



## Comparison of Some Numerical Simulation Techniques for COVID-19 Model in Iraq

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Article history: Received 20 July 2022, Accepted 24 October 2022, Published in July 2023.

[doi.org/10.30526/36.3.2945](https://doi.org/10.30526/36.3.2945)

### Abstract

The aim of our study is to solve a nonlinear epidemic model, which is the COVID-19 epidemic model in Iraq, through the application of initial value problems in the current study. The model has been presented as a system of ordinary differential equations that has parameters that change with time. Two numerical simulation methods are proposed to solve this model as suitable methods for solving systems whose coefficients change over time. These methods are the Mean Monte Carlo Runge-Kutta method (MMC\_RK) and the Mean Latin Hypercube Runge-Kutta method (MLH\_RK). The results of numerical simulation methods are compared with the results of the numerical Runge-Kutta 4th order method (RK4) from 2021 to 2025 using the absolute error, which proves that the MLH\_RK method is the best and closest to the expected values. The results have been discussed after being tabulated and represented graphically. Epidemic behavior for the next two years until 2025 has been projected using the proposed methods.

**Keywords:** Epidemic models, Coronavirus (COVID-19) model, Runge-Kutta method, Simulation process, Numerical simulation techniques.

### 1. Introduction

Coronavirus disease (COVID-19) is a new pandemic disease that began to appear in China, specifically in the city of Wuhan, and then spread rapidly around the world. This epidemic represented a global health problem, so some solutions and suggestions are discussed and studied to limit its spread as well as control it. Although, there are many researchers that have talked about this epidemiological model, studying its effects and the speed of its spread, as well as the number of people infected due to this epidemic and the extent of its impact in the future [1], The spread of



the coronavirus began in 2019-2020, and this new disease is considered as a type of (SARS-COV) and has the fastest spread compared to other viruses [2]. Specifically, it quickly and suddenly spread around the world on 29<sup>th</sup> March 2020 [3, 4]. The World Health Organization declared that this disease is a pandemic after spreading to 199 countries, as it first appeared in China in the city of Wuhan, and in early 2020, thousands of people died around the world [5]. The infection of this virus occurred unevenly in terms of damage, according to immunity and adherence to health prevention methods [5]. The spread of this virus has continuously led to great damage in most of the countries that have been affected. This has a significant impact on both global health and economic movement [6]. A large number of people have been infected with this epidemic as a result of mixing, interaction, and constant movement, just as some countries suffer from a lack of adherence to health prevention methods and a large number of them die. Some countries have adhered to the system of spacing, and A curfew was imposed for a specified period of time to limit the spread of the disease [7].

The epidemic model is the one that deals with a disease that spreads suddenly and rapidly and occupies large areas of society. These epidemiological models can be formulated as a system of nonlinear differential equations, and this epidemic model is considered a stochastic-deterministic model [8, 9]. Many researchers have studied analyzing the behavior of the epidemic and observing it over time to see whether it grows or settles in the population exposed to it. The SIR epidemic model was considered by the Banach contraction method, the Daftardar-Jafari method, and the Temimi-Ansari method [10]. LTAM was discussed for the first time to apply to the epidemic nonlinear model; this method is a merge of the Laplace transform with Tamimi and the Ansari iterative method [11]. The study's findings for the COVID-19 SIR epidemic model were designed with stochasticity in mind in order to eradicate the epidemic in Iraq [12]. To analyze the behavior of smoking habits, the Adomian decomposition method, variational iteration method, finite difference method, and Runge-Kutta method were used [13]. In addition, the Adomian decomposition method and variation iteration method were used for alcohol consumption [14]. Some researchers use the numerical Runge-Kutta method to analyze the behavior of obesity [15], smoking habits [13], influenza [16], and COVID-19 [17]. On the other hand, there are those who are interested in studying epidemiological models that have random coefficients and using suitable numerical simulation methods to solve them, such as [18-21].

The numerical method in this study is the Runge-Kutta method for the 4<sup>th</sup> order. It is considered one of the most efficient numerical methods for solving ordinary differential equations of different orders. High accuracy using this method can be achieved with order four to decrease the errors [22] and [9]. Four stages are considered in this method of order four [23]. Two numerical simulation methods are used, the first being the Mean Monte Carlo Runge-Kutta method (MMCRK), which is a reliable numerical simulation technique that merges two methods of different natures together in this study: the Monte Carlo simulation process (MC) and the Runge-Kutta method (RK) that are used to solve ordinary differential equations. Mahdi A. S. and Maha A. M. in 2019 discussed a modified numerical simulation technique for solving nonlinear epidemic models [19]. The second numerical simulation method is Mean Latin Hypercube Runge-Kutta (MLHRK). MLHRK is a numerical simulation method that is a mixture of the simulation method Latin Hypercube (LH) and the numerical method Runge-Kutta (RK). It is one of the reliable methods to solve such systems. Shatha J. M. and Maha A. M. (2021) studied the Mean Latin Hypercube Runge Kutta method to solve the influenza model. Emad T. G. and Maha A. M. discussed applying a suitable approximate-

simulation technique to the COVID-19 epidemic model with random parameters in 2022; see [20] and [21].

## 2. Mathematical Model of COVID-19

The mentioned model has been successfully used to study the people vaccinated against the COVID-19 epidemic in Iraq [24]. The population consists of five types of individuals  $S, V, A, I$  and  $R$  represent susceptible, vaccinated, asymptomatic, symptomatic, and the recovery respectively. These Individuals are functions according to time in the system. The governing equations for the epidemic under study are the nonlinear first-order ordinary differential equations [25].

$$\begin{aligned}
 S'(t) &= M - \tau S - \frac{\alpha(1+\beta A)S}{N} - \mu S + \gamma R, \\
 V'(t) &= \tau S - \frac{\rho\alpha(1+\beta A)V}{N} - \mu V, \\
 A'(t) &= \frac{\alpha(1+\beta A)S}{N} + \frac{\rho\alpha(1+\beta A)V}{N} - \delta A - \mu A, \\
 I'(t) &= \theta\delta A - \sigma I - \mu I \\
 R'(t) &= (1 - \theta)\delta A + \sigma I - \gamma R - \mu R,
 \end{aligned} \tag{1}$$

where **Tables 1** and **2** represent subpopulation  $S, V, A, I, R$  as the variables of model (1), and parameters  $M, \tau, \alpha, \beta, \mu, \gamma, \rho, \delta, \theta$  and  $\sigma$ . System (1) have the initial conditions for the system obtained from the World Health Organization website for Iraq data [4] as the folwing:

$S(0) = 500, V(0) = 30, A(0) = 36, I(0) = 24$  and  $R(0) = 10$ , with the predicted parameters that are given in **Table 2**.

**Table 1** Variables of COVID-19 model [25].

Variable	Definition
$S(t)$	People who are not infected but are vulnerable not to have immunity
$V(t)$	People vaccinated against coronavirus
$A(t)$	People infected with the virus without showing any symptoms
$I(t)$	Infected people have clear symptoms of infection in their bodies
$R(t)$	People who have recovered from the coronavirus or who died because of coronavirus infection

**Table 2** Parameters of COVID-19 model [25].

Parameter	Definition	Value	Source
$\alpha$	The rate of transmission people who are infected with this virus	0.8883	[26]
$\beta$	Correction factor for the rate of transmission of people without infection	0.45	[26]
$\mu$	The rate of natural death	0.00003349 day	[26]
$\gamma$	The rate of immunity	0.005	Assume
$1 - \rho$	The Vaccine efficacy and potency	0.8	Assume
$1/\delta$	The average period without symptoms of infection	7 days	[27]
$\theta$	The proportion of people does not show the effects of the symptoms of the virus, but it develops into a state of infection	0.2	[27]
$1 - \theta$	The proportion of individuals who recover but are asymptomatic	0.8	[27]
$M$	The Birth rate in the community	1500/day	Assume
$\tau$	The Vaccination rate against the virus	0.01 day	Assume
$1/\sigma$	The average rate of people recovering from infection with the virus	10 days	Assume

### 3. Numerical Method for Solving Covid-19 Model

RK4 is one of the numerical iterative methods with high accuracy. The nonlinear system (1) for the COVID-19 model can be solved by RK4 with the mentioned initial conditions. The general form of RK4 is:

$$y_{i+1} = y_i + \frac{h}{6}(l_1 + 2l_2 + 2l_3 + l_4), \tag{2}$$

where

$$\begin{aligned} S_{i+1} &= f(t_i, S_i, V_i, A_i, I_i, R_i), \\ &= S_i + \frac{1}{6}(lS_1 + 2lS_2 + 2lS_3 + lS_4) * h, \end{aligned} \tag{3}$$

$$\begin{aligned} V_{i+1} &= f(t_i, S_i, V_i, A_i, I_i, R_i), \\ &= V_i + \frac{1}{6}(lV_1 + 2lV_2 + 2lV_3 + lV_4) * h, \end{aligned} \tag{4}$$

$$\begin{aligned} A_{i+1} &= f(t_i, S_i, V_i, A_i, I_i, R_i), \\ &= A_i + \frac{1}{6}(lA_1 + 2lA_2 + 2lA_3 + lA_4) * h, \end{aligned} \tag{5}$$

$$\begin{aligned} I_{i+1} &= f(t_i, S_i, V_i, A_i, I_i, R_i), \\ &= I_i + \frac{1}{6}(lI_1 + 2lI_2 + 2lI_3 + lI_4) * h, \end{aligned} \tag{6}$$

$$\begin{aligned} R_{i+1} &= f(t_i, S_i, V_i, A_i, I_i, R_i), \\ &= R_i + \frac{1}{6}(lR_1 + 2lR_2 + 2lR_3 + lR_4) * h, \text{ for all } i = 1, 2, \dots, m. \end{aligned} \tag{7}$$

Now, the first iteration  $lS_1, lV_1, lA_1, lI_1$  and  $lR_1$  can be found as follows:

$$lS_1 = f_1(t_i, S_i, V_i, A_i, I_i, R_i), \tag{8}$$

$$lV_1 = f_1(t_i, S_i, V_i, A_i, I_i, R_i), \tag{9}$$

$$lA_1 = f_1(t_i, S_i, V_i, A_i, I_i, R_i), \tag{10}$$

$$lI_1 = f_1(t_i, S_i, V_i, A_i, I_i, R_i), \tag{11}$$

$$lR_1 = f_1(t_i, S_i, V_i, A_i, I_i, R_i). \text{ for all } i = 0, 1, \dots, m. \tag{12}$$

Also, the second iteration  $lS_2, lV_2, lI_2, lQ_2$  and  $lR_2$ , in the same way, is given as follows:

$$lS_2 = f_2\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_1, V_i + \frac{1}{2}h * lV_1, A_i + \frac{1}{2}h * lA_1, I_i + \frac{1}{2}h * lI_1, R_i + \frac{1}{2}h * lR_1\right), \tag{13}$$

$$lV_2 = f_2\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_1, V_i + \frac{1}{2}h * lV_1, A_i + \frac{1}{2}h * lA_1, I_i + \frac{1}{2}h * lI_1, R_i + \frac{1}{2}h * lR_1\right), \tag{14}$$

$$lA_2 = f_2\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_1, V_i + \frac{1}{2}h * lV_1, A_i + \frac{1}{2}h * lA_1, I_i + \frac{1}{2}h * lI_1, R_i + \frac{1}{2}h * lR_1\right), \tag{15}$$

$$lI_2 = f_2\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_1, V_i + \frac{1}{2}h * lV_1, A_i + \frac{1}{2}h * lA_1, I_i + \frac{1}{2}h * lI_1, R_i + \frac{1}{2}h * lR_1\right), \tag{16}$$

$$lR_2 = f_2\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_1, V_i + \frac{1}{2}h * lV_1, A_i + \frac{1}{2}h * lA_1, I_i + \frac{1}{2}h * lI_1, R_i + \frac{1}{2}h * lR_1\right). \tag{17}$$

for all  $i = 0, 1, \dots, m$ .

To get the third iteration,  $lS_3, lV_3, lA_3, lI_3$  and  $lR_3$ , follow the same way:

$$lS_3 = f_3\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_2, V_i + \frac{1}{2}h * lV_2, A_i + \frac{1}{2}h * lA_2, I_i + \frac{1}{2}h * lI_2, R_i + \frac{1}{2}h * lR_2\right), \tag{18}$$

$$lV_3 = f_3\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_2, V_i + \frac{1}{2}h * lV_2, A_i + \frac{1}{2}h * lA_2, I_i + \frac{1}{2}h * lI_2, R_i + \frac{1}{2}h * lR_2\right), \tag{19}$$

$$lA_3 = f_3\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_2, V_i + \frac{1}{2}h * lV_2, A_i + \frac{1}{2}h * lA_2, I_i + \frac{1}{2}h * lI_2, R_i + \frac{1}{2}h * lR_2\right), \tag{20}$$

$$lI_3 = f_3\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_2, V_i + \frac{1}{2}h * lV_2, A_i + \frac{1}{2}h * lA_2, I_i + \frac{1}{2}h * lI_2, R_i + \frac{1}{2}h * lR_2\right), \tag{21}$$

$$lR_3 = f_3\left(t_i + \frac{1}{2}h, S_i + \frac{1}{2}h * lS_2, V_i + \frac{1}{2}h * lV_2, A_i + \frac{1}{2}h * lA_2, I_i + \frac{1}{2}h * lI_2, R_i + \frac{1}{2}h * lR_2\right). \tag{22}$$

for all  $i = 0, 1, \dots, m$ .

To obtain the fourth iteration,  $lS_4, lV_4, lA_4, lI_4$  and  $lR_4$ , follow this:

$$lS_4 = f_4(t_i + h, S_i + h * lS_3, V_i + h * lV_3, A_i + h * lA_3, I_i + h * lI_3, R_i + h * lR_3), \tag{23}$$

$$lV_4 = f_4(t_i + h, S_i + h * lS_3, V_i + h * lV_3, A_i + h * lA_3, I_i + h * lI_3, R_i + h * lR_3), \tag{24}$$

$$lA_4 = f_4(t_i + h, S_i + h * lS_3, V_i + h * lV_3, A_i + h * lA_3, I_i + h * lI_3, R_i + h * lR_3), \tag{25}$$

$$lI_4 = f_4(t_i + h, S_i + h * lS_3, V_i + h * lV_3, A_i + h * lA_3, I_i + h * lI_3, R_i + h * lR_3), \tag{26}$$

$$lR_4 = f_4(t_i + h, S_i + h * lS_3, V_i + h * lV_3, A_i + h * lA_3, I_i + h * lI_3, R_i + h * lR_3). \tag{27}$$

for all  $i = 0, 1, \dots, m$ .

We substitute Eqs. (8), (13), (18) and (23) into Eq. (3) to find the numerical solutions of  $S_i$ . Also, we put Eqs. (9), (14), (19) and (24) into Eq. (4) to achieve the numerical solutions of  $V_i$ . In the same manner, we substitute Eqs. (10), (15), (20) and (25) into Eq. (5) to obtain the numerical solutions of  $A_i$  and substitute Eqs. (11), (16), (21) and (26) into Eq. (6) to find the numerical solutions of  $I_i$ . Finally, we substitute Eqs. (12), (17), (22) and (27) into Eq. (7) to get the numerical solutions of  $R_i$ , for all  $i = 0, 1, \dots, m$ .

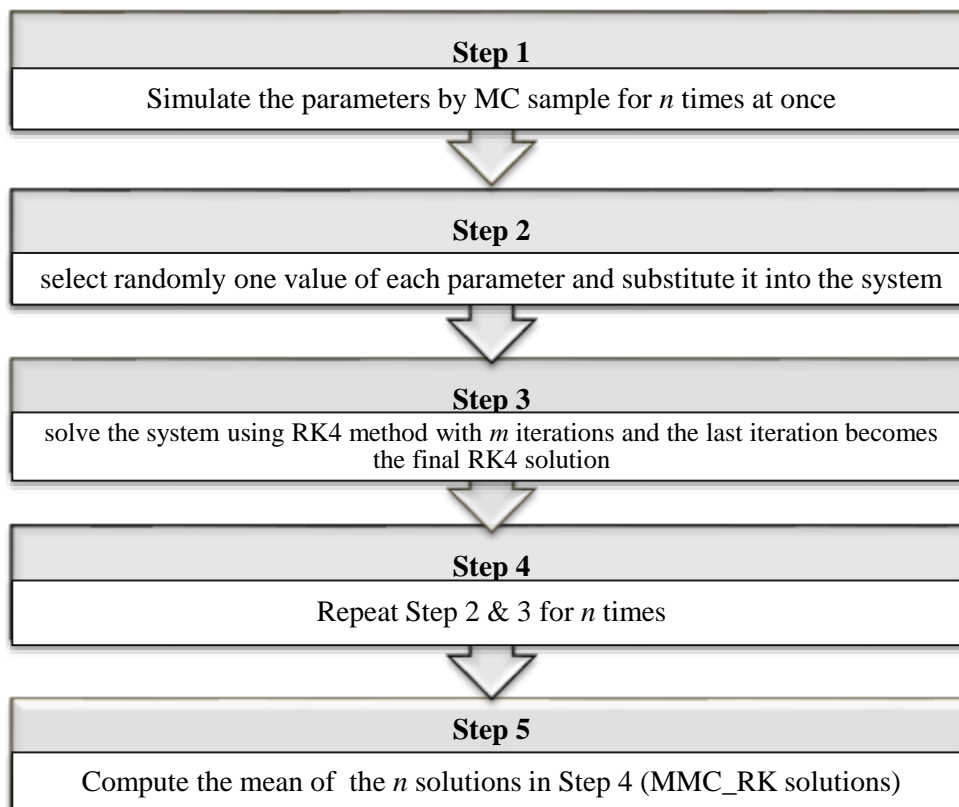
#### 4. Numerical Simulation Methods for Solving Covid-19 Model

##### 4.1 Mean Monte Carlo Range-Kutta (MMC\_RK)

Mean Monte Carlo Runge-Kutta (MMC\_RK) is an efficient numerical simulation method for solving such mathematical models under study. This method consists of mixing two different methods, one numerical, the Runge-Kutta method (RK), with the Monte Carlo simulation process (MC). MC estimates the model coefficients that are random variables, while RK is used to solve the model numerically. The average of the last RK iteration resulting from each MC repetition is considered the estimated approximate solution for the model under study.

Because the natural epidemic models have randomness in their coefficients, the MMC\_RK numerical simulation process is considered as more suitable method than the classical methods like RK4 that solve models depending on fixed parameters. The MMC\_RK method is explained in **Fig 1** and implemented by using MATLAB software. More details are shown in [19].

##### MMC\_RK Procedure

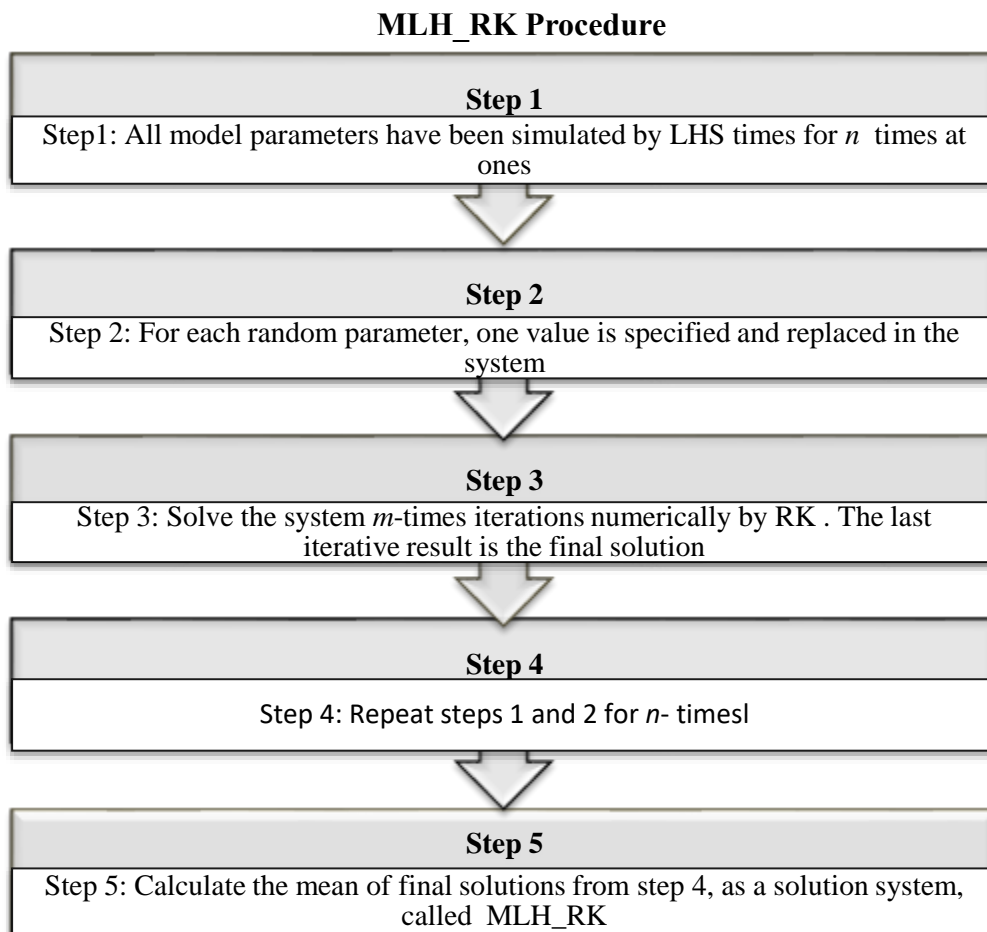


**Figure 1:** Steps of MMC\_RK process, [19].

#### 4.2 Mean Latin Hypercube Runge-Kutta (MLH\_RK)

Mean Latin Hypercube Runge-Kutta (MLH\_RK) is a numerical simulation method that is a mixture of a numerical method called Latin Hypercube (LH) and a numerical method called Runge-Kutta (RK). This method is implemented via the Matlab program, and more details are shown in [20]. LH estimates the coefficients of the model, which are considered random variables; MC estimates the model coefficients; and RK is used to solve the model numerically. The average of the last RK iteration results with each LH repetition is considered the estimated approximate solution for the model under study.

Everything we talked about before the method MMC\_RK applies to the method MLH\_RK. In addition to that, the MLH\_RK method is more accurate and faster than the MMC\_RK method because it simulates all model parameters at once. It also saves time and effort. **Fig 2** explains the MLHRK in greater detail.



**Figure 2:** Steps of MLH\_RK process, [20].

5. Results and Discussion

Numerical and numerical simulation solutions of the nonlinear of COVID-19 epidemic model in Iraq have been discussed and analyzed in this section. In this study, the real step size has been used such that  $h=0.02$  in a week, (52 weeks in a year, the data of the COVID-19 epidemic is taken from each week; therefore, in order to change the weeks to a months, the real step size is calculated as  $h = \frac{1}{52} \approx 0.02$ ) and  $h=0.08$  in a month, (12 month in a year, the data of the COVID-19 epidemic is taken from each month; therefore, in order to change the months to a year, the real step size is calculated as  $h = \frac{1}{12} \approx 0.08$ ).

**Table 3.** Numerical and numerical simulation results of COVID-19 model from 2021 to 2022

Model Variables	Step Size, $h$ (weekly & monthly)	Number of Iteration, $m$ (weekly & Monthly)	RK4 (1 years)	MMC_RK 100 rep. (1 years)	MLH_RK 100 rep. (1 years)
<b>S(t)</b>	0.08 (monthly)	150	111.2080	112.0276	112.02304
	0.02 (weekly)	600	111.6410	111.9771	111.9769
<b>V(t)</b>	0.08 (monthly)	150	46.2424	45.3405	47.1184
	0.02 (weekly)	600	46.2938	45.3136	47.0938
<b>A(t)</b>	0.08 (monthly)	150	198.0505	198.4761	198.4017
	0.02 (weekly)	600	197.6970	198.0655	197.9236
<b>I(t)</b>	0.08 (monthly)	150	38.2352	37.9597	38.6755
	0.02 (weekly)	600	36.0473	35.8729	36.1012
<b>R(t)</b>	0.08 (monthly)	150	205.2406	205.7047	205.4156
	0.02 (weekly)	600	205.6102	206.3006	205.3439

**Table 4.** Expected numerical simulation results of COVID-19 model from 2021 to 2025

Model Variables	Step Size, $h$ (weekly & monthly)	Number of Iteration, $m$ (weekly & monthly)	RK4 (4 years)	MMC_RK 100 rep. (4 years)	MLH_RK 100 rep. (4years)
<b>S(t)</b>	0.08 (monthly)	600	45.3077	45.7295	45.1721
	0.02 (weekly)	2400	45.4914	45.7972	45.3906
<b>V(t)</b>	0.08 (monthly)	600	34.9403	35.5509	35.3254
	0.02 (weekly)	2400	34.8710	35.6280	35.1763
<b>A(t)</b>	0.08 (monthly)	600	13.5280	13.7776	13.2342
	0.02 (weekly)	2400	13.4236	13.7370	13.4793
<b>I(t)</b>	0.08 (monthly)	600	9.3148	9.3368	9.3201
	0.02 (weekly)	2400	9.2985	9.3130	9.2956
<b>R(t)</b>	0.08 (monthly)	600	500.1596	500.4997	499.8646
	0.02 (weekly)	2400	500.4212	500.7103	500.4103



**Table 5.** Prediction intervals (5th percentile, 95th percentile) for MMC\_RK and MLH\_RK solutions

MMC_RK from 2021 to 2025 ( $t \leq 48$ )		
Subpopulation	(100 repetitions)	(1000 repetitions)
$S(t)$	(34.4889 , 56.9510)	(33.7740 , 58.7899)
$V(t)$	(22.5928 , 57.1467)	(22.0591 , 55.9641)
$A(t)$	(7.3331 , 21.2286)	(7.8735 , 20.6545)
$I(t)$	(5.0933 , 13.9210)	(5.5697 , 14.6953)
$R(t)$	(447.8911 , 628.1435)	(449.8386 , 628.6205)
MLH_RK from 2021 to 2025 ( $t \leq 48$ )		
Subpopulation	(100 repetitions)	(1000 repetitions)
$S(t)$	(35.4277 , 59.8350)	(33.5215 , 57.8323)
$V(t)$	(26.3581 , 56.7235)	(24.0661 , 56.6104)
$A(t)$	(6.4966 , 17.3059)	(6.5912 , 17.6509)
$I(t)$	(4.2058 , 12.3463)	(4.7953 , 12.5404)
$R(t)$	(414.8612 , 578.4889)	(410.9803 , 570.2245)

**Table 6.** Absolute error for MMC\_RK and MLH\_RK with RK4 from 2021 to 2022.

Model Variables	Step Size, $h$ (weekly & monthly)	Iterations (months)	MMC_RK	MLH_RK
$S(t)$	0.08 (monthly)	12	0.8196	0.81504
	0.02 (weekly)		0.3361	0.3359
$V(t)$	0.08 (monthly)	12	0.9019	0.8760
	0.02 (weekly)		0.9802	0.8000
$A(t)$	0.08 (monthly)	12	0.4256	0.3512
	0.02 (weekly)		0.3685	0.2266
$I(t)$	0.08 (monthly)	12	0.2755	0.04403
	0.02 (weekly)		0.1744	0.0539
$R(t)$	0.08 (monthly)	12	0.4641	0.1750
	0.02 (weekly)		0.6904	0.2663

**Table 7.** Absolute error  $E_h = \left| T_h - T_{\frac{h}{2}} \right|$  for MMC\_RK and MLH\_RK from 2021 to 2025

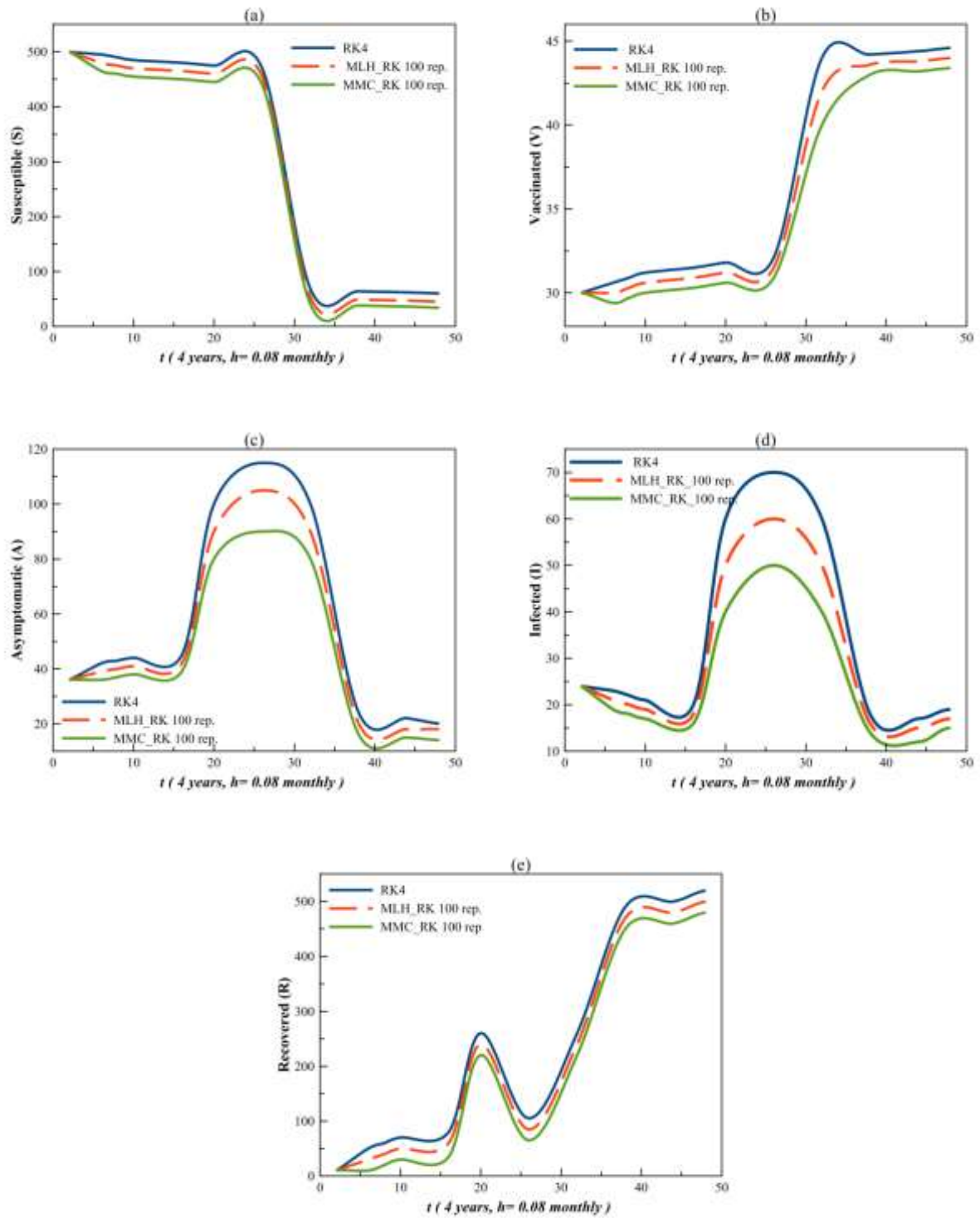
Model	Step Size, $h$		$E_h\text{-MMC\_RK}$	$E_h\text{-MLH\_RK}$
Variables	(weekly & monthly)	Number of Iterations	100 rep. (4 years)	100 rep. (4 years)
$S(t)$	0.08 <b>monthly</b>	600	0.045088	0.107386
	0.08/2	1200	0.022554	0.111144
	0.08/4	2400	0.019704	0.103381
$V(t)$	0.08 <b>monthly</b>	600	0.088598	0.109317
	0.08/2	1200	0.104216	0.039814
	0.08/4	2400	0.073518	0.029403
$A(t)$	0.08 <b>monthly</b>	600	0.027061	0.157000
	0.08/2	1200	0.013543	0.048095
	0.08/4	2400	0.010381	0.010124
$I(t)$	0.08 <b>monthly</b>	600	0.011903	0.010215
	0.08/2	1200	0.011887	0.014358
	0.08/4	2400	0.011402	0.009302
$R(t)$	0.08 <b>monthly</b>	600	0.332002	0.645725
	0.08/2	1200	0.121379	0.099979
	0.08/4	2400	0.109360	0.083376

**Table 3** shows the numerical simulation solutions of MMC\_RK and MLH\_RK for one year (2021–2022) with 100 repetitions in the interval [0, 1] and real step sizes of 0.02, 0.08, and 0.12 weekly and monthly, respectively. Table 4 also includes the results of the numerical simulations MMC\_RK and MLH\_RK with 1000 for the societal groups in the monthly interval [0, 48] for the future time until 2025.

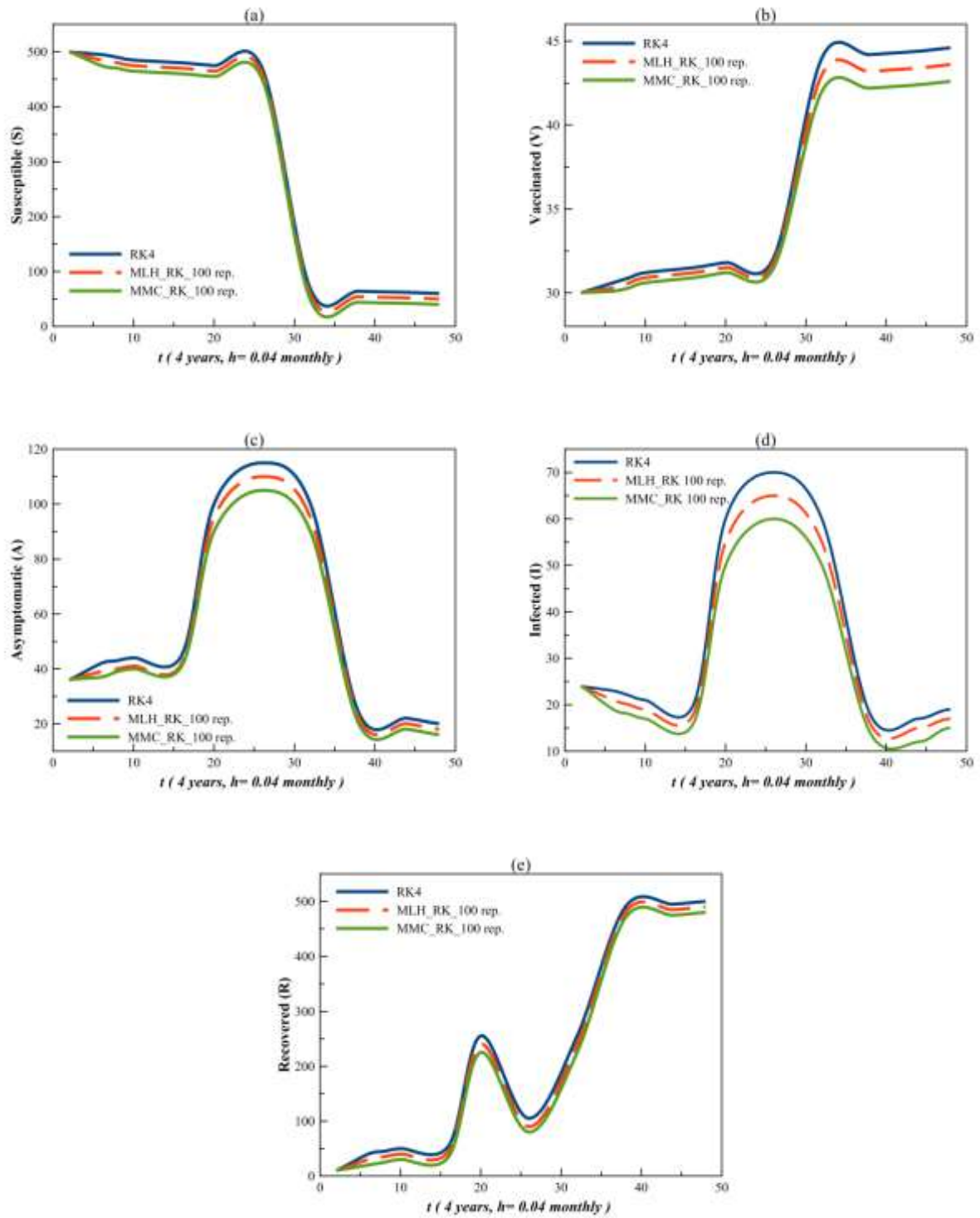
The expected approximate MMC\_RK and MLH\_RK results have been calculated in the prediction intervals that contain the minimum bound (5th percentile) and maximum bound (95th percentile) for MMC\_RK and MLH\_RK results in the future until 2025. MMC\_RK and MLH\_RK results must be inside the predicted intervals; see **Table 5**.

To compare the two numerical simulation methods, MMC\_RK and MLH\_RK, with the numerical RK4 method, the absolute error for,, and is calculated as a criterion for comparison from 2021 to 2022. In Table 6, it is clear that the MLH\_RK method is more accurate and reliable than the MMC\_RK method since the absolute error of the MLH\_RK results is less than the MMC\_RK results for all subpopulations of the studied model.

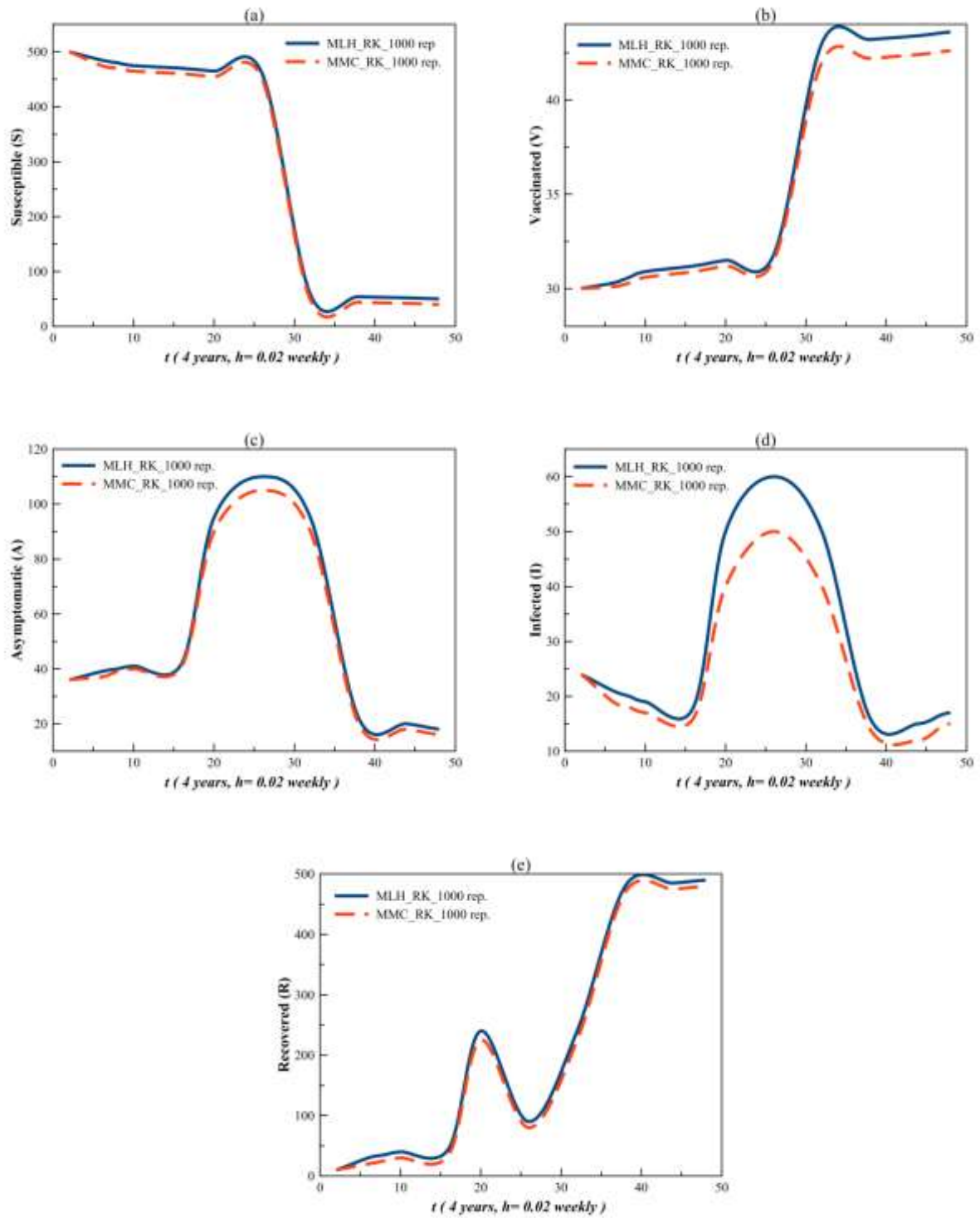
Table 7 shows the numerical stability of the numerical methods used in the current study. Table 7 also explains how the numerical simulation method (MLH\_RK) becomes more convergent as the step size is reduced, resulting in a smaller error between the proposed method and the actual method in step size. To prove the convergence of the methods used, see [28].



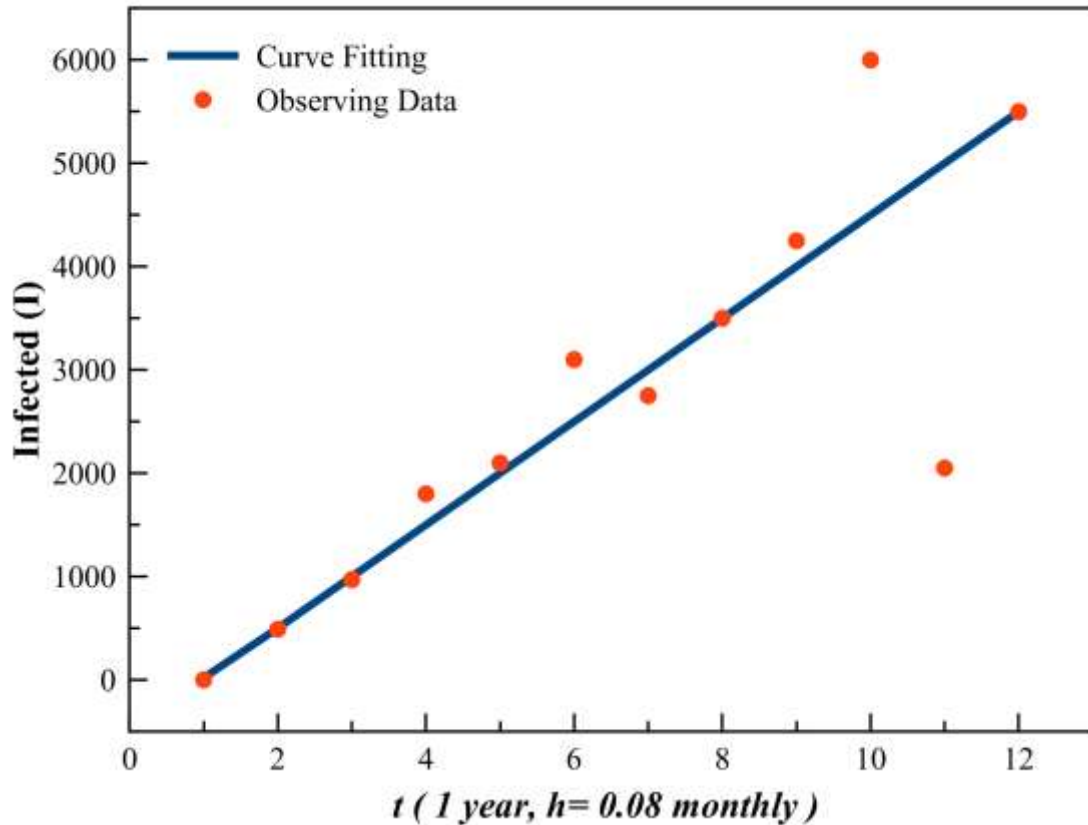
**Figure 3.** Comparison of numerical and numerical simulation solutions by using RK4, MMC\_RK and MLH\_RK of (a)  $S(t)$ , (b)  $V(t)$ , (c)  $A(t)$ , (d)  $I(t)$  and (e)  $R(t)$  from 2021 to 2025 when  $h = 0.08$  monthly in Iraq.



**Figure 4.** Comparison numerical simulation MMC\_RK and MLH\_RK results with numerical RK4 results for (a)  $S(t)$ , (b)  $V(t)$ , (c)  $A(t)$ , (d)  $I(t)$  and (e)  $R(t)$  from 2021 to 2025 when  $h = 0.04$  monthly in Iraq.



**Figure 5.** The numerical simulation results MMC\_RK and MLH\_RK of (a)  $S(t)$ , (b)  $V(t)$ , (c)  $A(t)$ , (d)  $I(t)$  and (e)  $R(t)$  from 20201to 2025 when  $h = 0.02$  weekly in iraq.



**Figure 6.** Curve fitting for Infected people  $I(t)$  with observing data from 2021 to 2022 when  $h = 0.08$  monthly in Iraq.

**Fig 3** shows the curves of the methods used in our study for 48 months, the interval 2021–2025, in which all groups of society are shown according to the impact of the virus on them. **Fig 3(a)**, which represents a group of people who are not infected with an epidemic but are susceptible to infection for this class for all RK4, MMC\_RK, and MLH\_RK methods, is used with step size weekly and monthly through 4 years. There is a sudden drop in the curve of this group for all the methods used in the study RK4, MMC\_RK, and MLH\_RK after the 33rd month, then it rises again after the 35<sup>th</sup> month to stabilize during the last months of our study. Because of continuous mixing between the people and the lack of commitment, people in the society can not continuous protect their health properly. Therefore, we can observe the sudden descent in the curve as a result of a large number of infections, particularly between the 25<sup>th</sup> and 35<sup>th</sup> month of the study period, to settle down after the end of 2025.

**Fig 3(b)** shows a curved group of vaccinated people against COVID-19 in Iraq, where we show that there is a simple rise in the curve for all RK4, MMC\_RK, and MLH\_RK methods used in the study from the beginning of the vaccine until the 25<sup>th</sup> month. The large number of people wanting to get the vaccine as a result of rising health and cultural awareness has resulted in a dramatic increase, particularly between the 27<sup>th</sup> and 35<sup>th</sup> month, after which the curve stabilized until the end of the study period.

**Fig 3(c)** depicts the subpopulation as asymptomatic with the epidemic but not showing symptoms of infection. There is a simple rise in the first study months, bringing the curve of this group to its highest level between the 15<sup>th</sup> and 30<sup>th</sup> month. Because of following health prevention methods, the instructions of the World Health Organization, and the demand for vaccination against

the pandemic, the curve begins to decline gradually until the 40<sup>th</sup> month and settles at the beginning of the 40<sup>th</sup> month until the end of the year 2025.

**Fig 3(d)** represents the number of people infected with the epidemic. The curve rose dramatically from the 15<sup>th</sup> month to the highest level in the 25<sup>th</sup> month, and then fell dramatically from the 33<sup>rd</sup> month to the 40<sup>th</sup> month to settle as a result of increased health awareness and following health guidelines, and more people are convinced to get the vaccine.

**Fig 3(e)** represents the group of people who have been cured of the disease, as they have been removed from the list of positive cases. There is a gradual rise of the curve of this group until the 20<sup>th</sup> month, then it comes down in the 25<sup>th</sup> month, then it rises dramatically to reach its highest level in the 40<sup>th</sup> month due to following World Health Organization guidelines, so more people became fully vaccinated, then the curve is still at the same high level until the end of the study period.

**Fig 4** shows the convergence of the methods that are used, where the result that has the smallest step size has the greatest convergence. The convergence between the numerical simulation methods and the numerical method Runge-Kutta (RK4), which represented the exact solution, in Figure 4, is greater than the convergence in **Fig 3** because the step size in **Fig 4** is smaller. Also, we notice that the MLH\_RK method is more convergent than MMC\_RK to RK4.

**Fig 5** explains the similarities in the behavior of the solution for the proposed numerical simulations using the MMC\_RK and MLH\_RK methods despite the change in the step size (weekly with 100 repetitions) for each subpopulation,  $S$ ,  $I$ , and  $R$  for COVID-19 model for four years from 2021 to 2025.

Finally, **Fig 6** shows the curve fitting of real observed data from the World Health Organization, utilizing the concept of linear regression for the class of people who suffer from infection during the 12 months from 2021 to 2022 using the Magic Plot program.

## 6. Conclusion

The epidemiological COVID-19 model in our current study has been solved for 48 months, from 2021 to 2022. Many methods are employed, including the numerical RK4 method and the other two numerical simulation methods MMC\_RK and MLH\_RK, to solve this model. In this study, we found convergence in the results for all methods that we used, but the MLH\_RK method is the closest to the numerical method (RK4); the curve of MLH\_RK results is more convergent with the curve of RK4 results than the curve of MMC\_RK results. Therefore, it is considered the most efficient approximation method for solving this model.

Also, we found that the epidemic model gives an impression of the impact of this virus on society. The results showed that the category of people not infected with the epidemic began to decrease during the study interval, while the category associated with vaccinated people increased. There is a gradual increase in the category of infected people who do not show symptoms because education does not adhere to health prevention methods, as well as social distancing. Then it decreases in the last months of the study period. When the category of infected people is clear and their symptoms are clear, there is a gradual increase in all methods (RK4, MMC\_RK, and MLH\_RK), then it decreases in the final months of the study interval due to a lack of people taking the virus vaccine.

Finally, in the category of people who have been cured of the disease, there is a clear increase for this class for all methods used for the study. Epidemic behavior for the next four years until 2025 has been projected using the proposed methods. The results of this study indicate a decrease in the epidemic rate in the future..

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