Analysis and Prediction of COVID-19 Outbreak by a Numerical Modelling

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Abstract

Pandemic COVID-19 is a contagious disease affecting more than 200 countries, territories, and regions. Recently, Iraq is one of the countries that have immensely suffered from this outbreak. The Kurdistan Region of Iraq (KRI) is also prone to the disease. Until now, more than 23,000 confirmed cases have been recorded in the region. Since the onset of the COVID-19 in Wuhan, based on epidemiological modelling, researchers have used various models to predict the future of the epidemic and the time of peak, yielding diverse numbers in different countries. This study aims to estimate the basic reproductive number [R_0] for COVID-19 in KRI, using the standard SIR (Susceptible-Infected-Removed) epidemic model. A system of nonlinear differential equations was formulated and solved numerically by the 4th order Runge-Kutta method. The reproductive numbers R_0 was estimated by the method of fitting the curves between the actual daily data and numerical solution by applying the least square method. For the analysis, data were taken for the duration of 165 days, from 1st of March to 12th August 2020, in a population of 5.2 million. It is concluded that the R_0 value was fluctuating during the outbreak, with an average of 1.33, predicting that infection cases will reach their maximum value of around 540,000 on the 5th of November 2020. Then, the spread of the disease will die out since the number of susceptible people will decrease to about 3.2 million. While the number of removed individuals will reach approximately to 1.5 million.

Keywords: COVID-19, Numerical Model, 4th order Runge-Kutta, SIR, Reproductive Number

تحليل وتنبؤ جائحة المرض COVID-19 بطريقة النمذجة العددية

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الخلاصة

انتشر جائحة مرض (COVID-19) في أكثر من 200 دولة وإقليم حول العالم. وفي الآونة الأخيرة ،
اصبح العراق أحد البلدان التي عانت بشدة من هذا المرض وكجزء من العراق تعرض أيضا إقليم كردستان
العراق (KRI) للإصابة بهذا المرض، حتى الآن حسب الاحصائيات تم تسجيل أكثر من 23000 حالة مؤكدة
في الإقليم منذ بداية ظهور (COVID-19) في مدينة وهان الصينية. و بناءاً على النمذجة الوبائية ، استخدم
الباحثون نماذج رياضية مختلفة للتنبؤ بمستقبل الوباء وتأريخ الوصول الى القمة. تهدف هذه الدراسة إلى تقدير
رقم التولد العددي (R_0) لـ (COVID-19) في إقليم كردستان العراق باستخدام نموذج الوباء القياسي SIR
[المعرض، المصاب والمزال]. تمت صياغة نظام المعادلات التفاضلية الغير الخطية وحلها عدديا بطريقة
Runge-Kutta من المرتبة الرابعة. تم تقدير رقم التولد العددي (R_0) بطريقة تنسيب المنحنيات بين البيانات
اليومية الفعلية والحل العددي من خلال استخدام طريقة المربع الادنى. للتحليل العددي ، تم أخذ البيانات لمدة
(165) يوما ابتداءا من 1 مارس إلى 12 أغسطس لعدد سكان يبلغ 5.2 مليون نسمة. وقد تم التوصل إلى أن
(R_0) تذبذبة بمتوسط حولي 1.33. واظهر التحليل العددي توقع أن تصل الحالات المصابة إلى 540000
مصاب في الخامس من نوفمبر 2020. وبعد ذلك سينخفض انتشار المرض بسبب تقليل الكثافة السكانية
المعرضين للإصابة إلى حوالي 3.2 مليون نسمة. بينما سيصل عدد الأشخاص الذين تمت شفائهم والذين
توفوا إلى ما يقرب 1.5 مليون نسمة.

Introduction

The coronavirus disease 2019 (COVID-19) is a contagious disease which can be transmitted through droplets, aerosols, and direct contact [1-3]. It is caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a novel coronavirus, which emerged in Wuhan during early December, 2019 [4, 5]. The symptoms of the infection include fever, cough, myalgia, fatigue, sputum production, headache, haemoptysis, diarrhoea, dyspnoea, and lymphopenia [6]. In more severe cases, COVID-19 can cause pneumonia and even death [7]. The incubation period is believed to extend to 14 days with a median time of approximately 5.2 days [8].

The COVID-19 has spread rapidly throughout the world as it has been found to have higher levels of transmissibility and pandemic risk than the SARS-CoV [9]. It has rapidly resulted in over 20 million confirmed cases and more than 750,000 deaths worldwide in less than 9 months [7]**.** Due to the sharp escalating level of spread on March 11, the World Health Organization (WHO) declared the COVID-19 outbreak as a global pandemic [10].

The epidemiological prediction based upon mathematical modelling plays a key role to understand the pathway of the epidemic and propose effective strategies in controlling the disease [11].
SIR is a commonly used model for the transmission of the disease from human to human [12]. SIR is considered to be one of the most reliable simple tools which consists of three compartments; susceptible, infected, and removed [11, 13, 14].
The basic reproduction number [R_0] is a measure to evaluate the transmissibility of the virus in a particular population. Sustainability of the transmission of the disease depends on R_0 value; when $R_0 > 1$, the disease is most likely developed to secondary cases. However, $R_0 \leq 1$ indicates that the secondary cases in the outbreak are declining [15].
SIR model has been used in several studies to analyse the spread of COVID-19 [16-18]. The evaluation of COVID-19 by modelling in KRI has not been conducted to predict the behaviour of the disease spreading. Therefore, in this study, a numerical model for predicting the outbreak has been used to estimate how the quarantine, easy restriction, and population mixing affect outbreak progression. Accordingly, the model paves the way for the authority in charge to manage measures-related policies which can control and eradicate the infection.

Materials and Methods

In this study, a coupled system of nonlinear differential equations derived by Kermack and McKendrick in 1927 [19] is used. The system consists of three differential equations based on the classification which divides the population into three compartments; Susceptible [S], Infected [I] and Removed [R], which is known as the SIR model, as shown in Figure 1. The interactions between the categories are controlled by a transmission rate [β] and recovery rate [γ].

Figure 1-Schematic diagram of SIR Model; S, susceptible; I, infected; R, removed; β, transmission rate and γ, recovery rate.

The independent variable is time [t] measured in days and the dependent variables are [S, I and R]. We consider three related sets of dependent variables. Equations 1, 2 and 3 are related to the rate of change of susceptible population, the rate of change of infected population, and the rate of change of removed population, respectively.

$$\frac{dS}{dt} = -\beta S(t)I(t) \tag{1}$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t) \tag{2}$$

$$\frac{dR}{dt} = \gamma I(t) \tag{3}$$

$$R_o = \frac{\beta}{\gamma} \tag{4}$$

Equation 4 represents the reproductive number [R_0], which is the key point to identify the epidemic occurrence and disease severity.

Assumptions

For simplifying the analysis, the following assumptions are made [20]:

1- The total population number [N] is constant, ignoring births, immigration, and natural death. Accordingly, the rate of change of [N] will be zero. This will lead to:

$$N = S + I + R \tag{5}$$

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{6}$$

2- The population is homogeneously distributed.

3- Recovered individuals become immune and, hence, remain in the removed compartment.

4- The removed compartment also includes the individuals who died from the disease.

Runge-Kutta 4th order method

The 4th order Runge-Kutta method for a system of differential equations has the following forms [21]:

$$S_{i+1} = S_i + \frac{1}{6}(K_1 + 2K_2 + 2K_3 + K_4)h \tag{7}$$

$$I_{i+1} = I_i + \frac{1}{6}(G_1 + 2G_2 + 2G_3 + G_4)h \tag{8}$$

$$R_{i+1} = R_i + \frac{1}{6}(L_1 + 2L_2 + 2L_3 + L_4)h \tag{9}$$

where:

$K_1 = f(t_i, S_i)$

$K_2 = f\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}K_1 h\right)$

$K_3 = f\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}K_2 h\right)$

$K_4 = f(t_i + h, S_i + K_3 h)$

$$G_1 = f(t_i, I_i)$$
$$G_2 = f\left(t_i + \frac{1}{2}h, I_i + \frac{1}{2}G_1 h\right)$$
$$G_3 = f\left(t_i + \frac{1}{2}h, I_i + \frac{1}{2}G_2 h\right)$$
$$G_4 = f(t_i + h, I_i + G_3 h)$$
$$L_1 = f(t_i, R_i)$$
$$L_2 = f\left(t_i + \frac{1}{2}h, R_i + \frac{1}{2}L_1 h\right)$$
$$L_3 = f\left(t_i + \frac{1}{2}h, R_i + \frac{1}{2}L_2 h\right)$$
$$L_4 = f(t_i + h, R_i + L_3 h)$$

In order to solve the system of equations 7 to 9 by applying the 4th order Runge-Kutta method, initial conditions are required. The data were obtained from the KRI official website [22] from 1/3/2020 to 12/8/2020. Taking the total population of KRI as N=5,200,000, $S=S[0]$, $I=I[0]=4$, $R[0]=0$. The model mainly depends on two parameters, namely [β], the transmission rate, and [γ], the recovery rate. Estimating the values of parameters is often a complicated task. Inaccurate parameters for estimating the model are less useful as a predictive tool, although it may still be possible to describe the general behaviour [19]. There are different approaches for estimating the parameters; the first one is to estimate parameters directly based on some experience. Since covid-19 is a new disease, it is difficult to adapt this approach. The second is to compare and fit actual data with a numerical solution by the method of trial and error, with the help of the least square method which has is in this study. The mentioned process of estimating the parameters is called calibrating the model [19].

Results

The results in Figure 2 show the number of infected individuals that were announced by the KRI, the Ministry of Health, for the period between 1st of March to 12th of August 2020 [22]. The number of confirmed cases started with 4 cases in the beginning of the outbreak in the region. In April, this number declined to its minimum value. While, at the start of May, the cases increased steadily, followed by a rocketed increase in June. Also, the number of infected cases increased from the first of August until preparing this article.
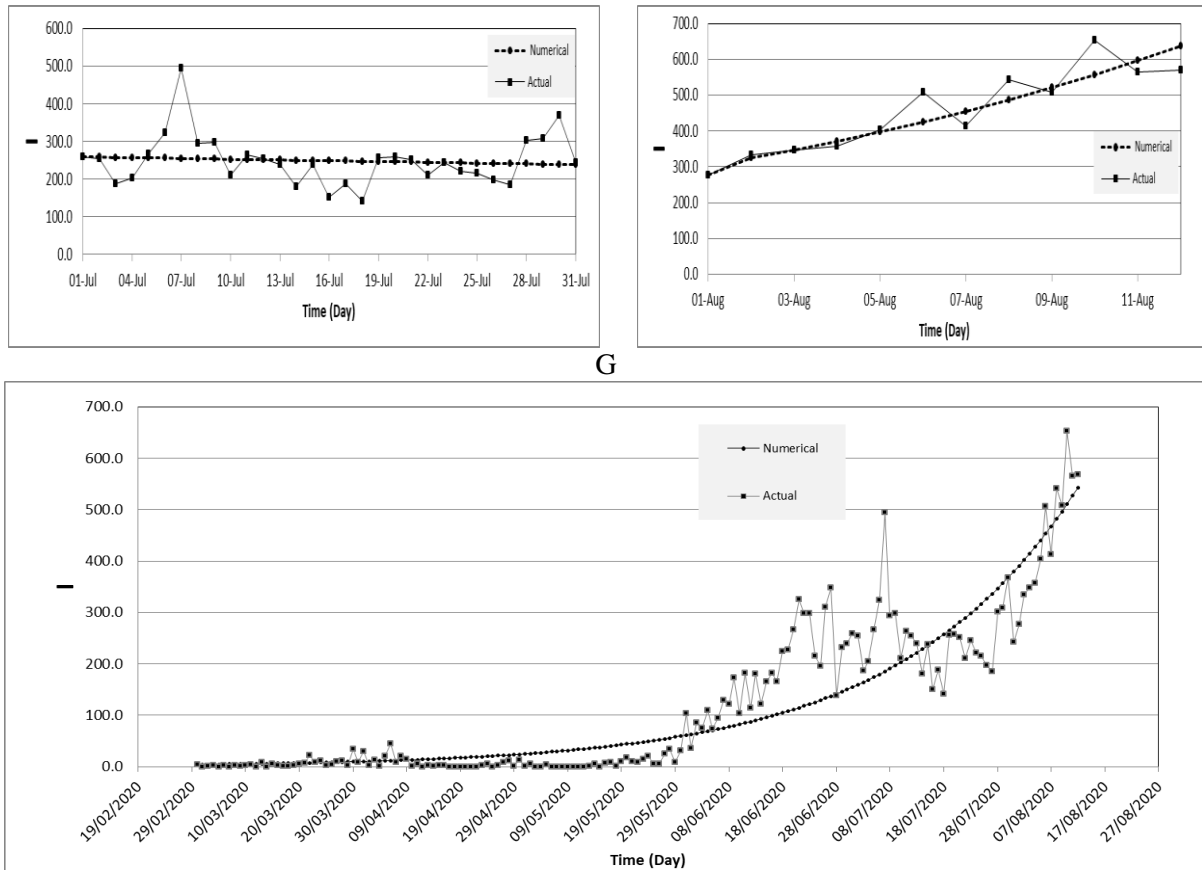

A

B

C

D

E

F

G
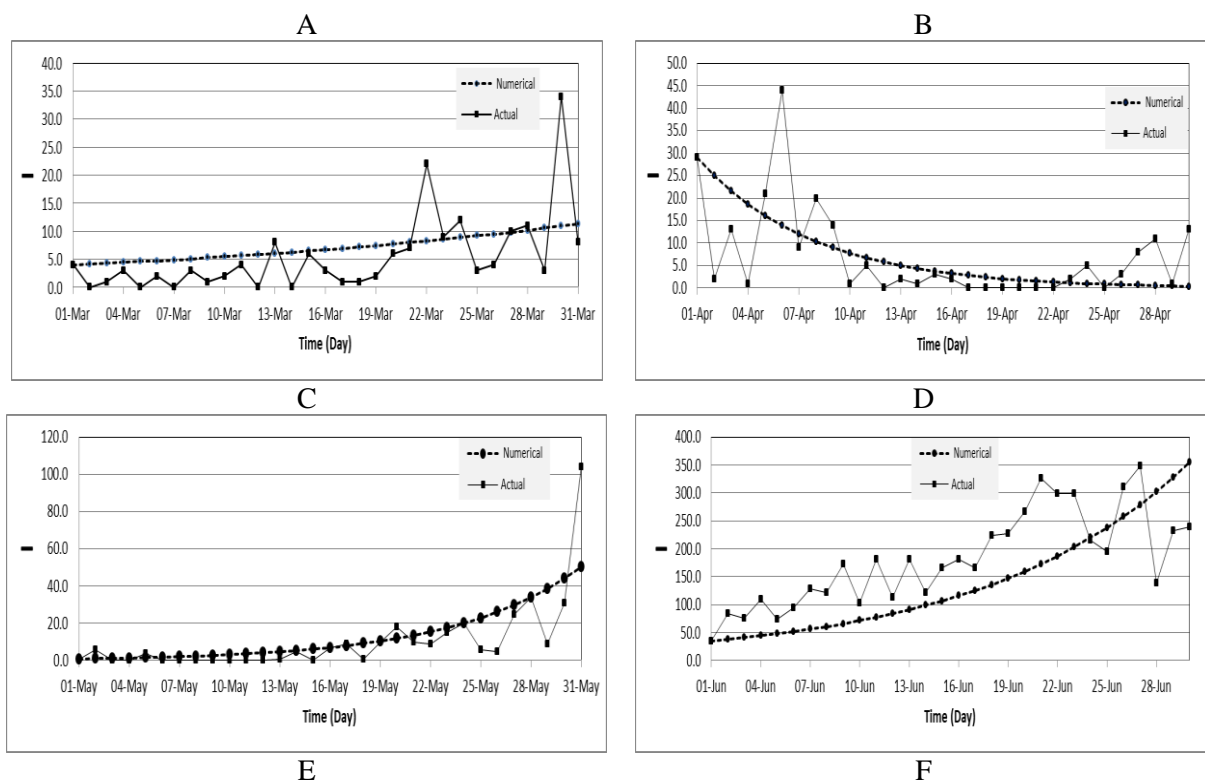
Figure 2-COVID-19 infected cases in KRI for the period from March to August 2020. X axis: Time [days], Y axis: number of infected cases. Monthly infected cases [A-F]: March [A], April [B], May [C] , June [D], July [E], August [F]. Total infected cases [G]. Actual monthly infected cases resembling the black line while the red line indicates the numerical results in KRI.

Figure -3 represents the results of R_0 value for each month as well as the whole period of the outbreak. April experienced the lowest value (0.063). May and June recorded the maximum values of 2.053 and 1.959, respectively. By using the overall data, the average R_0 value was estimated to be 1.327.
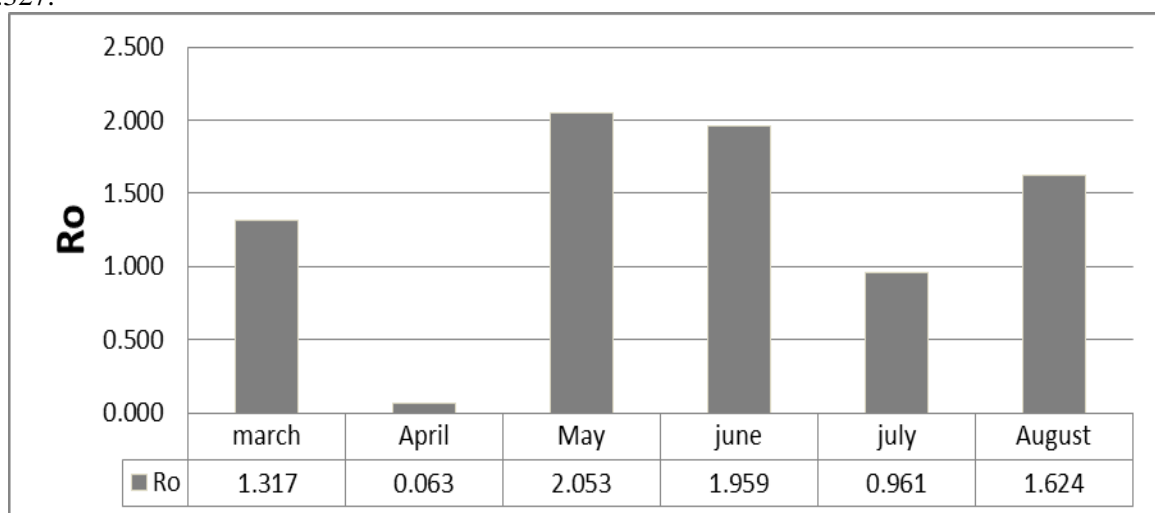

	march	April	May	june	july	August
■ Ro	1.317	0.063	2.053	1.959	0.961	1.624

Figure 3-The results of the basic reproduction number [R_0] during the outbreak of COVID-19 in KRI from the beginning of March until 12th of August 2020.

The general SIR model illustrated in figure 4 shows that the predicted infected cases will reach their maximum value of around 540,000 on the 5th of November 2020. Then, the spread of the disease

will die out since the number of the susceptible cases will decrease to about 3.2 million and the number of removed individuals will reach approximately to 1.5 million.
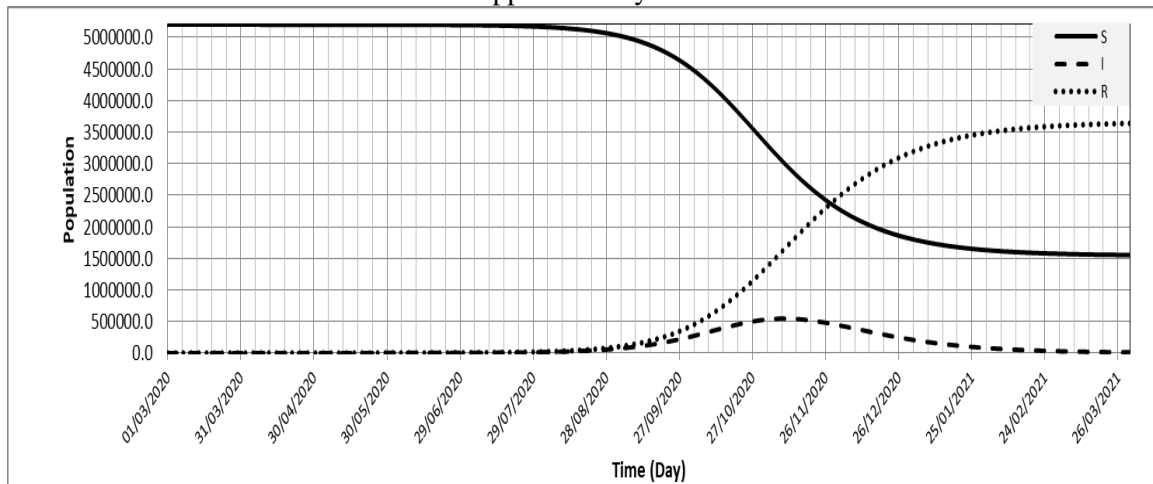

Figure 4-SIR model of prediction for COVID-19 outbreak in KRI [by using the mean of $R_0 = 1.327$]. X axis: Time [days], Y axis: population number. Blue line [S] resembles susceptible population, red line [I] represents infected cases, and green line [R] indicates removed population.

Discussion

The COVID-19 is spreading with astounding speed and it has severe consequences on health, economic, and social aspects. In the absence of population immunity, effective medicine, and vaccines, the spread of COVID-19 is still expanding exponentially in many countries. Numerical analysis will provide an early warning to the decision-making authority regarding the infected population and a prediction of the time frame for reaching the peak value. Also, it assists authorities to deal with measures amendment in a way fitting the dynamics of the spread of the disease [23, 24].

Numerical modelling has been revealed as a powerful tool to analyse disease behaviour and provide significant information for the authorities to take any necessary actions when needed. From the obtained results, the actual cases were compatible with the numerical analysis, due to the well-fitting characteristics of the used method [17]

In general, most models follow exponential growth. Surprisingly, due to the implementation of several restriction measures, the trend of numerical infected cases in April did not follow the exponential trend. Also, in July, due to high recovery rate, the curve remained nearly in a steady state. Similarly, Maier and Brockmann found that the exponential growth decreases by imposing restriction measures [25], which may lead to a proportional increase of the recovery cases.

Here, we estimated the R_0 in KRI from the beginning of COVID-19 attack and assessed the SIR model to predict the aftertime of the region in relation to COVID-19 disease. Data released by the Ministry of Health in KRI were used as a source for numerical modelling in this study. Based on these data, the estimated R_0 values during the time period of six months fluctuated between 0.063 and 2.053. As a consequence of strict restrictions which were implemented by KRI authority in April to contain the outbreak, the lowest estimated value of R_0 was recorded. While, the sudden and unplanned lifting of measures in May caused a dramatic increase in confirmed cases of COVID-19 [26], which resulted in a highest R_0. Studies also revealed that travel bans, border closing, lockdown, and social distancing are the most effective containment measures to enhance global readiness needed in response to COVID-19 [27]. The average of R_0 for the time period was around 1.33, which is approximately fit with WHO's declared lower value of 1.4-2.5 [28]. However, other studies estimated the maximum R_0 value to be around 6.7, with a similar minimum value to that found in our study [29]. R_0 values strongly are correlated with the implementation of COVID-19 restriction measures, which can be varied among different populations [30].

According to our data analysis, KRI has not reached the peak yet. It is estimated to reach the peak by the 5th of November 2020. However, the spread of the virus will gradually decrease, since the recovered population will increase and the number of susceptible individuals will decline. On the 26th

of November 2020, the number of susceptible individuals and recovered individuals will reach the same value.

Conclusions

In conclusion, the model can predict susceptible populations to SARS-CoV-2 infection along the time until the vaccine is available. The accuracy of the model depends on the quantity of confirmed data available. Therefore, it is important to increase the number of the diagnosis tests for the non-hospitalized population in the region and, as another source of data, use clinical manifestation-based technology of recording.

Conflict of interest

The authors declare no conflicts of interest.

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