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*Research article*

# Analysis coronavirus disease (COVID-19) model using numerical approaches and logistic model

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**Abstract:** The coronavirus disease (COVID-19) is a global health care problem that international efforts have been suggested and discussed to control this disease. Although, there are many researches have been conducted on the basis of the clinical data and recorded infected cases, there is still scope for further research due to the fact that a number of complicated parameters are involved for future prediction. Thus, mathematical modeling with computational simulations is an important tool that estimates key transmission parameters and predicts model dynamics of the disease. In this paper, we review and introduce some models for the COVID-19 that can address important questions about the global health care and suggest important notes. We suggest three well known numerical techniques for solving such equations, they are Euler's method, Runge–Kutta method of order two (RK2) and of order four (RK4). Results based on the suggested numerical techniques and providing approximate solutions give important key answers to this global issue. Numerical results may use to estimate the number susceptible, infected, recovered and quarantined individuals in the future. The results here may also help international efforts for more preventions and improvement their intervention programs. More interestedly, for both countries, Turkey and Iraq, the basic reproduction numbers $R_0$ have been reported recently by several groups, a research estimation by 9 April 2020 revealed that $R_0$ for Turkey is 7.4 and for Iraq is 3.4, which are noticeably increased from the beginning of the pandemic. In addition, on the basis of WHO situation reports, the new confirmed cases in Turkey on 11 April are 5138, and in Iraq on 29 May are 416, which can be counted as the peak value from the beginning of the disease. Thus, we investigate the forecasting epidemic size for Turkey and Iraq using the logistic model. It can be concluded that the suggested model is a reasonable description of this epidemic disease.

**Keywords:** coronavirus disease (COVID-19); mathematical modeling; computational simulations; Euler and Runge-Kutta Methods; logistic model

## 1. Introduction

There is a novel worldwide outbreak of a new type of coronavirus (2019-nCoV), COVID-19 is the new coronavirus that has spread among human beings specifically it was first detected in Wuhan in China and has now reached to 196 countries. COVID-19 is a respiratory virus that is transmitted through contact with an infected person through droplets when a person coughs or sneezes, or through saliva droplets [1]. More precisely, for both countries, Turkey and Iraq, the basic reproduction numbers $R_0$ have been reported by [2, 3], the estimation by 9 April 2020 revealed that $R_0$ for Turkey is 7.4 and for Iraq is 3.4 [2], obviously, the larger value of $R_0$, means the spreading is faster, and the harder it is to control the epidemic. Moreover, according to the daily data of the pandemic on the number confirmed new cases reported from WHO situation reports, the new cases in Turkey on 11 April are 5138 [4], and in Iraq on 29 May are 416 [5], which can be counted as the peak value from the beginning of the disease. Also, WHO declared that it is a pandemic disease. Governments in the world are under pressure to stop the infection. The cause of the current coronavirus infection has been determined as bats. In addition to that, some virologists who dealt with the gene sequence of novel coronavirus, after comparing coronaviruses in other creatures, their results revealed that bats and minks might be the couple probable hosts that were found to be most similar to those of the new coronavirus. It has been confirmed that COVID-19 is more contagious than SARS and MERS. The awareness of humanity is the only way to prevent the COVID-19 massive outbreak from turning into an economic, social, and security crisis that threatens world peace and prosperity. The WHO warned people that they must wash their hands frequently, and stay at home, for necessary stuff when they are out they have to wear mask and wear gloves [6].

Although a significant number of individuals are estimated to be infected with COVID-19 globally, sadly, there is no cure yet for it. Along with, the international organizations like the WHO play a vital role in reducing panic and removing stigma. Also, China as the main front line in the fight against the COVID-19 contagion, has made the greatest effort, achieved the most firsthand experience, and attained the most outstanding results. It stands ready to contribute its experience with the international community and enhance collaboration with other countries and international organizations to win the battle against the COVID-19. Furthermore, biomedical research cooperation is essential in any prevention and control efforts, especially in countries with low levels of public health emergency preparedness. For instance, Scientists at Harvard Medical School have joined forces with an expert team to work on diagnostic reagents. Beside this, international aid helps alleviate shortages of medical supplies [7].

There are some recently published works about the COVID-19 pandemic. One of the recent studies is about the prediction and control of covid-19 some models have been used based on dynamics to lessen the disease transmission three States in India have been forecast to control measure to reduce the contact of exposed and susceptible humans [8]. Also, another step forward work in this area is in the absence of vaccines or effective treatments in the world, in some countries like South Korea, Italy and Brazil some strategies have been adopted such as social isolation, lock-down of cities and border control to reduce the concerns of people [9]. Apart from this, COVID-19 outbreak in Canada using deep learning (DL) models key futures have been evaluated to predict the trends and possible stopping time of the novel COVID-19 outbreak around the world. The long short-term memory (LSTM) networks have been presented [10].While in another study it is dealt with how the transmission dynamics of infection took place in society, the mathematical modeling of fourteen nonlinear FDEs was presented [11].Furthermore, in another study a short - term predicting COVID-19 has been predicted in Brazil. As long as developing short-term forecasting models allow forecasting the number of future cases [12]. Back to predicting as it has been proposed that scientific community should come together provide novel and better methods, strategies, forecasting techniques and models, to understand and lessen the effects of this and future pandemics [13]. At this time in a different study an optimal regression tree algorithm has been applied to find the main causal variables that significantly affect the case fatality rates for different countries such as Canada, France, India, South Korea and the UK [14].

The COVID-19 mathematical modelling is confidentially working to comprehend and predict how infections spread. The use of mathematical models are to create a simplified depiction of infection spread in a population and to understand how an infection might increase in the future. These predictions could assist us to use public health resources such as vaccination programs, treatments, preventions and interventions. The development of computational models used to simulate dynamical equations for coronavirus disease. Clinicians and administrators are accepting the conclusions drawn from modeling, often without realizing the data are simulated. A new application for mathematical modeling is the determination of sample size requirement. Estimates of the population parameters can direct a simulation that increases one patient at a time until a statistically significant difference is detected between the experimental groups. A series of such simulations can give investigators a range and midpoint of a sample size that should satisfy the test of their hypothesis [15].

Covid-19 is novel and appeared at the end of 2019 for this reason there are not many imperial studies regarding coronavirus. Although, there are some studies that have been proposed in this field but are not sufficient. For example; a study has been conducted by Biao Tang , et al. in [16]. They suggested a deterministic compartmental model based on the clinical development of the disease, epidemiological status of the individuals, and intervention measures. According to their study, the estimations based on likelihood and model analysis show that the control reproduction number may be as high as 6.47. At the same time, Sha He1, et al. developed a model on the impact of the timing of working that is categorized on the disease transmission given different strength of protection and control measures [1]. On the other hand, Altaf Khan and Atangana proposed a model with the assumptions that the seafood market has enough source of infection that can be effective to infect people [17]. The reader can find more improvements for the COVID-19 models in [18–21].

Although, there are some mathematical modelling that have been proposed for new coronavirus disease prediction, but some of them can be further improved. Applying numerical methods to calculate some approximate solutions for this virus, could improve the predictions and estimations. A problem that has not been studied yet is Runge-Kutta methods for COVID-19. In a complicated coronavirus model, it is essential to find some numerical results more accurately and widely.

After announcing a curfew by the government for long time and banning travel between all Iraqi provinces, Iraqi citizens who have been abroad in the past fourteen days will be quarantined for fourteen days. The first case was in one of the provinces of Iraq in February; however, at the end of May it reached to 4848 Coronavirus cases since the epidemic began, according to the WHO. Initiation, Iraq reported 169 coronavirus deaths. Comparing infected coronavirus cases in Turkey in March and May, a few cases where confirmed but the number is increasing sharply in May to 158762 cases, and the number of death people is 4397.

The contribution of this work is applying the idea of Euler's method and Runge-Kutta methods to analyze the COVID-19 model equations and identifying the critical model elements. The main contributions in this work can be summarized as follows:

- The recently published papers about the COVID-19 have reviewed and discussed.
- The transmission rates are modeled as a system non-linear differential equations.
- The Runga Kutta and Euler method are suggested to find some numerical solutions for such equations.
- Another goal here is investigating forecasting epidemic size for Turkey and Iraq using the logistic model. The data for the confirmed cases in Turkey and Iraq have used in our computational simulations, some predications are discussed.
- Based on the computational simulations, the number of infected people has increased gradually until April 2020, then it will be decreased slightly after May 2020.

## 2. Metheods

Many scientific and technological problems are modeled mathematically by systems of ordinary differential equations, for example, chemical reactions, ecological interactions, biological process. Most realistic systems of ordinary differential equations do not have exact analytic solutions. Therefore, numerical techniques and computational tools help in providing model solutions [22].

There are many types of practical numerical methods that produce numerical approximations to solution of initial value problems (IVP) in ordinary differential equations. Historically, the ancestor of all numerical methods in use today was originated by Leonhard Euler in 1768, improved Euler's method and Runge-Kutta methods described by Carl Runge and Martin Kutta in 1895 and 1905 respectively. Accordingly, Euler's method, Runge–Kutta method of order two (RK2) and Runge–Kutta method of order four (RK4) can be easily used for solving non–linear system of infectious disease models with initial populations. More details and details regarding such numerical methods with application examples can be found in [23–26]. In this paper, we review some basic concepts for such numerical techniques.

### *2.1. Euler's method*

Euler's method is basic explicit method for solving systems of ordinary differential equations with initial conditions. More details and applications of this method can be seen in [27]. The basic Euler's method formula is given below:

$$u_{i+1} = u_i + hf(t_i, u_i), \tag{2.1}$$

to apply this formula for the following system of first order differential equations and $t \in [a, b] \subset \mathbb{R}$,

$$
\begin{aligned}
\frac{du_1}{dt} =& f_1(t, u_1, u_2, \dots, u_m), \\
\frac{du_2}{dt} =& f_2(t, u_1, u_2, \dots, u_m), \\
\frac{du_3}{dt} =& f_3(t, u_1, u_2, \dots, u_m), \\
&\vdots \\
\frac{du_m}{dt} =& f_m(t, u_1, u_2, \dots, u_m),
\end{aligned} \tag{2.2}
$$

with the initial conditions

$$u_i(a) = \alpha_i, \qquad \text{for } i = 1, 2, \dots, m. \tag{2.3}$$

Updating the function $u_1$ by $f_1$, $u_2$ by $f_2$ ,. . . , $u_m$ by $f_m$ and using the step size $h = \frac{b-a}{n}$, formula (2.1) takes the form

$$u_j(i+1) = u_j(i) + hf_j(t(i), u_1(i), u_2(i), \dots, u_m(i)), \tag{2.4}$$

where $i = 0, 1, \dots, n-1$ and $j = 1, 2, \dots, m$.

### 2.1.1. Advantages of Euler's method

Euler's method is easy to use and direct because in this method no integration appeared in calculation. It is also less time-consuming [27]. Moreover, Euler's method can be successfully applied to solve a problem where an analytic solution is impossible, for its recurring ability.

### 2.1.2. Disadvantages of Euler's method

Euler's method is less accurate and numerically unstable because $\frac{du}{dt}$ changes rapidly over an interval; this gives not a good approximation at the beginning of the process in comparison with the average value over the interval. The approximation error is proportional to the step size $h$. Hence, if $h$ is not small enough this method is too inaccurate [27,28].

## *2.2. Runge-Kutta method*

The Runge-Kutta method is the most popular numerical approach because it is quite accurate, stable and easy to program. This technique is the most widely used one since it gives starting values and is particularly suitable when the compilation of higher derivatives is complicated [27]. In this work, we review two types of Runge-Kutta method such as Runge-Kutta method of order two (RK2) and Runge-Kutta method of order four (RK4). They are effective numerical tools to solve high dimensional system of differential equations.

The idea of Runge-Kutta (RK) method is the same as Euler's method; that is, we update each unknown function $u_1$, $u_2$, $u_3, \dots$, and $u_m$, using the basic RK formulas and the appropriate right-hand-side function, $f_1$ or $f_2$ or $f_3$ . . . or $f_m$. We now consider the the two-stage RK method (known as the "midpoint method") [28]. For the midpoint method, if we denote the two update parameters as $k_1$ and $k_2$, then the basic second-order Runge-Kutta formulas are given below:

$$\begin{aligned} k_1 &= hf(t_i, u_i), \\ k_2 &= hf(t_i + 0.5h, u_i + 0.5k_1), \\ u_{i+1} &= u_i + k_2. \end{aligned} \tag{2.5}$$

To apply these formulas to the system (2.2), The parameters $k_1$ and $k_2$ for each unknown function should be computed. Consider an integer $n > 0$ and $h = \frac{b-a}{n}$ when $a \le t \le b$, and $u_i(a) = \alpha_i$ for each $i = 1, 2, \dots, m$. The values of the parameter $k_1$ for the unknown functions $u_1, u_2, \dots, u_{m-1}$, and $u_m$ are

$$k_{1,j} = hf_j(t(i), u_1(i), u_2(i), \dots, u_m(i)), \quad \text{for} \quad j = 1, 2, \dots, m. \tag{2.6}$$

Similarly, the values of $k_2$ are

$$k_{2,j} = hf_j(t(i) + 0.5h, u_1(i) + 0.5k_{1,1}, u_2(i) + 0.5k_{1,2}, \dots, u_m(i) + 0.5k_{1,m}), \tag{2.7}$$

for $j = 1, 2, \dots, m$. Finally, the values of the unknown functions at the next grid point are given:

$$u_j(i+1) = u_j(i) + k_{2,j}, \quad \text{for} \quad i = 0, 1, \dots, n-1 \tag{2.8}$$

It can be noticed that all the values $k_{1,1}, k_{1,2}, \dots, k_{1,m}$ should be computed before identifying the values $k_{2,j}$, for $j = 1, 2, \dots, m$.

Another method for a single first order equation is the classical Runge-Kutta method of order four, it is given by

$$\begin{aligned} u_0 &= \alpha, \\ k_1 &= hf(t_i, u_i), \\ k_2 &= hf(t_i + \frac{h}{2}, u_i + \frac{1}{2}k_1), \\ k_3 &= hf(t_i + \frac{h}{2}, u_i + \frac{1}{2}k_2), \\ k_4 &= hf(t_{i+1}, u_i + k_3), \\ u_{i+1} &= u_i + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4), \quad \text{for} \quad i = 0, 1, \dots, n-1, \end{aligned} \tag{2.9}$$

They can be used to solve the first-order initial-value problem given below:

$$\frac{du}{dt} = f(t, u), \qquad a \le t \le b, \qquad u(a) = \alpha. \tag{2.10}$$

We now consider the classic fourth-order Runge-Kutta method for the system of ODEs (2.2). Let $n$ be an integer $> 0$, set $h = \frac{b-a}{n}$, when $a \le t \le b$, and $u_i(a) = \alpha_i$ for each $i = 1, 2, \dots, m$. Suppose that the values $u_1(i), u_2(i), \dots, u_m(i)$ have been computed. We obtain $u_1(i+1), u_2(i+1), \dots, u_m(i+1)$ by first calculating

$$\begin{aligned} k_{1,j} &= hf_j(t_i, u_1(i), u_2(i), \dots, u_m(i)), \\ k_{2,j} &= hf_j(t_i + \tfrac{h}{2}, u_1(i) + \tfrac{1}{2}k_{1,1}, u_2(i) + \tfrac{1}{2}k_{1,2}, \dots, u_m(i) + \tfrac{1}{2}k_{1,m}), \\ k_{3,j} &= hf_j(t_i + \tfrac{h}{2}, u_1(i) + \tfrac{1}{2}k_{2,1}, u_2(i) + \tfrac{1}{2}k_{2,2}, \dots, u_m(i) + \tfrac{1}{2}k_{2,m}), \\ k_{4,j} &= hf_j(t_i + h, u_1(i) + k_{3,1}, u_2(i) + k_{3,2}, \dots, u_m(i) + k_{3,m}). \end{aligned} \tag{2.11}$$

Finally, the values of the unknown function at the next grid point are computed from

$$u_j(i+1) = u_j(i) + \frac{1}{6}(k_{1,j} + 2k_{2,j} + 2k_{3,j} + k_{4,j}), \tag{2.12}$$

for $i = 0, 1, \ldots, n-1$ and $j = 1, 2, \ldots, m$.

### 2.2.1. Advantages of Runge-Kutta method

Runge-Kutta method is easy to implement and stable since it gives reliable values starting values and particularly suitable when the computation of higher-order derivatives are complicated [27]. It scores over the earlier methods in obtaining a better approximation of the solution and at the same time, it doesn't need to know derivatives of $f$.

### 2.2.2. Disadvantages of Runge-Kutta method

Though the Runge-Kutta method is quite accurate, stable, and easy to program, it is also very laborious. It is a lengthy process and needs to check back the values computed earlier [27]. Also, error estimation is not easy to be done. Moreover, it does not work well for stiff differential equations [28].

## *2.3. Chemical kinetics*

The classical theory of chemical kinetics helps to understand and show the biological process in terms of mathematical modeling. The basic assumptions are introduced for set of components, reactions and their relations. We consider $n$ reversible reactions which are given below

$$\sum_{j=1}^{m} a_{ij}x_j \underset{k_i^-}{\overset{k_i^+}{\rightleftharpoons}} \sum_{j=1}^{m} b_{ij}x_j, \quad i = 1, 2, ..., n, \tag{2.13}$$

where $x_j$, $j = 1, 2, ..., m$ are chemical components, $a_{ij}$ and $b_{ij}$ are non–negative integers. The reaction constants are $k_i^+ > 0$ and $k_i^- \geq 0$. Using the idea of mass action law, the model reaction rates are expressed as follows

$$v_i = k_i^+ \prod_{j=1}^{m} x_j^{a_{ij}}(t) - k_i^- \prod_{j=1}^{m} x_j^{b_{ij}}(t). \tag{2.14}$$

Therefore, the model mathematical equations are defined below

$$\frac{dx}{dt} = \sum_{i \in J \subset \mathbb{R}} \pi_i v_i. \tag{2.15}$$

where $\pi_{ij} = b_{ij} - a_{ij}$, for $i = 1, 2, ..., n$ and $j = 1, 2, .., m$. Equation (2.15) can be written as follows:

$$\frac{dx_j}{dt} = h_j(x, k), \tag{2.16}$$

where $x \in \mathbb{R}^m$ and $k \in \mathbb{R}^n$. The more details and descriptions about chemical reactions and their differential equations with some applications in system biology can be found in [29–32].

## 3. Mathematical modeling for coronavirus disease

The current coronavirus outbreak becomes a global health care problem. There are some preventions announced as strategies for controlling the infection such as reducing contacts as much as possible and advice people to stay at home. Mathematical models for this virus are effectively role to show model dynamics and estimate the infected number in the future. Recently, a mathematical model was suggested for showing individual interactions and calculating the model reproduction number. The model is based on the clinical progression, epidemiological individuals and intervention measures. Accordingly, the model combined with the intervention compartments such as treatment, isolation (hospitalization) and quarantine [16]. More recently, the model has been updated for time-dependent dynamic system [20]. We develop the model diagram and the interaction individual components with their interaction rates given in Figure 1. The model includes eight groups (individuals): susceptible $S$, exposed $E$, symptomatic $I$, pre-symptomatic $A$, quarantine susceptible $S_q$, quarantine exposed $E_q$, hospitalized $H$ and recovered $R$. The model initial populations and interaction parameters are obtained for the confirmed cases in China. All parameter values and initial populations are given in Table 1. The estimated values were first defined in [16], then they were updated in [20]. We have mainly followed reference [20], and we used such values in our computational simulations. They used the Markov Chain Monte Carlo (MCMC) method to fit the model to the data, and assumed an adaptive Metropolis-Hastings (M-H) algorithm to carry out the MCMC procedure.

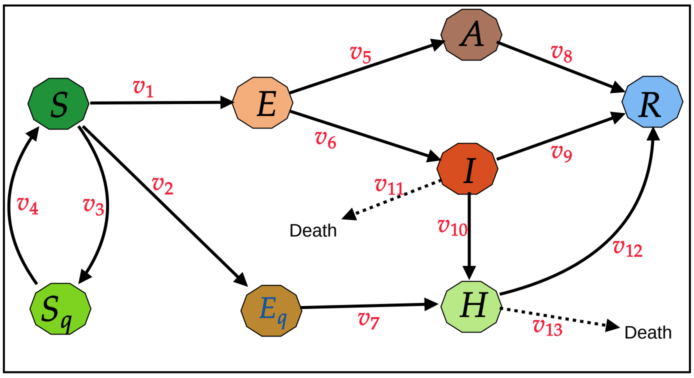


**Figure 1.** The model diagram the coronavirus disease (COVID-19) with interaction rates.

The model reactions for the COVID–19 with their rats are defined below:

$$\begin{aligned}
&S\xrightarrow{v_1}E,\quad S\xrightarrow{v_2}E_q,\quad S\xrightarrow{v_3}S_q.\quad S_q\xrightarrow{v_4}S,\\
&E\xrightarrow{v_5}A,\quad E\xrightarrow{v_6}I,\quad E_q\xrightarrow{v_7}H,\quad A\xrightarrow{v_8}R,\\
&I\xrightarrow{v_9}R,\quad I\xrightarrow{v_{10}}H,\quad I\xrightarrow{v_{11}}\text{Death},\quad H\xrightarrow{v_{12}}R,\\
&H\xrightarrow{v_{13}}\text{Death},
\end{aligned}\tag{3.1}$$

where $v_1 = k_1(1-k_3)U_1S(I+k_4A)$, $v_2 = k_1k_2U_1S(I+k_4A)$, $v_3 = k_2(1-k_1)U_1S(I+k_4A)$, $v_4 = k_5S_q$, $v_5 = k_3(1-k_6)$, $v_6 = k_3k_6$, $v_7 = k_7E_q$, $v_8 = k_9A$, $v_9 = k_8I$, $v_{10} = U_2I$, $v_{11} = k_{11}I$, $v_{12} = k_{10}H$, $v_{13} = k_{11}H$.

**Table 1.** The estimated initial populations and parameters for coronavirus disease (COVID-19) with their biological definitions that have been updated from the confirmed cases in China [20].

| Parameters | Biological definitions | Values |
|---|---|---|
| $S(0)$ | Initial susceptible individuals | 11081000 |
| $E(0)$ | Initial exposed individuals | 105.1 |
| $I(0)$ | Initial symptomatic individuals | 27.679 |
| $A(0)$ | Initial pre-symptomatic individuals | 53.839 |
| $S_q(0)$ | Initial quarantine susceptible individuals | 739 |
| $E_q(0)$ | Initial quarantine exposed individuals | 1.1642 |
| $H(0)$ | Initial hospitalized individuals | 1 |
| $R(0)$ | Initial recovered individuals | 2 |
| $k_1$ | Transmission per contact | $2.1011 \times 10^{-8}$ |
| $k_2$ | Quarantined exposed rate | $1.2858 \times 10^{-5}$ |
| $k_3$ | Transition rate between exposed and infected classes | $\frac{1}{7}$ |
| $k_4$ | The multiple of the transmissibility of $A$ to $I$ | 0.3 |
| $k_5$ | Quarantined uninfected contact rate | $\frac{1}{14}$ |
| $k_6$ | Probability of symptomatic among infected people | 0.86834 |
| $k_7$ | Transition rate between quarantined exposed quarantined infected classes | 0.1259 |
| $k_8$ | Recovery rate from symptomatic infected | 0.33029 |
| $k_9$ | Recovery rate from asymptomatic infected | 0.13978 |
| $k_{10}$ | Recovery rate from quarantined infected | 0.11624 |
| $k_{11}$ | Infected death rate | $1.7826 \times 10^{-5}$ |
| $a$ | Initial contact rate | 14.781 |
| $b$ | Minimum contact rate | 2.9253 |
| $d$ | Initial transition rate between symptomatic infected and quarantined infected class | 0.13266 |
| $1/e$ | The shortest period of diagnosis | 0.3654 |
| $r_1$ | Exponential decreasing rate of contact rate | 1.3768 |
| $r_2$ | Exponential decreasing rate of diagnose rate | 0.32029 |

The estimated values of initial populations and parameters given in Table 1. Using Eqs (2.14)–(2.16), the model dynamics are described by the following system of non–linear ordinary differential equations

$$\begin{aligned}
\frac{dS(t)}{dt} &= -(k_1U_1(t) + k_2U_1(t)(1-k_1))(I(t) + k_4A(t))S(t) + k_5S_q(t),\\
\frac{dE(t)}{dt} &= k_1U_1(t)(1-k_2)(I(t) + k_4A(t))S(t) - k_3E(t),\\
\frac{dI(t)}{dt} &= k_3k_6E(t) - (U_2(t) + k_8 + k_{11})I(t),\\
\frac{dA(t)}{dt} &= k_3(1-k_6)E(t) - k_9A(t),\\
\frac{dS_q(t)}{dt} &= (1-k_1)k_2U_1(t)(I(t) + k_4A(t))S(t) - k_5S_q(t),\\
\frac{dE_q(t)}{dt} &= k_1k_2U_1(t)(I(t) + k_4A(t))S(t) - k_7E_q(t),\\
\frac{dH(t)}{dt} &= U_2(t)I(t) + k_7E_q(t) - (k_{10} + k_{11})H(t),\\
\frac{dR(t)}{dt} &= k_8I(t) + k_9A(t) + k_{10}H(t),\\
U_1(t) &= (a-b)e^{-r_1t} + b. \quad U_2(t) = \frac{e}{1 + (\frac{e}{d} - 1)e^{-r_2t}}.
\end{aligned} \tag{3.2}$$

The model initial populations are expressed in the following equation

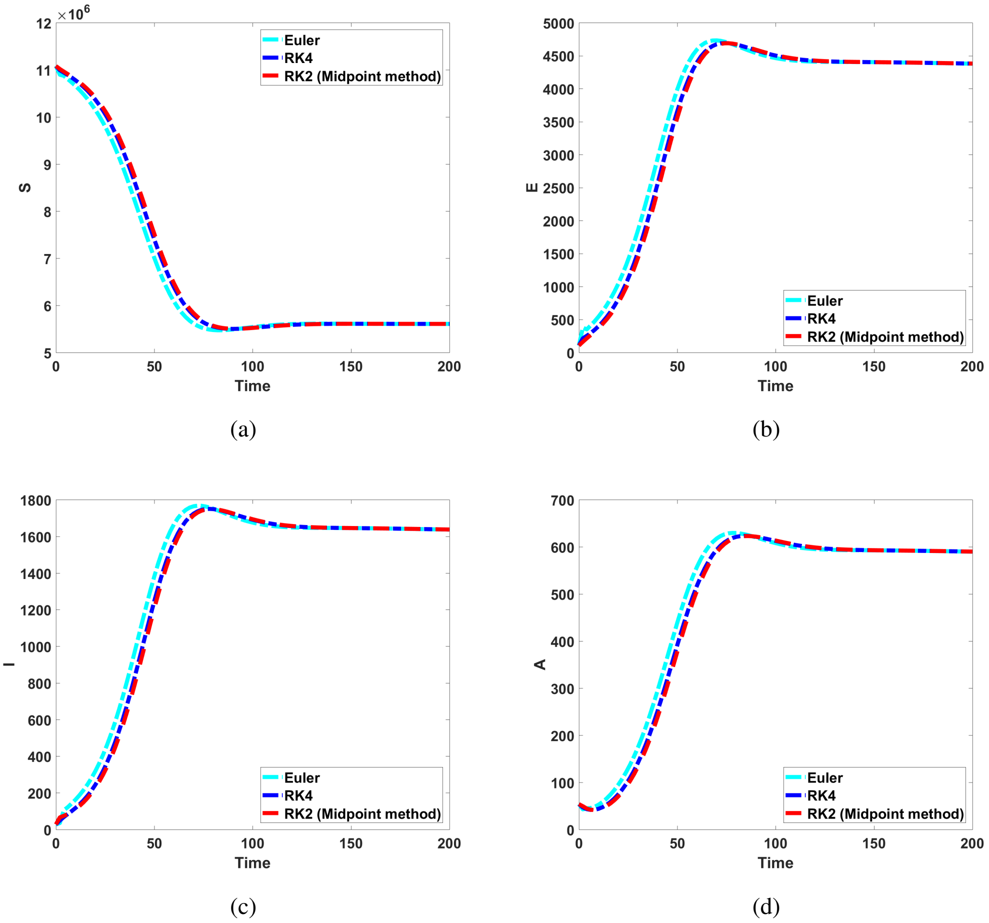
$$\begin{aligned}
&S(0) = S_0 > 0, \quad E(0) = E_0 > 0, \quad I(0) = I_0 > 0, \quad A(0) = A_0 > 0,\\
&S_q(0) = S_q^0 \geq 0, \quad E_q(0) = E_q^0 \geq 0, \quad H(0) = H_0 \geq 0, \quad R(0) = R_0 \geq 0.
\end{aligned} \tag{3.3}$$

The non–linear system of differential equations given in Eq (3.2) can not solved analytically. Therefore, the suggested numerical techniques given in this paper can provide some approximate solutions for the COVID-19 model states. We use MATLAB for calculating numerical predictions using initial populations and estimated parameters given in Table 1.

The high dimensional models of the spread of infectious diseases often can not be well understood only by biological approaches. This is why mathematical methods and computational simulations are effective tools that provide us more understanding and numerical predictions about model states. In this work, we applied three numerical approaches for describing the COVID-19 model dynamics and identifying critical model parameters. The numerical methods applied in this study are Euler method and Runge–Kutta method for order two and order four. The parameter values and initial populations in this study are obtained from the WHO situation report (the National Health Commission of the Republic of China ) presented in [16, 20]. We present these estimated values in Table 1.

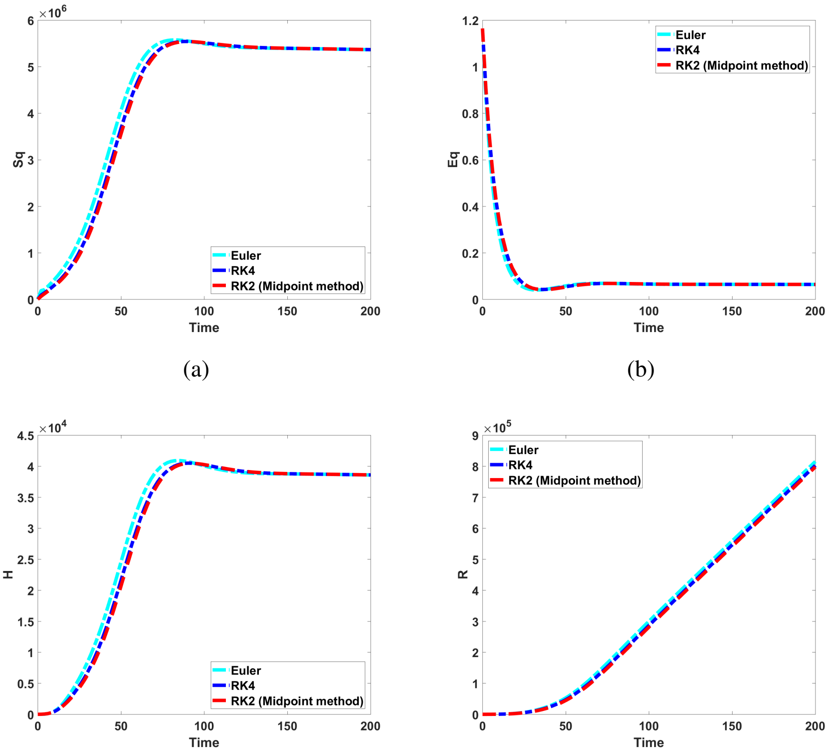
We calculate the numerical approximate solutions of the model Eq (3.2) for different parameters and initial populations using MATLAB, see Figures 2 and 3. Accordingly, this concludes that there is a different model dynamic for population model states. Numerical simulations are computed in two dimensional planes for the model variables using parameters and initial populations. More interestingly, there are a good agreement among all numerical approximate solutions based on the three proposed numerical approaches. Results in this study based on the computational simulations provide a good step forward in predicting the model dynamics in the future for development programs, interventions and health care strategies.

Particularly, results in Figure 2 show the numerical predictions for the number of susceptible, exposed, symptomatic infected and pre-symptomatic infected individuals. It is clear that there are a good agreement among the suggested numerical approaches and they become more stable after 100 days. In addition, the dynamics of quarantine susceptible and hospitalized people are gradually changed when $t \in [0, 100]$ then they become more flat. On the other hands, the number of quarantine exposed individuals become stable quickly after $t > 40$ but the number of recovered people increases slightly and it is stable very slowly, see Figure 3. All numerical approximate results are presented in Tables A1–A6.



(a) (b) (c) (d)

**Figure 2.** Numerical approximate solutions for the coronavirus disease model Eq (3.2) using Euler method, Runge-Kutta method for order two (RK2) and order four (RK4); (a): the number of susceptible populations $S$, (b): the number of exposed populations $E$, (c): the number of symptomatic populations $I$, (d): the number of pre-symptomatic populations $A$.



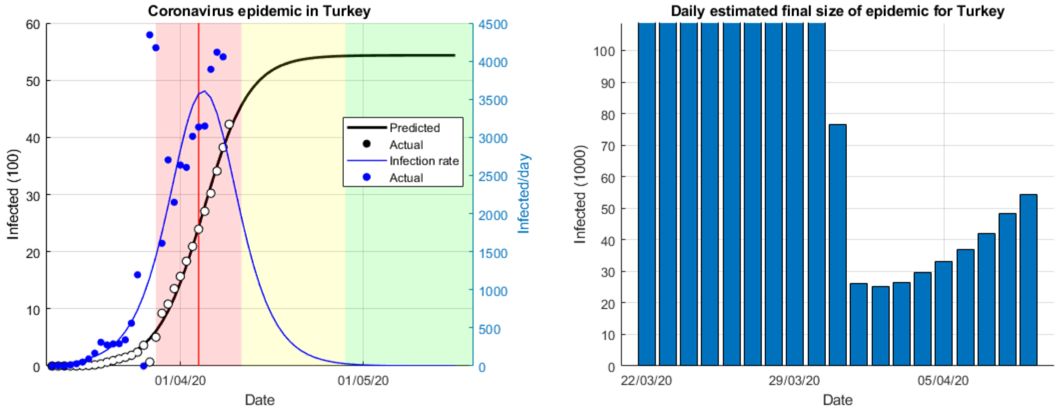
(a) (b)

(c) (d)

**Figure 3.** Numerical approximate solutions for the coronavirus disease model Eq (3.2) using Euler method, Runge-Kutta method for order two (RK2) and order four (RK4); (a): the number of quarantine susceptible populations $S_q$, (b): the number of quarantine exposed populations $E_q$, (c): the number of hospitalized populations $H$, (d): the number of recovered populations $R$.

## 4. Estimated infected people in Turkey and Iraq

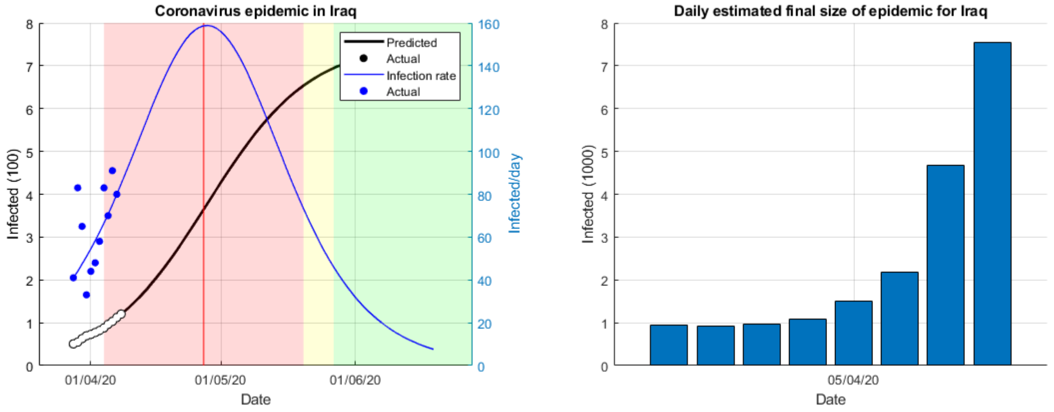
The function fitVirus03 applies a logistic model for estimation of final epidemic size from daily estimations [33]. The model is data–driven, so its forecast is as good as data are. Additionally, it is supposed that the model is a conceivable definition of the one-stage epidemic. In this section, we investigate the results of the two countries by the proposed model. All confirmed cases for Iraq and Turkey presented in Tables A7 and A8. We gave the results from 11 March 2020 to 9 April 2020 for Turkey. We demonstrated the results by Figure 4. We presented the results from 28 March 2020 to 4 April 2020 for Iraq. We demonstrated these results by Figure 5. Our results show that the infected rate is plotted with blue lines and blue dots are represented actual the daily number of cases. Separated phases given in Figures 4a and 5a are epidemic regions: red colors represent fast growth phase, yellow colors represent transition to steady-state and green colors show ending infected. Based on the computational results presented in Figures 4 and 5, the number of infected people in the two countries reached to the maximum on the April 2020, then it will gradually decreased and gets stable after June 2020.



(a) Predicted evaluation in Turkey

(b) The predicted final size in Turkey

**Figure 4.** Estimation of coronavirus COVID-19 epidemic size by the logistic model for Turkey.



(a) Predicted evaluation in Iraq

(b) The predicted final size in Iraq

**Figure 5.** Estimation of coronavirus COVID-19 epidemic size by the logistic model for Iraq.

## 5. Discussions

There are also many strategies and preventions as global efforts to reduce the impact of the COVID-19 around the world. Although, this pandemic becomes a global issue and speeding very fast but all clinical and theoretical studies give a great effort to control this disease. One of the theoretical tools that provide a wide range of predictions and estimations about this issue is mathematical modeling. Mathematical modeling with computational simulations give model predictions and identify key critical parameters. However, having many approaches for identifying such estimations and understanding this disease makes this issue remain unclear. Machine Learning (ML) and Cloud Computing effectively give predict growth of the epidemic and design strategies and policy to manage its spread [34]. This study provides an essential way to suggest more preventions compared to the previous approaches. Another step forward to analyze the dynamics of the COVOD-19 is using the idea of local sensitivity [35]. Based on this study, the sensitivity of each variable concerning the model parameters are calculated, and some model key elements are identified for more preventions and suggestions. More recent study about this issue is a qualitative and quantitative analysis for the model dynamics [36]. According to this study, some critical model parameters are identified, and this becomes an important tool to understand the global issue more effectively and widely. Comparing to all previous studies, our numerical approaches give a another great step forward to understand the model dynamics and predict the spreading of this disease on the community.

## 6. Conclusions

Global efforts around the world are focused and discussed several health care strategies for controlling the spreading of the new coronavirus on community. It can be seen that this virus becomes a public health threat and spreading easily among individuals. The coronavirus disease (COVID–19) model is a complicated one, and it requires some mathematical tools to have improvements about interventions and healthcare programs. The COVID-19 is modeled based on clinical data and reported cases in Wuham-China. The model equations are non-linear differential equations that numerical approaches are required to have some numerical solutions.

We applied the idea of Euler and Runge–Kutta methods to calculate some approximate solutions for each model state based on the reported cases. These provide us an important step forward to identify model critical elements and future model improvement. Computational results may help international efforts to reduce number of infected individuals from the disease and to prevent the conronavirus more widely on the community.

Accordingly, some findings and computational results are given based on the suggested approaches for the COVID-19 model. Firstly, the model dynamics of all compartments are computed using three different numerical techniques. The dynamics of all compartment are investigated, the results provide a great step forward to predict and analyze the population of each model state. All estimated parameters and initial populations obtained for the confirmed cases in China. Secondly, the number of infected and recovered people for confirmed cases in Iraq and Turkey are also discussed. The computations simulations obtained using Matlab.

Results in this study suggested that health care programs should more pay attention on the key critical model parameters. This may help community interventions that can reduce the impact of coronavirus disease. Computational results provide a key estimation and future predict easily about the number of infected individuals, susceptible individuals and recovered individuals. Accordingly, we have investigated forecasting epidemic size for Turkey and Iraq using the logistic model. It can be concluded that the suggested model is a reasonable description of this epidemic disease. Interestingly, the proposed steps here can further be developed and applied to a wide range of coronavirus models for different cases a round the world. They will be useful for future model improvements, interventions and vaccination programs.

## Conflict of interest

The authors declare that there are no competing interests.

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