



Research article

Computational simulations of the effects of social distancing interventions on the COVID-19 pandemic

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Abstract: The spread of the COVID-19 pandemic has been considered as a global issue. Based on the reported cases and clinical data, there are still required international efforts and more preventative measures to control the pandemic more effectively. Physical contact between individuals plays an essential role in spreading the coronavirus more widely. Mathematical models with computational simulations are effective tools to study and discuss this virus and minimize its impact on society. These tools help to determine more relevant factors that influence the spread of the virus. In this work, we developed two computational tools by using the R package and Python to simulate the COVID-19 transmissions. Additionally, some computational simulations were investigated that provide critical questions about global control strategies and further interventions. Accordingly, there are some computational model results and control strategies. First, we identify the model critical factors that helps us to understand the key transmission elements. Model transmissions can significantly be changed for primary tracing with delay to isolation. Second, some types of interventions, including case isolation, no intervention, quarantine contacts and quarantine contacts together with contacts of contacts are analyzed and discussed. The results show that quarantining contacts is the best way of intervening to minimize the spread of the virus. Finally, the basic reproduction number R_0 is another important factor which provides a great role in understanding the transmission of the pandemic. Interestingly, the current computational simulations help us to pay more attention to critical model transmissions and minimize their impact on spreading this disease. They also help for further interventions and control strategies.

Keywords: infectious disease; COVID-19 pandemic; basic reproduction number R_0 ; computational simulations; networks

1. Introduction

The spread of COVID-19 started in Wuhan, China in December 2019. The virus has spread throughout the world [1] and this pandemic has still been circulated with mutations of the novel coronavirus (e.g., Delta and Kappa variants) that continue to generate a constant health threat for upcoming seasons in various countries [2,3]. According to the Worldometer database from [4], on December 11, 2021, the total number of confirmed cases, deaths and recovered people were 269,764,557, 5,316,200 and 242,625,329, respectively. It can be seen that this disease still has not been controlled globally. To control this virus, more control strategies and preventions are needed due to its risk which is not only a medical problem.

Mathematical modeling approaches provide an essential range to identify the critical factors in the spread of coronavirus. Modeling this disease into a transmission network is an effective strategy that can help us to determine better relevant factors for spreading this pandemic. Computational simulations play an important role in identifying the model critical parameters and the model predictions. Individual interactions in a population may be represented in a network, with nodes representing people and edges representing contacts between them. Directly transmitted infectious disease and networks are deeply entwined [5]. Thus, social networks are critical factors of infectious disease transmission. Contact tracing, or identifying persons who have had contact with an infectious individual, is a typical way to detect newly infected people, usually before they become infectious. Contact tracing is applied effectively in the current epidemic's control [5]. Moreover, understanding the nature of human interaction patterns is critical for identifying the effects of the future epidemics and developing appropriate control strategies.

There are a variety of control strategies that help international efforts to minimize the impact of this pandemic on the community. Governments throughout the world have adopted measures such as quarantining, social distancing and using face masks to prevent the spread. These interventions include contact tracing, case isolation, quarantining of contacts, using personal protective equipment and policies that increase physical distance, such as schools and workplace closures and travel restrictions. From the above strategies, contact tracing probably is a good obvious measure. Firth et al. (2020) discussed that identifying the contacts of people decreases the size of simulated epidemics more than tracing just contacts [6]. According to another result reported in [7], defined tracing and quarantine techniques are the most effective way when integrated with additional control measures such as physical distance [6]. To prevent the spread of the COVID-19 pandemic, social distancing and isolation have been extensively used [8]. Block et al. (2020) showed that reducing interaction in social networks is another effective way to decrease transmission of the virus and also its risks [8].

There were many studies that suggested important control strategies to discuss analyzing the COVID-19 spread more widely and accurately. Interestingly, mathematical modeling approaches provide an essential range to identify the critical factors in this spreading [9]. By using different mathematical approaches, including the classical susceptible-infected-recovered (SIR) model and its derivatives, many investigators have been proposed to predict the outbreak of COVID-19. Different types of available models of the transmission of COVID-19 have been explained and described [9]. For example, an SIR model for forecasting the COVID-19 epidemic was proposed [3]. In addition, the impact of the first and second waves of COVID-19 in Italy was studied [10]. They explained some descriptive statistics with correlation analysis and tests of association. The relation between days of air pollution, wind resources and energy, and the diffusion of COVID-19 to provide insights into

sustainable policy to prevent future epidemics was discussed in [11]. A qualitative and quantitative analysis of COVID-19 has been discussed [12], and the researchers found some model critical parameters based on local sensitivities. Also, some model dynamics of the model compartments have been studied [13]. The techniques of sensitivity analysis were applied to the COVID-19 model given in [14]; they are useful approaches to identify the model critical transmissions. Some control strategies, including distancing strategies, were demonstrated in [7,8]. There is another work that proposed an effective and practical strategy to reduce the fatality rate for infectious diseases in society [15]. There is another study that uses physical mixing to monitor the biological transmissibility of social distancing interventions for the COVID-19 pandemic [16]. They have developed a new framework to approximate epidemic curves for Hong Kong by fitting the model curves with real confirmed data. In addition, a set of nonlinear differential equations with optimal strategies was used to limit the spread of the virus, diagnose the infectious and isolate infected people [17]. They used Pontryagin's maximum principle and solved the suggested equations by the finite difference method. Accordingly, a dynamical model of the COVID-19 pandemic was used to assess the impact of antiviral treatment, testing, hospitalization and social distancing [18]. The above techniques and suggested control strategies can significantly work in minimizing the impact of this virus on society. Also, they have played a great role during this pandemic, but there are still more computational techniques that should be studied and discussed, for instance, how some computational software packages such as R and Python can be used to understand this transmission and identify the critical model parameters.

In this study, there are some important questions that should be addressed and highlighted in regard to strategies to stop the spread of COVID-19. First, understanding the contact tracing and its levels are critical because it can be used to determine the transmission of this pandemic. The reader can see some various levels of contacts between individuals in [5] and [19]. Accordingly, to explain how contact tracing works for the transmission of the coronavirus, some scenarios are clearly suggested, including case isolation, no intervention, primary tracing (quarantine contacts) and secondary tracing (quarantine contacts and contacts of contacts). Second, isolating symptomatic persons and quarantining their contacts can also be addressed, which are common public health techniques for preventing the transmission of infectious diseases. Another question is about how to minimize the basic reproduction number (R_0) and its effect on spreading COVID-19.

There are some aims of the suggested tools and control strategies, such as extending the previous studies on the critical aspects of COVID-19 transmission dynamics. Therefore, we have considered different control strategies to minimize the impact of this transmission on the community. Another aim is to understand the impact of each model parameter on the virus transmission. Such parameters are clearly discussed and used in our computational simulations. For example, the basic reproduction number is identified as a critical model parameter, and this spreading can be controlled when the value of this parameter becomes smaller and smaller. Identifying such control parameters can be easily checked with the help of R and Python software. The current suggested tools help us to understand the transmission rates between the model compartments more easily and give a great step forward to identify the model critical parameters. Finally, some control scenarios are suggested and used in the simulations with the different parameter values.

The organization of this paper is as follows; in the next section, there will be an explanation about the methods and materials, including two computational tools, i.e., R and Python. In Section 3, commotional results are discussed. And, the paper ends with conclusions.

2. Methods

2.1. SIR model

The model transmissions between compartments of infectious disease are generally shown in terms of graphical representations using model nodes and links [20]. To better understand the spread of COVID-19, some epidemiological models have been suggested and studied. The SIR model is a common one and it has been widely used. The population here is divided into three compartments: susceptible people (S), infected people (I) and recovered people (R); the model network is shown in Figure 1.



Figure 1. SIR model diagram for infectious disease.

Using the kinetic equations based on the mass action law, the system of differential equations takes the form:

$$\begin{aligned} \frac{dS}{dt} &= -\alpha SI, \\ \frac{dI}{dt} &= \alpha SI - \beta I, \\ \frac{dR}{dt} &= \beta I. \end{aligned} \quad (1)$$

Therefore, at any time t , in the infection process, we have a constant total population $N(t) = S(t) + I(t) + R(t)$. The model parameters are $\alpha \wedge \beta$, and they are called the transmission rate and recovered rate, respectively [20,21]. There were also some other suggested models to discuss the spreading of diseases, such as the SIRD model and SEIR model given in [22]. Using a next-generation matrix technique, the basic reproduction number (R_0) for System (1) is given below:

$$R_0 = \frac{\alpha N}{\beta}.$$

This quantity plays a great role in determining the spread of the virus, and it provides a wide range of critical model parameter identifications. There are mainly two cases. First, if $R_0 > 1$, the disease will continue and spread more widely and many people will be infected from the disease. Second, if $R_0 < 1$, the disease will die out and it can be controlled shortly. The reader can see more details and some theoretical results about R_0 in [23,24]. In this section, two computational tools are developed and improved, entailing the use of R and Python to simulate the spread of the COVID-19 pandemic. Different control strategies are used to identify the model critical parameters. The current approaches provide great results to help us understand the spread of COVID-19 compared to the previous studies. This is because we can build all model compartments and their transmissions with the help of these packages. The developed tools here provide a good environment to check the disease control strategies and policies.

2.2. Computational simulation using R

The spread of COVID-19 and infected cases from this virus has become a global issue. Computational simulations play an important role in identifying the model critical parameters and the model predictions. Recently, researchers suggested and developed a model of the COVID-19 spread and simulated some real data using R ; see more details about the study in [6]. All data here were provided for R and they are available in [25]. They proposed a particular network to simulate how people can interact with each other effectively. The modeling process here starts from a particular network of people with some infected individuals. Then, the model progresses through daily time steps; a possibility of infection can be seen for each day. All model parameters that have been used in these simulations with their estimated values are given in Table 1. Individuals here are mainly classified as susceptible, infected and recovered people. Individuals may also be isolated or quarantined based on their isolation or quarantine duration. All infected persons who have not been separated or quarantined are considered infectors. Every day, all infectors' non-isolated, non-quarantined susceptibility contacts within the network are at danger of infection. While an infected person starts to show symptoms, the network transmissions begin to find the person's primary and secondary contacts. Contacts between individuals that have already recovered are excluded. Using the current proposed networks, many model transmission factors can be measured, such as interventions, the duration of outbreak, the number of infections from a starting point, the basic reproduction number (R_0), social distancing and the testing capacity (tests per day). The model network here has four alternative control scenarios. First, we have no intervention (i.e., no isolation or quarantine of persons). Second, there are some cases of isolation in which people separate before symptoms occur. Another control scenario is a primary contact tracing with quarantine, where persons isolate when symptoms appear and traced contacts are quarantined. The final control scenario is a secondary contact tracing; this is similar to the previous scenario together with contacts of contacts. Individuals who have been isolated and quarantined are placed in isolation for 14 days. Moreover, the other model parameters with their estimated values are shown in Table 1.

Table 1. Model parameters and their estimated values for the spread of the COVID-19 pandemic.

Parameters	Estimated values
Duration of outbreak (days)	30 days
Number of starting infections	3 cases
Reproduction number (R_0)	2, 2.8 and 3.2
Delay to isolation/quarantine	Short (0–2 days), Medium (2–5 days), Long (5–10 days)
Proportion of asymptomatic cases	0.3
Proportion of pre-symptomatic transmission	0.25
Proportion of contacts traced	0.8
Social distancing (% reduction in one-off contacts)	0%, 25% and 50%
Testing capacity (tests per day)	0, 50 and 100

Computational simulations here were obtained based on a variety of COVID-19 testing activities. With isolated or quarantined people, a testing time was provided for each person with the duration between confinement and testing. For more details, the reader can see the suggested computational package and its application to the spread of COVID-19 in [6].

2.3. Computational simulation using Python

Animated representations of spreading COVID-19 helps international efforts to understand the spread of this virus more widely and easily. Using a computational tool called Python helps us to simulate and predict the spread of the virus more generally and accurately. According to a report and some computational simulations that were published in the Washington Post, this pandemic can be further studied and there are many control strategies [26]. They discussed some model critical factors regarding the spread of this virus; all computational simulations were given based on some real data.

Here, in this study, we review the recently published work given in [26]; then, we propose some main steps of computational simulations for the COVID-19 pandemic; they are shown in Flowchart 1. The main steps in the flowchart can be explained and are given in more detail in Appendix A. Then, we improve and consider some other scenarios to see the topological changes of the model regarding the different values of R_0 . It is known that the basic reproduction number, or R_0 , is the most critical factor in determining how quickly a disease may spread among people. This quantity can be estimated here as 2.3, which means that each infected individual can infect 2.3 people on average throughout the duration of their disease. After getting infected with the virus, individuals either completely recovered or died. In this approach, we assume that once a person has been infected and recovered, they cannot be infected again. Similarly, quarantine is another important factor here that helps to decrease epidemics by reducing infected people's ability to transfer the virus to someone else. In addition, there may be more control strategies that can be used to minimize the impact of this virus on communities. Computational simulations here were obtained based on the proposed steps and equations using Python, as explained in Appendix A. The model parameters given in Table 2 with different situations are considered. We use different times (day = 15, 30 and 45) and different reproduction numbers ($R_0 = 2, 2.8 \wedge 3.2$). The transmission rate here depends on some model parameters given in Table 2.

Table 2. Parameter values used for computational simulations.

Parameters	Values	Sources
R_0	2.8	Assumed
Incubation	6	[27]
Percent mild	0.81	[28]
Mild recovery	(8,12)	[28]
Percent severe	0.14	[28]
Severe recovery	(21,42)	[26]
Severe death	(14,56)	[26]
Fatality rate	0.034	[26]
Serial interval	5	[27]

3. Results and discussions

According to the suggested computational simulation tools here, there are some significant results that can be useful to minimize the impact of this disease on society. From the first used technique, there are some control strategies, including contact tracing, quarantining individuals and testing capacity. First, the most effective control strategy is contact tracing. As it is clear that contacts between people play a great role in spreading this virus. Therefore, some different cases of reducing contacts are discussed in Figure 2. For example, Figure 2a shows the effects of reducing contacts by 0%, Figure 2b presents the effects of reducing contacts by 25% and Figure 2c shows the effects of reducing contacts by 50%. As a result, reducing such contacts may provide the different dynamics of this spreading, minimizing the number of infected people dramatically. On the other hand, reducing contacts by closing public places such as schools, universities and markets may have a negative impact on educational and economic sectors. Such strategies can be applied by using practical measures such as wearing masks, avoiding close encounters and social distancing. Accordingly, the first suggested strategy here was also discussed in [29]. They mention that the number of new infected cases increases because of the probability of susceptible people being infected by interacting with other infected people. However, if this scenario becomes unbearable and people begin ignoring the situation, the number of infected cases could increase exponentially. Finally, it can be concluded that reducing contacts has a great role in minimizing the spread of this virus. According to our computational results, the number of infected people can be significantly changed with the percentage of reducing contacts. When we increase this percentage of reducing contacts, the infected transmissions will be considerably reduced.

Another important control strategy for the spread of COVID-19 is quarantining individuals. This strategy is very important for identifying infected individuals and slow down the spread of the virus. Figure 3 shows three different time intervals. For example, Figure 3a stands for a very short period of delay to isolation (0–2 days), Figure 3b shows a medium period of delay to isolation (2–5 days) and Figure 3c gives a very long period of delay to isolation (5–10 days). Quarantining individuals with a very short period of delay to isolation (0–2 days) is very important for identifying contact tracing (see Figure 3a), because they remember who has had contact with them in a short period of time. Another study proposed a temporal deep learning method to identify disease progression and predict patient outcome at an early stage that helps target treatment and resource allocation [1]. The findings suggested that our control strategy is better for slowing down transmission of the virus. However, quarantine in a very long delay to isolation may not reduce the number of infected individuals significantly; see Figure 3c.

According to the second suggested method, there are also some other control strategies. The above-mentioned strategies and many other factors which can be used to decrease the value of the basic reproduction number (R_0). Also, some essential interventions for reducing transmissibility that effect the reproduction number (R_0) were studied in [19]. Figure 4 shows the topological changes of the subpopulations. For the proposed network when $R_0 = 2.8$, given the parameter values in Table 2, unfortunately, more than half of the total population is infected with COVID-19 after 45 days; see Figure 4c. Similarly, it is clear that the numbers of recovered and dead increase after three months of infection, while less people get infected and the pandemic will disappear gradually; see Figure 4e.

The testing capacity for COVID-19 is another important intervention for reducing the transmission of COVID-19; different scenarios about this strategy can be seen in Appendix B and

Figure 5. In addition, isolating infected individuals can be used as a control strategy; some isolation cases with periods of delay to isolation are explained in Appendix C and Figure 6. There are also some other scenarios for controlling this disease, such as no intervention, case isolation, primary tracing (quarantine contacts) and secondary tracing (quarantine contacts and contacts of contacts); see Appendix D and Figure 7. Also, when the value of R_0 becomes bigger, the spread of the virus becomes faster and more people get infected; see Figures 8 and 9 (Appendix E and F). These results provide a great environment for future predictions and can improve health care strategies theoretically and practically.

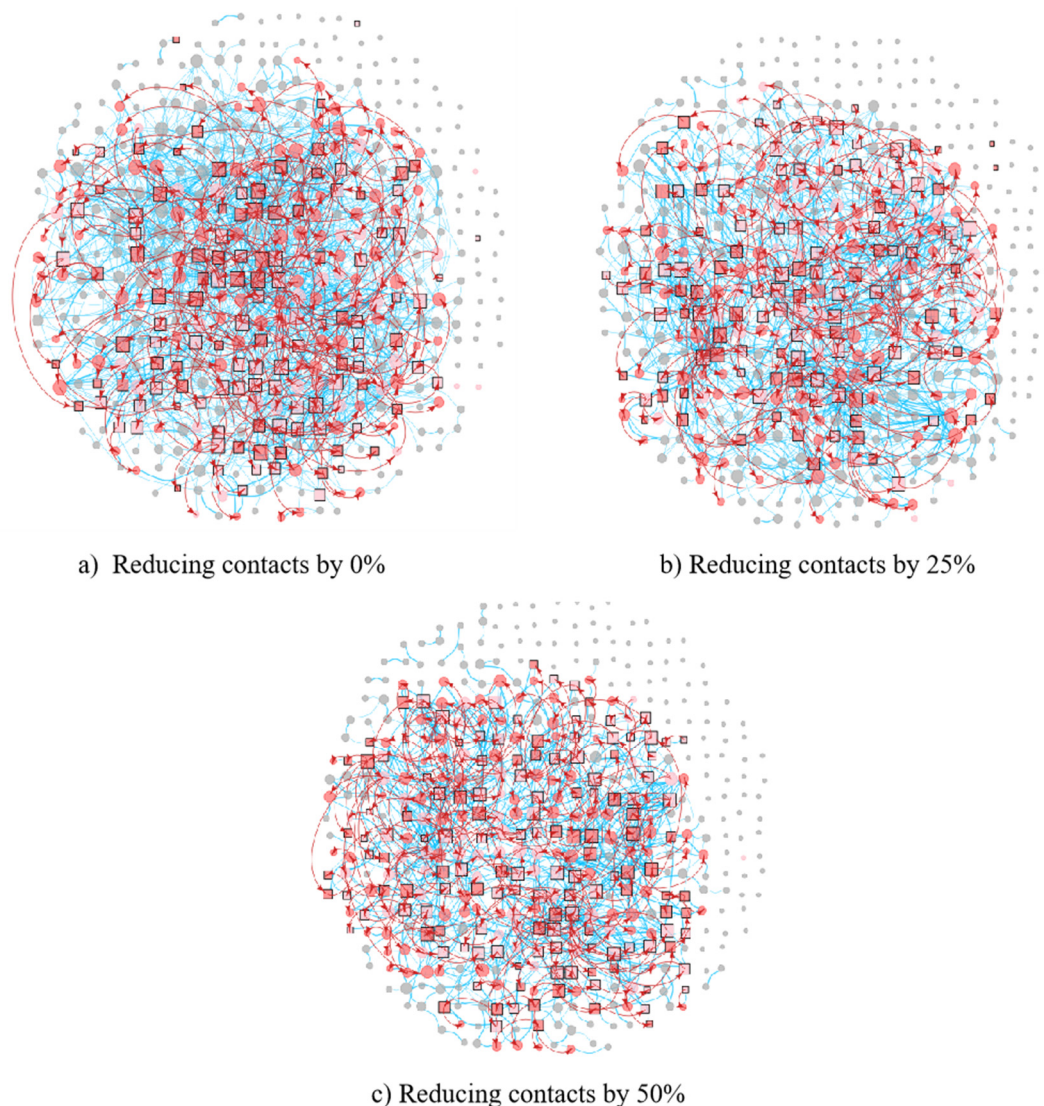


Figure 2. Effects of reducing percentages of contacts. a) 0% reduction of contacts, b) 25% reduction of contacts and c) 50% reduction of contacts. The gray circles, dark red circles and light red circles show uninfected individuals, currently infected individuals and previously infected individuals, respectively. The blue lines show contacts between individuals. The red lines show infections between individuals. The squares represent currently isolated/quarantined individuals.



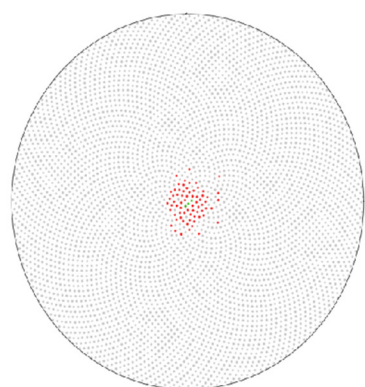
a) Quarantine contacts in a short periods (0 - 2 days) of delay to isolation

b) Quarantine contacts in a medium periods (2 - 5 days) of delay to isolation

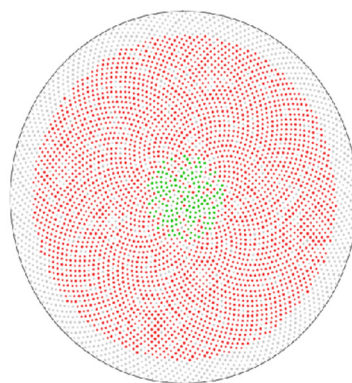


c) Quarantine contacts in a long periods (5 – 10 days) of delay to isolation.

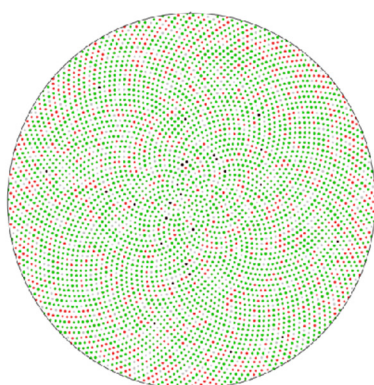
Figure 3. Intervention scenario of primary tracing (quarantine contacts). The periods of delay to isolation are a) short (0–2 days), b) medium (2–5 days) and c) long (5–10 days). The gray circles, dark red circles and light red circles stand for uninfected individuals, currently infected individuals and previously infected individuals, respectively. The blue lines show contacts between individuals. The red lines show infections between individuals. The squares represent currently isolated/quarantined individuals.



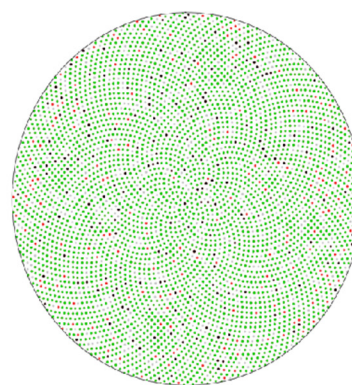
(a) Computational simulation at day 15 when: Infected = 214, Recovered = 3, Deaths = 0.



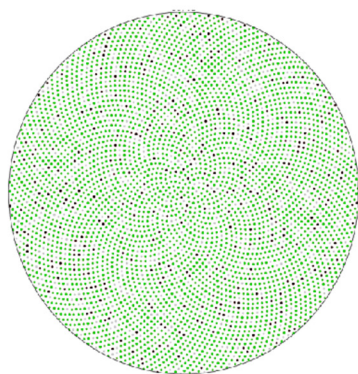
(b) Computational simulation at day 30 when: Infected = 3934, Recovered = 148, Deaths = 0.



(c) Computational simulation at day 45 when: Infected = 935, Recovered = 3121, Deaths = 26.



(d) Computational simulation at day 70 when: Infected = 193, Recovered = 3691, Deaths = 198.



(e) Computational simulation at day 90 when: Infected = 0, Recovered = 3740, Deaths = 342.

Figure 4. Computational simulations calculated when the basic reproduction number (R_0) is 2.8, and for different days (day = 15, 30, 45, 70 and 90). The gray circles, red circles, green circles and black circles stand for uninfected, currently infected, previously infected and dead individuals, respectively.

Finally, the suggested computational simulation tools provide a great environment to understand this pandemic more accurately. Although using such computational approaches may not give the real situation of the spread of this virus, they become good candidates to help international efforts and control strategies theoretically. For example, when we have only some initial parameters and real data,

then the simulation results can provide a good prediction and future model dynamics. Using different control parameters to minimize this spreading throughout the society is another result. Identifying and showing such critical model parameters in our computational simulations help one to see more sensitive elements in these transmissions. Consequently, the suggested tools can effectively work with model predictions and data fitting better than the existing models of differential equations. This is because using such models are computationally expensive and they include many parameters and constant rates.

4. Conclusions

Although the existing mathematical models with computational simulations provide a great reference when identifying the model critical parameters, there is still a need for more tools and approaches to understand this pandemic more widely and effectively. In this paper, two computational tools were discussed and analyzed in order to identify the model transmission rates and critical parameters. Our results provide a great environment for future predictions and improve health care strategies theoretically and practically. Some key measures that can be used for controlling strategies and preventions were highlighted and discussed. The model control parameters used in this study were case isolation, no intervention, quarantine contacts and quarantine contacts together with contacts of contacts, duration of outbreak, number of infections, basic reproduction number (R_0), social distancing and testing capacity. The disease transmission has been shown as a set of topological network features based on the suggested parameter values. Significantly, the quantity of the basic reproduction number gives a significant range to control this pandemic theoretically because the spread of this disease can be further controlled when the value of R_0 becomes smaller. However, more developed techniques with further transmission parameters will essentially be required to understand the impact of the COVID-19 pandemic on social, environmental, economical and institutional settings. Finally, the model results calculated here give more suggestions to control this pandemic more effectively and widely. They can also be used for further preventions and control strategies.

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Conflict of interest

The authors declare no conflict of interest.

Author contributions

Sarbaz Khoshnaw contributed to the conceptualization, validation, writing—review and editing and supervision. Azhi Mohammed contributed to the methodology, software, formal analysis, writing—original draft preparation and visualization. Both authors have read and agreed to the published version of the manuscript.

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