

An Efficient Analytical Simulation Algorithm For Solving an Epidemiological model

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ABSTRACT

Combining an analytical method which is Variation Iteration Method (VIM) with one of the simulation methods such as Monte Carlo (MC) method to create a new algorithm represents the idea of this research. where it can be applied to a mathematical system dealing with random variables and at the same time nonlinear. This algorithm is used for the first time in this study through which the parameters of this non-linear system are estimated using MC and then using VIM to obtain analytical solutions, this study gives an idea and impression about the behavior of this model in the future. The results are compared with the previous studies using the absolute error as well as the relative error, finally the results are put in tables and also represented graphically.

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1. Introduction

The importance of this study lies in knowing whether these social epidemics will continue to spread or will decline in the coming years, as these models are used to analyze infectious diseases and epidemics into stages. Several researchers have studied epidemiological models and their solutions, including Guerrero, Santonja and Villanueva in 2006 [1]. Sánchez, et al. The impact of cocaine use in Spain, in 2011 [2]. M. A. Mohammed, Noor, Siri and Ibrahim,

A new numerical proposal examines multidimensional random sampling to address cocaine use in Spain, in 2018 [3]. In 2010, a study of the impact of alcohol consumption and its effect on society by Santonja, et al. [4]. The social obesity model was also studied in 2010, specifically in the city of Valencia by Santonja, et al. [5]. In 2015. M. A. Mohammed, Noor, Ibrahim and Siri solved, study of a model for reducing obesity resulting from health awareness campaigns [6].

In 1997, Ji-Huan decided to study the analytical method is the Variational Iteration method (VIM), which is considered one of the appropriate and reliable methods for solving differential equations [7, 8]. This method has been widely used in scientific applications, including engineering, to solve equations of various types, including

linear, nonlinear, homogeneous, and non-homogeneous. The importance of this analytical method lies in the fact that it does not require special procedures and relies on iteration in its operation [9]. Autonomous ordinary differential systems one of the problems were solved by VIM in 1999 [7]. Also the differential equations of fractional order in 2000 [10].

Monte Carlo uses a traditional technique to generate random numbers for a sample of a probability distribution [11]. Many researchers have developed epidemiological models such as SIS, SIR, SEIR, and others, and have focused on studying them and epidemiological modeling, as these mathematical models are considered probabilistic and deterministic [12-14], see also [15, 16]. Various analytical methods have been used to solve epidemiological mathematical models, and some of these methods are Temimi-Ansari method, Daftardar- Jafari method, and Banach contraction method, [17], LTAM method for mixing Laplace transform with Tamimi and Ansari iterative method [18].

Several researchers have used methods to modify numerical simulations by combining two different approaches to obtain the best results, such as Mohammed, et al. in 2018 use Monte Carlo simulation technology and numerical iteration method which are Mean Latin Hypercube Finite Difference (MLH_FD), I studied a new numerical approach to solving a model of cocaine use in Spain [3]. The Mean Monte Carlo simulation with finite difference (MMC_FD) method to studying a non-linear epidemiological model through random sampling [19]. Integrating numerical simulation and shrinkage estimation techniques for solving epidemiological models was studied by Sabea, Mahdi A., and Maha A. Mohammed in 2024 [20].

This study includes several methods for solving the mathematical model used, including the analytical method (VIM), the Monte Carlo simulation method (MC), the numerical simulation method (MMC_FD), and finally the new approach method (MC_VI)

2. SEIRV Model incorporating a Holling type-II functional response

The epidemiological model [1] in this section divides the overall population N at time $t \geq 0$ into five segments, which are susceptible (S) 90 %, exposed (E) 5%, infected (I) 4%, recovered (R) 0 % and vaccinated (V) 1 %. Consequently,

$$N(t) = S(t) + E(t) + I(t) + R(t) + V(t)$$

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \beta \frac{SI}{1 + \alpha I} - (\mu + \gamma_2)S \\ \frac{dE}{dt} &= \beta \frac{SI}{1 + \alpha I} - (\alpha + \mu)E \\ \frac{dI}{dt} &= \alpha E - (\gamma_1 + \mu)I \\ \frac{dR}{dt} &= \gamma_1 I - (\mu + \gamma_2)R \\ \frac{dV}{dt} &= \gamma_2 S + \gamma_2 R - \mu V \end{aligned} \quad (1)$$

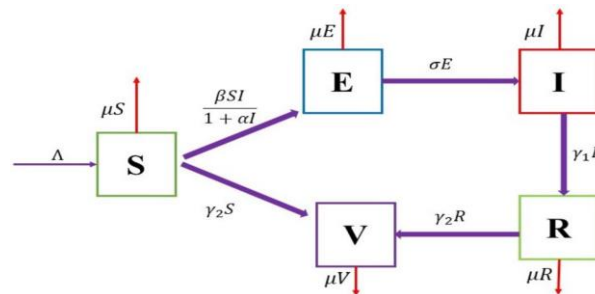


Fig. 1- This figure illustrates the relationship between the five social classes (susceptible, exposed, infected, recovered, vaccinated) and the effect of a type II Hollen response over time t .

Table 1- Parameters of SEIRV Model [1]

Notation	Definition	Value
Λ	Recruitment rates	0.056768
β	Transmission rates	0.065 (estimated)
σ	Latency period	1/5.669
γ_1	Recovery rate	0.5158 (estimated)
μ	Death rates	0.0170
γ_2	Vaccination rate	0.7571
α	Saturation rate	0.0010 (estimated)

3. Variation Iteration Method (VIM)

Using VIM to solve the system (1) under study with the initial conditions: $S_0(t)$, $E_0(t)$, $I_0(t)$, $R_0(t)$ and $V_0(t)$, and the predicted parameters that are given in Table 1: $\Lambda, \beta, \sigma, \gamma_1, \alpha, \mu, \gamma_2$ and $\alpha, m=10$ refers to numbers of years from 2006 to 2030. The zero terms become: $S_0(t) = 0.9$, $E_0(t) = 0.05$, $I_0(t) = 0.04$, $R_0(t) = 0$ and $V_0(t) = 0.01$ as following:

$$S_{k+1}(t) = S_k(t) + \int_0^t \lambda \left(S'_k(t) - \left(\Lambda - \beta \frac{S_k(t)I_k(t)}{1 + \alpha I_k(t)} - (\mu + \gamma_2)S_k(t) \right) \right) dt, \text{ for all } k \geq 0, \quad (2)$$

$$E_{k+1}(t) = E_k(t) + \int_0^t \lambda \left(E'_k(t) - \left(\beta \frac{S_k(t)I_k(t)}{1 + \alpha I_k(t)} - (\alpha + \mu)E_k(t) \right) \right) dt, \text{ for all } k \geq 0, \quad (3)$$

$$I_{k+1}(t) = I_k(t) + \int_0^t \lambda \left(I'_k(t) - (\alpha E_k(t) - (\gamma_1 + \mu)I_k(t)) \right) dt, \text{ for all } k \geq 0, \quad (4)$$

$$R_{k+1}(t) = R_k(t) + \int_0^t \lambda \left(R'_k(t) - (\gamma_1 I_k(t) - (\mu + \gamma_2)R_k(t)) \right) dt, \text{ for all } k \geq 0. \quad (5)$$

$$V_{k+1}(t) = V_k(t) + \int_0^t \lambda \left(V'_k(t) - (\gamma_2 S_k(t) + \gamma_2 R_k(t) - \mu V_k(t)) \right) dt, \text{ for all } k \geq 0. \quad (6)$$

The Lagrange multiplier is $\lambda = -1$. By substituting this value in all Eqs. (2-6), the zero terms become:

$$S_0(t) = 0.9, E_0(t) = 0.05, I_0(t) = 0.04,$$

$$R_0(t) = 0, V_0(t) = 0.1,$$

Now, to find $S_1(t)$, $E_1(t)$, $I_1(t)$, $R_1(t)$ and $V_1(t)$, in Eqs. (2-6), when substituting ($k=0$), the following has been obtained:

$$S_1(t) = 0.9 - 0.06199932t$$

$$E_1(t) = 0.05 - 0.09447554t$$

$$\begin{aligned}I_1(t) &= 0.04 + 0.17252354t \\R_1(t) &= 0.01099838t \\V_1(t) &= 0.1 + 0.35099838t\end{aligned}$$

Same way, when ($k=1$), Eqs. (2-6) the following has been gotten:

$$\begin{aligned}S_2(t) &= 0.9 - 0.06199932t + 0.00311026t^2 - 0.00012763t^3 \\E_2(t) &= 0.05 - 0.09447554t + 0.32148843t^2 + 0.68721148t^3 \\I_2(t) &= 0.04 + 0.17252354t + 0.73192231t^2 + 0.93762217t^3 \\R_2(t) &= 0.01099838t + 0.08051279t^2 + 0.43778921t^3 \\V_2(t) &= 0.1 + 0.35099838t + 0.74338629t^3\end{aligned}$$

when ($k=2$), can be achieve the following:

$$\begin{aligned}S_3(t) &= 0.9 - 0.06199932t + 0.00311026t^2 - 0.00012763t^3 + 1.99202672 \times 10^{-8}t^4 - 5.52507601 \times 10^{-10}t^5, \\E_3(t) &= 0.05 - 0.09447554t + 0.32148843t^2 + 0.68721148t^3 - 2.69344475 \times 10^{-8}t^4 + 3.50390346 \times 10^{-10}t^5 \\&\quad - 4.2405435 \times 10^{-13}t^6, \\I_3(t) &= 0.04 + 0.17252354t + 0.73192231t^2 + 0.93762217t^3 + 6.71214979 \times 10^{-9}t^4, \quad (9) \\R_3(t) &= 0.01099838t + 0.08051279t^2 + 0.43778921t^3 + 2.84480901 \times 10^{-9}t^4, \quad (10) \\V_3(t) &= 0.1 + 0.35099838t + 0.74338629t^3 + 7.5633901 \times 10^{-9}t^4. \quad (11)\end{aligned}$$

The procedures can be repeated to achieve the best approximate results:

$$S(t) = \lim_{k \rightarrow \infty} S_k(t), E(t) = \lim_{k \rightarrow \infty} E_k(t), I(t) = \lim_{k \rightarrow \infty} I_k(t), R(t) = \lim_{k \rightarrow \infty} R_k(t) \text{ and } V(t) = \lim_{k \rightarrow \infty} V_k(t).$$

4. Monte Carlo simulation process (MC)

The basic principle of Monte Carlo is the generation of random numbers that are uniformly distributed. This simulation is the basis of our study to solve the model used [22]. As following :

- Generating random numbers during the period (0,1).
- Any of these random numbers is considered a random variable and has its own regular distribution over the interval (0,1).
- Transforming these random variables with a standard uniform distribution into variables with a uniform distribution using the inverse transformation method (inversion method) [23].

5. Approximate Simulation Methods

In this section, we will use two approximate simulation methods, one for the proposed algorithm and the other for comparison purposes.

5.1 Mean Monte Carlo Finite Difference (MMC-FD)

One of the numerical simulation methods suitable for solving mathematical systems with random variables [24]. This method consists of a combination of two approaches: numerical (FD) and Monte Carlo simulation. This algorithm provides suitable approximate solutions by estimating the random coefficients of the system and then finding the solution using the FD method.

5.2 A New Algorithm Analytical Simulation Method (VIM-MC)

Monte Carlo Variation Iteration Method (VIM-MC) is a new approach that combines the Monte Carlo simulation method (MC) with a semi-analytical method which is Variation Iteration Method (VIM). The system parameters n

are re-estimated as random variables using Monte Carlo simulation, then these parameters are simulated m times, and the average solution for each simulation is taken.. This average represents the estimated solution of the system, short name VIM-MC method. The VIM-MC method is programmed via MATLAB software, for more details [19].

VIM-MC Procedure

Step 1 Using Monte Carlo, we simulate the system parameters n times simultaneously.

Step 2 For each parameter, we randomly select one value and then enter it into the system..

Step 3 solving the system by using VIM method with m iterations and the last iteration become the final VIM solution.

Step 4 Repeat Step 2 and Step 3 for n times.

Step 5 Compute the mean of the n solutions in Step 4 to gets solutions of (VIM-MC).

6. Results and Discussion

This section contains figures and tables showing the results of the exercise system used in the study over a 12-year period, using monthly and weekly step counts. The results showed a decrease in the percentage of the S group, which is clear evidence of their exposure to infection and their transition to the E group, which begins to increase gradually due to mixing and non-compliance with health prevention methods over time. This indicates a rise in the percentage of actually infected individuals (I), reaching its peak in the middle of the study period, which represents the highest level of infection in the study population. After that, it gradually decreases, and members of the group move to the R group after acquiring natural immunity and the effect of the natural response factor. At the same time, a clear increase appears in the vaccinated group (V), which helps to reduce the number of people exposed to infection.

Table 2 - Analytical simulation solutions of SEIRV Model incorporating a Holling type-II functional response from 2020 to 2026

Model variables	VIM (6 iter.)	Step size, h Monthly, Weekly	MMC-FD 6 years	VIM-MC 6 years
$S(t)$	0.0500	0.08 monthly	0.048901	0.050331
		0.02 weekly	0.049002	0.050774
$E(t)$	0.0120	0.08 monthly	0.010982	0.011884
		0.02 weekly	0.010601	0.011552
$I(t)$	0.0050	0.08 monthly	0.003781	0.003994
		0.02 weekly	0.003692	0.003774
$R(t)$	0.1650	0.08 monthly	0.165004	0.164882
		0.02 weekly	0.165102	0.165114
$V(t)$	0.8700	0.08 monthly	0.871332	0.868909
		0.02 weekly	0.871603	0.868786

Table 3 - Expected approximate solutions of SEIRV Model incorporating a Holling type-II functional response from 2020 to 2032

Model variables	VIM (12 iter.)	Step sizes, h	MMC-FD 12 years	VIM-MC 12 years
$S(t)$	0.0340	0.08 monthly	0.034102	0.034774
		0.02 weekly	0.034121	0.034884
$E(t)$	0.0020	0.08 monthly	0.002102	0.002224
		0.02 weekly	0.002051	0.002114
$I(t)$	0.0005	0.08 monthly	0.000512	0.000544
		0.02 weekly	0.000501	0.000502
$R(t)$	0.1920	0.08 monthly	0.191876	0.191774
		0.02 weekly	0.191992	0.191884
$V(t)$	0.9780	0.08 monthly	0.975408	0.974684
		0.02 weekly	0.975335	0.974616

Table 4 - Absolut error for MMC-FD and VIM-MC compared with VIM from 2020 to 2026

Model variables	Step sizes, h	MMC-FD 6 years	VIM-MC 6 years
$S(t)$	0.08 monthly	0.001099	0.000443
	0.02 weekly	0.000998	0.000774
$E(t)$	0.08 monthly	0.001018	0.000116
	0.02 weekly	0.001399	0.000448
$I(t)$	0.08 monthly	0.001219	0.001006
	0.02 weekly	0.001308	0.001226
$R(t)$	0.08 monthly	0.000004	0.000118
	0.02 weekly	0.000102	0.000114
$V(t)$	0.08 monthly	0.001332	0.001091
	0.02 weekly	0.001603	0.001214

Figure 1, illustrates the behavior and impact of the epidemic on the community groups during the study period. We observe that the curve of the S group decreases and individuals move to the E and I groups. The curve of the E group rises until it reaches its peak in the middle of the study period, then it gradually decreases. In the same way, the curve of the I group rises and then decreases after the middle of the study period. The interpretation of this behavior indicates the transfer of the group members to the R group, whose curve rose until the end of the study period. Finally, the curve of the vaccinated group also rose until the end of the period. This comes as a result of people's awareness and their willingness to take the necessary vaccines.

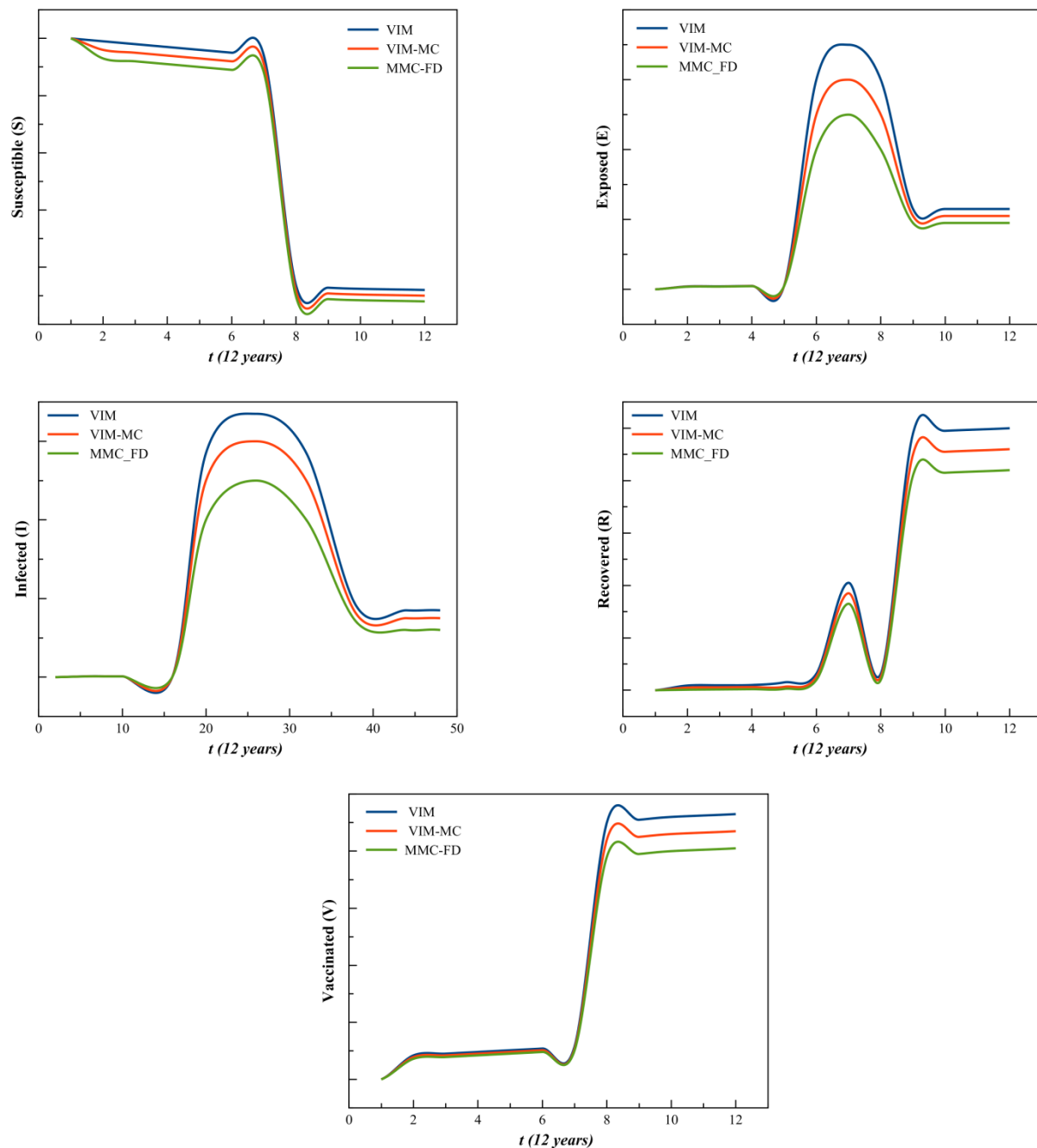


Fig. 2 - Curves of approximate simulation methods VIM-MC and MMC_FD compared with VIM of (a) $S(t)$, (b) $E(t)$, (c) $I(t)$, (d) $R(t)$ and (e) $V(t)$ through 12 years with step size $h = 0.8$ monthly and $m = 100$ repetitions.

SEIRV epidemiological models are among the most effective mathematical tools for understanding and interpreting the spread of epidemics and infectious diseases in the community. In this study, a natural response, specifically the Hollen response type II, was integrated with the epidemiological model, which illustrates the extent of transmission under saturation conditions. This study included the use of three methods to analyze the model used in the study. The first is the VIM analytical method, whose results we treat as real values, as it is a more accurate and reliable method. The second is the MMC-FD numerical simulation method for the purpose of comparison. The last is the proposed VIM-MC method, with a comprehensive comparison between the results of these methods using absolute error. The results indicate that the S community category gradually decreases over time, indicating the transfer of

elements from this group of healthy individuals to the E group of susceptible individuals. We observe a gradual rise in the curve of this category according to the expected behavior of this model, where the number of infections increases on average over the time period and then decreases afterward. This is due to the transfer of elements from this category to the R group of recovered individuals as a result of the use of medical precautions, natural response, and adherence to health prevention methods. Finally, there is a clear increase in the V group of vaccinated individuals over time, which indicates the extent of the impact of natural immunity and vaccination in reducing the spread of viral infection. The clear effect of the presence of a type II Hollen response function in reducing the number of injuries is that it provides a more realistic result of the saturation phenomenon compared to other models.

The VIM method showed approximate results for the analytical solutions of the model with high accuracy and efficiency with a lower number of iterations, giving stable and smooth results. This gives a better and more general understanding of the behavior of the epidemic without the need for intensive numerical solutions. All of this depends largely on the initial values and the number of iterations, which leads to slight differences when compared with other methods used in solving the model under study.

Regarding the numerical simulation method MMC_FD, it showed high accuracy results for all segments of society, especially when using small time intervals and when the step size is smaller, but at the same time it requires a great deal of effort in the calculations, especially if the study period is longer with random parameters in the mathematical system used.

The results indicate that combining a semi-analytical method (VIM) with a simulation method (Monte Carlo) is an effective approach. VIM provides rapid solutions and a general overview of the model's behavior, while simulation yields more accurate results, allowing for the estimation of system parameters. Furthermore, the presence of the Hollin response enhances interaction between individuals, particularly in crowded or communication-difficult environments. In general, the VIM-MC hybrid method is a reliable tool for studying complex mathematical systems with random variables as their coefficients. The proposed method can realistically and flexibly describe the dynamics of epidemic spread. This work can also be further developed in the future by incorporating other factors such as seasonal variations, community behavior, or real-world data.

7. Conclusion

This study includes the analysis and study of a SEIRV-type epidemiological model with the addition of a nonlinear normal response function, namely the Hollen response of type II, in order to describe the dynamics and behavior of the spread of the epidemic more accurately. This hybridization allowed us to demonstrate the extent of the impact of the saturation phenomenon on the spread of infection, which is considered an advanced step compared to the rest of the models.

This research employed two approaches to solve the mathematical model: the semi-analytical VIM method, whose results are treated as real values and considered a reliable tool for comparing results from other methods, and the numerical simulation method MMC_FD. The comparison demonstrated that the new and proposed VIM_MC approach is highly efficient compared to the VIM method, using the absolute error as the comparison criterion. Introducing the natural response greatly helps in reducing infection transmission rates and thus reducing the increase in the number of infected individuals (I) as well as the number of those susceptible to infection (E). This is a result of the saturation effect, which gives a better understanding of the strategy for controlling epidemics.

Based on the above, it can be said that the proposed algorithm is an effective tool for studying the spread of epidemics, and that combining analytical methods and simulation methods provides accuracy and efficiency. This algorithm can be applied to other different epidemiological models.

8. Future recommendations

- Using analytical and other methods and

combining them with different simulation methods.

- Other epidemiological models can be used and studied using the same proposed method.
- The study could be expanded to include system parameter analysis.
- Enter real data for more accurate results.

In conclusion, this study presents a new approach that combines analytical and simulation methods, which can be relied upon in the future to understand and combat the spread of epidemics, predict their behavior, and analyze their dynamics.

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