



## Integrating Numerical Simulation and Shrinkage Estimation Techniques for Solving Epidemiological Models: A Case Study on COVID-19

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### ABSTRACT

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This investigation introduces a novel methodology that integrates numerical simulation with shrinkage estimation techniques to solve systems of nonlinear equations, marking its inaugural application to epidemiological models. Focused on the Susceptible-Vaccinated-Asymptomatic-Infected-Recovered (SVAIR) model for COVID-19, originally developed in late 2021, this research employs two numerical simulation methods within a statistical shrinkage framework to approximate solutions. The proposed methodology juxtaposes traditional numerical methods with an innovative shrinkage estimation formula, blending classical and simulation techniques to address the unique challenges posed by epidemiological data. Through meticulous comparison, it is demonstrated that the solutions derived from the advanced shrinkage approach exhibit greater efficiency and proximity to actual values than those obtained through conventional simulation methods. This efficiency not only underscores the potential of the proposed methods to enhance accuracy but also highlights their capacity to conserve time, resources, and effort across diverse practical applications. The findings advocate for the adoption of the approximate shrinkage method as a superior alternative for analyzing epidemic systems, given its demonstrated closeness to exact solutions.

## 1. INTRODUCTION

Many epidemics that appeared during the current century represent the greatest threat to the world because they are fast and contagious. It also had a significant impact on the expanding economy and population, causing travel to halt in several places [1-3]. Among these diseases is the coronavirus, which began in 2019, especially in Wuhan, a city in China. The coronavirus is among the deadliest and fastest-growing diseases [4]. The World Health Organisation (WHO) declared in 2020 that this epidemic is a pandemic because it is spreading rapidly and significantly throughout the world [5-7]. The global pandemic, exacerbated by inadequate health facilities and rapid virus spread, resulted in thousands of deaths worldwide due to inadequate social distancing, health prevention measures, and WHO directives [5, 8]. Many researchers have been interested in the study of epidemiological modelling for different formulations of epidemic models, such as Susceptible-Infected-Susceptible (SIS), Susceptible-Infected-Recovered (SIR), Susceptible-Exposed-Infectious-Recovered (SEIR), and so on. The epidemiological mathematical models as stochastic-deterministic models are considered by several researchers [1, 5, 9-11].

There are various ways to solve the epidemiological mathematical models. Regarding analytical techniques such as the Banach contraction method, Temimi-Ansari method, and

Daftardar-Jafari approach [12]. The LTAM method combines Laplace transform and Tamimi-Ansari repetitive techniques [13]. Kareem and Al-Azzawi [14] studied a model of stochastic differential equations that describe COVID-19's spread in 2021. Shafeeq et al. [15] applied the vaccination mathematical model for bifurcation analysis in 2022 to the COVID-19 pandemic. A delayed epidemiological model with the effect of delaying vaccination and awareness efforts until 2023 was studied by Yaseen et al. [16] for Hopf bifurcation and stability. Similar to this, semi-analytic techniques such as Sabaa and Mohammed [17] in 2020. Additionally, the numerical techniques, for example, the 4<sup>th</sup> order algorithm of Runge-Kutta [18]. Mohammed and Mohammed [19] also talked about the numerical Runge-Kutta method for the 2021 nonlinear model of influenza solving. Using a trustworthy RK4 numerical approach, Ghadeer and Mohammed [20] investigated the nonlinear mathematical model of COVID-19 in 2022.

Some authors modified numerical simulation techniques to combine two different methodologies and get the best results for epidemiological models. Two examples of these techniques are the methodology of simulating Monte Carlo and the method of numerical iteration. In 2018, Mohammed et al. [21] examined the Mean Latin Hypercube (MLH) Finite Difference method (FD) as a hybrid numerical strategy to solve the cocaine usage model in Spain. Additionally, in 2019, a nonlinear epidemic model was sampled at random using the

Mean Monte Carlo (MMC) simulation with the finite difference approach [22]. The other effective numerical simulation strategies used the MMC Runge-Kutta method [23] and the MLH Runge-Kutta method [24] to solve the influenza model. Researchers [24, 25] discussed using suitable techniques to approximate the 2022 epidemic model simulation with randomised parameters.

Numerous techniques are employed in this research. The first one involves solving the model under investigation numerically using the finite difference approach. Furthermore, our work employs two numerical simulation techniques: the MLH\_FD and the MMC\_FD [26]. The novel techniques, known as the approximate shrunken method (ASM), are used with the mathematical COVID-19 model [27]. ASM is a statistical shrinkage estimation method like the MLH\_FD or the MMC\_FD. They are a mix of the traditional FD and numerical simulation techniques. In solving such problems, these recently suggested techniques are more precise and dependable than previous numerical simulation techniques.

These systems under study are characterised by the fact that their parameters change with time, so they need special methods to solve them using simulation techniques and numerical simulation methods to address the problem of changing the parameters of the system under study. The previous numerical simulation methods solved the problem of changing the parameters of the epidemiological system and similar systems with a percentage error, and the proposed methods to solve this problem came with a lower error while giving an estimated solution that is closer to reality than the solutions of the previous methods of the previous studies mentioned above.

The following are included in this research: The COVID-19 mathematical model is presented in Section 2. Section 3 shows the derivation of the numerical approach RK4. Numerical simulation approaches are covered in Section 4. Either the MLH\_FD or the MMC\_FD and the new approximate shrunken approaches employed in our work to solve the epidemic model are presented in Section 5. The description, tables, and graphic representation of the employed methodologies are included in Section 6. Ultimately, the work's final result is explained in Section 7.

## 2. COVID-19 MATHEMATICAL MODEL

The model under study has been successfully used for people vaccinated against the COVID-19 coronavirus; for more details, refer to the study made by Yang et al. [28]. Five categories of people make up the population: susceptible, vaccinated, asymptomatic, symptomatic, and recovering, represented by the letters  $S$ ,  $V$ ,  $A$ ,  $I$ , and  $R$ , respectively. These categories are defined as functions of time, illustrating the temporal progression of the epidemic through a non-linear set of first-order ordinary differential equations.

The variables  $S$ ,  $V$ ,  $A$ ,  $I$  and  $R$  are represented in Table 1 and parameters are shown in Table 2.

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

**Table 1.** Model variables for COVID-19 [28]

Variable	Definition
$S(t)$	Those who are not ill but run the risk of losing their immunity.
$V(t)$	Individuals who received a coronavirus vaccine COVID-19.
$A(t)$	Individuals having the infection but not exhibiting any symptoms.
$I(t)$	Those who are infected and their symptoms are evident to them.
$R(t)$	Individuals who have either recovered from the virus or lost their lives due to the infection.

**Table 2.** Coefficients of the COVID-19 model [28]

Parameter	Definition	Value
$\alpha$	Rate at which symptomatic patients are transmitted	0.8883
$\beta$	Adjustment factor for the rate of transmission of asymptomatic individuals	0.45
$\mu$	The typical death rate	0.00003349_day
$\gamma$	The percentage of immunity against infection	0.005
$1 - \rho$	Vaccine potency and effectiveness	0.8
$\frac{1}{\delta}$	The typical amount of time without illness symptoms	7_day
$\theta$	The percentage of individuals who do not exhibit the virus's symptoms before they become symptomatic cases	0.2
$1 - \theta$	Percentage of asymptomatic people who get better	0.8
$M$	Community's birth rate	1500_day
$\tau$	Rate of vaccination against the pathogen	0.01_day
$\frac{1}{\sigma}$	The typical percentage of individuals who recover from a viral illness	10_days

System (1) uses the following beginning state values to compare the trends of the number of distinct populations within 350 days with and without vaccination interventions. These initial state variables are taken from Yang et al. [28] and make up the system defined:

$$S_0 = 50000000, V_0 = 0, A_0 = 1000, I_0 = 100, R_0 = 50 \tag{2}$$

The anticipated parameters are listed in Table 2.

## 3. A NUMERICAL APPROACH TO COVID-19 MODEL SOLVING

The FD is a numerical method that gives accurate approximation solutions and can also be used to solve non-linear systems of differential equations. The simplicity of the FD is one of its main advantages. A further benefit is the ease with which high-order approximations can be obtained, leading to high-order spatial discretization accuracy. Moreover, in this study, the epidemiological mathematical model is a nonlinear multiparameter system (1). As well, FD is preparing an accurate numerical solution quickly using MATLAB software in our work. With the initial circumstances, the current system can be solved via FD; the

zero terms are in Section 2. This study suggests that the genuine step size ( $h$ ) should be 0.02 weekly, 0.08 monthly, and so on. The numerals  $m=52,12$  denote the weeks and months, in that order, that make up a year.

FD becomes stable if the errors of FD at any stage of the computation are not magnified, and FD is a converged method when the numerical solution is closer to the truth or exact solution as the computation progresses. In the present research, the exact solution of the current model is unavailable, and FD is an iteration numerical method to solve the current model; therefore, the criteria for FD convergence is that the difference between any two successive results is tinny.

In order to find the Backward Finite Difference (BFD), it can be utilised in the first one, as below:

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

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

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

$$I_1(t) = I_0(t) + h(\theta\delta A_0(t) - \sigma I_0(t) - \mu I_0(t)) \quad (6)$$

$$R_1(t) = R_0(t) + h((1 - \theta)\delta A_0(t) + \sigma I - \gamma R_0(t) - \mu R_0(t)) \quad (7)$$

The first iteration  $S_1, V_1, A_1, I_1$  and  $R_1$  are computed using Eqs. (3)-(7) to provide the subsequent outcomes:  $S_1=49959826.9800989, V_1=40000, A_1=1027.65762186108, I_1=101.48466604$  and  $R_1=59.91906604$ .

The other terms are now found by using the Central Finite Difference (CFD) in the following manner:

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

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

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

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

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

#### 4. MODIFIED NUMERICAL SIMULATION TECHNIQUES FOR COVID-19 MODEL SOLVING

Two updated techniques of numerical simulation for the model (1) have been discussed and used in this work. The numerical simulation techniques exhibit similar convergence and stability to those of the FD. In the current study, the difference between the sequential numerical solutions is so small when the step size ( $h$ ) approaches zero; this is the convergence criteria used to determine when a sufficient

numerical solution is reached.

#### 4.1 MMC\_FD

One effective numerical simulation technique for resolving these kinds of mathematical problems is MMC\_FD [22]. This approach combines two distinct approaches: the Monte Carlo simulation process, and the numerical FD. The random-variable model coefficients are estimated using the Monte Carlo simulation approach. Firstly, generate the random numbers using the Monte Carlo simulation technique; the random number generated follows the standard uniform distribution on zero-one; that is  $\zeta \in (0,1)$ . Then the simulated random number generated is transformed to follow the uniform distribution on the created interval ( $a,b$ ) from the neighborhood of estimated values of parameters (from the previous study) via the inverse transform method (inversion method). Define the created interval that has the form:

$$a = \text{estimated parameter} - 0.2 \times \text{estimated parameter}$$

$$b = \text{estimated parameter} + 0.2 \times \text{estimated parameter}$$

The estimated parameters from the previous study are mentioned in Table 2 [28]. Therefore, the simulated parameter by the inverse transform method has the following formula:

$$b_i = F^{-1}(\zeta) = a + (b - a)\zeta$$

where,  $\zeta$  is the random number generated and simulated by Monte Carlo, such that  $\zeta \in (0,1)$ .  $b_i$  is the modified parameters,  $a$  and  $b$  are the lower and upper bounds of the created interval ( $a, b$ ).  $F$  is the uniform probability distribution on ( $a, b$ ). With  $i = 1, 2, \dots, m$ , to calculate  $S_i, V_i, A_i, I_i$  and  $R_i$ , they are taken into account as numerical COVID-19 model solutions.

The modified parameters  $b_i$  (with  $i$  being the number of parameters) of the model are defined as follows:

$$b1 = (\alpha - 0.2\alpha) + ((\alpha + 0.2\alpha) - (\alpha - 0.2\alpha)),$$

$$b2 = (\beta - 0.2\beta) + ((\beta + 0.2\beta) - (\beta - 0.2\beta)),$$

$$b3 = (\tau - 0.2\tau) + ((\tau + 0.2\tau) - (\tau - 0.2\tau)),$$

$$b4 = (\rho - 0.2\rho) + ((\rho + 0.2\rho) - (\rho - 0.2\rho));$$

$$b5 = (\delta - 0.2\delta) + ((\delta + 0.2\delta) - (\delta - 0.2\delta)),$$

$$b6 = (\vartheta - 0.2\vartheta) + ((\vartheta + 0.2\vartheta) - (\vartheta - 0.2\vartheta)),$$

$$b7 = ((1 - \rho) - 0.2(1 - \rho)) + (((1 - \rho) + 0.2(1 - \rho)) - ((1 - \rho) - 0.2(1 - \rho))),$$

$$b8 = (\sigma - 0.2\sigma) + ((\sigma + 0.2\sigma) - (\sigma - 0.2\sigma)),$$

$$b9 = (\gamma - 0.2\gamma) + ((\gamma + 0.2\gamma) - (\gamma - 0.2\gamma)),$$

$$b10 = (\mu - 0.2\mu) + ((\mu + 0.2\mu) - (\mu - 0.2\mu)),$$

$$b11 = (M - 0.2M) + ((M + 0.2M) - (M - 0.2M)).$$

Suppose that the number of simulations for the model parameters is  $k = 100, 1000$ , and the real step sizes in the current work is  $h = 0.02$  with 52 weeks, and  $h = 0.08$  with 24 months) whereas the number of iterations of numerical method is  $m = \text{length of the interval under study}/h$ .

The model is solved numerically using FD. All the processes are repeated for each repetition  $j$  when  $j = 1, \dots, k$  and  $i = 1, \dots, m$  (number of iteration). Then the last-iteration numerical results are collected for each repetition. By averaging the outcomes of the most recent FD iteration with each Monte Carlo repeat, the approximate solution that has

been estimated for the model under study is found. Due to the time variety for model coefficients, the MMC\_FD numerical simulation process is thought to be more dependable than traditional methods. Since the coefficients in natural epidemic models are random, the MMC\_FD numerical simulation process is thought to be a better approach than traditional techniques like FD, which solve models with set parameters. MATLAB software is used to implement the MMC\_FD method [22].

#### 4.2 MLH\_FD

The MLH finite difference numerical simulation approach combines a numerical method known as the FD with simulation processes using Latin hypercube sampling (LHS) [21]. It is regarded as one of the most trustworthy techniques for resolving a set of first-order nonlinear ordinary differential equations. While FD is used to solve the model numerically, LHS is used to estimate the model's coefficients, which are regarded as random variables. The mean of the final FD iteration results for each LHS repeat represents the approximate solution that has been estimated for the model that is being studied. The previously discussed MMC\_FD method is similar to the MLH\_FD method. The difference in the solution procedures of MLH\_FD is in the use of the LHS simulation method to estimate the coefficients of the model [21]. Furthermore, MLH\_FD is quicker and more accurate than the MMC\_FD approach, because it simulates model parameters simultaneously. MATLAB software is used to implement this integrated method; otherwise, the implementation details for MLH\_FD are the same as those for MMC\_FD, which were discussed in the preceding section.

### 5. ASM

Two novel approaches are developed in this section to solve the models under consideration, particularly the epidemic models. These techniques are regarded as a novel approach between numerical simulation and statistics since they have proven to be successful and efficient in producing superior accuracy compared to the updated numerical simulation techniques. Indeed, the shrinkage estimation method consists of the actual or classical value multiplied by a weighting function  $w$  and prior values for the estimator multiplied by  $(1 - w)$ ; it is believed that the prior value (from the previous study) is close to the true or exact value of the estimator. In general, the advantage of the shrinkage estimation method is that it gives the estimator more accuracy than the classical estimation method. In addition, the prior information in the estimation method reduces the costs of time and money. In the current work, FD has been considered the actual value, and MMC\_FD and MLH\_FD have been suggested as prior values (since their methods were suggested in a previous study). The mean of the solutions  $\widehat{Sol}_{ASM}$  is considered an estimate solution for the system under study when a weighting function  $0 \leq w \leq 1$  is used. The proposed formula is as follows:

$$\widehat{Sol}_{ASM} = W(\text{actual/classical value}) + (1 - W)(\text{prior value})$$

#### 5.1 ASM\_MMCFD

The statistical form for shrinkage estimation,

ASM\_MMCFD, is a novel strategy that combines numerical simulation techniques, called MMC\_FD in the current work, with the traditional approximation method, or FD in the current study. When it comes to solving the nonlinear mathematical systems under consideration, this freshly created technology performs more accurately and reliably than earlier numerical simulation techniques such as MMC\_FD and MLH\_FD. Between statistical and approximate approaches, ASM\_MMCFD provides different estimation values. The MATLAB software was utilised to compute this approach, which was then used as the algorithm that follows demonstrates:

Step 1: A model's parameters have been simulated  $n$  times using Monte Carlo (with  $n$  being the number of repetitions).

Step 2: A single value is obtained from Step 1 for each random parameter in the system, and that value is then changed to a specific distribution (uniform distribution).

Step 3: FD is used to numerically solve the system  $m$  times through iterations, by using BFD for the first time and CFD for other times. The ultimate solution that is chosen is the last iterative result, which yields the numerical solutions.

Step 4: For  $n$  repetitions, Steps 1 and 2 are repeated again.

Step 5: The final average outcomes in Step 4 are calculated, which allows MMC\_FD to identify a solution for the system under consideration.

Step 6: The proposed algorithm is used as follows:

$$\widehat{Sol}_{ASM\_MMCFD} = W(FD) + (1 - W)(MMC\_FD)$$

Since the solution of the system for ASM\_MMCFD is called the estimate solution  $\widehat{Sol}_{ASM\_MMCFD}$  when  $w$  is a weight function, with  $0 \leq w \leq 1$ .

#### 5.2 ASM\_MLHFD

Another proposed method is ASM\_MLHFD, which combines the standard numerical method FD with another numerical simulation methodology, MLH\_FD, to develop a novel shrinkage estimation statistical algorithm. When addressing such mathematical models, our suggested procedure performs more accurately and efficiently than existing approximation simulation techniques. ASM\_MLHFD produces alternative estimation values between statistical and approximate techniques. The MATLAB software is used to accomplish this strategy, as seen in the following algorithm:

Step 1: LHS has simulated every model parameter  $n$  times (with  $n$  being the number of repetitions) at once.

Step 2: For each random parameter (uniform distribution), the system specifies and replaces a single value.

Step 3: FD is used to numerically solve the system  $m$  times through iterations, by using BFD for the first time and CFD for other times. The final solution is the last iterative outcome to obtain the numerical solutions.

Step 4: For  $n$  repetitions, Steps 1 and 2 are repeated again.

Step 5: The mean of the final data in Step 4 should be calculated using MLH\_FD to discover results for the system under consideration.

Step 6: The updated algorithm is applied as follows:

$$\widehat{Sol}_{ASM\_MLHFD} = W(FD) + (1 - W)(MLH\_FD)$$

Estimate solution  $\widehat{Sol}_{ASM\_MLHFD}$  is the name for the system solution of ASM\_MLHFD, with  $w$  being a weight function, and  $0 \leq w \leq 1$ .

**6. RESULTS AND DISCUSSION**

The epidemic model's approximate simulation values used to examine individuals who had COVID-19 vaccinations are covered in this part, along with an analysis of them. For the research period spanning from the beginning of 2021 to the end of 2022, Table 3 and Table 4 present approximate simulation findings over a two-year period with  $h = \{0.02, 0.08\}$  step size in week and month using 100 repetitions. It should be noted that Table 5 shows a numerical comparison between the numerical technique FD and the suggested approximation shrinking methods ASM\_MMCDFD and ASM\_MLHFD, as well as the numerical simulation approaches MMC\_FD, MLH\_FD, and  $S, V, A, I,$  and  $R$ . Additionally, Table 6 and Table 7 show the outcomes of the approximate simulation solution with 1000 repetitions regarding the social groupings  $S, V, A, I$  and,  $R$  for the years 2025 and after. The absolute error of the proposed methods is less than that of the other methods used for all groups of pollution. Since ASM\_MLHFD has the lowest absolute error number among the suggested approaches, it can be concluded that it is the most accurate and dependable approach. The test method for the convergence and stability of iterative methods, which has been applied in Table 8, the details of the method can be seen in the source [29]. Table 8 explains the stability of the new algorithms ASM\_MMCDFD and ASM\_MLHFD that the current study uses, as well as how the approximation shrunken technique (ASM\_MLHFD) is reducing the step size more than other methods. To demonstrate the convergence of the employed approaches, when  $k = 1, 2, \dots$ , the error between the recommended method in step size  $h$  with that in step size  $h/2k$ , is denoted by  $E_h$  [29]. In this study, the error of simulation numerical methods is called the convergence error.

The prediction intervals (5<sup>th</sup> percentile, 95<sup>th</sup> percentile) for the results of MMC\_FD, MLH\_FD, ASM\_MMCDFD, and

ASM\_MLHFD up until 2025 include the minimum bound (5%) and maximum bound (95%). The results of these methods must be inside the predicted intervals (Tables 9 and 10).

Another measure, mean squared error (MSE), is used, due to the availability of simulation and randomness in the proposed methods. Therefore, this measure is more suitable than the rest of the other measures that depend on exact values not available in the system under study. The suggested form of MSE in the present work is as follows:

$$MSE_{ASM} = \sum_{w=0.1}^1 \frac{(\widehat{Sol}_{ASM}(w) - FD)^2}{10},$$

$$w = 0.1, 0.2, \dots, 1$$

Table 11 displays the MSE results of the new algorithms ASM\_MMCDFD and ASM\_MLHFD compared with FD. Then it can be noted that the approach method ASM\_MLHFD has the smallest error when the step size  $h = 0.02$  is weekly and there are 1000 repetitions with 208 iterations.

Table 8 presents the residual error  $|ASM_{i+1} - ASM_i|$  for comparison between the proposed methods as to which is better. On the other hand, it proves the stability and convergence of these methods, as we notice that the error between every two successive results is very small and there is no gap for ten successive steps under conditions of 1000 repetitions through two years for the subpopulation  $I(t)$ . The results indicated the stability and convergence of these methods; ASM\_MLHFD has a smaller error than ASM\_MMCDFD. The residual error for other subpopulations can also be found to lead to a similar conclusion. Under different conditions, ASM\_MLHFD proved to be better than ASM\_MMCDFD.

**Table 3.** Estimated COVID-19 model simulation results after two years of (24, 104) iterations

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

**Table 4.** Approximate simulation results of the COVID-19 model after two years of (24, 104) iterations

Model Variables	Step Size	FD (2 years)	ASM_MMCDFD (100 Repetitions)	ASM_MLHFD (100 Repetitions)
$S(t)$	0.08 (monthly)	38071016.66343352	38071016.65930412	38071016.66109873
	0.02 (weekly)	38070276.77017017	38070276.75302661	38070276.76903357
$V(t)$	0.08 (monthly)	10553860.66802990	10553860.64810284	10553860.65903982
	0.02 (weekly)	10553798.07126030	10553798.04968830	10553798.06752017
$A(t)$	0.08 (monthly)	858150.28334196	858150.26889502	858150.27994930
	0.02 (weekly)	858658.95841104	858658.94323870	858658.95129034
$I(t)$	0.08 (monthly)	70272.14889928	70272.13906561	70272.14208755
	0.02 (weekly)	70314.83744996	70314.82609875	70314.83480975
$R(t)$	0.08 (monthly)	407636.46528549	407636.43732093	407636.45930567
	0.02 (weekly)	407887.56435948	407887.53580647	407887.55670321

**Table 5.** Absolute error within two years for ASM\_MLHFD, MLH\_FD, MMC\_FD, and ASM\_MMCFD compared with FD

Model Variables	Step Size	MMC_FD (100 Repetitions)	MLH_FD (100 Repetitions)	ASM_MMCFD (100 Repetitions)	ASM_MLHFD (100 Repetitions)
$S(t)$	0.08 (monthly)	0.08330511	0.00459702	0.00412940	0.00233479
	0.02 (weekly)	0.06004857	0.03009794	0.01714356	0.00113660
$V(t)$	0.08 (monthly)	0.03856189	0.03082729	0.01992706	0.00899008
	0.02 (weekly)	0.05183007	0.02674218	0.02157200	0.00374013
$A(t)$	0.08 (monthly)	0.07276862	0.02853649	0.01444694	0.00339266
	0.02 (weekly)	0.04808625	0.02826896	0.01517234	0.00712070
$I(t)$	0.08 (monthly)	0.03929750	0.01644987	0.00983367	0.00681173
	0.02 (weekly)	0.02840545	0.01713391	0.01135121	0.00264021
$R(t)$	0.08 (monthly)	0.03538336	0.02663659	0.02796456	0.00597982
	0.02 (weekly)	0.06699347	0.05119116	0.02855301	0.00765627

**Table 6.** Anticipated COVID-19 model numerical simulation results with (48, 208) iterations (2021 - 2025)

Model Variables	Step Size	FD (Four Years)	MMC_FD (1000 Repetitions)	MLH_FD (1000 Repetitions)
$S(t)$	0.08 (monthly)	5596247.41805423	5523824.21037309	5554322.54786577
	0.02 (weekly)	5594499.20621553	5535150.0856032	5570547.90651805
$V(t)$	0.08 (monthly)	11390855.697436	11318213.417702	11335644.830232
	0.02 (weekly)	11389578.4470469	11314056.243055	11340525.023144
$A(t)$	0.08 (monthly)	9679318.64840848	9638924.64702312	9653421.10234362
	0.02 (weekly)	9678455.6118537	9611283.4570231	9642301.80122570
$I(t)$	0.08 (monthly)	2329257.57547543	2298435.1304572	2304572.3900318
	0.02 (weekly)	2329410.25714638	2284373.8130920	230076.75502584
$R(t)$	0.08 (monthly)	20919855.5339504	20453182.2704518	20554608.4509824
	0.02 (weekly)	20923589.5192151	2036458.4302958	20471066.0931247

**Table 7.** Estimated COVID-19 model simulation results with (48, 208) iterations (2021 - 2025)

Model Variables	Step Size	FD (Four Years)	ASM_MMCFD (1000 Repetitions)	ASM_MMCFD (1000 Repetitions)
$S(t)$	0.08 (monthly)	5596247.41805423	5574645.69053531	5585089.06476432
	0.02 (weekly)	5594499.20621553	5561233.90871235	5581467.09734521
$V(t)$	0.08 (monthly)	11390855.697436	11380132.70765231	11388250.12407854
	0.02 (weekly)	11389578.4470469	11367910.51012435	11378311.71298450
$A(t)$	0.08 (monthly)	9679318.64840848	9665121.52034513	9672540.04503211
	0.02 (weekly)	9678455.6118537	9655713.70487620	9667045.88530127
$I(t)$	0.08 (monthly)	2329257.57547543	2311452.61437041	2320765.00765931
	0.02 (weekly)	2329410.25714638	2314642.45032168	2322745.39045612
$R(t)$	0.08 (monthly)	20919855.5339504	20643527.20487594	20849036.90485761
	0.02 (weekly)	20923589.5192151	20534817.49085632	20734918.03756029

**Table 8.** Residual error  $|ASM_{i+1} - ASM_i|$  for methods with 1000-repetitions through two years for subpopulation  $I(t)$

Real Step Size	ASM-MMCFD Results	ASM-MLHFD Results
0.08 (monthly)	0.01666544	0.01393020
0.02 (weekly)	0.01523048	0.01207432
0.08 (monthly)	0.01469597	0.01187046
0.02 (weekly)	0.01392549	0.01036521
0.08 (monthly)	0.01012994	0.00820355
0.02 (weekly)	0.00934875	0.00674032
0.08 (monthly)	0.00813537	0.00587609
0.02 (weekly)	0.00760342	0.00438721
0.08 (monthly)	0.00645293	0.00382014
0.02 (weekly)	0.00432701	0.00225618

**Table 9.** Prediction intervals of MMC\_FD and MLH\_FD results

MMC_FD from 2021 to 2025 ( $t \leq 48$ )		
Subpopulation	(100 Repetitions)	(1000 Repetitions)
$S(t)$	(1672933.76258185, 28152829.0835285)	(1754203.70242891, 25014911.2078358)
$V(t)$	(4854332.12987130, 19907265.14562321)	(4914287.04244360, 201826524.1592367)
$A(t)$	(2526701.92714029, 14027604.9421523)	(2912593.10100395, 14259301.2041330)
$I(t)$	(783250.04730922, 3925657.20437419)	(443503.12514210, 3763219.01559544)
$R(t)$	(2730187.32175010, 46520652.1040678)	(3981302.03099372, 43217383.1570850)
$S(t)$	(1593762.12557087, 26140582.0313621)	(1684705.3193358, 27023049.0124453)
$V(t)$	(5913025.11470490, 20132284.3951547)	(6553372.14235131, 21032513.3021521)
$A(t)$	(2632071.26573405, 11075975.0123805)	(2997241.19872519, 12276377.9946024)
$I(t)$	(379785.39352095, 3189805.23854122)	(473091.72607831, 3850660.14783108)
$R(t)$	(2901088.21938931, 33981746.0342931)	(3230620.15092162, 36930477.95427287)

**Table 10.** Prediction intervals of ASM\_MLHFD and ASM\_MMCFD results

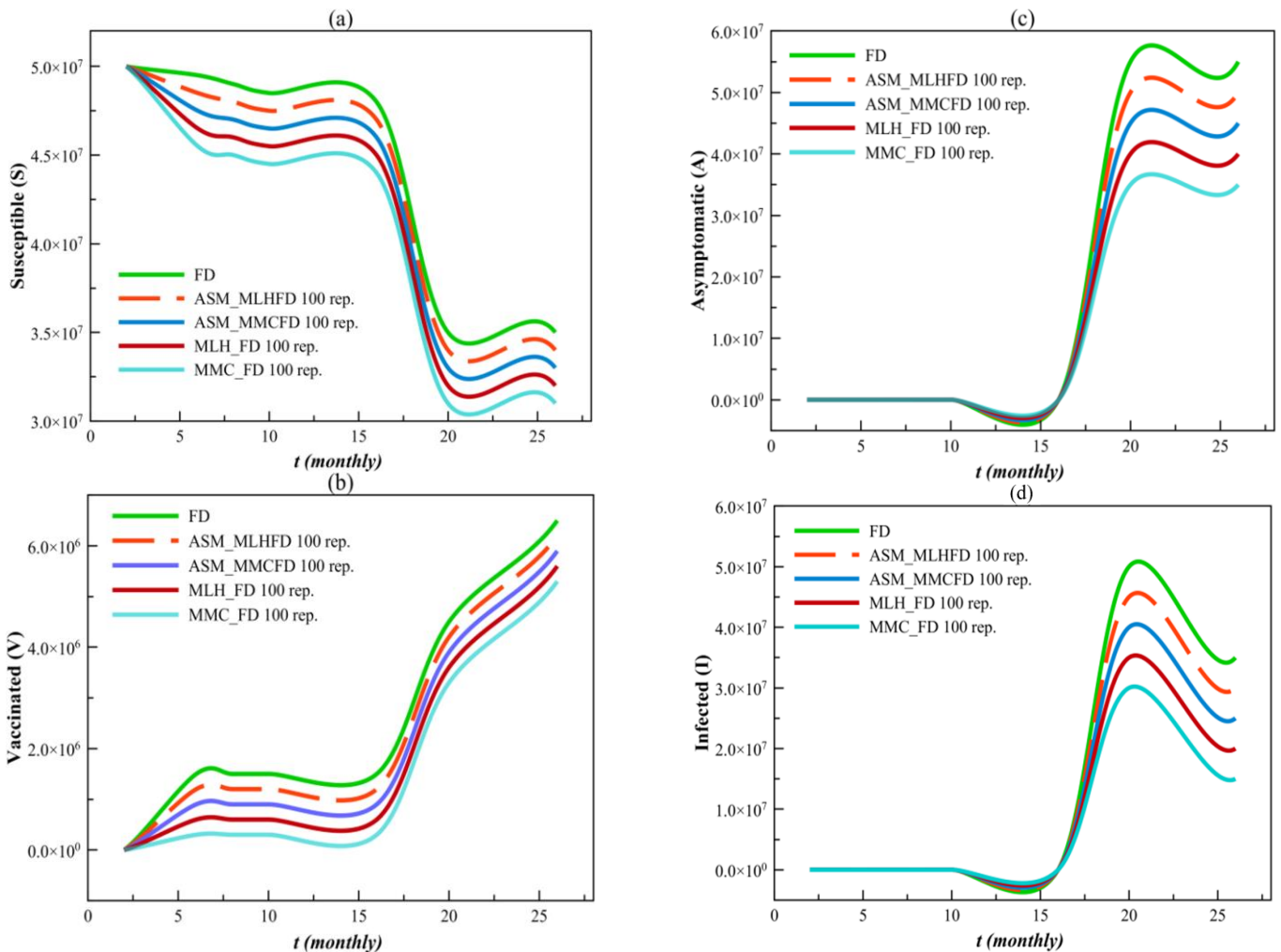
ASM_MMCFD from 2021 to 2025 ( $t \leq 48$ )		
Subpopulation	(100-Repetitions)	(1000-Repetitions)
$S(t)$	(3950853.19810822, 8355942.10072372)	(3932267.80917685, 8945320.92304827)
$V(t)$	(10913288.1892918, 11689684.1091632)	(11007744.06092943, 11905732.1603113)
$A(t)$	(8233120.10583944, 11710580.0648323)	(8234522.38043491, 11649250.3038142)
$I(t)$	(270458.91055872, 2817817.93681025)	(284825.98708533, 2849618.70397891)
$R(t)$	(2973142.15008971, 25132787.24283071)	(2703462.93051224, 25928150.72950831)

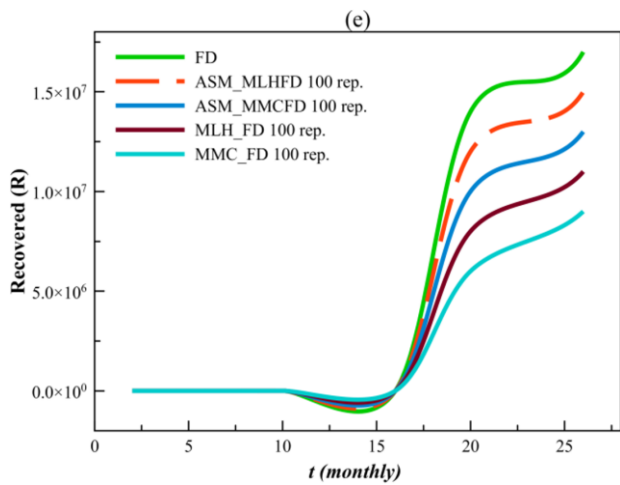
  

ASM_MLHFD from 2021 to 2025 ( $t \leq 48$ )		
Subpopulation	(100-Repetitions)	(1000-Repetitions)
$S(t)$	(2943174.25839341, 19788642.09436108)	(3033499.13964752, 25023841.02057831)
$V(t)$	(843790.52226933, 11579276.0110593)	(789038.10282076, 13489552.13040319)
$A(t)$	(370172.16010234, 16581299.26135940)	(621193.72131032, 17216089.0837042)
$I(t)$	(110188.33132253, 2900366.13318390)	(287403.01870354, 3225683.210328872)
$R(t)$	(1543908.02479968, 24966325.13512590)	(2386531.07820631, 25236288.51056642)

**Table 11.** MSE of the vaccine model of the COVID-19 pandemic for ASM\_MMCFD and ASM\_MLHFD through four years

Model Variables	Step Size	$m$ Iterations	Present ASM_MMCFD Results		Present ASM_MLHFD Results	
			100 Repetitions	1000 Repetitions	100 Repetitions	1000 Repetitions
$S(t)$	0.08 monthly	48	0.00363453	0.00312174	0.00029865	0.00018854
	0.02 weekly	208	0.00293345	0.00230821	0.00022671	0.00012389
$V(t)$	0.08 monthly	48	0.00863045	0.00693878	0.00518570	0.00340532
	0.02 weekly	208	0.00631062	0.00451512	0.00355874	0.00239670
$A(t)$	0.08 monthly	48	0.00923731	0.00641730	0.00034628	0.00024133
	0.02 weekly	208	0.00729035	0.00487783	0.00028201	0.00019780
$I(t)$	0.08 monthly	48	0.00732361	0.00569011	0.00421838	0.00354622
	0.02 weekly	208	0.00573012	0.00430936	0.00302557	0.00220514
$R(t)$	0.08 monthly	48	0.01332731	0.01172313	0.00942925	0.00640313
	0.08 weekly	208	0.01024522	0.00943924	0.00731737	0.00434077





**Figure 1.** Comparison of approximate simulation method curves during two years and 100 repetitions

Figure 1 displays the curves of the methods applied over a two-year period with 100 repetitions and a monthly step size of  $h=0.08$  to solve the COVID-19 mathematical model. The curves in Figure 1(a) depict the group  $S(t)$  of people who are not currently infected with the pandemic but could do so at any time. The curve for this group starts out slowly and decreases until the tenth month, then starts to gently climb and continues until the fifteenth month. Following that, mixing and non-compliance with health prevention measures cause the wave to begin to increase, which causes the curve to sharply decline. It doesn't end until the twentieth month, when it starts to stabilise a little. Group  $V(t)$  of individuals receiving COVID-19 vaccinations exhibits a distinct and progressive rise in their curve until the fifteenth month. After that, as seen in Figure 1(b), it keeps rising until the end of the research period. The epidemic-affected individuals  $I(t)$  are shown in Figure 1(d). While Figure 1(c) is linked to the group of individuals  $A(t)$  who are virus carriers but do not exhibit signs of illness. Due to the influence and efficacy of the vaccination on society, it is evident that the curve increases gradually and slightly until the fifteenth month, at which point it increases more sharply to the end of the study interval.

Figure 1(e) shows how this group's  $R(t)$  curve correlates with the group of individuals who were taken off the infection list. Between the fifteenth month and the conclusion of the study period, there is a discernible increase in this category's curve.

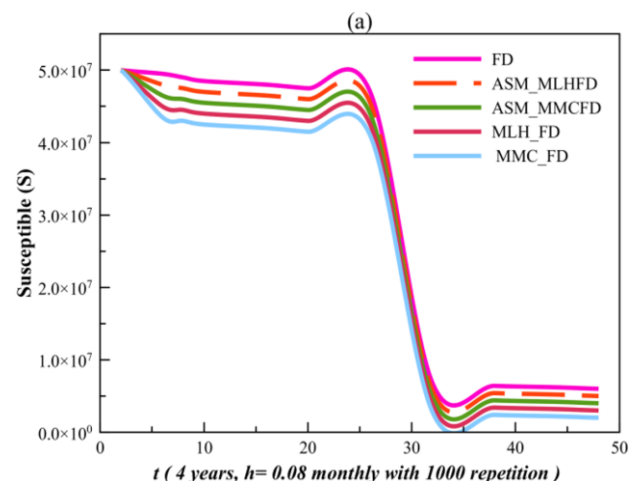
The COVID-19 epidemic's mathematical model's curve, which has 1000 repeats over four years, from 2021 to 2025, is depicted in Figure 2. This curve in Figure 2(a) is linked to those who do not have the infected  $S(t)$  virus. The group's curve gradually begins to fall for all numerical simulation methods utilized throughout the study's initial few months (step size  $h = 0.08$ ) and monthly for the following four years. The curve then sharply declines as a result of mixing and noncompliance with health-preventive measures, and then stabilizes in the final few months of the study due to people's willingness to receive the COVID-19 vaccination. It is observed that the degree to which the FD numerical method and the suggested methods, ASM\_MLHFD and ASM\_MMCFD, resemble those of other numerical simulation techniques. This group's curve, shown in Figure 2(b), represents individuals who received 1000 repetitions of the COVID-19  $V(t)$  vaccine. It is evident that this category's curve rises noticeably in the first few months for

ASM\_MMCFD, ASM\_MLHFD, FD, MMC\_FD, and MLH\_FD within four years. After that, due to the rise in the number of people receiving vaccinations against this disease at the halfway point of the study period, the curve starts to rise sharply and continues to rise.

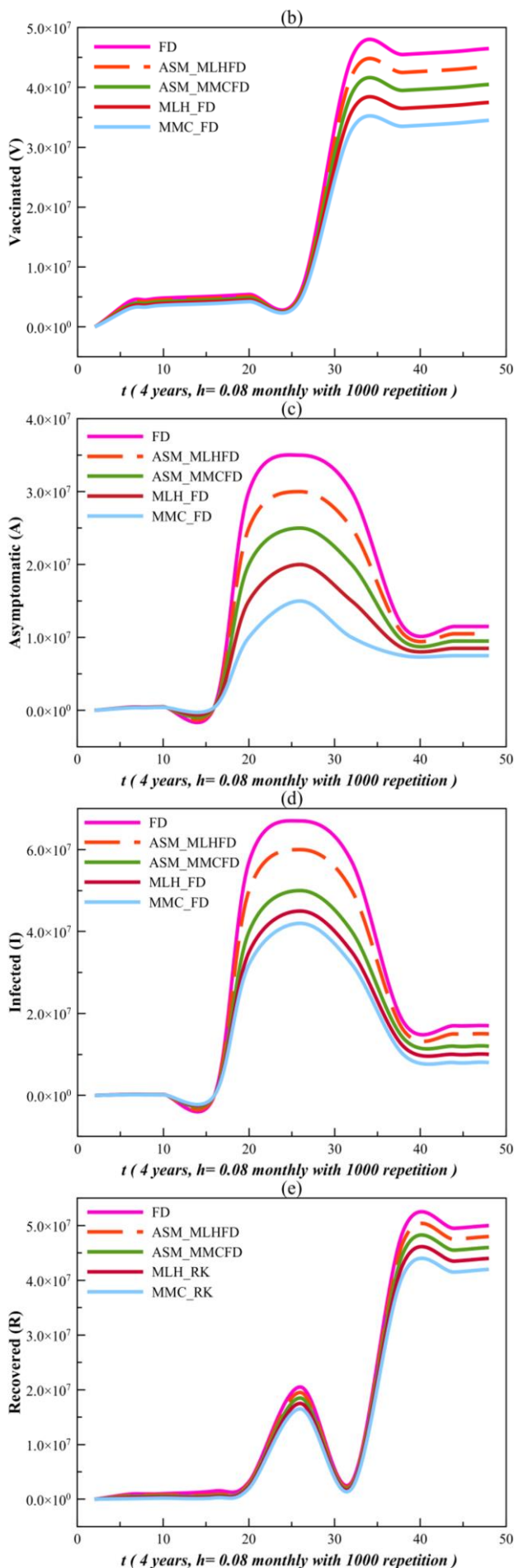
Finally, the curve stabilizes at the end of the study period. Furthermore, we observe with great clarity how near the FD curve the novel approach ASM\_LH and ASM\_MC curves are to the curve from the other approximation simulation techniques.

The curve of this group  $A(t)$ , shown in Figure 2(c), relates to individuals who carry the virus but do not exhibit symptoms of infection with the epidemic. Due to mixing and non-compliance with health preventative strategies, midway through the research period, specifically in the 20<sup>th</sup> month, there is a spike in the maximum level. After that, the curve declines until the forty-first month, when it levels out and stays that way until the study's conclusion. It is also observed that, in comparison to the other approaches, the suggested method ASM\_MLHFD's curve more closely converges with the numerical method FD's curve. The infected individuals depicted in Figure 2(d) exhibit symptoms of infection  $I(t)$ . It is observed that for all approaches (ASM\_MLHFD, ASM\_MMCFD, FD, MMC\_FD, and MLH\_FD) with 1000 repetitions and a step size of  $h=0.08$  weekly, the curve of this category grows. This increase peaks in the twentieth month of the study period, and subsequently decreases until the 40<sup>th</sup> month, when it stabilizes until the study period's conclusion. Additionally, the ASM\_MLHFD and ASM\_MMCFD suggested approaches converge more than the curves from the other methods. Figure 2(e) shows that the curves for this group of individuals who were removed from the infection list indicate that they either entirely recovered from the pandemic or, as a result, they experienced  $R(t)$ . The amount of rise and decrease in this category's curve, however, differs for each of the four research years within the 48-month study period. The rise begins in the 20<sup>th</sup> month and continues until the 25<sup>th</sup>, after which it decreases once more at the end of the 30<sup>th</sup> month, before rising significantly to reach its peak height in the 40<sup>th</sup> month and stabilizing in the final months of the study. The suggested algorithm, ASM\_MLHFD's curve continues to resemble the FD curve more than the other numerical simulation methods.

Additionally, Figure 2 illustrates how, at  $h=0.08$  weekly with 1000 repeats, the approximation simulation algorithms ASM\_MLHFD, ASM\_MMCFD, MMC\_FD, and MLH\_FD converge.







**Figure 2.** Comparison of approximation curves for simulation techniques from 2021 to 2025

The model solution for the numerical simulation methods and the suggested estimating methods in Table 6 and Table 7 are all found to fit within the Table 8 and Table 9 forecast timeframe. Conversely, the WHO's data for the previous and present years, as demonstrated in Figures 1 and 2, clearly indicates that the forecast of the COVID-19 epidemic's behavior for this study fits that of other studies in the same field.

## 7. CONCLUSION

The shrinkage estimation is characterized by being more efficient than the classical estimations, as previous studies have proven, and for the first time, it is employed in the proposed formation as a special formula that combines numerical simulation methods and classical numerical methods to give a new approximate approach that appears to provide improved performance over other methods that were used to solve the nonlinear system.

A new style of numerical simulation method in the form of shrinkage estimation has been proposed to estimate the solution of the system of differential equations. Using a uniform distribution and a real step size, a sample size is proposed as the number of iterations for the numerical method used. The proposed numerical simulation methods via the estimation method fare better than the classical numerical simulation methods in the current study. Moreover, it's applications in various life sciences, especially epidemiological models.

This study's mathematical model is COVID-19, which is written as a set of ordinary differential equations in order one that are nonlinear. There will be a 48-month study term from 2021 to 2025. To solve the system under study, a variety of techniques are employed, including MMC\_FD and MLH\_FD, numerical simulation techniques, and the numerical method FD. Finally, the two proposed methods, ASM\_MLHFD and ASM\_MMCFD, give the best convergence in the results under the current study, where the closest approximation is the shrunken approach, ASM\_MLHFD. It notes that increasing the number of iterations with the proposed methods leads to a slight increase in the accuracy of the results, which indicates that these methods do not require many iterations, which saves time, cost, and effort in their practical applications in life.

An impression of the virus's effects on society is provided by this study. The findings indicate that over the study period, there was a decline in the category  $S(t)$  of individuals who were not affected by the epidemic. While category  $V(t)$  is linked to those who have received vaccinations, we observe a gradual rise in this category due to the influence and efficacy of the vaccine on society. Similarly, category  $A(t)$ , which is made up of infected individuals who do not exhibit symptoms, shows a gradual increase in this category due to noncompliance with social distancing and health prevention measures. When people are informed to get vaccinated against the virus, we observe a progressive decline in all ways under observation, even though category  $I(t)$  of those who are infected and their symptoms and indications are evident to them. In summary, there has been a noticeable rise in the category  $R(t)$  of individuals who have either recovered from their illness or passed away from it, a trend that is evident across all study techniques.

This study has the importance of predicting the behavior of the outbreak of the epidemic in the near future within a specific time period under study. This prediction appears in the form

of a predictive period that has minimum and maximum limits for each category of society, as shown in Table 8 and Table 9.

It is suggested that ASM can be used to replace the FD method with another numerical or approximate method, replace the Monte Carlo/Latin Hypercube simulation technique with other kinds of simulation techniques, and use different distributions for the simulated parameters that have a probability distribution.

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