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Estimation of the epidemiological model with a system of differential equations (SIRD) using the Runge-Kutta method in Iraq

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Abstract

In this paper, we will use the SIRD model to discuss the development of the Corona pandemic in Iraq; through a system of non-linear differential equations, we will use the (Runge-Kutta) method as a solution to the system of various non-linear equations such as the SIRD model, and the parameters used are based on This paper deals with confirmed cases of injury, recovery and deaths from the accurate data available for the period from (February 24, 2020) to (February 22, 2022), and we also present an estimate of the Basic Reproduction number (R_0) for the (SIRD) model.

Keywords: Ordinary Differential Equation, Solving differential equations, Runge-Kutta, epidemic, SIRD model, COVID-19
2020 MSC: 34A05

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1 Introduction

An epidemiological model (SIRD) with Ordinary Differential Equation (ODE) [15] was used. The mathematical principles on which epidemiological models are based are similar; they are based on an attempt to understand how individuals move between prominent cases and monitor the rate of transmission. Individuals are based on this basis and according to the model. The proposed (SIRD) [9, 11, 16, 18] is either exposed to infection and symbolized by the symbol (S), or infected and symbolized by the symbol (I), or the hospitalized and symbolized by the symbol (R) and will be clarified later, which contains fixed and time-varying parameters. The parameters in the model are conditional on the initial epidemic values; that is, it reflects the clinical development of the disease. The parameter that is usually identified and diagnosed in epidemiological models is the primary reproduction number (R_0) [4], which represents the number of people infected as a result of infection from an infected person, and the parameter (R_0) controls the speed of virus spread.

Epidemics have always been a source of great concern to the human race, like the Spread of the Black Death in Europe in the fourteenth century constituted about a third of the European population and the yellow fever epidemic in the United States in 1793. Furthermore, recent events remind us that epidemics represent a real problem for health

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institutions continuously facing emerging diseases. In (2020) [12] studied the patterns of the Spread of epidemic diseases such as the Coronavirus from mathematical modelling. In (2020) [15] used the (SIRD) and (Gaussian-SIRD) models to predict the trends of coronavirus disease (Covid-19) in Kuwait. In (2020) [8]. Using the SIRD model (susceptible - recovered - deceased). The official data of the epidemic in Italy was used to determine the parameters of this model. In (2020) [18] fitted an epidemiological model to the transmission dynamics of COVID-19) during a period. The values of the model parameters were estimated using the method of reducing the sum of error squares using the optimization algorithm (Levenberg-Marquardt), and the differential equations were solved in the proposed model using the method (Runge-Kutta) of the fourth degree. Moreover, in (2021) [10] proposed a modified version to analyze and predict the Spread of (COVID-19) from the differential model (SEIRD) (exposed to infection).

2 The (SIRD) model

It is a fragmented model used in epidemiology to design the Spread of disease. The model divides the population into four groups: (susceptible, infected, recovered, and dead) contains the mortality parameter.

Either the basic assumptions [7] on which the SIRD model is based are [17]:

1. The recovered people will no longer be susceptible to infection again.
2. The number of deaths due to other causes (causes other than infection or the disease under study) is neglected.
3. The area under study is closed and isolated from other areas, meaning that:

   $$S_t + I_t + R_t + D_t = \text{Constant}.$$

   Since: Constant represents the total population (N) which is closed. The size of the community is fixed (i.e. the area is affected by restrictions on movement, and sometimes with people not leaving their areas).
4. People are identical to each other (i.e., different demographic factors or health conditions are not considered), i.e. the population is homogeneously mixed.
5. The effect of the vaccination campaign does not depend.
6. Individual populations are randomly distributed over the area, allowing for a fixed identification of communication between those exposed to infection and the injured.
7. The virus kills about (α) of the infected individuals. The model can be described according to a globally effective scheme, as shown in Figure 1.

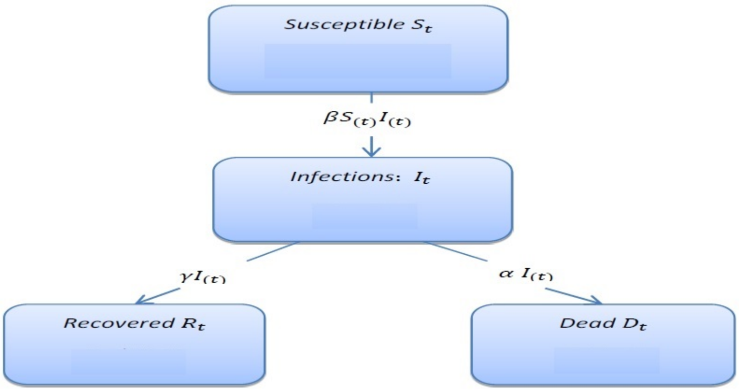

Figure 1:

The SIRD model is a dynamic system that consists of a set of differential equations (ODE) [14], and we can described through the following four equations [1, 6, 16]:

$$\frac{dS_{(t)}}{dt} = S'_t = -\frac{\beta}{N} S_{(t)} I_{(t)}, \tag{2.1}$$

$$\frac{dI_{(t)}}{dt} = I'_t = \frac{\beta}{N} S_{(t)} I_{(t)} - \gamma I_{(t)} - \alpha I_{(t)}, \tag{2.2}$$

$$\frac{dR_{(t)}}{dt} = R'_t = \gamma I_{(t)}, \tag{2.3}$$

and

$$\frac{dD_{(t)}}{dt} = D'_t = \alpha I_{(t)}. \tag{2.4}$$

The conditions for initial values [5] are as follows:

$$S_{(t=0)} = S_0 > 0 \quad I_{(t=0)} = I_0 > 0 \quad R_{(t=0)} = R_0 = 0 \quad D_{(t=0)} = D_0 = 0$$

Table 1: presents the description of the state variables and parameters of the SIRD model

code	**description**
S_t	Number of people exposed to infection at time t
I_t	Number of infected individuals at time t
R_t	The number of people recovered at the time t
D_t	The number of people death at time t
β	infection transmission rate
γ	Recovered rate
α	Death rate
N	The size of the population under study
β^{-1}	Average infection as a result of contact with an infected person
$(\gamma+\alpha)^{-1}$	The average time it takes an infected person to leave the injury category
R_0	The basic Reproduction number

3 Discrete-time SIRD model

[3] Equations (2.1) to (2.4) convert the system of Ordinary Differential Equations (ODE) to a system of discrete-time equations using ($\Delta t = 1$) and adding the finite difference system, resulting in the following equations [15]:

$$S_{(t+1)} = S_{(t)} - \frac{\beta}{N} S_{(t)} I_{(t)}, \tag{3.1}$$

$$I_{(t+1)} = I_{(t)} + \frac{\beta}{N} S_{(t)} I_{(t)} - \gamma I_{(t)} - \alpha I_{(t)} \tag{3.2}$$

$$R_{(t+1)} = R_{(t)} + \gamma I_{(t)}, \tag{3.3}$$

$$R_{(t+1)} = R_{(t)} + \alpha I_{(t)}, \tag{3.4}$$

and

$$\begin{bmatrix} S_{(t+1)} - S_{(t)} \\ I_{(t+1)} - I_{(t)} \\ R_{(t+1)} - R_{(t)} \\ D_{(t+1)} - D_{(t)} \end{bmatrix} = \begin{bmatrix} \Delta S_{(t)} \\ \Delta I_{(t)} \\ \Delta R_{(t)} \\ \Delta D_{(t)} \end{bmatrix} \tag{3.5}$$

The cumulative counter of confirmed cases at time (t) [3] can be expressed as follows:

$$C\Delta X = \sum_{i=0}^{t} \Delta X_{(t)} \tag{3.6}$$

where $X = I, R, D$ and

$\Delta X_{(t)}$: represents a vertical vector ($t \times 1$) that includes all new cases reported up to time (t),

$C\Delta X_{(t)}$: Represents a vertical vector ($t \times 1$) containing the cumulative numbers of confirmed cases up to time (t).

4 Basic Reproduction number (R_0)

The basic Reproduction number (R_0) is defined as the average number of susceptible individuals in a homogeneous population that an infected person will transmit at any given period of infection. This measure helps determine whether an infectious disease can spread between a group of individuals or not, in other words, the speed of infection spread, that is, a description of the nature of the Spread. The Basic Reproduction Number is extracted as follows [3, 8]:

$$R_0 = \frac{\beta}{\gamma + \alpha}. \tag{4.1}$$

It represents the basic Reproduction number at the beginning of the epidemic, as ($S \approx N$). The basic reproduction number at time (t) is extracted from the following equation:

$$R_{0(t)} = \frac{\beta}{\gamma + \alpha} S_{(t)}. \tag{4.2}$$

5 Estimation of the parameters

Parameters in dynamical systems is a broad field that includes many different properties of mathematical and statistical analysis, using Matlab ode45 software, a system of differential equations is solved with given initial values of parameters and state variables.

5.1 Solving differential equations

Solving differential equations is very important, as differential equations are mathematical tools of importance in many physical, engineering, social and economic issues and environmental phenomena. There are many ways to find the approximate numerical solution to the problem of exceptional values [10].

5.1.1 Rung Kota (R.K)

It is one of the most well-known iterative methods for approximating Ordinary Differential Equations (ODE). It is accurate and has better approximation properties than other methods. This method has been designed to increase the accuracy of the numerical solution to the system of various non-linear equations. This method is characterized by its ease because it does not require the calculation of higher derivatives. In order to obtain approximate estimates of the initial value problem, there are several formulas for this method, including the Runge- Kutta (R.K) method of the fourth degree, which is the most common. As the initial value problem is: by following the general scheme of the Rang-Kutta method for (z) from the stages, as follows [2, 10, 13]:

$$X(t_{n+1}) = X(t) + T \sum_{i=1}^{z} b_i K_i \tag{5.1}$$

where $X = (S, I, R, D)$: represents the state vector

b_i, c_i : represent the real coefficients.

$$\begin{aligned} K_1 &= f(t_n, x_n) \\ K_2 &= f(t_n + c_2 T, x_n + a_{21} T K_1) \\ &\vdots \\ K_z &= f(t_n + c_z T, x_n + a_{z1} T K_1 + a_{z2} T K_2 + \ldots + a_{z,z-1} T K_{z-1}) \end{aligned} \tag{5.2}$$

$$K_i = f\left(t_n + c_z T, x_n + T \sum_{j=1}^{i-1} a_{ij} K_j\right) \tag{5.3}$$

where:

$$i = 1, 2, 3, ..., z; \quad j = 1, ..., i-1,$$

a_{ij} : represents the coefficient matrix of the Rang Kota (R.K) method.

6 Data description

The data adopted in this paper is based on real recorded cases collected from (https://github.com/ CSSEGISand-Data) Which includes confirmed cases, recovery cases, and deaths due to infection with the Corona virus (COVID-19).

7 Results

Table 2 shows the results of the numerical solution using the (R.K) method in Iraq (12/2/2022).

Table 2:

β	γ	α	R_0	CFR	R_I^2	R_R^2	R_D^2
0.1255	0.13335	0.03114	0.99	0.04	0.9571	0.9583	0.9746

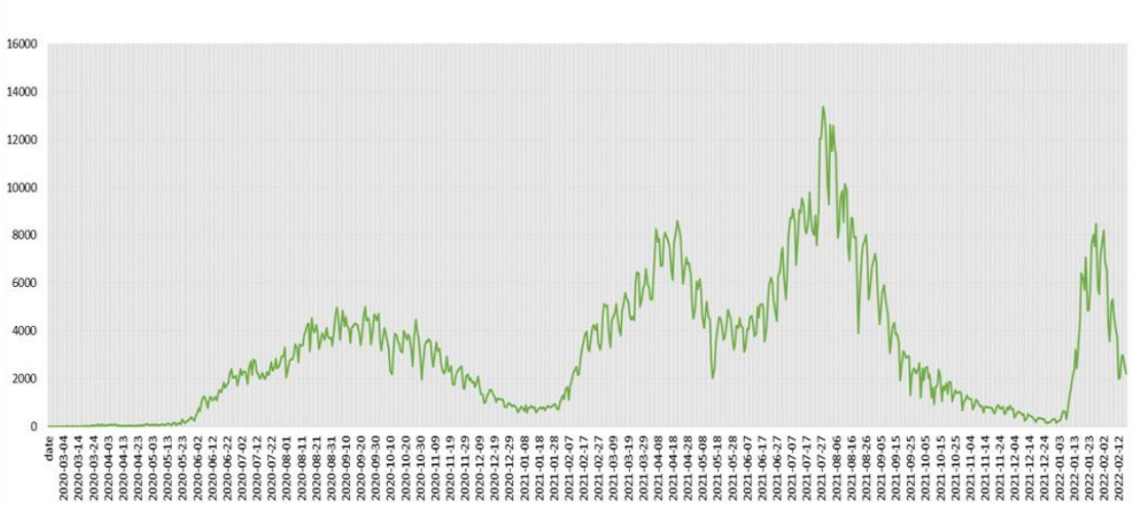

Figure 2: represents the scheme of the basic reproduction number as a function of time (t) according to (R.K) method for the period (4/3/2020) to (12/2/2022) in Iraq.

Calculating the coefficient of determination for the prescriptive variables of the SIRD model, as shown in table 2. The results of the (Runge-Kutta) method: the case rate, the contact rate, the cure rate and the death rate for Coronavirus (COVID-19) were calculated using the (Runge-Kutta) method in the (MatLab) program, and the results are based on the accurate data collected for Iraq, And the population size (N) represents the size of Iraq's population in the year (2020), as it reached (41756241). The initial values were used, and the cumulative number (total cases) was calculated daily from the epidemic's beginning to (12/2/2022).

The contact rate was (0.1255), as for the recovery rate, it amounted to (0.13335). In contrast, the deaths amounted to (0.03114). Through it, the primary reproduction number is calculated, whose value reached (0.99), which are values less than one, and through it, it becomes clear to us that the Coronavirus is stable and that Spread is reduced. And average infection as a result of contact with an infected person (7.968), the average time it takes an infected person to leave the injury category (6.0793). From Figure 2 we see the basic reproduction number extracted by (R.K) method, we see that the peak of the epidemic was on (6/8/2021).

8 Conclusion

It is possible that the analysis presented in this paper will be useful for gaining a general understanding of the evolution of the spread of the epidemic, as well as for predicting the variables of the SIRD model. Calculation of parameters also provides informative evolution of disease time series. And test the accuracy of the model.

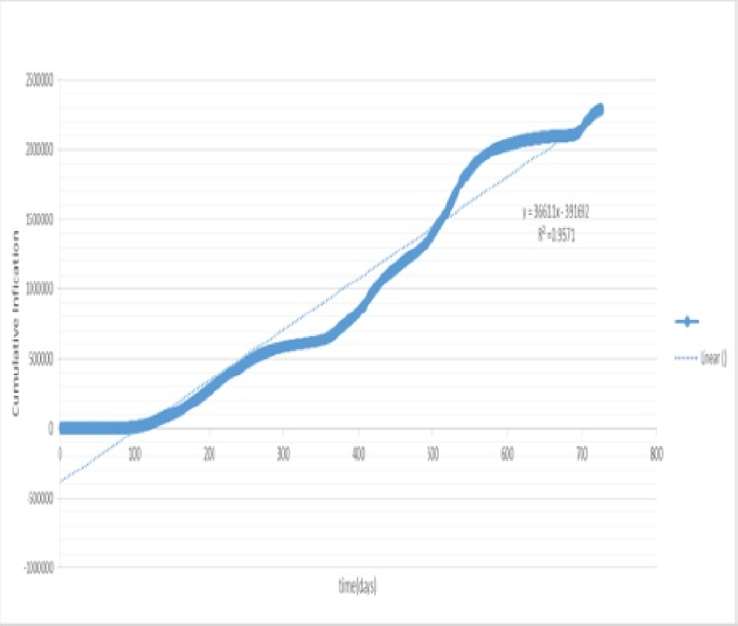

Figure 3: represents the cumulative numbers of people infected with Corona virus using the (R.K) method for the (SIRD) model until (2/2/2022), the starting date was (24/2/2020) with the appearance of the first case in Iraq.

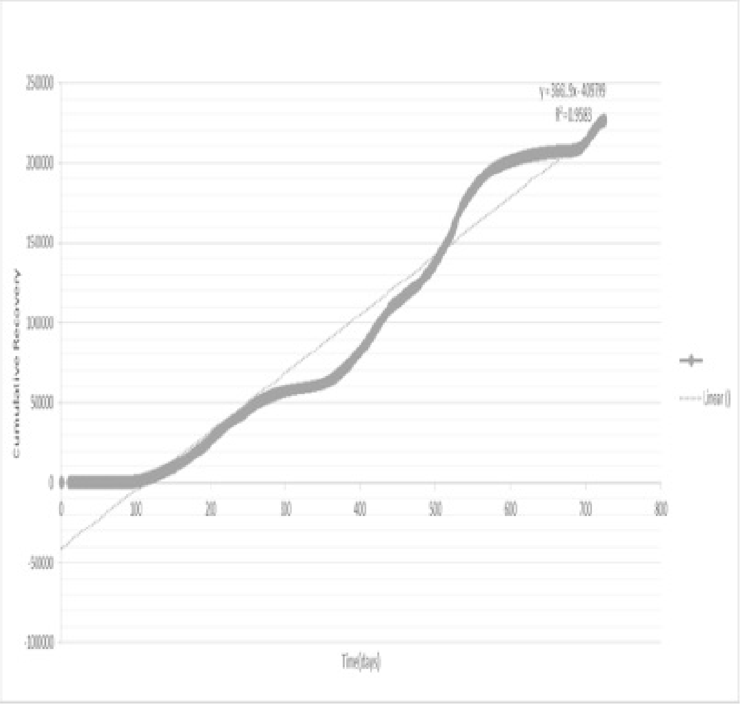

Figure 4: represents the cumulative numbers of patients with corona virus with the regression equation using the (R.K) method for the (SIRD) model until (2/2/2022) the starting date was (6/3/2020) the first case of recovery in Iraq.

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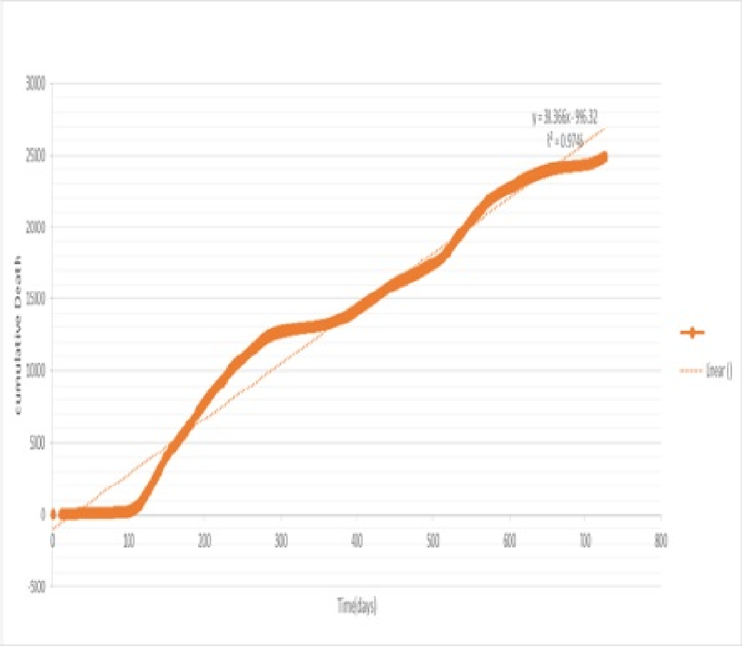

Figure 5: represents the cumulative numbers of deaths as a result of infection with the Corona virus using the (R.K) method for the (SIRD) model until (2/2/2022) the starting date was (4/3/2020) the first death in Iraq.

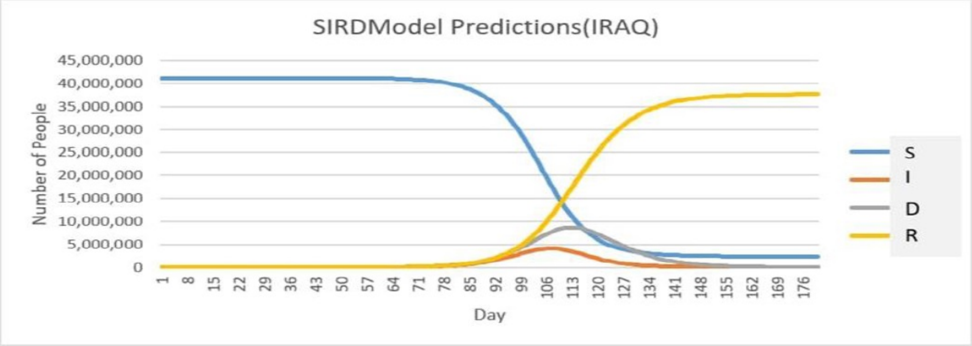

Figure 6: represents the numerical solution of the SIRD model to predict using the Rang Kota method. The number of individuals infected with Coronavirus (COVID-19) is represented by the curve in (red), as for the number of deaths resulting from infection in (black) and healing processes in (yellow) which is increasing significantly. While the color (blue) indicates the number of individuals exposed to infection, which is decreasing significantly.

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