A RELIABLE NUMERICAL SIMULATION TECHNIQUE FOR SOLVING COVID-19 MODEL

MAHDI A. SABEA, MAHA A. MOHAMMED[*]

Department of Mathematics, College of Education for Pure Science / Ibn al-Haytham, University of Baghdad, 47146,

Baghdad, Iraq

Abstract. The nature of epidemiological models is characterized by randomness in their coefficients, while the classical or analytical and numerical methods deal with systems with fixed coefficients, which makes these methods inappropriate for solutions of epidemiological systems that have coefficients that change with time. For that, the numerical simulation methods that deal with time change are more appropriate than other ways. The aim of the research is to apply some of these methods to the COVID-19 system. Two efficient methods used for previous studies are used to solve this system, which are Monte Carlo Finite Difference Method and Mean Latin Hypercube Finite Difference Method. For the sake of comparison, a numerical method, the finite difference method, is used to solve this system. We have reached good results that give an analysis and impression of the behavior of the Covid 19 epidemic since its inception and predict its behavior for the next years. All results have been written in graphs and tabulated.

Keywords: COVID-19; epidemiology diseases; finite difference method; numerical simulation techniques.

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1. INTRODUCTION

Throughout history, many epidemics appeared and posed a real threat to the world, as well as greatly affected economic and population growth, and caused trips to stop in some cities. This

[*]Corresponding author

E-mail address: mahasssa@yahoo.com

epidemic may be contagious or transmitted in other ways. Among these diseases is the Black Death, which spread widely in Europe, malaria, the plague in Africa, SARS in China from 2002 to 2003, AIDS and cancer, etc. [1-3]. At the beginning of 2019, the Coronavirus appeared, specifically in the Chinese city of Wuhan, and this epidemic is considered one of the most dangerous and fastest spreading epidemics, and it is of the SARS-CV type [4, 5]. In the year 2020, on March 29, the epidemic spread significantly and rapidly throughout the world, which led to the suspension of flights through airports, land transport between countries, schools and universities, and most jobs with direct mixing [6, 7]. The World Health Organization declared this epidemic to be a pandemic after it infected 199 countries around the world and caused the death of thousands of people [8]. The emergence of the epidemic coincided with the period of spring festivals and celebrations in Asia, and this helps to spread the epidemic due to the mixing of many people, especially on flights with all countries of the world. This is considered one of the reasons for the spread of the virus to the rest of the world [9]. As a result of the lack of health facilities in some countries, including developing countries, and the severity and speed of the virus's spread, the virus turned into a global pandemic that caused the death of thousands of people around the world because they did not receive appropriate treatment is social distancing and adherence to health prevention ways and the directive of the World Health Organization [6, 9].

One of the most prominent epidemics that researchers have been interested in is Covid 19 since 2020. Among these researches that have been formulated in the form of a system of differential equations to study the behavior of the spread of the epidemic are [10-16] and see [17, 18]. As well, there are those who are interested in predicting the behavior of the epidemic among them; the stochasticity in COVID -19 SIR epidemic model was discussed in Iraq to die out the epidemic in [19, 20], see also [21, 22].

In general, from the research that focused on studying the approximate methods (analytical and numerical) for solving epidemiological systems: SIR epidemic model was studied by Temimi-Ansari method, Daftardar-Jafari method, and Banach contraction method, [23]. For the first time, LTAM was discussed to solve the nonlinear epidemic model, this method is combine

Laplace transform with Tamimi and Ansari iterative method, [24]. Shurowq K. Shafeeq, S.K., et al., discussed Bifurcation analysis of a vaccination mathematical model with application to COVID-19 pandemic in [25].Sabaa and Mohammed discussed in 2020 the approximate solutions of the nonlinear smoking habit model [26]. Shatha and Maha discussed Runge-Kutta numerical method for solving nonlinear influenza model in 2021 [27]. Emad and Maha studied COVID-19 model using Runge-Kutta numerical method in 2022 [10, 11].

On the other hand, there is interest in numerical simulation approach for the behavior of epidemics and estimating the behavior of epidemics for the future. Among these researchers who developed a new approach linking transaction simulation of the epidemic system with methods for solving these systems, where the simulation method was used Monte Carlo Process (MC) with numerical method which is Finite Difference Mehod (FD), and other to use a more efficient simulation method, which is Latin Hypercub Sampling (LHS) with numerical methods for both. The most famous numerical simulation methods in our search are Mean Latin Hybercub Finite Difference Method (MLH_FD) [28], Mean Monte Carlo Finite Difference Mehod (MMC_FD) [29], Mean Monte Carlo Runge-Kutta method (MMC_RK) [30], Mean Latin Hypercube Runge-Kutta (MLH_RK) [31] had been imployed.

The importance of our study is to find easy, fast, effective, and suitable ways to solve specific models that have some difficulties in solving, since these systems by their nature, are nonlinear, as well as have random coefficients, two numerical simulation processes MLH_FD and MMC_FD have been used to apply to Covid 19 model. For our search, Mean Monte Carlo Finite Difference Mehod (MMC_FD), Mean Latin Hybercub Finite Difference Method (MLH_FD), have been used.

The search division is as follows: define the mathematical model used of COVID-19 in Section 2, the numerical finite difference method and the analytical variation iteration method have applied to COVID-19 model in Section 3. Section 4 exhibits two numerical simulation methods MMC_FD and MLH_FD to solve the nonlinear COVID-19 model respectively. Section 5 discusses the findings and results of proposed methods that represent in tables and graphs. Lastly, the summary and conclusion of the research, are in Section 6.

2. COVID-19 MATHEMATICAL MODEL

The epidemic model in our study includes the COVID-19 of people vaccinated against the Coronavirus epidemic [32]. The population consists of five types of individuals S, V, A, I, and R represent susceptible, vaccinated, asymptomatic, symptomatic, and recovery respectively. These individuals are dependent on time. The nonlinear epidemic model under study consists of ordinary differential equations of first order [33].

$$S'(t) = M - \tau S - \frac{\alpha(1+\beta A)S}{N} - \mu S + \gamma R,$$

$$V'(t) = \tau S - \frac{\rho\alpha(1+\beta A)V}{N} - \mu V,$$

$$A'(t) = \frac{\alpha(1+\beta A)S}{N} + \frac{\rho\alpha(1+\beta A)V}{N} - \delta A - \mu A, \qquad (1)$$

$$I'(t) = \theta\delta A - \sigma I - \mu I$$

$$R'(t) = (1-\theta)\delta A + \sigma I - \gamma R - \mu R$$

where Tables 1 and 2 represent subpopulation S, V, A, I, R as the variables of the model (1), and parameters M, τ, α, β, μ, γ, ρ, δ, θ and σ sequentially. System (1) must be solved according to the initial conditions from the World Health Organization website is the source of initial values of the system are taken from [33].

$$S(0) = 50000000, V(0) = 0, \ A(0) = 1000, \ I(0) = 100 \text{ and } R(0) = 50 \qquad (2)$$

with the predicted parameters that are given in Table 2.

Table 1. Variables of COVID-19 model [33]

Variable	Definition
$S(t)$	People who are not infected, but are vulnerable to not having immunity
$V(t)$	People vaccinated against coronavirus
$A(t)$	People infected with the virus without showing any symptoms
$I(t)$	Infected people and symptoms of infection are clear to them
$R(t)$	People who have recovered from the virus

Table 2. Parameters of COVID-19 model [33]

Parameter	Definition	Value
α	The rate of transmission people infected with this virus	0.8883
β	The correction factor for the rate of movement of people without infection	0.45
μ	The rate of natural death	0.00003349 day
γ	The rate of immunity	0.005
$1 - \rho$	Vaccine efficacy and potency	0.8
$\dfrac{1}{\delta}$	The average period without symptoms of infection	7 days
θ	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
$1 - \theta$	Infected people do not show symptoms of infection and then recover	0.8
M	Birth rate in the community	1500/day
τ	Vaccination rate against the virus	0.01 day
$\dfrac{1}{\sigma}$	The average rate of people recovering from infection with the virus	10 days

3. NUMERICAL METHOD FOR SOLVING COVID-19 MODEL

Epidemiological mathematical model in our study is a nonlinear system (1) of the Covid-19 with the estimated parameters that are explained in Table 2. It can be solved via the Finite Difference Method (FD) the initial conditions. The zero terms are in (2). The real step size h is proposed in this study as $0.02, 0.08$, and $m = 52, 12$ refers the numbers of weeks and months respectively through one year. In order to find $S_1(t), V_1(t), A_1(t), I_1(t)$ and $R_1(t)$, Backward Finite Difference (BFD) can be utilized as below:

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$$S_1(t) = S_0(t) + h\left(M - \tau S_0(t) - \frac{\alpha(1+\beta A_0(t))S_0(t)}{N} - \mu S_0(t) + \gamma R_0(t)\right), \tag{3}$$

$$V_1(t) = V_0(t) + h\left(\tau S_0(t) - \frac{\rho\alpha(1+\beta A_0(t))V_0(t)}{N} - \mu V_0(t)\right), \tag{4}$$

$$A_1(t) = A_0(t) + h\left(\frac{\alpha(1+\beta A_0(t))S_0(t)}{N} + \frac{\rho\alpha(1+\beta A_0(t))V_0(t)}{N} - \delta A_0(t) - \mu A_0(t)\right), \tag{5}$$

$$I_1(t) = I_0(t) + h(\theta\delta A_0(t) - \sigma I_0(t) - \mu I_0(t)). \tag{6}$$

$$R_1(t) = R_0(t) + h\left((1-\theta)\delta A_0(t) + \sigma I - \gamma R_0(t) - \mu R_0(t)\right). \tag{7}$$

The first iteration $S_1(t), V_1(t), A_1(t), I_1(t)$ and $R_1(t)$ are calculated from Eqs. (3-7) to obtain the following results: $S_1(t) = 49959826.9800989$, $V_1(t) = 40000$, $A_1(t) = 1027.65762186108$, $I_1(t) = 101.48466604$ and $R_1(t) = 59.91906604$.

Now, the Central Finite Difference (CFD) is applied to find the other terms as the follows:

$$S_{i+1}(t) = S_{i-1}(t) + 2h\left(M - \tau S_i(t) - \frac{\alpha(1+\beta A_i(t))S_i(t)}{N} - \mu S_i(t) + \gamma R_i(t)\right), \tag{8}$$

$$V_{i+1}(t) = V_{i-1}(t) + 2h\left(\tau S_i(t) - \frac{\rho\alpha(1+\beta A_i(t))V_i(t)}{N} - \mu V_i(t)\right), \tag{9}$$

$$A_{i+1}(t) = A_{i-1}(t) + 2h\left(\frac{\alpha(1+\beta A_i(t))S_i(t)}{N} + \frac{\rho\alpha(1+\beta A_i(t))V_i(t)}{N} - \delta A_i(t) - \mu A_i(t)\right), \tag{10}$$

$$I_{i+1}(t) = I_{i-1}(t) + 2h(\theta\delta A_i(t) - \sigma I_i(t) - \mu I_i(t)), \tag{11}$$

$$R_{i+1}(t) = R_{i-1}(t) + 2h\left((1-\theta)\delta A_i(t) + \sigma I - \gamma R_i(t) - \mu R_i(t)\right), \tag{12}$$

for all $i = 1,2, \dots, m$. To find $S_1, S_2, \dots, S_m$, $V_1, V_2, \dots, V_m$, $A_1, A_2, \dots, A_m$, $I_1, I_2, \dots, I_m$ and $R_1, R_2, \dots, R_m$ that consider as numerical solutions for COVID-19 Model.

4. NUMERICAL SIMULATION METHODS FOR SOLVING COVID-19 MODEL

In this section, two numerical simulation techniques are proposed, Monte Carlo simulation (MC) or Latin Hyber Cube simulation process (LH) merge a numerical method Finite Difference (FD). Mean Monte Carlo Finite Difference (MMC_FD) and Mean Latin Hyber Cube Finite Difference (MLH_FD) are named for these numerical simulation techniques.

The simulation processes MC or LH can simulate the random coefficients for the model. With each repetition, a numerical method FD is used for solving the model numerically using simulated system parameters. The average of the last FD iteration results with each MC or LH repetition is computed as the estimated approximate solution for the system under search.

The randomness in the system coefficients represents the nature of epidemic models, so, MMC_FD and MLH_FD numerical simulation methods are more suitable methods than the FD method, due to the FD method being dedicated to solving models with constant coefficients while MMC_FD and MLH_FD are dedicated to solving models with random variables. The MMC_FD and MLH_FD methods are performed using MATLAB software, more details are found in [28] and [29].

5. RESULT AND DISCUSSION

The results of numerical and numerical simulation methods for the nonlinear Coronavirus model are discussed and analyzed in this section. The initial conditions of the system are taken from [33]. In this study, 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 contains the FD numerical and MMC_FD and MLH_FD numerical simulation results with $p = 100$ repetitions of COVID-19 model for two years from the beging of 2021 to the end of 2022. On the other hand, Table 4 gives the expected numerical simulation results with $p = 1000$ repetitions for variables $S(t), V(t), A(t), I(t)$ and $R(t)$ of COVID-19 model in the next four years, the study interval is 2021 to 2025, which is also seen in Figure 1.

In Table 5, the absolute error criterion for two years from the beging of 2021 to the end of 2022 is used to compare the numerical simulation methods proposed in this study with the numerical FD method which is considered as the exact solution for this system. The results

mentioned in Table 5 show that the error of the MLH_FD method is smaller than the error of the MMC_FD method which indicates that the MLH_FD method is more efficient than the MMC_FD method because it has the lowest absolute error.

It is clear that prediction intervals (5th percentile as a minimum result, 95th percentile a maximum result) for MMC_FD and MLH_FD expected results have been accounted for in Table 6. All these MMC_FD and MLH_FD expected results to fall within these estimated intervals in Tables 6.

Table 7, explain the stability of the approximate simulation methods which are used in the study and how close the numerical simulation method (MLH_FD) is every time we reduce the step size more than MMC_FD, such that E_h is the error between the proposed method in step size h and step size $h/2q$, $q = 1,2, ...,$ to prove the convergence of the used methods [29].

Table 3. Numerical and numerical simulation results of COVID-19 model in two years

Model Variables	Step Size, h (monthly& weekly)	Time	FD (2 years)	MLH_FD (100 repetition)	MMC_FD (100 repetition)
$S(t)$	0.08 (monthly)	24	38071016.66343352	38071016.65883650	38071016.58012841
	0.02 (weekly)	104	38070276.77017017	38070276.74007223	38070276.71012160
$V(t)$	0.08 (monthly)	24	10553860.66802990	10553860.63720261	10553860.62946801
	0.02 (weekly)	104	10553798.07126030	10553798.04451812	10553798.01943023
$A(t)$	0.08 (monthly)	24	858150.28334196	858150.25480547	858150.21057334
	0.02 (weekly)	104	858658.95841104	858658.93014208	858658.91032479
$I(t)$	0.08 (monthly)	24	70272.14889928	70272.13244941	70272.10960178
	0.02 (weekly)	104	70314.83744996	70314.82031605	70314.80904451
$R(t)$	0.08 (monthly)	24	407636.46528549	407636.43864890	407636.42990213
	0.02 (weekly)	104	407887.56435948	407887.51316832	407887.49736601

Table 4. Expected numerical simulation results (100 rep.) in four years from 2021 to 2025

Model Variables	Step Size, h (monthly & weekly)	Time	FD (4 years)	MLH_FD (1000 repetition)	MMC_FD (1000 repetition)
$S(t)$	0.08 (monthly)	48	5596247.41805423	5554322.54786577	5523824.21037309
	0.02 (weekly)	208	5594499.20621553	5570547.90651805	5535150.0856032
$V(t)$	0.08 (monthly)	48	11390855.697436	11335644.830232	11307213.417702
	0.02 (weekly)	208	11389578.4470469	11340525.023144	11314056.243055
$A(t)$	0.08 (monthly)	48	9679318.64840848	9653421.10234362	9638924.64702312
	0.02 (weekly)	208	9678455.6118537	9642301.80122570	9611283.4570231
$I(t)$	0.08 (monthly)	48	2329257.57547543	2304572.3900318	2298435.1304572
	0.02 (weekly)	208	2329410.25714638	230076.75502584	2284373.8130920
$R(t)$	0.08 (monthly)	48	20919855.5339504	20554608.4509824	20453182.2704518
	0.02 (weekly)	208	20923589.5192151	20471066.0931247	2036458.4302958

Table 5. Absolute error for MMC_FD and MLH_FD with FD throught two years

Model Variables	Step Size, h (monthly & weekly)	Time	MLH_FD (100 repetition)	MMC_FD (100 repetition)
$S(t)$	0.08 (monthly)	24	0.00459702	0.08330511
	0.02 (weekly)	108	0.03009794	0.06004857
$V(t)$	0.08 (monthly)	24	0.03082729	0.03856189
	0.02 (weekly)	108	0.02674218	0.05183007
$A(t)$	0.08 (monthly)	24	0.02853649	0.07276862
	0.02 (weekly)	108	0.02826896	0.04808625
$I(t)$	0.08 (monthly)	24	0.01644987	0.03929750
	0.02 (weekly)	108	0.01713391	0.02840545
$R(t)$	0.08 (monthly)	24	0.02663659	0.03538336
	0.02 (weekly)	108	0.05119116	0.06699347

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Table 6. Prediction intervals (5th percentile, 95th percentile) for MMC_FD and MLH_FD

solutions with 48 months with h=0.08

MLH_FD from 2021 to 2025 ($t \leq 48$)		
Subpopulation	**Mean** **MLH_FD** **(100 repetitions)**	**Prediction intervals** **(100 repetitions)**
$S(t)$	5554322.54786577	(1435090.42128167 , 26021301.73208561)
$V(t)$	11335644.83023271	(5279581.25095422 , 18880838.96929031)
$A(t)$	9653421.10234362	(2305560.36249567 , 11204393.56146084)
$I(t)$	2304572.3900318	(315287.719890118 , 3138151.22521585)
$R(t)$	20471066.0931247	(2337184.64747243 , 36049014.36118590)
MMC_FD from 2021 to 2025 ($t \leq 48$)		
Subpopulation	**Mean** **MLH_FD** **(100 repetitions)**	**Prediction intervals** **(100 repetitions)**
$S(t)$	5523824.21037309	(1394807.03878321 , 25130099.48022151)
$V(t)$	11307213.417702	(5934287.76820442 , 18045760.13022874)
$A(t)$	9638924.64702312	(2545687.02033021, 11834502.47230394)
$I(t)$	2298435.1304572	(324756.40329118 , 3590422.14320885)
$R(t)$	20453182.2704518	(2529055.39012451, 36382207.37480203)

Table 7. Absolute error $E_h = \left| T_h - T_{\frac{h}{2}} \right|$ for MMC_FD and MLH_FD through two years

Model **Variables**	**Step Size, h** **(monthly & weekly)**	**Number of** **Iterations (m)**	$E_h\_MMC\_FD$ **100 rep.**	$E_h\_MLH\_FD$ **100 rep.**
	0.08 (monthly)	150	0.00087135	0.00699431
$S(t)$	0.08/2	300	0.00079702	0.00588563
	0.08/4	600	0.00017641	0.00520223

	0.08 (monthly)	150	0.00041902	0.00069881
$V(t)$	0.08/2	300	0.00024882	0.00044212
	0.08/4	600	0.00017512	0.00024212
	0.08 (monthly)	150	0.00462423	0.00692062
$A(t)$	0.08/2	300	0.00386289	0.00390911
	0.08/4	600	0.00310220	0.00181253
	0.08 (monthly)	150	0.00110737	0.00186231
$I(t)$	0.08/2	300	0.00096313	0.00220781
	0.08/4	600	0.00074066	0.00182013
	0.08 (monthly)	150	0.00905204	0.00485206
$R(t)$	0.08/2	300	0.0048506 1	0.00244731
	0.08/4	600	0.00120753	0.00090547

Figure 1 shows the curves of the methods used in our study for the interval 2021 to 2025 with step size $h = 0.08$ monthly and $p = 100$ repetitions, in which all groups of society are shown according to the impact of the virus on them. Figure 1(a), represents a group of people $S(t)$ who are not infected by an epidemic but are susceptible to infection. A sudden descent in the curve of this group for all the methods used in the study MLH_FD, MMC_FD, and FD after 33th months, then it rises again after 35th months to stabilize during the last months of our study. Because of continuous mixing between the people and the lack of commitment to ways to prevent health properly in our society observe the descent of a sudden in the curve as a result of a large number of infections, particularly between the 25th and 35th months of the study period to settle down after the end of 2025.

Figure 1(b), shows a curved group $V(t)$ of people vaccinated against COVID-19, where we see there is a simple rise of the curve for all the methods with (100 repetition) used in the study with the beginning of the vaccine until the month 25. The large number of people wanting to get the vaccine as a result of rising awareness of health and culture has led to a curved rise

dramatically, especially in the period between month 27 and month 35, then the curve settles until the end of the study period.

As for Figure 1(c), this curve represents the subpoplution asymptomatic $A(t)$ with the epidemic without appearing symptoms of the infection, there is high simple in the first study months, bringing the curve of this group to the highest level between months 15 and month 30, then declines gradually until the month 40 to settle at the beginning of the month 40 until the end of the year 2025. This is as a result of following the instructions of the World Health Organization, such as social distancing, non-mixing, continuous sterilization, etc., as well as the demand for vaccination.

Figure 1(d), this curve represents the infected people $I(t)$ with the epidemic, the curve has risen from month 15 dramatically to reach the highest in month 25, and after that, the curve declines dramatically from month 33 until month 40 to settle after the result of increased awareness of health and follow the guidelines of health and turn out so much to get the vaccine.

Figure 1(e), represents the group of people $R(t)$ who have been cured of the disease, as they have been removed from the list of injuries. There is a gradual rise of the curve of this group until the month 20 to come down in month 25 then rises dramatically to reach its highest level in month 40 due to following World Health Organization guidelines, then it follows still in the same high level until the end of the study period.

Figure 2 shows the converegence of the methods which are used with $p = 1000$ repetitions, where we notice that the smaller step size has the greater the convergence, the convergence in Figure 2 is more between the numercal simulation methods and the numerical method Finte Difference (FD), which represented the exact solution, compared to the Figure 1 because of a small of step size, also we notice that MLH_FD method is more converge than MMC_FD to FD. Also, explains the stability in the behavior of numerical simulation methods MMC_FD and MLH_FD despite the change in the step size ($h = 0.04$ monthly with 1000 repetitions) for each subpopulations $S(t), V(t), A(t), I(t)$, and $R(t)$ for COVID-19 model for four yeas from 2021 to 2025.

Finally, Figure 3 shows the curve fitting of real observing data from the World Health Organization for the class of people who suffer from infection during the period of 52 weeks from the beging of 2021 using magic plot program.
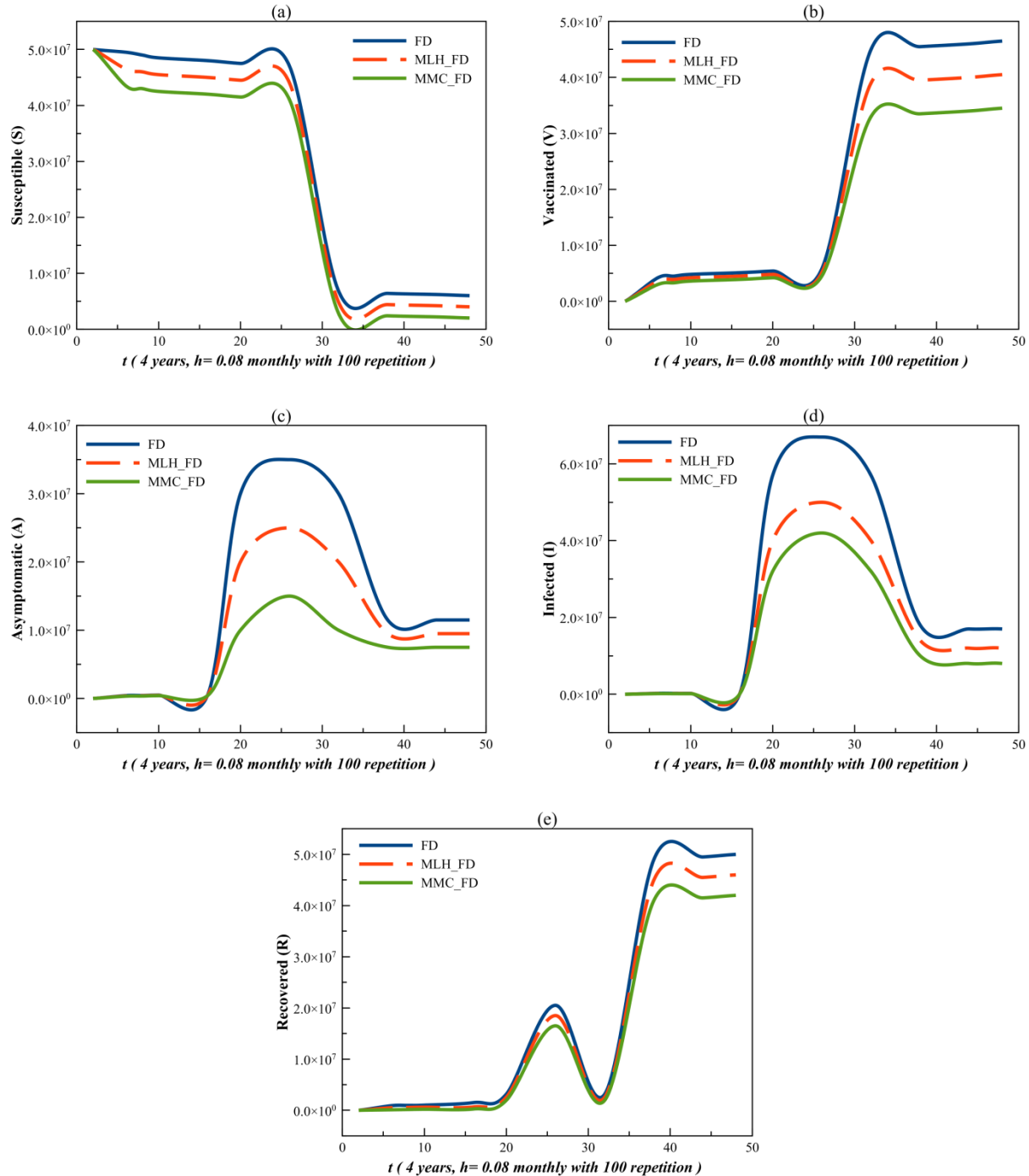

Figure 1. Curves of approximate simulation solutions of subpopulations $S(t)$, $V(t)$, $A(t)$,

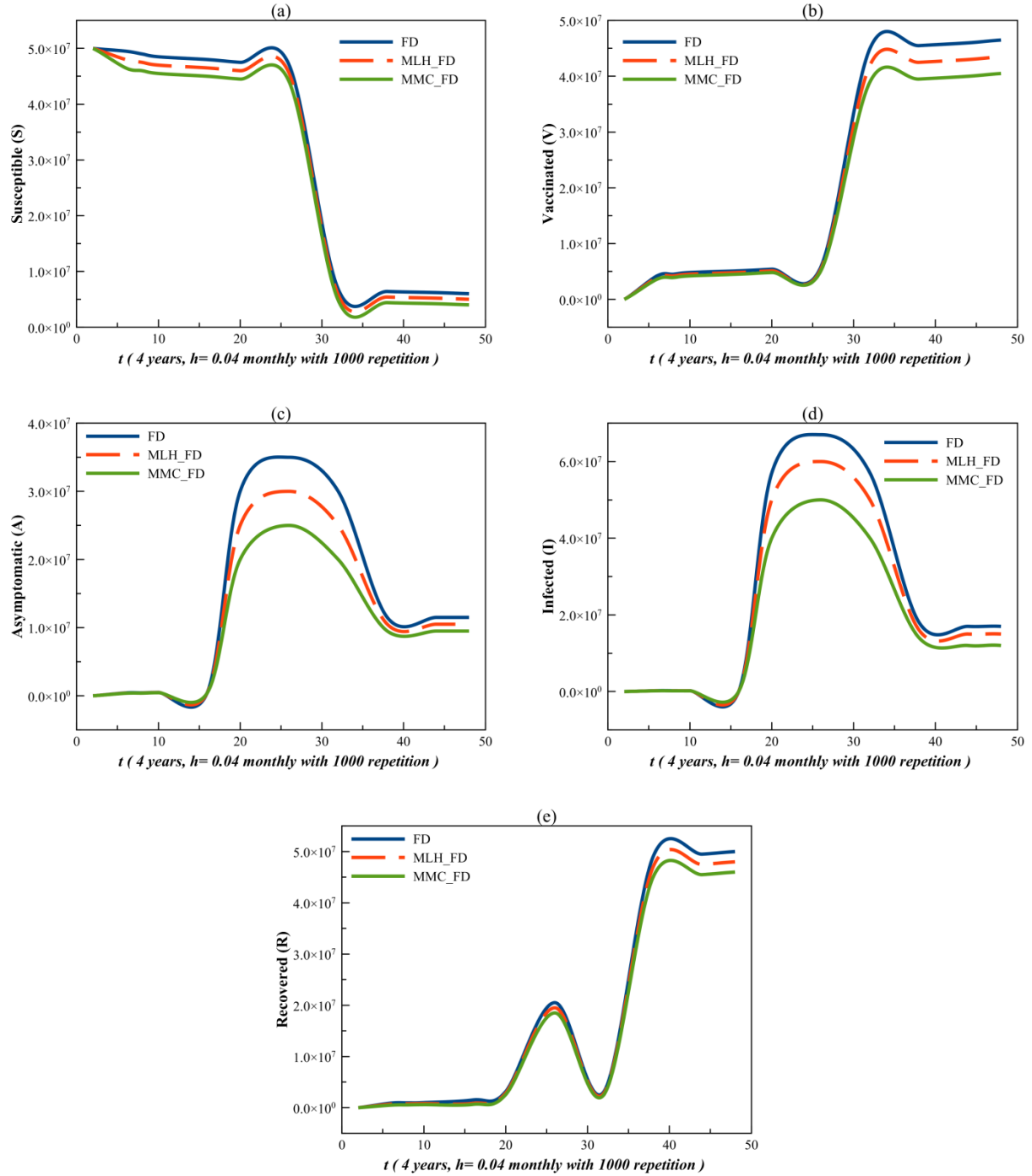$I(t)$ and (e) $R(t)$ in 4 years when $h = 0.08$ monthly with $p = 100$ repetitions.

Figure 2. Curves of approximate simulation solutions of subpopulations $S(t), V(t), A(t),$

$I(t)$ and $R(t)$ in 4 years when $h = 0.04$ monthly with $p = 1000$ repetitions.
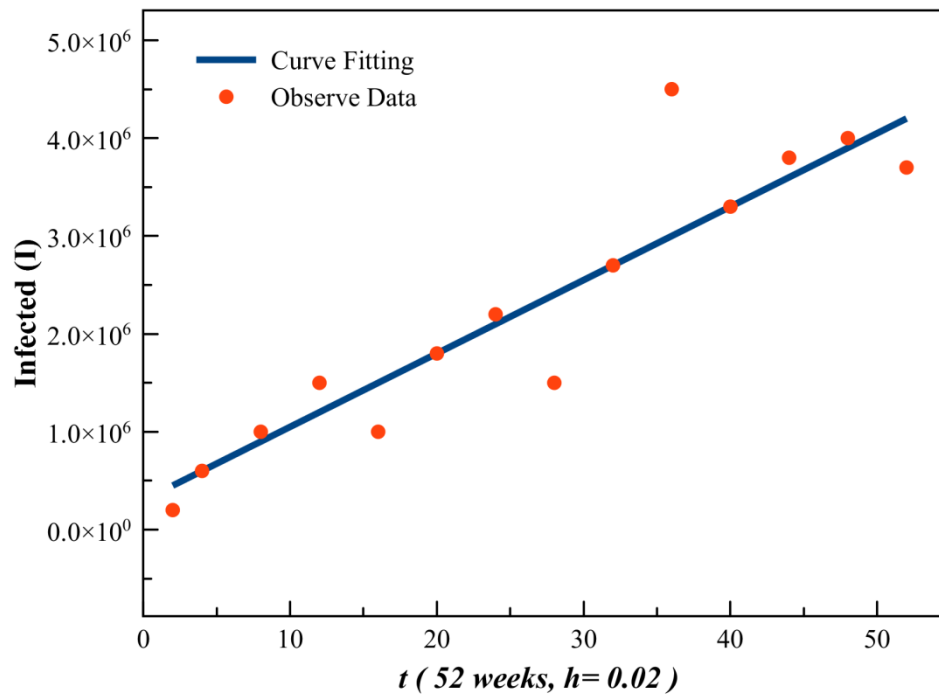
Figure 3. Curve fitting for subpopulation $I(t)$ with observing data through one year when

$h = 0.02$ weekly.

6. CONCLUSION

In our research paper, two reliable numerical simulation methods which are MMC_FD and MLH_FD methods have been applied to the COVID-19 epidemic model. These methods have been utilized to solve the COVID-19 model for four years from 2021 to 2025. Our work is including the numerical FD method used for comparison purposes. By a comparison tool between the numerical simulation methods which are used in our study and FD, it has been found that the MLH_FD method is more efficient than the MMC_FD because it has the lowest absolute error during the study period and the curve of MLH_FD method is more converge for curve of FD than other method MMC_FD. One of the benefits of the proposed MMC_FD and MLH_FD methods is that it gives a prediction of the future behavior of the epidemic by giving an anticipation period for approximate solutions. Good findings have been getting when using

MMC_FD and MLH_FD methods, which give an analysis and impression of the behavior of the Covid 19 epidemic since its inception and predict its behavior for the future to 2025.

Studying this epidemic model gives us an idea and impression of the impact of this virus on the population. The results of the group of healthy people $S(t)$ is decreasing until 2025, while the group of vaccinated people $V(t)$, is increasing in this group gradually until the end of the study period as a result of the impact and effectiveness of the vaccine on society. The group of infected people without showing symptoms $A(t)$, and the group of infected people $I(t)$, in these groups of people, there is an increase in the number of infections clearly during the study period from 2021, then a decline is showing at the end of the study period in 2025 . Finally, in the group of people who have fully recovered from infection with the virus $R(t)$, it is noticeable that there is an increase in this group of people and it persists until the end of the study period. The results of this study indicate a decrease in the epidemic rate in the few next years.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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