expressed dynamically using differential equations. However, in all of the models discussed in these studies, it was assumed that the total population is constant in the absence of disease. Although COVID-19 was treated as a seasonal disease at the beginning of the epidemic, now it is well known that unlike the seasonal diseases, the dynamics of the spread need to be examined in a long period of time. Therefore, the assumption of constant population in epidemic models used for diseases that cause short-term epidemics may not be suitable for COVID-19. In the epidemic model that is discussed in this paper, a variable population is considered to obtain a more realistic approach to explain the dynamics of the spread. In the models given by Arino and Portet ([3]), Ndairou et al. ([7]) and Liu et al. ([6]), it is assumed that the virus is not transmitted during the incubation period. However, it is known that the new type of coronavirus, which is known to be transmitted

*Corresponding author, e-mail: edemirci@ankara.edu.tr

through droplets, is contagious also during the incubation period ([9]). This fact is also taken into account in the model to be discussed in this paper. In the study by Vega ([8]), simulations based on a SIRD model including social isolation term were made. However, the incubation period of the virus was not taken into account in this study. We propose a mathematical model consisting of ordinary differential equations in which demographic parameters for the population, transmission of the virus in the incubation period, social isolation parameter and vaccination are all considered.

The study divided into four sections: In the first section, we give a brief review of the models used for COVID-19 and give the motivation for model proposed in this study. In the second section, the model is constructed, fixed points of the system are evaluated and local stability analysis of the disease-free equilibrium point is given. The third section is devoted to the numerical solution of the model. In the last section, conclusions of this study are provided.

2. MODEL FORMULATION AND ANALYSIS

In this study, we construct a compartment model where the total population at time t, $N(t)$, is divided into five partitions depending on their epidemiological states: $S(t)$, $E(t)$, $I_1(t)$, $I_2(t)$ and $R(t)$. $S(t)$ is composed of susceptible individuals in the population. Three infective groups are used in the model. The first one, $E(t)$, consists of the exposed individuals. They are infected by the virus, but due to the incubation period of the virus they are not generally contagious until the last two days of this period ([10]). If a person is in $E(t)$, then it is known that the diagnosis rate of that person is quite low. However, that person can still transmit the virus to the susceptible individuals. The other two infectious groups, $I_1(t)$ and $I_2(t)$ are composed of diagnosed individuals with SARS-COV2 and undiagnosed individuals (both symptomatic and asymptomatic), respectively. According to the official policies applied by almost every country in the world, the diagnosed individuals are isolated from the rest of the population for a period that they become uncontagious. This period is updated by the officials time to time depending on the dominant variant of the virus that is effective in the country. Based on this fact, we assume that the diagnosed individuals are not contagious for the population. In the beginning of the COVID-19 pandemic, it was thought to be a seasonal epidemic. However, as the process progressed, it was understood that the pandemic would last for a long time. In most of the given models for short term epidemics, total population is assumed to be constant. But for COVID-19 models, it would not be realistic to ignore the demographic properties of the population. In the models given in [11] and [12], demographic effects are considered but the equation governing the total population is given in the form

$$\frac{dN}{dt} = \Lambda - \mu N, \tag{1}$$

where Λ and μ represent the new births per unit of time and natural death rate of the population, respectively. In the model we propose, a more general equation for the total population is considered for the disease-free case:

$$\frac{dN}{dt} = \big(b(N) - d(N)\big)N, \tag{2}$$

where $b(.)$ and $d(.)$ are functions of N representing the birth and death rates, respectively. The functions b and d are assumed to be non-negative definite, differentiable functions which does not contradict with the biological facts. We also assume that $\exists K > 0$ such that $b(K) = d(K)$, where K represents the carrying capacity of the population. The model is given by the following system of ordinary differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= b(N)N - \frac{(\beta_1 E + \beta_2 I_2)\xi S}{N} + r_{-1}R - \big(\mu + d(N)\big)S, \\
\frac{dE}{dt} &= \frac{(\beta_1 E + \beta_2 I_2)\xi S}{N} - \big(\gamma_1 + \gamma_2 + d(N)\big)E,
\end{aligned} \tag{3}$$

$$\frac{dI_1}{dt} = \gamma_1 E + \gamma_3 I_2 - (d(N) + \theta + r_1)I_1,$$

$$\frac{dI_2}{dt} = \gamma_2 E - \big(\gamma_3 + r_2 + d(N)\big)I_2,$$

$$\frac{dR}{dt} = r_1 I_1 + r_2 I_2 - (d(N) + r_{-1})R + \mu S.$$

with non-negative initial conditions

$$S(0) = S_0, E(0) = E_0, I_1(0) = I_{10}, I_2(0) = I_{20}, R(0) = R_0. \quad (4)$$

Flow diagram of the model is given in Figure 1.

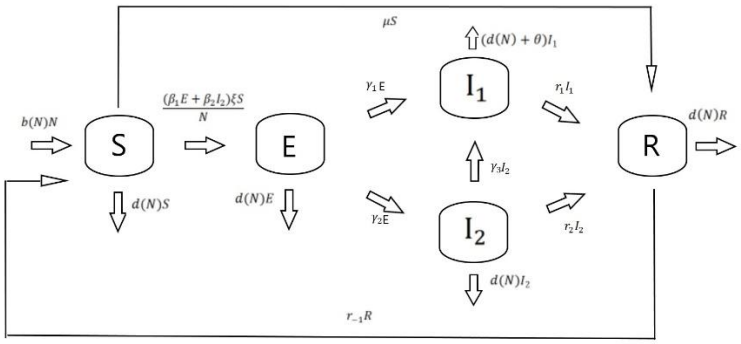

Figure 1. *Flow diagram of the model given by (3)*

The parameters β_1 and β_2 are transmission rates arising from contact with exposed (E) and undiagnosed infected individuals (I_2), respectively. Due to social isolation recommendations that are officially made, people limit the number of people they are in contact with and they are more reluctant to enter uncontrolled areas as they were before the outbreak. For this reason, a frequency-dependent contamination term is used in model (3) instead of a density-dependent contamination term, which is frequently used in airborne transmitted diseases. r_{-1}, μ, γ_1, γ_2, γ_3, r_1 and r_2 represent waning immunity rate, effective vaccination rate, the rate of being diagnosed within the incubation period, the rate of being undiagnosed within the incubation period, diagnosing rate after the incubation period, recovery rate for diagnosed infected individuals and recovery rate for undiagnosed infected individuals, respectively. Recovered group is composed of the immune individuals in the population. Immunity can be gained by vaccination or recovering from the infection with immunity. However, in the proposed model the individuals who once been infected and are no longer contagious are also considered as immune, although some symptoms associated with the disease may persist. The parameter ξ, $0 \leq \xi \leq 1$, is used to reflect social isolation effect to the model. $\sqrt{\xi}$ indicates the proportion of individuals who continue their social lives unprotected from COVID-19. If all of the population lives unprotected (without using face masks, without following social distancing rules, etc.), then the value of ξ is assumed to be 1. As the protection level increases then ξ will decay to zero, proportionally. θ denotes the COVID-19 related death rate. Let $R_+^{5*} = \{(S, E, I_1, I_2, R)^T \in R^5 : S, E, I_1, I_2, R \geq 0 \; and \; S + E + I_1 + I_2 + R > 0\}$.

Theorem 1. There is a unique solution of IVP (3)-(4) and the solution remains in R_+^{5*}.

Proof. Existence and uniqueness of the solution of (3)-(4) can easily be seen. We need to show that the domain R_+^{5*} is positively invariant. Since,

$$\left.\frac{dS}{dt}\right|_{S=0} = b(E + I_1 + I_2 + R)(E + I_1 + I_2 + R) + r_{-1}R \geq 0,$$

$$\left.\frac{dE}{dt}\right|_{E=0} = \frac{\beta_2 I_2 \xi S}{S + I_1 + I_2 + R} \geq 0,$$

$$\left.\frac{dI_1}{dt}\right|_{I_1=0} = \gamma_1 E + \gamma_3 I_2 \geq 0,$$

$$\left.\frac{dI_2}{dt}\right|_{I_2=0} = \gamma_2 E \geq 0,$$

$$\left.\frac{dR}{dt}\right|_{R=0} = r_1 I_1 + r_2 I_2 + \mu S \geq 0,$$

on each hyperplane bounding the non-negative orthant, the vector field points into R_+^{5*} and R_+^{5*} is positively invariant.

$N(t) = S(t) + E(t) + I_1(t) + I_2(t) + R(t)$, therefore, $N(t)$ also remains non-negative. For simplicity in calculations in the equilibrium point analysis, henceforth, we use the system

$$\begin{aligned}
\frac{dS}{dt} &= b(N)N - \frac{(\beta_1 E + \beta_2 I_2)\xi S}{N} + r_{-1}(N - S - E - I_1 - I_2) - \big(\mu + d(N)\big)S, \\
\frac{dE}{dt} &= \frac{(\beta_1 E + \beta_2 I_2)\xi S}{N} - \big(\gamma_1 + \gamma_2 + d(N)\big)E, \\
\frac{dI_1}{dt} &= \gamma_1 E + \gamma_3 I_2 - (d(N) + \theta + r_1)I_1, \\
\frac{dI_2}{dt} &= \gamma_2 E - \big(\gamma_3 + r_2 + d(N)\big)I_2, \\
\frac{dN}{dt} &= \big(b(N) - d(N)\big)N - \theta I_1,
\end{aligned} \tag{5}$$

which is equivalent to system (3) with the initial conditions:

$$S(0) = S_0, E(0) = E_0, I_1(0) = I_{10}, I_2(0) = I_{20}, \mathrm{N}(0) = N_0. \tag{6}$$

Equilibrium points of system (5) are evaluated by letting

$$\frac{dS}{dt} = 0,$$

$$\frac{dE}{dt} = 0,$$

$$\frac{dI_1}{dt} = 0,$$

$$\frac{dI_2}{dt} = 0,$$

$$\frac{dN}{dt} = 0.$$

The disease-free equilibrium (DFE) point of system (5) is

$$F_0^* = \left(S_0^*, E_0^*, I_{1,0}^*, I_{20}^*, N_0^*\right) = \left(\frac{(b + r_{-1})K}{\mu + b + r_{-1}}, 0,0,0, K\right), \tag{7}$$

where $b := b\,(K) = d\,(K)$ and the endemic equilibrium of system (5) is

$$F^* = (S^*, E^*, I_1^*, I_2^*, N^*)$$

where

$$I_1^* = a_1 N^*,$$

$$I_2^* = a_1 a_2 N^*,$$

$$E^* = a_1 a_2 a_3 N^*,$$

$$S^* = a_4 N^*,$$

and N^* is the positive solution of the equation:

$$b(N^*) - a_4[a_1 a_2 \xi(\beta_1 a_3 + \beta_2) + d(N^*) + r_{-1} + \mu] + r_{-1}[1 - a_1(1 + a_2 + a_2 a_3)] = 0. \tag{8}$$

Here,

$$a_1 = \frac{b(N^*) - d(N^*)}{\theta},$$

$$a_2 = \frac{d(N^*) + \theta + r_1}{a_3\gamma_1 + \gamma_3},$$

$$a_3 = \frac{d(N^*) + \gamma_3 + r_2}{\gamma_2},$$

$$a_4 = \frac{(\gamma_1 + \gamma_2 + d(N^*))a_3}{\xi(\beta_1 a_3 + \beta_2)}.$$

Basic reproduction number, R_0, for epidemic models is an important threshold value that helps us understand the future of the disease. The biological interpretation of R_0 is the number of secondary infections that are caused by one infected individual introduced to a susceptible population. For models with multi infective groups, using the Next Generation Matrix (NGM) method to calculate R_0 is more convenient ([13]). Before applying NGM method to the model, we first need to verify that for the disease-free model, the DFE is locally asymptotically stable. With the assumption b′(K) < d′(K), it is easy to show that NGM method can be applied to the model given by (5). This assumption is biologically valid for growing populations. We consider the infectious classes and define $X = (E, I_1, I_2)$. Let the matrices $\mathcal{F}_i$ and $\mathcal{V}_i$ represent the new infections introduced to a class and the compartmental transitions, respectively, are defined as

$$\mathcal{F}_i(X) = \begin{pmatrix} \frac{\beta_1 E + \beta_2 I_2}{N}\xi S \\ 0 \\ 0 \end{pmatrix},$$

$$\mathcal{V}_i(X) = \begin{pmatrix} (d(N) + \gamma_1 + \gamma_2)E \\ -\gamma_1 E - \gamma_3 I_2 + (d(N) + \theta + r_1)I_1 \\ -\gamma_2 E + (\gamma_3 + d(N) + r_2)I_2 \end{pmatrix}.$$

The NGM for system (5) is the matrix FV^{-1}, where

$$F = \left[\frac{\partial \mathcal{F}_i(X)}{\partial x_i}\right]_{F_0^*}, V = \left[\frac{\partial \mathcal{V}_i(X)}{\partial x_i}\right]_{F_0^*}.$$

Hence, the basic reproduction number of system (5) is

$$R_0^* = \frac{\xi\beta_1(b + r_{-1})}{(b + r_{-1} + \mu)(b + \gamma_1 + \gamma_2)} + \frac{\xi\beta_2\gamma_2(b + r_{-1})}{(b + r_{-1} + \mu)(b + \gamma_1 + \gamma_2)(b + \gamma_3 + r_2)}.$$

Theorem 2. Let $b\,(.)$ and $d\,(.)$ be positive definite and differentiable functions. Assume that there exists a $K > 0$ such that $b\,(K) = d\,(K) = b$ and $b'\,(K) < d'\,(K)$. The DFE of the system given by (5) is locally asymptotically stable if $R_0^* < 1$.

3. NUMERICAL SIMULATIONS OF THE MODEL

In this section, we first construct the demographic functions $b\,(.)$ and $d\,(.)$ using the data of Turkey between the years 2006 and 2019 ([14]). We use the software Mathematica for calculations in this study. Using linear regression, the birth rate and death rate functions are obtained as follows:

$$b\,(N) = 9.738213863922327 \times 10^{-5} - 6.709683343532898 \times 10^{-13}N,$$

$$d\,(N) = -1.608685714474 \times 10^{-5} + 3.8017993601939726 \times 10^{-13}N.$$

Vaccination against COVID-19 first started in December, 2020, almost one year after the virus is identified. However, it took longer for communities to reach vaccines. In Turkey, although the first vaccine application was made in January, it took August to reach significant vaccination rates in the community. For this reason we first assume that the effective vaccination rate is zero. For the parameter values in Table 1 and μ = 0, the basic reproduction number is evaluated as $R_0^* = 1.88804$. The positive equilibrium point for these parameter values is $(S^*, E^*, I_1^*, I_2^*, N^*)$ where

$$S^* = 1.64777 \times 10^7,$$

$$E^* = 1.48516 \times 10^6,$$

$$I_1^* = 5.14193 \times 10^6,$$

$$I_2^* = 85616.6,$$

$$N^* = 3.1147 \times 10^7.$$

Table 1. *Model parameters used for the numerical solution*

$\theta = 0.489011 \times 10^{-3}$	$\gamma_2 = 0.014$
$r_1 = 0.142857$	$\gamma_3 = 0.1$
$r_2 = 0.142857$	$\beta_1 = 0.3$
$r_{-1} = 0.435747 \times 10^{-2}$	$\beta_2 = 0.26$
$\gamma_1 = 0.011$	$\xi = 0.15$

For the same parameter values, as the daily effective vaccination rate μ increases, R_0^* value decreases, and for the values of $\mu > 0.0039$, $R_0^* < 1$.

Solving system (5) with the initial conditions

$$(S_0, E_0, I_{10}, I_{20}, N_0) = (82094772, 424090, 212045, 424090, 83154997),$$

we obtain I_1 as shown in Figure (2).

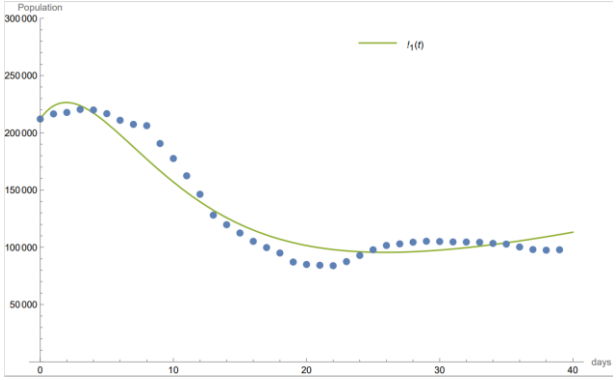

Figure 2. *Diagnosed individuals with COVID-19 evaluated from system (5) and reported number of active cases between December 12, 2020 and January 22, 2021 in Turkey*

4. CONCLUSIONS

In this study, we introduce a novel mathematical model to explain the spread of SARS-COV2 in a varying population. We use a compartment model with three infectious classes. The first one is the exposed group which is composed of the individuals who are in the first stage of the disease. The virus is in its incubation period and diagnosing rate of the individuals in this group is quite low. However, people in this class are contagious. We divide the infectious individuals into two groups after the incubation period. The first group is composed of infected individuals who are diagnosed with COVID-19 and we assume that, due to the isolation rules, they are not contagious. The second class is composed of the individuals who are not diagnosed with COVID-19 but infectious (both symptomatic and asymptomatic), and they can transmit the disease. The model contains social isolation and vaccination terms which are considered as the most effective control mechanisms for COVID-19 pandemic. Official policies about the social isolation rules and the rate of efficient vaccination change from time to time in every country. Also, the virus evolves and its spreading rate changes. Therefore, when using real data to estimate the future of the pandemic it would be more appropriate to use time periods with similar properties (social isolation rules, vaccination rate, variant of virus).

CONFLICTS OF INTEREST

No conflict of interest was declared by the authors.

ACKNOWLEDGEMENTS

This research is supported by The Scientific and Technological Research Council of Turkey (TUBITAK) within the scope of the 1001-Scientific and Technological Research Project (120F307).

REFERENCES

[1] Brauer, F., Castillo-Chavez, C., and Feng, Z., Mathematical Models in Epidemiology, First Edition, Springer-Verlag New York, (2019).

[2] Nistal, R., De la Sen, M., Gabirond, J., Alonso-Quesada, S., Garrido, A.J., Garrido, I., "A Study on COVID-19 Incidence in Europe through Two SEIR Epidemic Models Which Consider Mixed Contagions from Asymptomatic and Symptomatic Individuals", Applied Sciences, 11: 6266, (2021). DOI: 10.3390/app11146266

[3] Arino, J., Protet, S., "A simple model for COVID-19", Infectious Disease Modelling, 5: 309-315, (2020).

[4] Cakir, Z., Savas, H. B., "A mathematical modelling for the COVID-19 pandemic in Iran", Ortadogu Tıp Dergisi, 12(2): 206-210, (2020).

[5] Ivorra, B., Ferrandez, M. R., Vela-Perez, M., Ramos, A. M., "Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections. The case of China", Communications in Nonlinear Science and Numerical Simulation, 88: 105303, (2020).

[6] Liu, Z., Magal, P., Seydi, O., Webb, G., "A COVID-19 epidemic model with latency period", Infectious Disease Modelling, 5: 323-337, (2020).

[7] Ndairou, F., Area, I., Nieto, J. J., Torres, D. F. M., "Mathematical modeling of COVID-19 transmission Dynamics with a case study of Wuhan", Chaos, Solitons & Fractals, 135: 109846, (2020).

[8] Vega, D.I., "Lockdown, one, two, none, or smart. Modeling containing COVID-19 infection. A conceptual model", Science of the Total Environment, 730: 138917, (2020).

[9] https://www.who.int/docs/default-source/coronaviruse/situationreports/20200402-sitrep-73-covid-19.pdf?sfvrsn=5ae25bc76. Access date: 25.06.2020

[10] https://www.cdc.gov/coronavirus/2019-ncov/daily-life-coping/contact-tracing.html. Access date: 10.02.2022

[11] Ahmed, I, Modu, G. U., Yusuf, A., Kumam, P., Yusuf, I., "A mathematical model of Coronavirus Disease (COVID-19) containing asymptomatic and symptomatic classes", Results in Physics, (2021). DOI: 10.1016/j.rinp.2020.103776

[12] Riyapan, P., Shuaib, S. E., Intarasit, A., "A Mathematical Model of COVID-19 Pandemic: A Case Study of Bangkok, Thailand", Computational and Mathematical Methods in Medicine, (2021). DOI: https://doi.org/10.1155/2021/6664483

[13] Van den Driessche P., Watmough J., "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission", Mathematical Biosciences, 180(1-2): 29–48, (2002).

[14] https://data.tuik.gov.tr/Bulten/Index?p=Olum-ve-Olum-Nedeni-Istatistikleri-2019-33710. Access date: 15.11.2022