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Article

A Numerical Efficient Technique for the Solution of Susceptible Infected Recovered Epidemic Model

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Abstract: The essential features of the nonlinear stochastic models are positivity, dynamical consistency and boundedness. These features have a significant role in different fields of computational biology and many more. The aim of our paper, to achieve the comparison analysis of the stochastic susceptible, infected recovered epidemic model. The stochastic modelling is a realistic way to study the dynamics of compartmental modelling as compared to deterministic modelling. The effect of reproduction number has also observed in the stochastic susceptible, infected recovered epidemic model. For comparison analysis, we developed some explicit stochastic techniques, but they are the time-dependent techniques. The implicitly driven explicit technique has developed for the stochastic susceptible, infected recovered epidemic model. In the support, some theorems and graphical illustration has presented. Also, the time efficiency of this method makes it easy to find the solution of the stochastic system. The comparison with other techniques shows the efficacy and reliability of the designed technique.

Keywords: Epidemiolocal model; stochastic differential equations; stochastic techniques; convergence analysis

1 Introduction

Kermack et al. [1] have found from 1930 to 1940. There were in print a chain of papers titled "contributions to the mathematical theory of epidemics". Also known as a forerunner in mathematical comprehension of plagued diseases. Dickman et al. [2] have found further reprinting in the discipline of epidemiological modelling. Bailey et al. [3] have presented the mathematical study of the disease started to gain flow in the mid-20th century, and resultantly a huge variety of old models have been propagated, numerically probed and employed to contagious diseases. Allen et al. [4] have explained the above cycle of plague through his random models by forming an equation called stochastic differential equations (SDEs), and the same was resultant of an assumption that the processes happen with a distribution

method with the same ratio. Baumann et al. [5] have focused the previous work mainly on the SIR model. It was explained and explored on the same level with the same result through a hybrid model of SDEs. Anyway, this was not the only way to define randomness into the SIR models. The people are divided into three categories as follows: χ_1(t) (susceptible) heathy but may be open to diseases, $\chi_2(t)$: (infected) who are sick and may transfer it further and χ_3(t): (removed) who are sick but got the immunity against it. In order to calculate several people, which are receptive of the subject disease or gradually became healthy at the due time intervals is detained. Dietz et al. [6] have presented SIR modelling for contagious diseases, may be proved as the most suitable models. In other fields such as research and health, much work has been made by the blessings of the subjective model and obtained encouraging results, regarding medical care for certain disease during a plague. Besides these models, SIS similar to SIR model also covers the medical cares of those persons, who are no longer communicable. These persons fall in victim due to some reasons once again. Generally, frostily can be detected with the appliance of the SIS model. Moreover, there is found another model known as the SEIR model in update and dignified form. It can be applied to the people who are whether receptive of infection, exposed to an infection or recovered. The SIR model might be used in order to regulate the variety of seasonal alternation and changes. Oksendal et al. [7] have found a successful tool which has been prominent now to withdraw comprehensive intuition about epidemic diseases is mathematical modelling. The evolution of the mathematical modelling and the feasible duplications permits for examining the reactivity and contrasting of connection in physical models. Bayram et al. [8] have studied different models of diseases dynamics. It is crystal clear that analytical solutions do not possess by nonlinear initial value problems (IVP'S). The schemes which are presented the classical explicit finite-differences like Runge-Kutta and Euler methods violate the dynamical properties as mentioned above by using different type step sizes. Allen et al. [9] have found that these methods proved to be less advantage and dependent numerical instability. Arif et al. [10] have found explicit solutions of the stochastic differential equations do not exist due to non-differentiable term of Brownian motion. To integrate such type of equations, we need to use different stochastic numerical techniques. Cresson et al. [11] have found: is there any stochastic techniques in literature preserve the essential features of computational biology systems? No doubt, we have seen in literature numerical techniques such as Euler and Runge-Kutta never maintain essential features of computational biology systems in the deterministic modelling. If we talk about existing stochastic techniques such as Euler Maruyama, stochastic Euler and stochastic Runge-Kutta does not maintain the essential features of computational biology systems in the stochastic case. There is much gap in the literature and indeed to research more: Could we develop the essential features preserving the stochastic technique in computational biology systems? The major outbreak of this paper is to introduce stochastic nonstandard finite difference technique (S-NSFD) under rules defined by Mickens in a stochastic sense.

The flow of paper has based on the following sections:

In Section 2, described the deterministic epidemic model. In Sections 3 and 4 explains the construction way of stochastic epidemic model, equilibria and their stability. In Section 5, explains the existing stochastic numerical techniques and proposed stochastic technique for stochastic susceptible, infected recovered epidemic model and their convergence analysis. Finally, in Section 6, we will reach our conclusion and some future directions.

2 Deterministic Epidemic Model

We shall consider susceptible, infected recovered model epidemic in this section. For taking arbitrary time t, the variables are designated as S(t) (denotes the susceptible group in time t), I(t) (denotes the infectious groups in time t), R(t) (denotes the recovered group in time t). The model parameters are described as η (denote the intrinsic growth rate of susceptible), α (denotes the maximum value of per capita reduction rate), υ (denotes the natural recovery rate from infection) and ξ (denotes the mortality rate of the recovered population). The governing equations of the epidemic model as follows:

$$S' = \eta - \frac{\alpha SI}{1 + \alpha I} - \xi S. \tag{1}$$

$$\mathrm{I}' = \frac{\alpha \mathrm{SI}}{1+\alpha \mathrm{I}} - \upsilon \mathrm{I} - \xi \mathrm{I}. \tag{2}$$

$$\mathrm{R}' = \upsilon \mathrm{I} - \xi \mathrm{R}. \tag{3}$$

where the section for the systems (1)–(3) is $\Omega = \left\{ (S, I, R) : \mathrm{S} + I + R \leq \frac{\eta}{\xi},\ \mathrm{S} \geq 0, \mathrm{I} \geq 0,\ \mathrm{R} \geq 0 \right\}$. The solutions of systems (1)–(3) will be closed and lie in section Ω. So, this section is also called feasible and non-negative invariant section.

2.1 Equilibria of Model

The systems (1)–(3) has three types of equilibria, such as trivial equilibria (TE), disease-free equilibria (DFE) and endemic equilibria (EE) as follows:

TE is $C = (S, I, R) = (0, 0, 0)$.

DFE is $\mathrm{D} = (S^{\mathrm{o}}, \mathrm{I}^{\mathrm{o}}, \mathrm{R}^{\mathrm{o}}) = \left(\frac{\eta}{\xi}, 0, 0 \right)$.

EE is $\mathrm{E} = (S^*, \mathrm{I}^*, \mathrm{R}^*)$.

where,

$S^* = \frac{(1+\alpha \mathrm{I}^*)\eta}{\alpha \mathrm{I}^* + \xi(1+\alpha \mathrm{I}^*)}$, $I^* = \frac{\alpha\eta - \xi(\xi+\upsilon)}{\alpha(1+\xi)(\xi+\upsilon)}$, $R^* = \frac{\upsilon \mathrm{I}^*}{\xi}$, $\mathrm{R}_{\mathrm{o}}^{\mathrm{d}} = \frac{\alpha\eta}{(\upsilon+\xi)\xi}$.

Note that $\mathrm{R}_{\mathrm{o}}^{\mathrm{d}}$ is reproduction number of susceptible infected recovered epidemic model.

3 Stochastic Epidemic Model

For this, we shall suppose a vector $\mathrm{W} = [S,\ \mathrm{I},\ \mathrm{R}]^{\mathrm{T}}$, the possible expectation of models (1)–(3) as presented in Tab. 1.

The expectation and variance of the stochastic epidemic model is defined as

$\mathrm{E}^*[\Delta \mathrm{W}] = \sum_{\mathrm{i}=1}^{6} \mathrm{P_i T_i}$.

$$\text{Expectation} = \mathrm{E}^*[\Delta \mathrm{W}] = \begin{bmatrix} \mathrm{P}_1 - \mathrm{P}_2 - \mathrm{P}_3 \\ \mathrm{P}_2 - \mathrm{P}_4 - \mathrm{P}_5 \\ \mathrm{P}_4 - \mathrm{P}_6 \end{bmatrix} \Delta \mathrm{t}.$$

$$\text{Var} = \mathrm{E}^*\left[\Delta \mathrm{W} \Delta \mathrm{W}^{\mathrm{T}}\right] = \sum_{\mathrm{i}=1}^{6} \mathrm{P_i}[\mathrm{T_i}][\mathrm{T_i}]^{\mathrm{T}}.$$

$$\mathrm{E}^*\left[\Delta \mathrm{W} \Delta \mathrm{W}^{\mathrm{T}}\right] = \begin{bmatrix} \mathrm{P}_1 + \mathrm{P}_2 + \mathrm{P}_3 & -\mathrm{P}_2 & 0 \\ -\mathrm{P}_2 & \mathrm{P}_2 + \mathrm{P}_4 + \mathrm{P}_5 & -\mathrm{P}_4 \\ 0 & -\mathrm{P}_4 & \mathrm{P}_4 + \mathrm{P}_6 \end{bmatrix} \Delta \mathrm{t}.$$

$$\text{Stochastic drift} = \mathrm{f}(\mathrm{W}(\mathrm{t}), \mathrm{t}) = \frac{\mathrm{E}^*[\Delta \mathrm{W}]}{\Delta \mathrm{t}}.$$

$$\text{Stochastic diffusion} = \mathrm{L}(\mathrm{W}(\mathrm{t}), \mathrm{t}) = \sqrt{\frac{\mathrm{E}^*[\Delta \mathrm{W} \Delta \mathrm{W}^{\mathrm{T}}]}{\Delta \mathrm{t}}}.$$

The SDE of the systems (1)–(3) as follows:

$$\mathrm{dW}(\mathrm{t}) = \mathrm{f}(\mathrm{W}(\mathrm{t}), \mathrm{t})\mathrm{dt} + \mathrm{L}(\mathrm{W}(\mathrm{t}), \mathrm{t})\mathrm{d}\psi(\mathrm{t}). \tag{4}$$

With initial conditions $\mathrm{W}(0) = \mathrm{W_o} = [0.5, 0.3,\ 0.2]^{\mathrm{T}}$, $0 \leq \mathrm{t} \leq \mathrm{T}$ and the representation ψ is called the Brownian motion.

3.1 Euler Murayama Technique

Raza et al. [12,13] have found the construction of the system (4) and taking numeric values of parameters presented in Tab. 2 as

Table 1: Transition probabilities

T_i = Transitions	P_i = Probabilities
$T_1 = (\Delta W)_1 = [1,0,0]^T$	$P_1 = \eta\Delta t$
$T_2 = (\Delta W)_2 = [-1,1,0]^T$	$P_2 = \frac{\alpha SI}{1+\alpha I}\Delta t$
$T_3 = (\Delta W)_3 = [-1,0,0]^T$	$P_3 = \xi S\Delta t$
$T_4 = (\Delta W)_4 = [0,-1,1]^T$	$P_4 = \upsilon I\Delta t$
$T_5 = (\Delta W)_5 = [0,-1,0]^T$	$P_5 = \xi I\Delta t$
$T_6 = (\Delta W)_6 = [0,0,-1]^T$	$P_6 = \xi R\Delta t$

$$W_{n+1} = W_n + G_1(W_n, t)\Delta t + G_2(W_n, t)\Delta\psi_n. \tag{5}$$

So, the time step size is presented by 'Δt' and $\Delta\psi_n$ is standard normal distribution i.e., $\Delta\psi_n \sim N(0,\ 1)$. The solution of system (5), i.e., DFE is $D = (1,0,0)$ and EE is $E = (0.9048,\ 0.07937,\ 0.01587)$. The simulation of Euler's Murayama technique at the equilibria of the model as presented in Fig. 1.

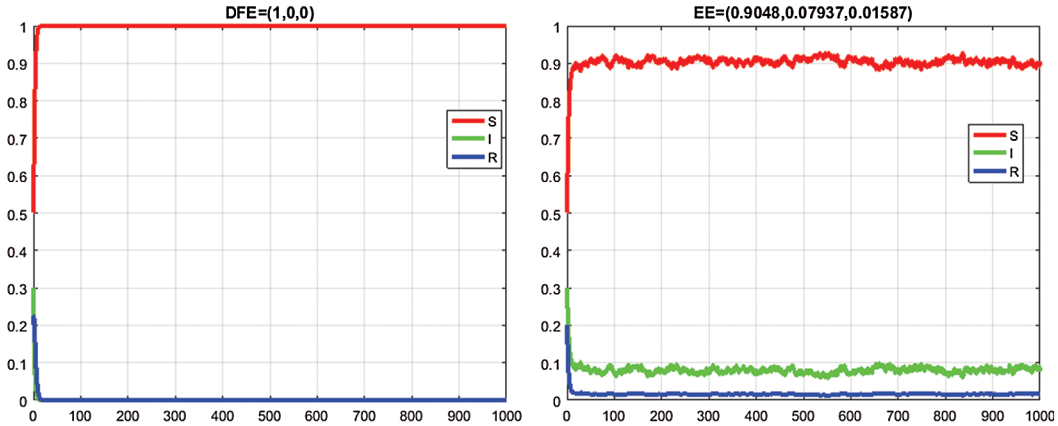

Figure 1: (a) Solution of the stochastic epidemic model for DFE (b) Solution of the stochastic epidemic model for EE

4 Parametric Perturbation in Model

Arif et al. [14] have presented this idea, and we could choose parameters from the systems (1)–(3) and change into the random parameters with small noise as $\alpha dt = \alpha dt + \rho d\psi$ and $\upsilon dt = \upsilon dt + \rho_1 d\psi$. So, the stochastic epidemic of the systems (1)–(3) is as follows:

$$dS = \left(\eta - \frac{\alpha SI}{1+\alpha I} - \xi S\right)dt - \frac{SI\rho d\psi}{1+\alpha I}. \tag{6}$$

$$dI = \left(\frac{\alpha SI}{1+\alpha I} - \upsilon I - \xi I\right)dt + \frac{SI\rho d\psi}{1+\alpha I} - \quad I\rho_1 d\psi. \tag{7}$$

$$dR = (\upsilon I - \xi R) + I p_1 d\psi. \tag{8}$$

The Brownian motion is denoted *by* $\psi(t)$, ρ and ρ_1 are the randomness of each equation of system (6)–(8). Due to non-integrable term of Brownian motion, we shall use stochastic techniques to find the results of the systems (6)–(8).

4.1 Stochastic Threshold Dynamics

Theorem: If $\rho^2 < \frac{\alpha}{k}$ and $R_o^d < 1$, then in the systems (6)–(8) infected compartment tend to zero exponentially almost sure.

Proof: We shall consider that $(S(t), I(t), R(t))$ is a solution of systems (6)–(8) and by Ito's formula, where $f(I) = \ln(I)$.

$$d\ln(I) = f'(I)dI + \frac{1}{2} f''(I) I^2 \left(\frac{\rho^2 I^2}{(1+\alpha I)^2} \right) dt.$$

$$d\ln(I) = \left[\frac{\alpha S}{1+\alpha I} - (\upsilon + \xi) - \frac{1}{2}\left(\frac{\rho^2 S^2}{(1+\alpha I)^2} \right) \right] dt + \left(\frac{S\rho}{1+\alpha I} - \rho_1 \right) d\psi.$$

$$\ln I(t) = \ln I(0) + \int_0^t \left(\frac{\alpha S}{1+\alpha I} - \frac{1}{2}\frac{\rho^2 S^2}{(1+\alpha I)^2} \right) dt - [(\upsilon + \xi)]t + \int_0^t \left(\frac{S\rho}{1+\alpha I} - \rho_1 \right) d\psi .$$

where $M(t) = \int_0^t \left(\frac{S\rho}{1+\alpha I} - \rho_1 \right) d\psi$ is the local continuous martingale with $M(0) = 0$.

If $\rho^2 > \frac{\alpha\xi}{\eta}$,

$$\ln I(t) \le \left(\frac{\alpha^2}{2\rho^2} - 1 \right) t + M_1(t) + \ln I(0).$$

$$\frac{\ln I(t)}{t} \le -\left((\upsilon + \xi) - \frac{\alpha^2}{2\rho^2} \right) + \frac{M_1(t)}{t} + \frac{\ln I(0)}{t}$$

if $\lim_{t\to\infty} \frac{M_1(t)}{t} = 0$.

$$\lim_{t\to\infty} \sup \frac{\ln I(t)}{t} \le -\left((\upsilon + \xi) + {\rho_1}^2 - \frac{\alpha^2}{2\rho^2} \right) < 0.$$

When $\rho^2 > \frac{\alpha^2}{2(\nu + {\rho_1}^2)}$ and $\lim_{t\to\infty} I(t) = 0$ almost sure.

If $\rho^2 < \frac{\alpha\xi}{\eta}$, then

$$\ln(I(t)) \le \left(\frac{\alpha\eta}{\xi} - \frac{1}{2}\rho^2 \left(\frac{\alpha\eta}{\xi}\right)^2 - (\upsilon + \xi) \right) t + M_1(t) + \ln I(0).$$

$$\frac{\ln I(t)}{t} \le (\upsilon + \xi) \left[\frac{\alpha\eta}{\xi(\upsilon + \xi)} - \frac{1}{2(\upsilon + \xi)} \rho^2 \left(\frac{\alpha\eta}{\xi}\right)^2 - 1 \right] \frac{M_1(t)}{t} + \frac{\ln I(0)}{t}. \tag{9}$$

By taking the superior limit on both sides of (9), we have

$$\lim_{t\to\infty} \sup \frac{\ln I(t)}{t} \le (\upsilon + \xi)\left(R_o^d - 1 \right), \text{ then when } R_o^d < 1 \text{ we get } \lim_{t\to\infty} \sup \frac{\ln I(t)}{t} < 0.$$

$$\Rightarrow \lim_{t\to\infty} I(t) = 0 \text{ almost sure}$$

$$R_o^S = R_o^d - \frac{1}{2(\upsilon+\xi)}\rho^2\left(\frac{\alpha\eta}{\xi}\right)^2 < 1.$$

Note that R_o^S is the stochastic reproduction number of the susceptible, infected recovered epidemic model will decide the extinction and persistence of disease. The reproduction number $R_o^S = 0.9625 < 1$ means existing parameter values are helpful to control disease in a population otherwise in case if $R_o^S = 1.1156 > 1$ means the disease is endemic in the population. The dynamics of reproduction number has a vital role in the study of computational biology systems.

4.2 Stochastic Euler Technique

This technique is presented for the systems (6)–(8) as follows:

$$S^{n+1} = S^n + h\left[\eta - \frac{\alpha S^n I^n}{1+\alpha I^n} - \xi S^n\right] - \frac{hS^n I^n \rho \Delta\psi_n}{1+\alpha I^n}. \tag{10}$$

$$I^{n+1} = I^n + h\left[\frac{\alpha S^n I^n}{1+\alpha I^n} - \upsilon I^n - \xi I^n\right] + \frac{hS^n I^n \rho \Delta\psi_n}{1+\alpha I^n} - h\rho_1 \Delta\psi_n I^n. \tag{11}$$

$$R^{n+1} = R^n + h[\upsilon I^n - \xi R^n] + h\rho_1 \Delta\psi_n I^n. \tag{12}$$

The time step size represented by h and $\Delta\psi_n \sim N(0,1)$.

4.3 Stochastic Runge Kutta Technique

This technique is presented for the systems (6)–(8) as follows:

Stage-1

$$A_1 = h\left[\eta - \frac{\alpha S^n I^n}{1+\alpha I^n} - \xi S^n\right] - \frac{hS^n I^n \rho \Delta\psi_n}{1+\alpha I^n}.$$

$$B_1 = h\left[\frac{\alpha S^n I^n}{1+\alpha I^n} - \upsilon I^n - \xi I^n\right] + \frac{hS^n I^n \rho \Delta\psi_n}{1+\alpha I^n} - h\rho_1 \Delta\psi_n I^n.$$

$$C_1 = h[\upsilon I^n - \xi R^n] + h\rho_1 \Delta\psi_n I^n.$$

Stage-2

$$A_2 = h\left[\eta - \frac{\alpha(S^n + \frac{A_1}{2})(I^n + \frac{B_1}{2})}{1+\alpha(I^n + \frac{B_1}{2})} - \xi(S^n + \frac{A_1}{2})\right] - \frac{h(S^n + \frac{A_1}{2})(I^n + \frac{B_1}{2})\rho\Delta\psi_n}{1+\alpha(I^n + \frac{B_1}{2})}.$$

$$B_2 = h\left[\frac{\alpha(S^n + \frac{A_1}{2})(I^n + \frac{B_1}{2})}{1+\alpha(I^n + \frac{B_1}{2})} - \upsilon(I^n + \frac{B_1}{2}) - \xi(I^n + \frac{B_1}{2})\right] + \frac{h(S^n + \frac{A_1}{2})(I^n + \frac{B_1}{2})\rho\Delta\psi_n}{1+\alpha(I^n + \frac{B_1}{2})} - h\rho_1\Delta\psi_n(I^n + \frac{B_1}{2})$$

$$C_2 = h\left[\upsilon(I^n + \frac{B_1}{2}) - \xi(R^n + \frac{C_1}{2})\right] + h\rho_1\Delta\psi_n(I^n + \frac{B_1}{2}).$$

Stage-3

$$A_3 = h\left[\eta - \frac{\alpha(S^n + \frac{A_2}{2})(I^n + \frac{B_2}{2})}{1 + \alpha(I^n + \frac{B_2}{2})} - \xi(S^n + \frac{A_2}{2})\right] - \frac{h(S^n + \frac{A_2}{2})(I^n + \frac{B_2}{2})\rho\Delta\psi_n}{1 + \alpha(I^n + \frac{B_2}{2})}.$$

$$B_3 = h\left[\frac{\alpha(S^n + \frac{A_2}{2})(I^n + \frac{B_2}{2})}{1 + \alpha(I^n + \frac{B_2}{2})} - \upsilon(I^n + \frac{B_2}{2}) - \xi(I^n + \frac{B_2}{2})\right] + \frac{h(S^n + \frac{A_2}{2})(I^n + \frac{B_2}{2})\rho\Delta\psi_n}{1 + \alpha(I^n + \frac{B_2}{2})} - h\rho_1\Delta\psi_n(I^n + \frac{B_2}{2})$$

$$C_3 = h\left[\upsilon(I^n + \frac{B_2}{2}) - \xi(R^n + \frac{C_2}{2})\right] + h\rho_1\Delta\psi_n(I^n + \frac{B_2}{2}).$$

Stage-4

$$A_4 = h\left[\eta - \frac{\alpha(S^n + A_3)(I^n + B_3)}{1 + \alpha(I^n + B_3)} - \xi(S^n + A_3)\right] - \frac{h(S^n + A_3)(I^n + B_3)\rho\Delta\psi_n}{1 + \alpha(I^n + B_3)}.$$

$$B_4 = h\left[\frac{\alpha(S^n + A_3)(I^n + B_3)}{1 + \alpha(I^n + B_3)} - \upsilon(I^n + B_3) - \xi(I^n + B_3)\right] + \frac{h(S^n + A_3)(I^n + B_3)\rho\Delta\psi_n}{1 + \alpha(I^n + B_3)} - h\rho_1\Delta\psi_n(I^n + B_3)$$

$$C_4 = h[\upsilon(I^n + B_3) - \xi(R^n + C_3)] + h\rho_1\Delta\psi_n(I^n + B_3).$$

Final stage

$$\left.\begin{aligned} S^{n+1} &= S^n + \frac{1}{6}[A_1 + 2A_2 + 2A_3 + A_4] \\ I^{n+1} &= I^n + \frac{1}{6}[B_1 + 2B_2 + 2B_3 + B_4] \\ R^{n+1} &= R^n + \frac{1}{6}[C_1 + 2C_2 + 2C_3 + C_4] \end{aligned}\right\} \tag{13}$$

The time step size represented by h and $\Delta B_n \sim N(0, 1)$.

4.4 *Stochastic NSFD Technique*

This technique is presented for the systems (6)–(8) as follows:

$$S^{n+1} = \frac{S^n + h\eta}{\left(1 + \frac{h\upsilon I^n}{1 + \alpha I^n} + \frac{hI^n\rho\Delta\psi_n}{1 + \alpha I^n} + h\xi\right)}. \tag{14}$$

$$I^{n+1} = \frac{I^n(1 + \alpha I^n) + \alpha h S^n I^n + h S^n I^n \rho\Delta\psi_n}{(1 + \alpha I^n)(1 + h\upsilon + h\rho_1\Delta\psi_n + h\xi)}. \tag{15}$$

$$R^{n+1} = \frac{R^n + h\upsilon I^n + h\rho_1\Delta\psi_n I^n}{(1 + h\xi)}. \tag{16}$$

The time step size represented by h and $\Delta\psi_n \sim N(0, 1)$.

4.5 Convergence Analysis

In this section, we have proved essential features of our proposed stochastic technique, namely as stochastic nonstandard finite difference technique (S-NSFD) for computational biology systems. First theorem for positivity, second for boundedness, third and fourth for dynamical consistency as follows:

Theorem: The systems (14)–(16) has a non-negative solution (S^n, I^n, R^n) $\in R^3_+$ on $n \geq 0$, For any given initial value (S^n (0), I^n (0), R^n (0)) $\in R^3_+$ almost sure.

Theorem: The region $\Omega = \{(S^n , I^n , R^n) \in R^3_+ : S^n \geq 0, I^n \geq 0, R^n \geq 0, S^n + I^n + R^n \leq k\}$ for all $n \geq 0$ is a non-negative invariant set for the systems (14)–(16).

Proof. The systems (14)–(16) may be written as:

$$\frac{S^{n+1} - S^n}{h} = \eta - \frac{\alpha S^n I^n}{1 + \alpha I^n} - \xi S^n - \frac{S^n I^n \rho \Delta\psi_n}{1 + \alpha I^n}.$$

$$\frac{I^{n+1} - I^n}{h} = \frac{\alpha S^n I^n}{1 + \alpha I^n} - \upsilon I^n - \xi I^n + \frac{S^n I^n \rho \Delta\psi_n}{1 + \alpha I^n} - \rho_1 \Delta\psi_n I^n.$$

$$\frac{R^{n+1} - R^n}{h} = \upsilon I^n - \xi R^n + \rho_1 \Delta\psi_n I^n.$$

By adding above-mentioned all the equations, we have

$$\frac{S^{n+1} - S^n}{h} + \frac{I^{n+1} - I^n}{h} + \frac{R^{n+1} - R^n}{h} = \eta - \frac{\alpha S^n I^n}{1 + \alpha I^n} - \xi S^n - \frac{S^n I^n \rho \Delta\psi_n}{1 + \alpha I^n} + \frac{\alpha S^n I^n}{1 + \alpha I^n} - \upsilon I^n - \xi I^n + \frac{S^n I^n \rho \Delta\psi_n}{1 + \alpha I^n} - \rho_1 \Delta\psi_n I^n + \upsilon I^n - \xi R^n + \rho_1 \Delta\psi_n I^n.$$

$$\frac{(S^{n+1} + I^{n+1} + R^{n+1}) - (S^n + I^n + R^n)}{h} = \eta - \xi(S^n + I^n + R^n).$$

$$(S^{n+1} + I^{n+1} + R^{n+1}) = (S^n + I^n + R^n) + h\eta - h\xi(S^n + I^n + R^n).$$

$$(S^{n+1} + I^{n+1} + R^{n+1}) \leq \frac{\eta}{\xi} + h(\eta - \xi(\frac{\eta}{\xi})).$$

$$(S^{n+1} + I^{n+1} + R^{n+1}) \leq \frac{\eta}{\xi}.$$

Almost surely.

Theorem: The discrete dynamical systems (14)–(16) has the same equilibria as that of the continuous dynamical systems (6)–(8) for all $n \geq 0$.

Proof. For solving the systems (14)–(16), we get three equilibria as follows:

TE is $C = (S^n , I^n , R^n) = (0, 0, 0)$.

DFE is $D = (S^n , I^n , R^n) = (\frac{\eta}{\xi}, 0, 0)$.

EE is $E = (S^n , I^n , R^n)$.

where,

$$S^n = \frac{(1 + \alpha I^n)\eta}{\alpha I^n + \xi(1 + \alpha I^n)}, \; I^n = \frac{\alpha\eta - \xi(\xi + \upsilon)}{\alpha(1 + \xi)(\xi + \upsilon)}, \; R^n = \frac{\upsilon I^n}{\xi}.$$

Almost surely.

Theorem: Brauer et al. [15] have presented the eigenvalues of the discrete dynamical systems (14)–(16) lies in the unit circle for all $n \geq 0$.

Proof: We consider F, G and H from the systems (14)–(16) as follows:

$$\mathrm{F}=\frac{S+\mathrm{h}\eta}{1+\dfrac{\mathrm{h}\alpha\mathrm{I}}{1+\alpha\mathrm{I}}+\mathrm{h}\xi+\dfrac{\mathrm{hI}\rho\Delta\psi_{\mathrm{n}}}{1+\alpha\mathrm{I}}}$$

$$\mathrm{G}=\frac{\mathrm{I}+\dfrac{\mathrm{h}\alpha\mathrm{SI}}{(1+\alpha\mathrm{I})}+\dfrac{\mathrm{hSI}\rho\Delta\psi_{\mathrm{n}}}{(1+\alpha\mathrm{I})}}{(1+\mathrm{h}\upsilon+\mathrm{h}\xi+\mathrm{h}\rho_1\Delta\psi_{\mathrm{n}})}$$

$$\mathrm{H}=\frac{\mathrm{R}+\mathrm{h}\upsilon\mathrm{I}+\mathrm{h}\rho_1\Delta\psi_{\mathrm{n}}}{1+\mathrm{h}\xi}.$$

The Jacobean matrix defined as

$$\mathrm{J}=\begin{bmatrix}\dfrac{\partial\mathrm{F}}{\partial\mathrm{S}} & \dfrac{\partial\mathrm{F}}{\partial\mathrm{I}} & \dfrac{\partial\mathrm{F}}{\partial\mathrm{R}}\\ \dfrac{\partial\mathrm{G}}{\partial\mathrm{S}} & \dfrac{\partial\mathrm{G}}{\partial\mathrm{I}} & \dfrac{\partial\mathrm{G}}{\partial\mathrm{R}}\\ \dfrac{\partial\mathrm{H}}{\partial\mathrm{S}} & \dfrac{\partial\mathrm{H}}{\partial\mathrm{I}} & \dfrac{\partial\mathrm{H}}{\partial\mathrm{R}}\end{bmatrix}$$

$$\text{where},\ \frac{\partial\mathrm{F}}{\partial\mathrm{S}}=\frac{1}{\left(1+\mathrm{h}\xi+\dfrac{\mathrm{h}\alpha I}{1+\alpha I}+\dfrac{\mathrm{h}I\rho\Delta\psi_{\mathrm{n}}}{1+\alpha I}\right)}$$

$$\frac{\partial\mathrm{F}}{\partial\mathrm{I}}=\frac{-(S+\mathrm{h}\eta)[(1+\alpha I)(\mathrm{h}\alpha)-\mathrm{h}\alpha^2 I+(1+\alpha I)\mathrm{h}\rho\Delta\psi_{\mathrm{n}}-\mathrm{h}I\rho\Delta\psi_{\mathrm{n}}\alpha]}{\left(1+\mathrm{h}\xi+\dfrac{\mathrm{h}\alpha I}{1+\alpha I}+\dfrac{\mathrm{h}I\rho\Delta\psi_{\mathrm{n}}}{1+\alpha I}\right)^2(1+\alpha I)^2},\ \frac{\partial\mathrm{F}}{\partial\mathrm{R}}=0.$$

$$\frac{\partial\mathrm{G}}{\partial\mathrm{S}}=\frac{\mathrm{h}\alpha I+\mathrm{h}I\rho\Delta\psi_{\mathrm{n}}}{(1+\alpha I)(1+\mathrm{h}\upsilon+\mathrm{h}\xi+\mathrm{h}\rho_1\Delta\psi_{\mathrm{n}})},$$

$$\frac{\partial\mathrm{G}}{\partial\mathrm{I}}=\frac{(1+\alpha I)(\mathrm{h}\alpha S)-\mathrm{h}^2\alpha SI+(1+\alpha I)\mathrm{h}S\rho\Delta\psi_{\mathrm{n}}-\mathrm{h}SI\rho\Delta\psi_{\mathrm{n}}\alpha}{(1+\mathrm{h}\upsilon+\mathrm{h}\xi+\mathrm{h}\rho_1\Delta\psi_{\mathrm{n}})(1+\alpha I)^2},\ \frac{\partial\mathrm{G}}{\partial\mathrm{R}}=0.$$

$$\frac{\partial\mathrm{H}}{\partial\mathrm{S}}=0,\frac{\partial\mathrm{H}}{\partial\mathrm{I}}=\frac{\mathrm{h}\upsilon+\mathrm{h}\rho_1\Delta\psi_{\mathrm{n}}}{1+\mathrm{h}\xi},\ \frac{\partial\mathrm{H}}{\partial\mathrm{R}}=\frac{1}{1+\mathrm{h}\xi}.$$

Now we want to linearize the model about the equilibria of the model for disease-free equilibrium $\mathrm{D}=(S^{\mathrm{n}},\ I^{\mathrm{n}},\ R^{\mathrm{n}})=\left(\dfrac{\eta}{\xi},0,0\right)$ and $\mathrm{R}_{\mathrm{o}}^{\mathrm{S}}<1$.

The given Jacobean is

$$\mathrm{J}=\begin{bmatrix}\dfrac{1}{1+\mathrm{h}\eta} & 0 & 0\\ 0 & \dfrac{\mathrm{h}\alpha\eta+\mathrm{h}\eta\rho\Delta\psi_{\mathrm{n}}}{\xi(1+\mathrm{h}\upsilon+\mathrm{h}\xi+\mathrm{h}\rho_1\Delta\psi_{\mathrm{n}})} & 0\\ 0 & \dfrac{\mathrm{h}\upsilon+\mathrm{h}\rho_1\Delta\psi_{\mathrm{n}}}{1+\mathrm{h}\xi} & \dfrac{1}{1+\mathrm{h}\xi}\end{bmatrix}$$

The eigenvalues of Jacobean matrix are

$$\lambda_1 = \frac{1}{1+h\eta} < 1 \; \lambda_2 = \frac{h\alpha\eta + h\eta\rho\Delta\psi_n}{\xi(1+h\upsilon+h\xi+h\rho_1\Delta\psi_n)} < 1, \quad R_o^S < 1, \; \lambda_3 = \frac{1}{1+h\xi} < 1.$$

This is the guarantee to the fact that all eigenvalues of the Jacobean lie in the unit circle. So, the system (8) is linearizable around D.

5 Numerical Experimentations

Imane et al. [16] have given the values of parameters presented in Tab. 2, for the results of the techniques mentioned above.

Table 2: Parameter values

Parameters	Values (years)
η	0.5
ξ	0.5
α	DFE = 0.6 EE = 0.7
υ	0.1
ρ	0.02
ρ_1	0.05

5.1 Euler Maruyama Technique

The results of the system (5) presented in Fig. 2.

5.2 Stochastic Euler Technique

The results of the system (10)–(12) presented in Fig. 3.

5.3 Stochastic Runge Kutta Technique

The results of the system (13) presented in Fig. 4.

5.4 Stochastic NSFD Technique

The results of the system (14)–(16) presented in Fig. 5.

5.5 Contrast Section

We shall make a comparison of deterministic and stochastic susceptible infected recovered model by using existing stochastic and proposed techniques. The comparison results of the system are presented in Fig. 6.

5.6 Covariance of Compartments

We shall discuss the proportion among the compartment of the susceptible infected recovered model in this section. For this, we shall calculate the correlation coefficient, and its results are displayed in Tab. 3.

In the Tab. 3, we concluded that the inverse proportion hold in the susceptible compartment and others. It means that we can analyze the ratio of the susceptible compartment will increase with the decrease in remaining compartments of the model. So, in the end, we can get the condition that population will be disease-free.

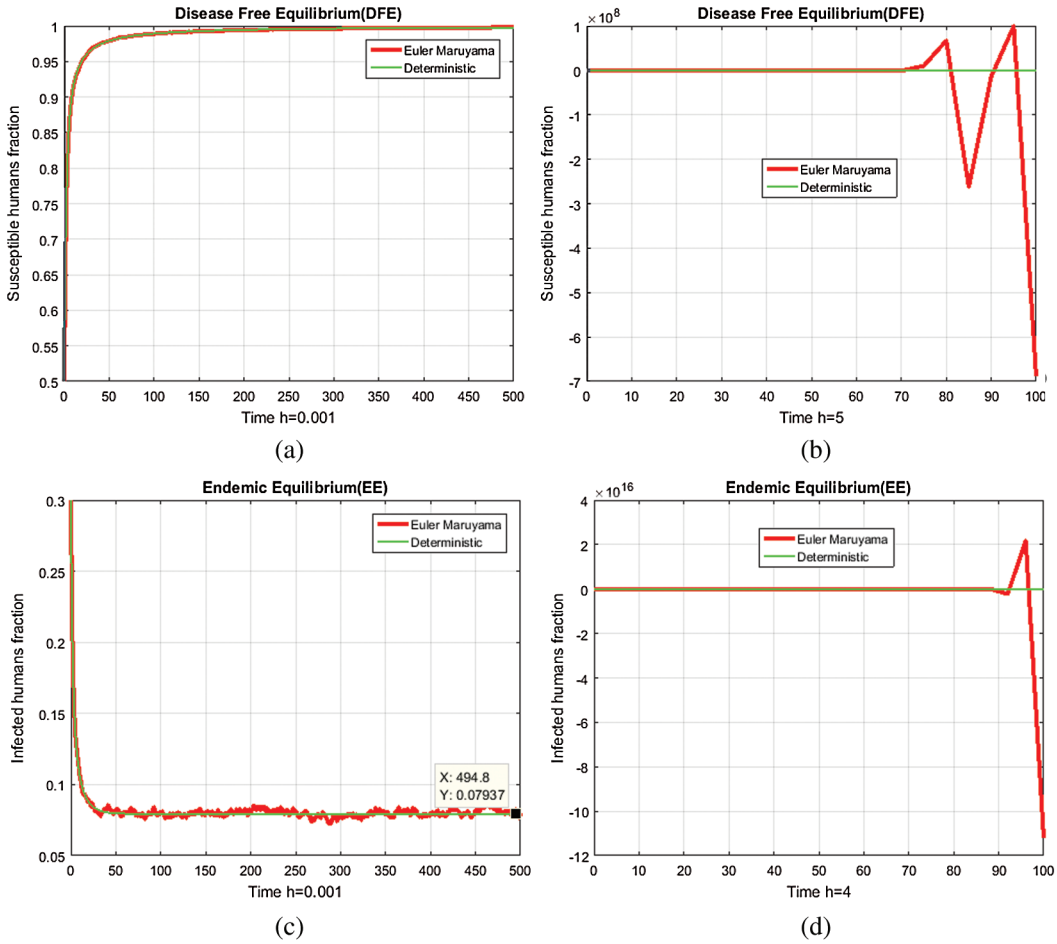

Figure 2: (a) Susceptible humans at h = 0.001 (b) Susceptible humans at h = 5 (c) Infected humans at h = 0.001 (d) Infected humans at h = 4

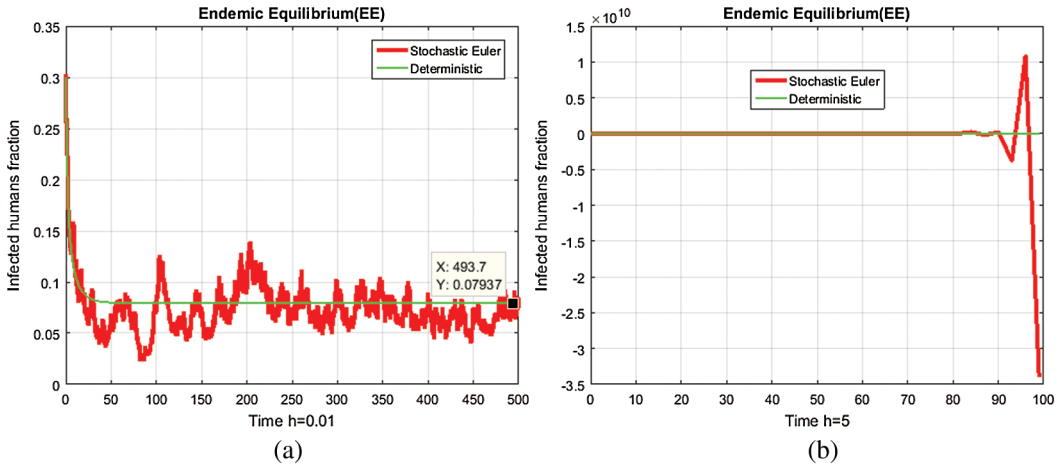

Figure 3: (a) Infected humans at h = 0.01 (b) Infected humans at h = 5

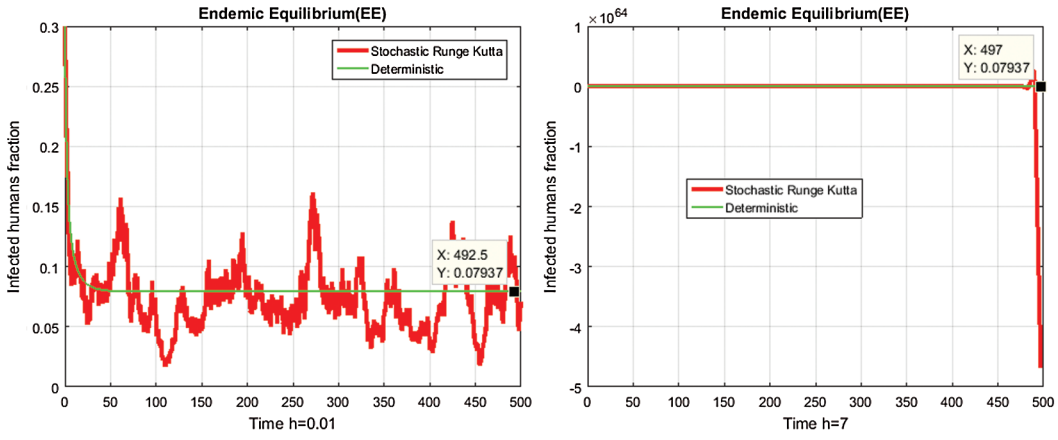

Figure 4: (a) Infected humans at h = 0.01 (b) Infected humans at h = 7

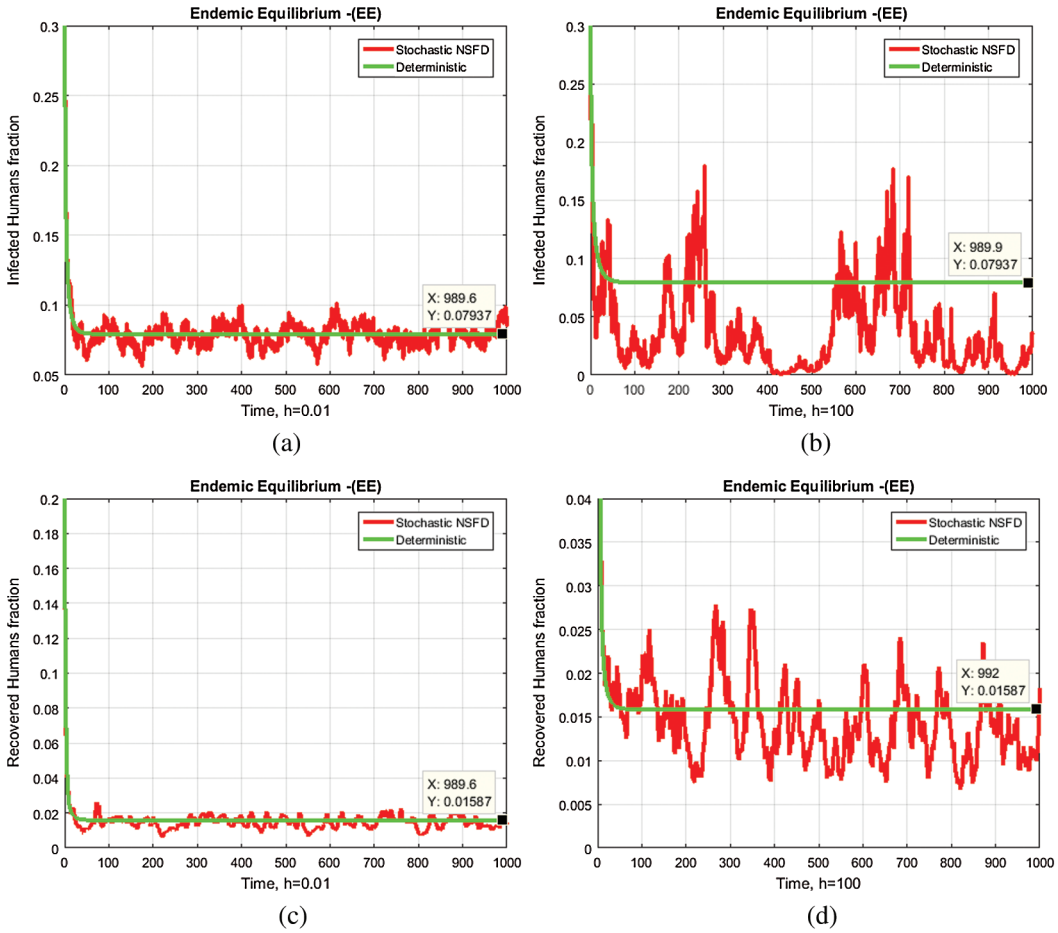

Figure 5: (a) Infected humans at h = 0.01 (b) Infected humans at h = 100 (c) Recovered humans at h = 0.01 (d) Recovered humans at h = 100

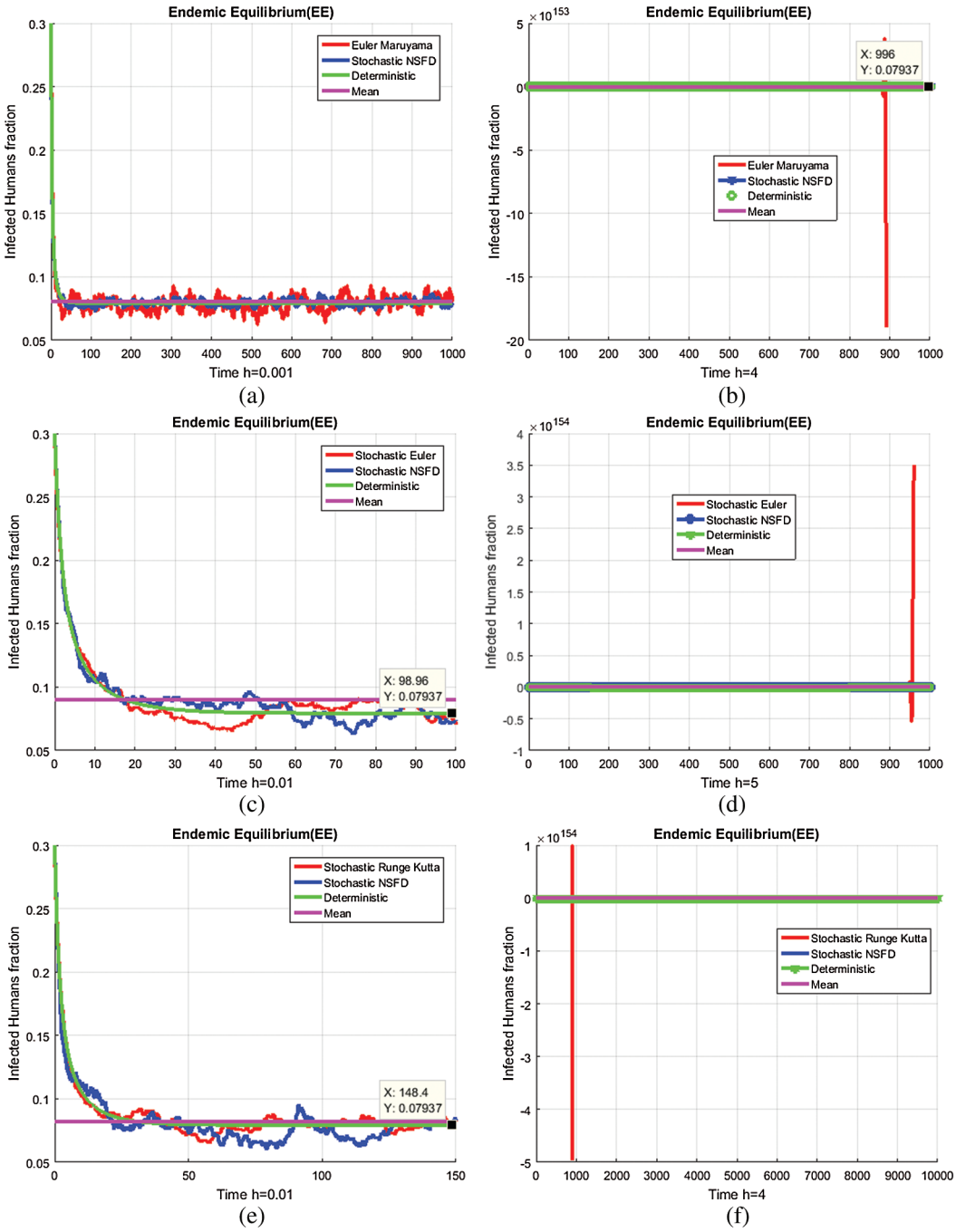

Figure 6: Contrast in results of stochastic NSFD with explicit stochastic techniques (a) Infected humans fraction with Euler Mayuyama and its average at h = 0.001 (b) Infected humans fraction with Euler Mayuyama and its average at h = 4 (c) Infected humans fraction with stochastic Euler and its average at h = 0.01 (d) Infected humans fraction with stochastic Euler and its average at h = 5 (e) Infected humans fraction with stochastic Runge Kutta and its average at h = 0.01 (f) Infected humans fraction with stochastic Runge Kutta and its average at h = 4

Table 3: Correlation coefficient

Sub-Populations	Correlation Coefficient (ρ)	Relationship
(S, I)	-0.9961	Inverse
(I, R)	0.9792	Direct
(S, R)	-0.9932	Inverse

5.7 Results and Discussion

The Euler Maruyama technique converges to the equilibria of the model in Figs. 2a and 2c at h = 0.001. A little bit change in the time step size the given technique shows the divergence in Figs. 2b and 2d. The stochastic Euler technique converges to equilibria of the model in Fig. 3a at h = 0.001. In the same manner, a little bit change in the step size the given technique shows the divergence in Fig. 3b. The stochastic Runge Kutta technique converges to equilibria of the model in Fig. 4a at h = 0.001. A little bit change in the step size the given technique shows the divergence in Fig. 4b. So above discussion, we can analyze that these techniques are time-dependent and conditionally convergent. The stochastic NSFD technique converges to equilibria of the model in Fig. 5 at any time step size. In Fig. 6, we have shown the comparison of stochastic NSFD with existing stochastic explicit techniques for different time-step sizes. We have a conclusion that stochastic NSFD always preserves the essential properties of epidemiological systems as positivity, boundedness and dynamical consistency. Also, we have to claim that deterministic solutions are called the mean of stochastic solutions. This is the beauty of stochastic NSFD as compared to other stochastic explicit techniques.

6 Conclusion and Directions

We have claimed that stochastic results are more accurate and well significant according to nature. No doubt, deterministic results are called the mean of stochastic results. Also, we have discussed the efficiency of stochastic techniques. The explicit stochastic techniques violate the dynamical properties presented by Mickens in a stochastic context.

On the other hand, essential features of computational biology systems such as non-negativity and dynamical consistency have followed by stochastic NSFD [17]. For future work, we shall make a comparison in delay and fractional computational biology systems [18]. Also, the implementation of proposed stochastic nonstandard finite difference technique could be a new significant affiliation in all different computational biology systems.

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