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DYNAMICAL MODEL FOR COVID-19 IN A POPULATION

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Abstract. In this paper a new mathematical model for COVID-19, including improved people who are susceptible to get infected again, is given. And it is used to investigate the transmission dynamics of the corona virus disease (COVID-19). Our developed model consists of five compartments, namely the susceptible class, $S(t)$, the exposed class, $E(t)$, the infected class, $I(t)$, the quarantine class, $Q(t)$ and the recover class, $R(t)$. The basic reproduction number is computed and the stability conditions of the model at the disease free equilibrium point are obtained. Finally, We present numerical simulations based on the available real data for Kerman province in Iran.

Keywords: Dynamical model, Asymptotically stability, The basic reproduction number.
2020 MSC: Primary 34A34, 34D20, 37G10

1. Introduction

Corona virus disease (COVID-19) is an infectious disease caused by a newly discovered Corona virus. Corona viruses are a large family of zoonotic viruses, i.e, they are transmitted from animals to human [7]. Most people infected by COVID-19 virus will experience mild to moderate respiratory illness and recover without requiring special treatment. Older people and those with underlying medical problems like diabetes, cardiovascular disease, cancer and chronic respiratory disease are more likely to develop serious illness.
On average it takes 5- 6 days from when some one is infected with the virus for the symptoms to show, however it can takes up to 14. In mild cases, it can take people one to two weeks to recover, while serious cases can take six weeks or more. Most common symptoms are:
fever, dry cough, tiredness.
less common symptoms are:
aches and pain, sore throat, diarrhoea, conjunctivitis, headache, lose of taste and smell, a rash on skin or discoloration of fingers or toes.
Serious symptoms:
difficulty breathing or shortness of breath, chest pain or pressure, loss of speech.

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One of the best methods to investigate the condition of epidemic in population is mathematical modeling. Mathematical model is a powerful tool that effectively helps in investigation of real world phenomenon and processes [3, 4, 8, 9, 12, 20]. Since the beginenning of the pandemic, many mathematical models have been introduced and numerical results have been tested in some population. Researchers suggested mathematical models to analyze the dynamical behavior and spread of the novel virus which can help to predict the future of pandemic [15]. Many mathematical models provide more insight on how to control the disease spread [16, 17]. Fanelli and Piazza [10] studied a novel compartmental model describing the transmission patterns of COVID-19 in three highly infected countries. In [23], Zhang et al., using SIR model investigated how crowding of infected individuals effects the susceptibles or population. This effect is addressed by a nonlinear incidence rate. In [13] and [25], an SIR model with random perturbation for COVID-19 is formulated and some basic properties like unique positive solution and exponential stability is investigated. Sitthiwirattham et al. introduced an SEIR discrete model [18]. Nazir et al. divided population into five compartments including, susceptibles, exposed people, E, symptomatic people, I, asymptomatic infected people A_p and removed people, R in [19]. In addition, they considered the rate of changes of reservoir of virus in the model. Bushnaq et.al. concidered an SEIR model to control the spread of COVID-19. authors used two control variables in the form of media campaigns, social distancing and face mask use [6]. In [22] an SEIR model is considered. Authors used the method of Sobol to compute the sensitivity indices. Zhang et al. introduced an SEIQR model in [24]. Their model is described by a system of fractional-order differential equations model. Dynamical behaviour and numerical approximation are studied by this model. They applied the adaptive predictor–corrector algorithm and fourth-order Runge–Kutta method to simulate the proposed mode. In [21] Zeb et al. introduced a mathematical model by incorporating isolation. They used the nonstandard finite difference (NSFD) scheme and Runge-Kutta fourth order method to calculate numerical solutions. In the analysis of mathematical models of corona virus, the reproductive number has a significant role in describing the nonlinear dynamics of the model. One of the most popular methods to calculate the basic reproduction number is Watmough method [5] which is used in [1] and [2].

In all of previous models the researchers have considered various compartments but, they did not consider the possibility of getting infected again shortly after recovery. This seems that it is an important factor. The introduced model in this paper contains, re-infection parameter.

The paper is organized as follows. In section 2, the mathematical model is introduced. The basic reproduction number is obtained in section 3. In section 4, disease free equilibrium point stability conditions are investigated and at the last section, using numerical simulation, we analyze the model in the endemic equilibrium point.

2. Mathematical model

In this paper we introduce a model, based on Kermack and McKendrick model [14]. In this model, the population is divided in 5 compartments.
$S(t)$ is the number of Susceptibles at the time t. E is exposed compartment. Infection in people of this class is hidden. A fraction ϵ of these individuals become symptomatic at time t. And a fraction k of them left the exposed class and recovered without any symptoms at time t. People in this class can transmit the infection to healthy individuals with transmission rate β_1.
$I(t)$ is the number of infectives at time t. $Q(t)$ is the number of infective people who are in critical conditions and hospitalized at time t.
The last class is recovered, $R(t)$. Members of this class recover with temporary immunity.
We assume that the birth and natural mortality rate in the population are equal. Thus, the size of population is constant, K. According to the above description, we denote the transmission rate (per capite) by β_2. γ is the recovery rate. The mortality rate because of disease is considered μ_1 and μ_2 in classes I and Q, respectively. η is fraction of infective members who are hospitalized. a fraction θ of recovered individuals become susceptible again. The mathematical model $SEIQRS$ is as follows:

$$\begin{cases} \dfrac{dS}{dt} = -S(\beta_1 E + \beta_2 I + \beta_3 Q) + \theta R, \\ \dfrac{dE}{dt} = S(\beta_1 E + \beta_2 I + \beta_3 Q) - (\gamma + \epsilon)E, \\ \dfrac{dI}{dt} = \epsilon E - (\gamma + \mu_1 + \eta)I, \\ \dfrac{dQ}{dt} = \eta I - (\gamma + \mu_2)Q, \\ \dfrac{dR}{dt} = \gamma(E + I + Q) - \theta R, \end{cases}$$

In this model the transmission rate in infective class is more than exposed and quarantine classes, hence consider $\beta_1 = \frac{1}{4}\beta_2$ and $\beta_3 = \frac{1}{10}\beta_2$.
With the above assumptions $K = S(t) + E(t) + I(t) + Q(t) + R(t)$.

Hence, the differential equation system is reduced to:

$$\begin{cases} \dfrac{dS}{dt} = -S(\beta_1 E + \beta_2 I + \beta_3 Q) + \theta K - \theta(S + I + Q + E), \\ \dfrac{dE}{dt} = S(\beta_1 E + \beta_2 I + \beta_3 Q) - (\gamma + \epsilon)E, \\ \dfrac{dI}{dt} = \epsilon E - (\gamma + \mu_1 + \eta)I, \\ \dfrac{dQ}{dt} = \eta I - (\gamma + \mu_2)Q, \end{cases}$$

3. Basic reproduction number

In this section we would like to calculate the basic reproduction number R_0. For this purpose, we use the method of P. Van Den Driessche and James Watmough [5].

We sperate the dynamic into two parts. The first matrix which we denote it by F is the matrix of transition rate and the second matrix which is denoted by T is a matrix of infection rates. Hence

$$F = \begin{pmatrix} -(\beta_1 E_0 + \beta_2 I_0 + \beta_3 Q_0) & 0 & 0 & 0 \\ 0 & \beta_1 S_0 & \beta_2 S_0 & \beta_3 S_0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

and

$$T = \begin{pmatrix} -\theta & 0 & 0 & 0 \\ 0 & -(\gamma + \epsilon) & 0 & 0 \\ 0 & 0 & -(\gamma + \mu_1 + \eta) & 0 \\ 0 & 0 & \eta & -(\gamma + \mu_2) \end{pmatrix},$$

Where, S_0 is the inatial value of susceptible people at the beginning of endemic and $E_0 = I_0 = Q_0 = 0$.

Thus

$$FT^{-1} = \begin{pmatrix} A & 0 & 0 & 0 \\ 0 & B & C & D \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

where,

$A = \frac{\beta_1 E_0 + \beta_2 I_0 + \beta_3 Q_0}{\theta}$,
$B = -\frac{\beta_1 S_0}{\gamma+\epsilon} - \frac{\beta_2 S_0 \epsilon}{(\gamma+\epsilon)(\gamma+\mu_1+\eta)} - \frac{\beta_3 S_0 \epsilon \eta}{(\gamma+\epsilon)(\gamma+\mu_1+\eta)(\gamma+\mu_2)}$,
$C = \frac{\beta_2 S_0}{\gamma+\mu_1+\eta} - \frac{\beta_3 S_0}{(\gamma+\mu_1+\eta)(\gamma+\mu_2)}$,
$D = \frac{\beta_3 S_0}{\gamma+\mu_2}$.

FT^{-1} is called next generation matrix for the model. R_0 is the maximum eigenvalue of FT^{-1} [5].

$$R_0 = \frac{S_0}{\gamma+\epsilon}(\beta_1 + \frac{\beta_2\epsilon}{\gamma+\mu_1+\eta} + \frac{\beta_3\epsilon\eta}{(\gamma+\mu_1+\eta)(\gamma+\mu_2)}).$$

.

4. Dynamic of model analysis

From the biological consideration , the phase space of the model is
$T_0 = \{(S, E, I, Q, R) : 0 < S + E + I + Q + R \leq K\}$
The model has a disease free equilibrium point, $p_0 = (K, 0, 0, 0)$. Also if $\theta(K - S^* - Q^* - E^*) > S^*(\beta_1 E^* + \beta_3 Q^*)$, then the endemic equilibrium point $p_1 = (S^*, E^*, I^*, Q^*)$ exists, where:
$S^* = \frac{(\gamma+\epsilon)(\gamma+\mu_1+\eta)(\gamma+\mu_2)}{\beta_1(\gamma+\mu_2)(\gamma+\mu_1+\eta)+\beta_2\eta\epsilon}$,
$E^* = \frac{(\gamma+\mu_1+\eta)}{\epsilon} I^*$,
$Q^* = \frac{\eta I^*}{\gamma+\mu_2}$
and
$I^* = \frac{-S^*(\beta_1 E^*+\beta_3 Q^*)+\theta K-\theta(S^*+Q^*+E^*)}{\beta_2 S^*+\theta}$.
Theorem. If $R_0 < 1$ and $\gamma - \epsilon > \beta_1 K$ then the disease free equilibrium point p_0 is asymptotically stable.
Proof: Linearizing of the model in p_0 is given the following characteristic equation

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0,$$

where:
$a_1 = -\beta_1 K + (3\gamma + \epsilon + \eta + \mu_1 + \mu_2)$,
$a_2 = -(-\beta_1 K - (\gamma + \epsilon))(2\gamma + \mu_1 + \mu_2 + \eta) + (\gamma + \mu_2)(\gamma + \mu_1 + \eta) - \epsilon\beta_2 K$,
$a_3 = (-\beta_1 K + (\gamma + \epsilon))(\gamma + \mu_1 + \eta)(\gamma + \mu_2) - \eta\epsilon\beta_3 K - \beta_2 K\epsilon(\gamma + \mu_2)$.
Since $R_0 < 1$, $a_1 > 0$ and $a_2 > 0$.
Also, $\beta_1 - \gamma + \epsilon < 0$ so
$a_3 > (\gamma + \epsilon - \beta_1 k)(\gamma + \mu_1 + \eta)(\gamma + \mu_2) - \eta\epsilon(\gamma + \mu_2) - \epsilon(\gamma + \mu_2)(\gamma + \mu_1 + \eta) =$
$(\gamma + \epsilon - \beta_1 k)(\gamma + \mu_1 + \eta)(\gamma + \mu_2) - \epsilon(\gamma + \mu_2)(\gamma + \mu_1 + 2\eta) > 0$.
We can check easily that $a_1 a_2 > a_3$. Hence, using Routh-Hutwitz theorem [11], the disease free equilibration point p_0 is asymptotically stable.

Remark 4.1. At the beginning of outbreak, if $R_0 < 1$, the epidemic dose not happen.

5. Numerical stability analysis and simulations

It is difficult to analyse the stability of endemic equilibrium point analytically. Hence, one has to resort to numerical calculations.
According to statistics provided by Kerman university of medical sciences from 20 April 2020 to 3 June 2020, the parameters γ, η, θ, ϵ, μ_1 and μ_2 can be estimated. But, it is not easy to estimate parameter β_2. Using the equations

in the model and the data, the mean value of 5.97×10^{-8} with a standard deviation of 1.61×10^{-8} can be obtained. The results can be seen in table 1.

TABLE 1. Parameter description

Parameter	Value	Definition
γ	0/071	recovery rate
β	5.97×10^{-8}	infection rate
η	0/02	transmission rate for I to Q
θ	0/1	transmission rate from R to S
ϵ	0/06	transmission rate from E to I
μ_1	0/001	mortality rate because of disease in I class
μ_2	0/1	mortality rate because of disease in Q class

The population of Kerman province is considered 3,165,000. According to data, the initial values are $S_0 = 3163759$, $E_0 = 718$, $I_0 = 513$ and $Q_0 = 10$. Basic reproduction number is $R_0 = 1.3142$. As you see $R_0 > 1$. We can easily check that p^* is asymptotically stable. Therefore, epidemic occurs and the population tends to reach endemic equilibrium point. It also stays near that.

5.1. **solution curves.** In this part, according to the above information, the solution curves are described. Here we use RK4 method to perform the numerical simulations. Most of individuals were found susceptible, in the first days in a locality. Over time, healthy people become infected through contact with patients. Hence, the number of people in classes E, I and as a result, the population of hospitalized people is increased. Therefore, susceptibility is decreasing and as a result healthy population also declines, as shown in figure **??**. Hence the exposed, the infected and the quarantined classes are growing up, see figures **??**, **??** and **??** respectively. As you see, the number of individuals in exposed class is growing up rapidly. Many people in the population present in this compartment. Therefore, a large number of people in the infected community are asymptomatic. The number of infected individuals is increasing. The number of symptomatic infected people reaches 3000. Similarly, the number of people hospitalized increases to 180.

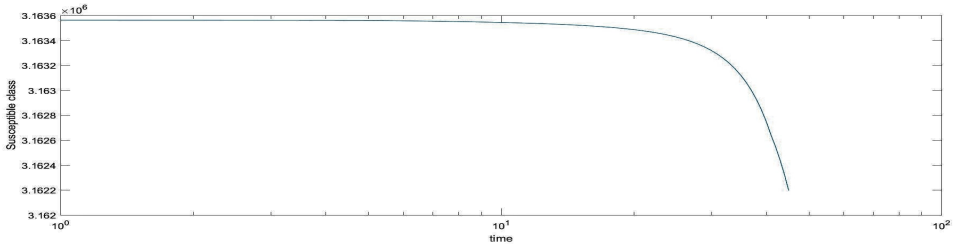

FIGURE 1. Dynamical behavior of the susceptible class (population).

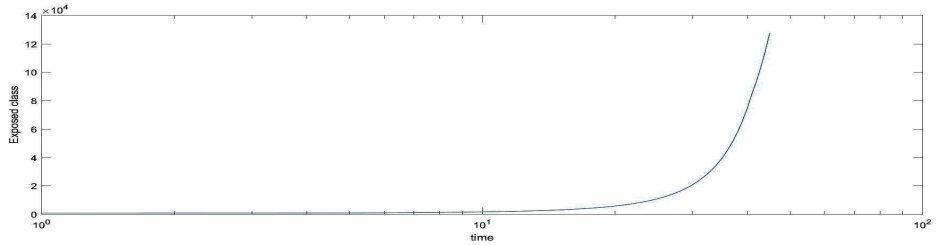

FIGURE 2. Dynamical behavior of the exposed class.

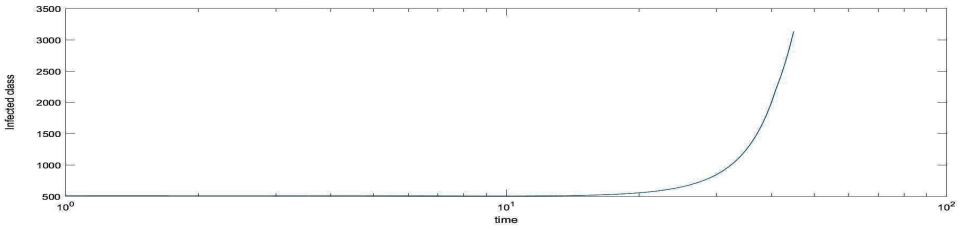

FIGURE 3. Dynamical behavior of the infected class.

5.2. **parameter study.** In the above assumptions, infection period is considered 14 days. While for different people it can be variable. In this section, it is assumed that the length of this period will be shorter or longer with different strategies such as vaccines or drugs, etc. Accordingly, the rate of transmission disease and basic reproduction number are changed. In the following diagrams, the relationship between the length of infection period with β_2 and R_0 has been shown in figures **??** and **??**, respectively.
First figure shows the relationship between the length of infection period, T, and β_2.Indeed, As T increases, the amount of β_2 also increases. The minimum value of β_2 is happened in $T = 6$ which $\gamma = 0.16$. In this case, as shown in

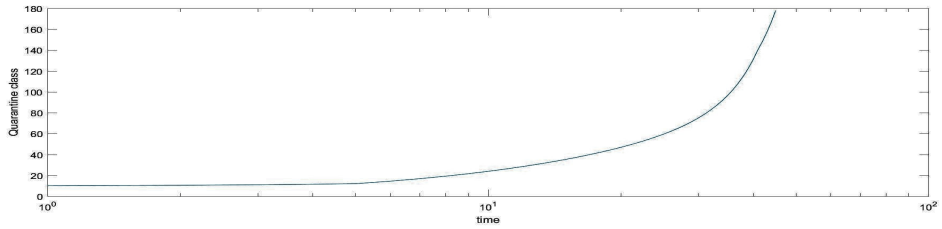

FIGURE 4. Dynamical behavior of the quarantine class.

figure 2, R_0 is near 1 and Epidemic do not occur. Also the endemic equilibrium point is unstable. The endemic equilibrium point is unstable until the length of infection is 12 days and then this equilibrium point is asymptotically stable. Hence, at $T = 12$ a bifurcation occur. Therefore, if the duration of the infection can be reduced by different methods, the epidemic will be eliminated.

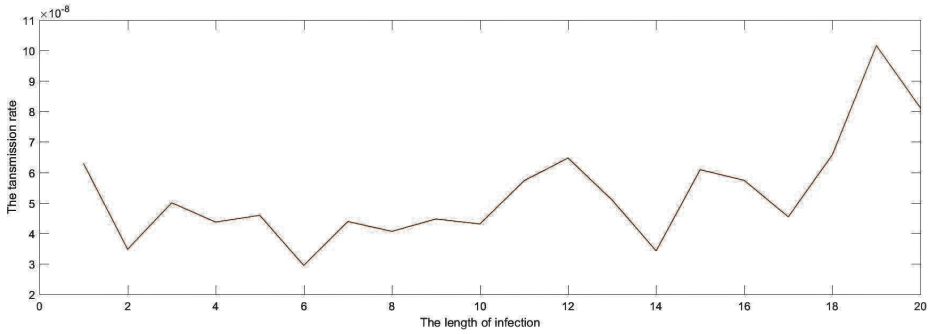

FIGURE 5. The relationship between the length of infection and β.

6. Conclusion

We established a new model by considering re-infection after recovery for the transmission dynamics of COVID-19. Disease free equilibrium point stability conditions were investigated. Also, according to the statistics of infections from 20 April to 3 June 2020 in Kerman province and using numerical simulations, we analyzed the solution of the dynamical model.

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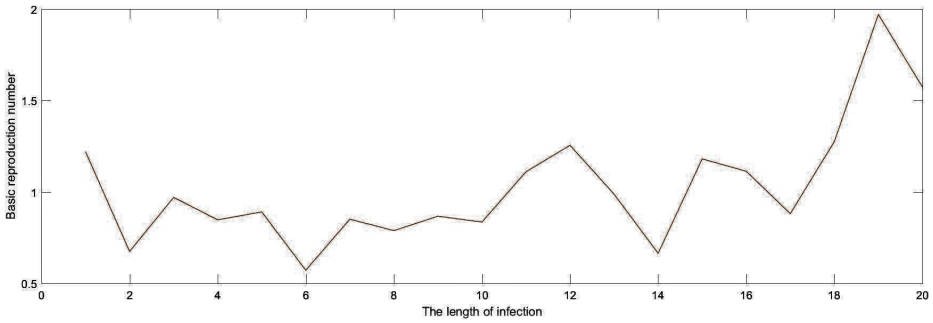

FIGURE 6. The relationship between the length of infection and R_0.

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