Mathematical Modeling and Analysis for COVID-19 Model by Using Implicit-Explicit Rung-Kutta Methods

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ABSTRACT

One of the most common health care problems globally is COVID-19, and also there are an international effort to monitor it have been proposed and discussed. Despite the fact that many studies have been performed based on clinical evidence and confirmed infected cases. However, there is room for additional research since a range of complex criteria are included for later research forecast. As a consequence, mathematical modelling mixed with the numerical simulations is an effective method for estimating main propagation parameters and forecasting disease model dynamics. We study and present some models for the COVID-19 in this paper, which can answer significant questions concerning global health care and implement important notes. The IMEX Runge–Kutta and classical Runge–Kutta methods are two well-known computational schemes to find the solution for such system of differential equations. The results, which are based on these numerical procedures suggested and provide estimated solutions, provide critical answers to this global problem. The amount of recovered, infected, susceptible, and quarantined people in the expectation can be estimated using numerical data. The findings could also aid international efforts to increase prevention and strengthen intervention programs. The findings could also support international efforts to increase prevention and strengthen intervention programs. It is clearly that the proposed methods more accurate and works in a very large interval in time with a few step sizes. That is consequently beginning to a decrease in the computational price of the method. Numerical experiments show that there is a good argument and accurate solutions for solving this type of problem.

Keywords COVID-19, Mathematical model, Runge-Kutta method, Numerical simulation, Model dynamics, Comparison simulations.

1. Introduction

COVID-19 is a modern coronavirus that has expanded among humans and was 1st recognized in Wuhan, China. Furthermore, has presently expanded to 196 countries, today along with that the new version of this disease is appear. COVID-19 will be known as a respiratory illness that is transferred through communication by the infected body or by saliva droplets during somebody sneezes or coughs [1]. More specifically, the simple replication numbers R_0 for both Turkey and Iraq have been stated by [2, 3], and the estimate through 9 April 2020 confirmed that the value of R_0 for Iraq is 3.4 and the value of R_0 for Turkey is 7.4 [3]. Furthermore, according to daily pandemic data on the amount of approved new cases recorded from WHO, the number of new cases in Iraq on 29 May was 416 [6] also in Turkey on 11 April was 5138 [5], which can be recognized as the peak value behind the epidemic began.

It has since been designated a pandemic disease by the WHO. Governments all over the world are under pressure to avoid the spread of the disease. The WHO warned people to clean their hands regularly and rest at home if they can; if they must go out, they must wear a mask and gloves [4]. Investigators at Harvard Medical School, for instance, possess pulled up among a skilful organization to improve characteristic reagents. Furthermore, foreign assistance aids in the alleviation of medical supply shortages [5]. A few articles on the COVID-19 pandemic have recently been published. One of the most modern investigations focused on the control and prediction of covid-19, in which fascinating models based on the dynamics were practiced to reduce infection transmission in the three Indian countries [9]. Moreover, in the truancy of treatments or prosperous treatments in world, fascinating nations, such as Italy, South Korea and Brazil, offered measures for example city lock-downs with border protection and social isolation for helping

public solicitudes [10]. The Long-short term memory systems were defined previously [11]. It is dealt with in another report. The mathematical simulation of fourteen nonlinear FDEs [6] was introduced to show how the transference dynamics of disease happened in community. In addition, COVID-19 has been predicted in Brazil in a short-term analysis. However, producing short term forecasting models provide for a forecast of possible cases [7]. To return to the subject of prediction, it has been suggested that the scientific community work together to develop new and improved approaches, tactics, forecasting procedures, and diagrams to fully agree and decrease the consequences of that also expected pandemics [8].

At the same time, during a separate investigation, the optimal regression tree description has been used to recognize significant variables which have a significant impact on case fatality rates in various countries, including Canada, South Korea, India, United Kingdom and France [9]. COVID-19 mathematical modelling is working behind the scenes to better understand and forecast how infections spread. Mathematical models have been used to create a reduced description of disease developed in the community also to realize how a disease could raise in future. Certain estimates can support us to make more regular use of public health supplies such as vaccines, medications, interventions and preventions. Estimates of population parameters can be used to guide a simulation which combines individual case at the moment ere a statistically important variation among the innovative organizations is mentioned. A list of these simulations will provide researchers with a midpoint and sample size range that will enable them to test their hypothesis [10]. Since Covid-19 is a new virus that only arose in the last months of 2019, there are some magnificent studies on it. Moreover, some studies in this area have been suggested, they are inadequate. As an illustration, a thought was managed by Biao Tang. in [11]. Altaf Khan and Atangana, on the

other hand, suggested a model based on the premise that the seafood industry has enough sources of infection to infect people [12]. More modifications for the COVID-19 models can be found in [13-16].

While several mathematical models have been proposed for the prediction of new coronavirus diseases, some of them can still be improved. Numerical approaches may be used to determine some estimated solutions for this virus, which could help to boost forecasts and estimates. The IMEX Runge-Kutta methods for COVID-19 are a challenge that has yet to be investigated. In a complicated coronavirus model, it's critical to get more precise and widespread numerical results. Iraqi people who have been away in the last 14 days that must be quarantined for 14 days later the government declared a curfew for a long time also prevented journey among all Iraqi regions. In February,2020, the first case occurred in one of Iraq's provinces. Concerning to the WHO, the cases of Coronavirus has raised to 4848 since the outbreak began in April. Iraq had 169 coronavirus deaths at the time of the outbreak. When analysing infected coronavirus cases between May and March in Turkey, just some cases were approved, however the number of cases increased dramatically in May, to 158762, with 4397 deaths. This work contributes by analysing the COVID-19 model also determining the primary model components by using IMEX Runge-Kutta methods. This work's key contributions can be summarized as some points: the first point is COVID-19 has been studied and discussed in recently published articles. And the second one is the transmission rates are calculated using a collection of nonlinear differential equations. And the third point is to find numerical solutions for such equations, the IMEX Runge-Kutta methods are recommended. And the last point is according to numerical simulations, each quantity of infected people has regularly extended until April 2020, behind that marginally reduce after May 2020.

2. THE PROPOSED METHOD

High order implicit-explicit Runge Kutta (IMEX-RK) techniques are used for solving stiff problems. Whenever first-order IMEX-RK techniques have generally been applied to deals with the stiff terms of the chemistry implicitly in combustion simulations and hypersonic flow, two IMEX-RK techniques are fourth-order accurate. As a result, there have been several studies that have attracted much interest, and many numerical schemes, like the Euler method, Runge Kutta method, multistep schemes [17-20], Finite difference method [21,34-40], and Finite element methods [22-25], have been proposed over time. Consider the numerical form for the ordinary differential equations in the following system:

$$\frac{dx(t)}{dt} = F_{Im}(t, x(t)) + F_{Ex}(t, x(t)). \qquad (2.1)$$

Splitting the right-hand side of (2.1) into stiff and non-stiff is a key idea for the proposed process. An explicit Runge-Kutta (ERK) technique is applied for finding the solution for the non-stiff part $F_{Ex}(t, x(t))$ and a diagonally implicit Runge Kutta (DIRK) technique is manipulated for finding the solution for the stiff part $F_{Im}(t, x(t))$. A common s-stage implicit-explicit Runge-Kutta (IMEX-RK) technique involves an s-stage of both ERK and DIRK technique including the same weighting coefficients b_i, for $i = 1, 2, \dots, s$. An Implicit-Explicit Runge-Kutta scheme to the system (2.1) will be of the follow form [26, 27].

c_1	a_{11}	0	0	$\cdots$	0
c_2	a_{21}	a_{22}	0	$\cdots$	0
c_3	a_{31}	a_{32}	a_{33}	$\cdots$	0
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$
c_s	a_{s1}	a_{s2}	a_{s3}	$\cdots$	a_{ss}
	b_1	b_2	b_3	$\cdots$	b_s

$\hat{c}_1$	0	0	0	$\cdots$	0
$\hat{c}_2$	$\hat{a}_{21}$	0	0	$\cdots$	0
$\hat{c}_3$	$\hat{a}_{31}$	$\hat{a}_{32}$	0	$\cdots$	0
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$
$\hat{c}_s$	$\hat{a}_{s1}$	$\hat{a}_{s2}$	$\hat{a}_{s3}$	$\cdots$	0
	b_1	b_2	b_3	$\cdots$	b_s

The explicit and implicit components are indicated by the letters (Ex) and (Im). The Implicit-Explicit scheme, defined by its Butcher coefficients $(A^{[Ex]}, A^{[Im]}, b^{[Ex]}, b^{[Im]}, c^{[Ex]}, c^{[Im]})$ will be of the form:

$$x^{n+1} = x^n + \Delta t \sum_{i=1}^{s} \left(b_i^{[Im]} k_i^{[Im]} + b_i^{[Ex]} k_i^{[Ex]} \right), (2.2)$$

where $k_i^{[Im]}$ and $k_i^{[Ex]}$ are the discrete counterparts of the stiff and nonstiff operators respectively in (2.2), F_{Im} and F_{Ex},

$$k_i^{[Im]} = F_{Im}(t_i + c_i \Delta t, x_i(t)),$$
$$k_i^{[Ex]} = F_{Ex}(t_i + c_i \Delta t, x_i(t)),$$

and the values of the stages are as follows:

$$x_i = x^n + \Delta t \sum_{j=1}^{s} \left(a_{ij} k_i^{[Im]} + \hat{a}_{ij} k_i^{[Ex]} \right). \qquad (2.3)$$

The above expression, using DIRK schemes for the implied part, gives

$$x_i = x^n + \Delta t \sum_{j=1}^{i-1} \left(a_{ij} k_i^{[Im]} + \hat{a}_{ij} k_i^{[Ex]} \right) + \Delta t a_{ii} k_i^{[Im]}. (2.4)$$

In order to deal with the case of a linearly implicit case, we use

$$(I - \Delta t a_{ii} K) x_i = x^n + \Delta t \sum_{j=1}^{i-1} \left(a_{ij} k_i^{[Im]} + \hat{a}_{ij} k_i^{[Ex]} \right), (2.5)$$

3. THE SUGGESTED COVID-19 COMPARTMENT MODEL

The current coronavirus outbreak has turned into a worldwide health-care issue. Some procedures for managing the disease have been announced, for example limiting communications as much as they can also advising people to stay at home. The benefit of using the mathematical models for this virus are in demonstrating model dynamics and forecasting the number of infected people for the prospect. In the result, the model included compartments for quarantine, isolation (hospitalization) and treatment [11]. That model has recently been revised to include a time-dependent dynamic system [16].

In Figure (1), we establish the model diagram as well as the interaction individual components and their interaction rates. Exposed E, susceptible S, pre-symptomatic A, symptomatic I, quarantine exposed E_q, quarantine susceptible S_q, recovered R and hospitalized H are the eight classes (individuals) in the model.

For the recorded situations in China, that model initial populations and interaction parameters were obtained. Table (1) and Table (2) lists all parameter values and the initial populations respectively. The estimated values were specified first in [11] and then modified in [16]. In our numerical simulations, we mostly followed reference [28, 29], and we used those values. Based on the COVID-19 model that suggested in [28, 29] the model diagram described in Figure (1), and for more simplifications we introduce new variables $\{x_i : i = 1,2,3,\dots,8.\}$, so we suppose that $x_1 = S, x_2 = E, x_3 = I, x_4 = A, x_5 = S_q, x_6 = E_q, x_7 = H$, and $x_8 = R$, then the model parameters, and variables with their definitions and estimating values are given in Table (1) and Table (2) respectively.
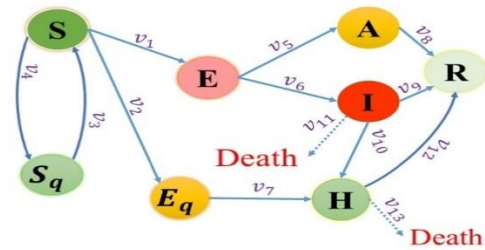

Fig. 1. COVID-19 transmission model structure[28, 29].

Table 1: The Model parameters with their estimating values[28, 29].

Parameters	Biological definition	Values
k_1	Contact rate.	14.782
k_2	Possibility of transmitting per contact.	2.1011×10^{-8}
k_3	Exposure rate of those who have been quarantined.	1.8887×10^{-7}
k_4	Individuals who have been exposed to the virus are more likely to become sick.	$\frac{1}{7}$
k_5	The multiplier of A to I transmissibility.	0.3
k_6	The rate for which uninfected contacts who had been quarantined were released into the broader community.	$\frac{1}{14}$
k_7	Infected individuals' chances of developing symptoms.	0.86834
k_8	Symptomatic infected people's transfer levels to quarantined infected people's class.	0.13266
k_9	Transition rate from quarantined exposed to quarantined contaminate. .individuals	0.1259
k_{10}	Symptomatic infected individual's recovery rate.	0.33029
k_{11}	Asymptomatic infected individual's recovery rate.	0.13978
k_{12}	Infected individuals who have been quarantined recovery rate.	0.11624
k_{13}	Death rate due to disease.	1.7826×10^{-5}

Table 2: The Model populations(variables) with their estimating initial values[28, 29].

Following[28, 29] and replacing the logistic model, the system of nonlinear differential equations of the Figure (1) based on mass action law can be defined as follows:

$$\frac{dx_1}{dt} = k_6 x_5 - k_1 x_1 (x_3 + k_5 x_4)\big(k_2(1 - k_3) + k_2 k_3 + k_3(1 - k_2)\big),$$

$$\frac{dx_2}{dt} = k_1 k_2 (1 - k_3) x_1 (x_3 + k_5 x_4) - x_2 (k_5(1 - k_7) + k_4 k_7),$$

$$\frac{dx_3}{dt} = k_4 k_7 x_2 - (k_{10} x_3 + k_8 x_3 + k_{13} x_3),$$

$$\frac{dx_4}{dt} = k_5(1 - k_7) x_2 - k_{11} x_4, \qquad (3.1)$$

$$\frac{dx_5}{dt} = k_1 k_3 (1 - k_2) x_1 (x_3 + k_5 x_4) - k_6 x_5,$$

$$\frac{dx_6}{dt} = k_1 k_2 k_3 x_1 (x_3 + k_5 x_4) - k_9 x_6,$$

$$\frac{dx_7}{dt} = k_9 x_6 + k_8 x_3 - (k_{12} x_7 + k_{13} x_7),$$

$$\frac{dx_8}{dt} = k_{11} x_4 + k_{10} x_3 + k_{12} x_7.$$

Based on Table (2) the initial populations can be expressed as follows:

$$x_1(0) = x_1^0 > 0, \quad x_2(0) = x_2^0 > 0, \quad x_3(0) = x_3^0 > 0,$$
$$x_4(0) = x_4^0 > 0, x_5(0) = x_5^0 \geq 0, \quad x_6(0) = x_6^0 \geq 0,$$
$$x_7(0) = x_7^0 \geq 0, x_8(0) = x_8^0 \geq 0. \qquad (3.2)$$

The Eq. (3.1) is a non–linear system of differential equations that cannot be solved analytically. As a result, the computational techniques proposed in this paper might be able to provide some approximations for the COVID-19 model states. We calculate numerical predictions in MATLAB using the initial populations and estimated parameters mentioned in Table (2) and Table (1). Only biological methods are also insufficient to comprehend the high-dimensional models of infectious disease transmission. Mathematical approaches and mathematical models are also useful techniques for properly interpreting model states and making numerical predictions.

4. IMPLICIT–EXPLICIT (IMEX) RUNGE KUTTA METHOD

This section aims to solve the model equations of COVID-19 applying the high-order IMEX-RK techniques. This can be gained by recalling (3.1) and,

for brevity's part, writing it as

Variables	Biological definition	Initial population values
$x_1(0)$	Initial susceptible individuals.	11.081×10^6
$x_2(0)$	Individuals that were first revealed.	105.1
$x_3(0)$	Infected individual who was symptomatic. at first	27.679
$x_4(0)$	Initial pre-symptomatic infected individuals.	53.839
$x_5(0)$	Initial quarantined susceptible individuals.	739
$x_6(0)$	Initial quarantined exposed individuals.	1.1642
$x_7(0)$	initial individuals that were hospitalized.	1
$x_8(0)$	Initial individuals that were recovered.	2

$$F_{Im}(t, x(t)) = \begin{bmatrix} k_6 x_5 \\ -x_2(k_5(1 - k_7) + k_4 k_7) \\ k_4 k_7 x_2 - (k_{10} x_3 + k_8 x_3 + k_{13} x_3) \\ k_5(1 - k_7) x_2 - k_{11} x_4 \\ -k_6 x_5 \\ -k_9 x_6 \\ k_9 x_6 + k_8 x_3 - (k_{12} x_7 + k_{13} x_7) \\ k_{11} x_4 + k_{10} x_3 + k_{12} x_7 \end{bmatrix},$$

$$F_{Ex}(t, x(t)) = \begin{bmatrix} -k_1 x_1(x_3 + k_5 x_4)\big(k_2(1 - k_3) + k_2 k_3 + k_3(1 - k_2)\big) \\ k_1 k_2 (1 - k_3) x_1 (x_3 + k_5 x_4) \\ 0 \\ 0 \\ k_1 k_3 (1 - k_2) x_1 (x_3 + k_5 x_4) \\ k_1 k_2 k_3 x_1 (x_3 + k_5 x_4) \\ 0 \\ 0 \end{bmatrix}.$$

Consider the system (3.1), and replacing preceding equations in (3.1), this leads us to

$$\frac{dx}{dt} = F_{Im}(t, x(t)) + F_{Ex}(t, x(t)), \qquad (4.1)$$

where

$$x(t) = [x_1(t)\ x_2(t)\ x_3(t)\ x_4(t)\ x_5(t)\ x_6(t)\ x_7(t)\ x_8(t)]^T,$$

A key idea for the proposed method is to split the right-hand side of (4.1) into stiff $F_{Im}(t, u(t))$ and nonstiff $\big(F_{Ex}(t, u(t))\big)$.

c_1	1/4	0	0	0	0
c_2	0.34114705729739	1/4	0	0	0
c_3	0.80458720789763	−0.07095262154540	1/4	0	0
c_4	−0.52932607329103	1.15137638494253	−0.80248263237803	1/4	0
c_5	0.11933093090075	0.55125531344927	−0.1216872844994	0.20110104014943	1/4
	0.11933093090075	0.55125531344927	−0.1216872844994	0.20110104014943	1/4

and

$\hat{c}_1$	0	0	0	0	0

$\hat{c}_2$	0.39098372452428	0	0	0	0
$\hat{c}_3$	1.09436646160460	0.33181504274704	0	0	0
$\hat{c}_4$	0.14631668003312	0.69488738277516	0.46893381306619	0	0
$\hat{c}_5$	−1.33389883143642	2.90509214801204	−1.06511748457024	0.27210900509137	0
	0.11933093090075	0.55125531344927	−0.1216872844994	0.20110104014943	1/4

Algorithm 1 IMEX-RK(5, 4, 4)
1: Input x_0,no of stages, no of iterations, Time
2: Put $h = $ Time/no of iterations
3: The matrices $A^{[E]}$, $A^{[I]}$, $b^{[E]}$ and $b^{[I]}$ can be obtained in the Butcher Table.
4: **for** n = 0 : (no of iterations) $- 1$ **do**
5:   accum1 $\leftarrow x_n$
6:   **for** $i = 0$: (no of stages) $- 1$ **do**
7:     accum2 $\leftarrow x_n + h \cdot (A^{[I]}_{ij} \cdot \mathbf{F}_{Im}(:, \mathbf{u}_n))$.
8:     **for** $j = 0$: $(i - 1)$ **do**
9:       accum2 $\leftarrow$ accum2$+h \cdot (A^{[Im]}_{ij} \cdot k^{[Im]}_j + A^{[Ex]}_{ij} \cdot k^{[Ex]}_j)$.
10:     **end do**
11:     $k^{[Im]}_i \leftarrow F_{Im}(:, $ accum2$)$.
12:     $k^{[Ex]}_i \leftarrow F_{Ex}(:, $ accum2$)$.
13:     accum1$\leftarrow$ accum1$+h \cdot (b^{[Im]}_i \cdot k^{[Im]}_i + b^{[Ex]}_i \cdot k^{[Ex]}_i)$.
14:   **end do**
15:   $x_{n+1} \leftarrow$ accum1.
16: **end do**

5. NUMERICAL EXPERIMENTS

The aim of this section is to explain the performance of a presented method using a Matlab programming implementation. For solving (3.1) and (4.1), the IMEX - RK (4, 5, 5) and the classical Runge Kutta method ERK4 are used, where 4 is the order of the scheme and 5 is the number of steps implicit and explicit schemes.
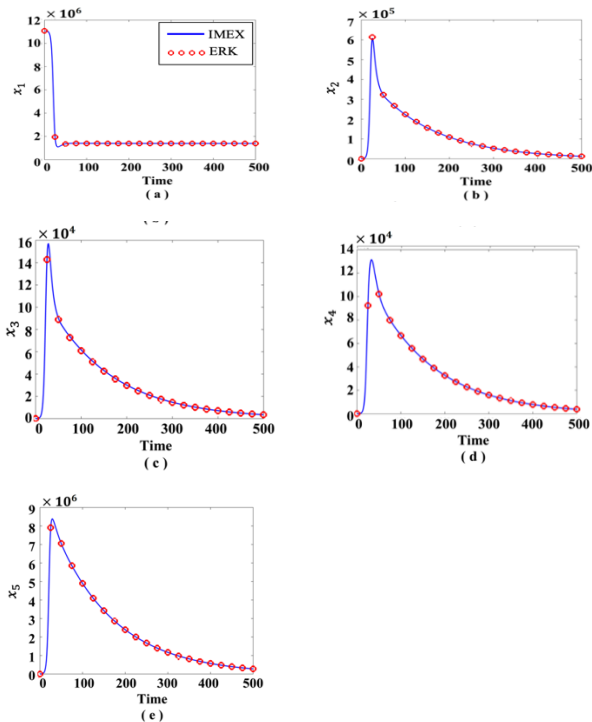

Fig. 2. Numerical approximate solutions for COVID-19 model Eq. (3.1) using IMEX-RK method of order four (IMEX-RK (4,5,5)) and classical RK of order four (ERK4); (a): the number of susceptible populations x_1, (b): the number of exposed populations x_2, (c): the number of symptomatic populations x_3, (d): the number of pre-symptomatic populations x_4. (e): the number of quarantine susceptible populations x_5.

Table 3: Comparing results by using IMEX-RK (4,5,5) and ERK4 methods for x_1, and x_2 compartments.

Time	ERK4 $h = 0.01$		IMEX-RK (4,5,5) $h = 1$	
	x_1	x_2	x_1	x_2
0	1.1081e7	105.1	1.1081e7	321240
50	1335988	323469	1356499	222716
100	1393144	223929	1402766	155988
150	1393100	156616	1397655	109198
200	1393100	109537	1395255	76417.9
250	1393100	76610.3	1394100	53466.7
300	1393100	53581.2	1393544	37403.2
350	1393100	37474.7	1393288	26163.2
400	1393100	26209.8	1393155	18299.7
450	1393100	18331.1	1393088	12799.0
500	1393100	12820.8	1393055	105.1

Table 4: Comparing results by using IMEX-RK (4,5,5) and ERK4 methods for x_3, and x_4 compartments.

Time	ERK4 $h = 0.01$		IMEX-RK (4,5,5) $h = 1$	
	x_3	x_4	x_3	x_4
0	27.679	53.839	27.679	53.839
50	88961.5	102160.0	90257.9	102766.0
100	60940.6	66686.4	61704.6	66986.8
150	42622.3	46641.4	43125.5	46839.1
200	29810.0	32621.0	30146.4	32752.5
250	20849.1	22815.1	21076.4	22903.2
300	14581.9	15956.9	14736.5	16016.1
350	10198.6	11160.2	10304.3	11200.2
400	7132.88	7805.48	7205.5	7832.5
450	4988.74	5459.15	5038.72	5477.43
500	3489.12	3818.13	3523.58	3830.51

Here, we used two numerical approaches to describe the COVID-19 model dynamics. In this analysis, IMEX-RK and classical Runge–Kutta methods are used. The National Health Commission for Republic to the China (WHO) situation report shown in[11, 16] provided the initial populations and parameter values for this analysis. Table (1) and Table (2) summarizes the approximate values. Figures (2) and (3) show how we used MATLAB to measure the numerical results for the model Eq. (3.1) for initial populations and several parameters. As a result, the population model states have a distinct model dynamic. The results of this research, which are focused on theoretical simulations, are a significant step ahead in divining

potential model dynamics to the community projects, therapies, also health-care procedures. The numerical estimates for the number of symptomatic infected, susceptible exposed,

Table 5: Comparing results by using IMEX-RK (4,5,5) and ERK4 methods for x_5, and x_6 compartments.

Time	ERK4		IMEX-RK (4,5,5)	
	$h = 0.01$		$h = 1$	
	x_5	x_6	x_5	x_6
0	739.0	1.1642	739.0	1.1642
50	7056211	0.083811	7047822	0.0835313
100	4897644	0.055706	4895500	0.0555338
150	3425444	0.038957	3425555	0.0388761
200	2395755	0.027247	2396522	0.0272075
250	1675599	0.019056	1676400	0.0190367
300	1171911	0.013328	1172577	0.0133176
350	819631	0.009321	820118	0.0093156
400	573250	0.006519	573584	0.0065158
450	400931	0.004559	401151	0.0045572
500	280411	0.003189	280550	0.0031873

Table 6: Comparing results by using IMEX-RK (4,5,5) and ERK4 methods for x_7, and x_8 compartments.

Time	ERK4		IMEX-RK (4,5,5)	
	$h = 0.01$		$h = 1$	
	x_7	x_8	x_7	x_8
0	1	2	1	2
50	115085	2059944	115346	2047899
100	73989.6	4365344	74086.5	4357900
150	51737.9	5965411	51801.0	5960600
200	36185.4	7084499	36226.6	7081400
250	25308.1	7867177	25334.7	7865211
300	17700.5	8414588	17717.5	8413366
350	12379.7	8797444	12390.5	8796699
400	8658.37	9065211	8665.12	9064777
450	6055.66	9252499	6059.82	9252244
500	4235.33	9383477	4237.84	9383355

and pre-symptomatic infected individuals are shown in Figure (2). It is clearly that the numerical methods suggested are in good agreement, and the number of susceptible exposed become more stable after 50 days, meanwhile the number of symptomatic infected, and pre-symptomatic infected individuals are become decreasing after 50 days. Furthermore, as t ϵ [0, 70], the dynamics of quarantine susceptible and hospitalized people start shifting and become flatter. On the other hand, after t > 40, the number of quarantined individuals stabilizes rapidly, however,

the amount of recovered people rises slightly and stabilizes slowly, as shown in Figure (3).

6. CONCLUSION

Global programs are focusing on and discussing a variety of health-care methods for preventing the spread of the latest coronavirus in the population. As can be shown, this virus has the potential to become a public health threat, spreading quickly among individuals. There are also several programs and preventative measures in place as part of global initiatives to minimize the COVID-19's global effects. Mathematical modeling is one of the theoretical tools that can be used to make a broad range of predictions and estimates about this problem. Computational simulations combined with mathematical modelling include model predictions and define key critical parameters.

Confirmed cases and clinical data in Wuhan are applied to the model of COVID-19. Moreover, the differential equations of this model are nonlinear that needs numerical solutions. On the basis of the reported cases, we used IMEX-RK and classical Runge–Kutta schemes to evaluate the approximations for every model state. These are a big step forward in terms of identifying model basic elements and improving the model in the future. The results of computational work could help global attempts to lessen the number of people that have been infected with the virus and to restrict this coronavirus from spreading within the community. The dynamics of each compartment are analysed, and the results show that it is possible to foretell and examine the population of all model state. They proposed method [28] for solving this type of problem has some disadvantages due to stability. We address this challenge by employing Implicit Explicit Runge kutta method. This scheme can be provided another significant step forward in understanding model dynamics and predicting disease transmission in the population. Another interesting of this scheme is to use a small sample in the population instead of the

large sample. This is consequently managing to a decrease within the computational expense and save data.

The findings of that work indicated that healthcare operations must focus more on the original model parameters. This model can be estimated by using finite element methods see [35-39].

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