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Non-standard computational analysis of the stochastic COVID-19 pandemic model: An application of computational biology

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Abstract The present study is conducted to analyse the computational dynamical analysis of the stochastic susceptible-infected-recovered pandemic model of the novel coronavirus. We adopted two ways for stochastic modelling like as transition probabilities and parametric perturbation techniques. We applied different and well-known computational methods like Euler Maruyama, stochastic Euler, and stochastic Runge Kutta to study the dynamics of the model mentioned above. Unfortunately, these computational methods do not restore the dynamical properties of the model like positivity, boundedness, consistency, and stability in the sense of biological reasoning, as desired. Then, for the given stochastic model, we developed a stochastic non-standard finite difference method. Following that, several theorems are presented to support the proposed method, which is shown to satisfy all of the model's dynamical properties. To that end, several simulations are presented to compare the proposed method's efficiency to that of existing stochastic methods.

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1. Introduction

On 31 December2019, the World Health Organization (WHO) confirmed a new coronavirus in Wuhan City, Hubei Province, China [1,2]. The international committee on virus taxonomy designated (SRARS-CoV2) as a coronavirus causing severe acute respiratory syndrome [3,4]. Initially, it was traced out in Wuhan city of China and after that moved to other nations of the world so rapidly proved itself contagious. Concerning its origin, there are various arguments. Some called bats [5,6], and some considered the seafood market [7] as its origin. A significant reason for its spread is international traveling of any form [8]; thus, immigration has the most prominent role in spreading. The non-human origin of 2019-nCoV as many infected cases confirmed their presence in local fish and wildlife markets in Wuhan [9,10]. Many researchers suggested its human-to-human transmission [11,12]. A brief history of these patients revealed that they worked in the livestock market. Reportedly, some were severely infected by the attack of pneumonia and indicated early symptoms of the disease on December 8, 2019. On January 7, 2020, Chinese establishments figured out the causative agent behind this pneumonia and named it SARS CoV-2, a new addition to Coronaviridae. COVID-19 is the clinical designation, and on March 11, the WHO declared a global pandemic as the agent responsible for the outbreak [36]. Since then, the death toll surged up to 0.2 million; however, infected were calculated about 3 million in number. Coronavirus diseases are zoonotic, meaning they can be transmitted from animals to humans [37]. Symptoms may vary from mild (common cold) to severe (severe acute respiratory syndrome) and (Middle East respiratory syndrome) as caused by other members of SARS, MERS- CoV [38]. Transmission of these viruses is considered from animals to humans and from humans to humans. The former is unknown. However, some researchers affirm that this transmission could be possible through secretions of the animal body either from the digestive or from the respiratory tract. Later, through direct or indirect contact of an infected individual to the healthier one [39]. Modeling is a versatile field of mathematics that relates the physical phenomenon to calculated deduction, hence, improving learning. Nowadays, health agencies worldwide collect data related to death and recoveries, the number of testing individuals, symptomatic, asymptomatic people due to coronavirus, and publishing it daily. This stage of calculation required an appropriate modeling procedure that awards accuracy to the data compilation. For that purpose, low and high dimensional models are most recommendable to study and forecast pandemics as the previous one dealt with the minimal compartments and later with maximum parameters [40]. Several models on the COVID-19 have been published to provide the best information with high precision, as presented in [41–45]. This SIR model was chosen because it simulates the maximum number of COVID-19 patients and the time required to reach pandemic levels. Currently, this pandemic destroyed health, economic and industrial sectors and confined the society in their residences throughout the world. Scientists perceive many ways and are continually working to contain and cure the virus and ensure the safety of ordinary people as much as possible. Individuals who suffered from this disease experienced mild to severe respiratory disorders along with aches, pains, nasal congestion, sore throat, diarrhea, etc. [13] depicted the involvement of mathematical models in solving real-life issues, especially infectious disease transmission dynamics. Recently, these models are modified and extended to non-integer order and non-local derivatives of fractional disorders that enable them to predict precautionary measures to ensure the safety of maximum people. Additionally, these models are a reliable source of strategy formulation to control and eliminate diseases from society like COVID-19. Shereen et al. [13] studied the characteristics, region, and transmission of coronavirus in the human population. However, Tahir et al. [14] investigated middle east respiratory syndrome (MERS) due to coronavirus in humans. In [15], Zhao et al. applied mathematical modeling to study the dimensions of the coronavirus pandemic. Shim et al. [16] extended their work by investigating the transmission dynamics of 2019-nCoV in South Korea. In [17], predict some containment strategies through mathematics and determine artificial intelligence structure for data-driven predictions of 2019-nCoV, respectively. Chen et al. [18] developed a mathematical model for the transmission of COVID-19. The methods which enable a reliable prediction of COVID-19 will thus be of considerable benefit for convincing public opinion why such measures should be adhered to in the last decade. In evaluating their potential future effects, the modeling of viral diseases such as COVID-19 is extremely significant. Artificial Intelligence (AI) techniques have the potential to lead to the development of high-quality predictive models. New mathematical models are developed that could be used for simulation to predict the future actions of the spread. Only a few models have been proposed for COVID-19 propagation and are being used for decision-making. In a recent study, Ndairou et al. [19] developed a self-contained system of mathematical models to investigate the spread of COVID 19 in Wuhan, China. Prem et al. [20] examined the status of COVID-19 in Wuhan. In another analysis, the transmission dynamics of COVID-19 were analyzed by Mizumoto and Chowell [21] on the international shipping company Diamond Princess Cruises Ship. Hellewell et al. [22] identified the successful COVID-19 isolation technique. Kucharski et al. [23] proposed a mathematical model-basedCOVID-19 analysis, in which the authors considered all positive cases in Wuhan, China, until March 5, 2020. A big parameter to examine the essence of an infectious disease is the basic reproduction number. Liu et al. [24] examined the prospective numerical value of the COVID-19 basic reproductive number in their work. Fanelli and Piazza [25] examined and predicted the existence of COVID-19 with mathematical modeling in three of the most affected countries by March 2020. In recent research, Chakraborty and Ghosh [26] also considered a hybrid ARIMA-WBF model that predicted the emergence of multiple COVID-19 countries globally. As the existence of and destruction of COVID-19 depends on the varying parameters of the environment (i.e., Personal immunity, history, preservation of the necessary hygiene of the pandemic region, etc.), the entire disease environment in the world cannot be defined using a single model (see Fig. 1).

Deterministic modeling is one of the major innovations to study the dynamics of infectious diseases like dengue, influenza, Spanish flu, HIV/AIDS, Zika virus, and COVID-19. Each type of modeling could be extended with the utilization of the idea of deterministic modeling. So, stochastic modeling is more

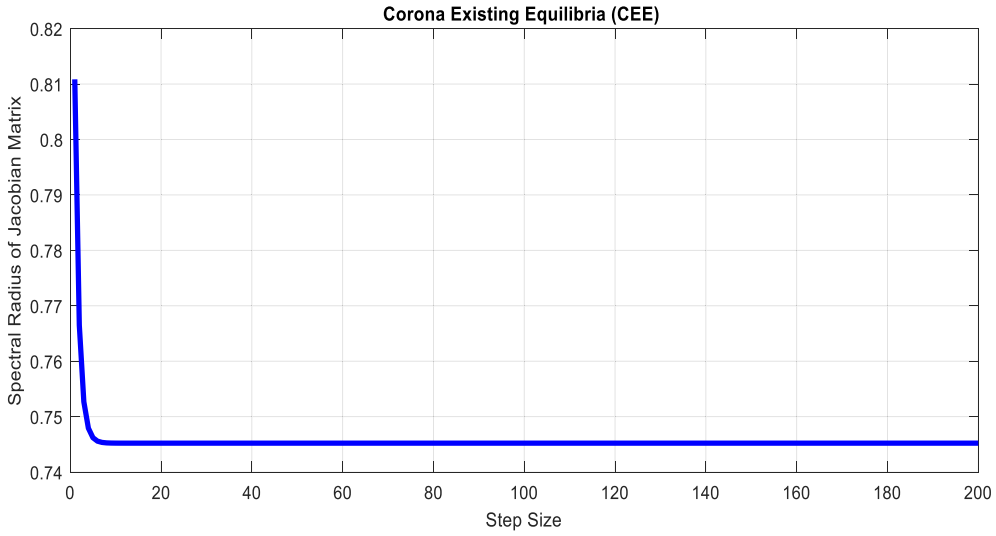

Fig. 1 Time-plot of the largest eigenvalue for the system (18–20) at the equilibria E_2, and temporal step sizes k in $[0, 200]$.

realistic, probabilistic, and close to nature. In other words, stochastic modeling is the true sense to study the dynamics of infectious diseases and their results close nature of physical phenomena. In this case, we considered the stochastic modeling of the coronavirus in the human population. Our primary objective is to conduct a structure-preserving analysis on the stochastic coronavirus model. That is the reason we are motivated to study the non-standard computational analysis of the stochastic COVID-19 model (see Table 1).

The following sections outline the paper's flow: Section 2, fundamental properties of the model is presented. In Section 3, the model's transition probabilities, parametric perturbation and reproduction dynamics are presented. In Section 4, the implementation of the well-known methods, stochastic non-standard finite difference method, convergence analysis, and comparative analysis of the stochastic model is presented. Finally, the conclusion is presented in Section 5.

2. Formulation of the model

In this part, we studied the dynamics of a coronavirus in humans with the case of the mathematical model in which the human population is divided into three components of sub-populations as presented in [27]. Let us consider population function, which is presented by $N(t), t \geq 0$ as defined $N : [0, \infty) \to \mathscr{R}$. Also, the non-negative differential function of each component of the population as $S, I, R : [0, \infty) \to \mathscr{R}$. The representation of the components of the human population is described as S(t) (denotes the susceptible humans who shall have the maximum probability to catch the fatal virus), I(t) (denotes the infected humans who have convicted with the virus), and R(t) (denotes the recovered humans who have got the vaccination or delay strategies and due to their internal level of immunity).

Table 1 Physical interpretation of the parameters.

c	represented the convex incidence rate under the law of mass action.
δ	denotes the rate at which infected humans die due to coronavirus.
α	represented the rate of humans after recovery may become susceptible.
μ	the rate at which humans die from other diseases and natural incidences.
β	the rate of humans may recover from the infection due to vaccination, hospitalization, social distancing, travel restrictions, quarantine, etc.
b	the rate of infected human's immigrant to one location to another.

The model of the differential equations as follows:

$$S^{'}(t) = \mathrm{a} - cS(t)I(t)(1 + \gamma I(t)) - \mu S(t) + \alpha R(t), \forall t \geq 0, \quad (1)$$

$$I^{'}(t) = cI(t)S(t)(1 + \gamma I(t)) - (\beta + \mu + \delta - b)I(t), \forall t \geq 0, \quad (2)$$

$$R^{'}(t) = \beta \mathrm{I(t)} - (\alpha + \mu)R(t), \forall t \geq 0, \quad (3)$$

Obviously, the identity $N(t) = S(t) + I(t) + R(t)$ is satisfied at all the time $t \geq 0$. Let S_0, I_0 and R_0 are non-negative numbers that correspond to the initial sizes of each population component. To put it another way, the conditions listed below are met:

$$S_0 = S(0), I_0 = I(0), T_0 = T(0), R_0 = R(0), \quad (4)$$

2.1. Fundamental properties

The state variables described in Eqs. (1–3) exhibits the non-negative solution for all time t ≥ 0 with non-negative initial conditions.

Lemma 1. *For all $t \geq 0$, the S, I, R has unique solutions with the given initial conditions and satisfy the inequality of boundedness* $\lim_{t \to \infty} Sup N(t) \leq \frac{a}{\mu}$ [33].

Proof. After adding the system (1–3), the total population of the model as follows:

$$\frac{dN}{dt} \leq a - \mu N - (\delta - b) \leq a - \mu N$$

$$\frac{dN}{dt} \leq a - \mu N \tag{5}$$

$$N(t) \leq N(0)e^{-\mu t} + \frac{a}{\mu} \tag{6}$$

Thus, for any finite time interval, the solution of the system (1–3) is bounded.

Lemma 2. *The given region* $\Gamma = \{S(t), I(t), R(t) \epsilon R_+^3 : S(t) + I(t) + R(t) \leq \frac{a}{\mu}\}$ *is positively invariant.*

Proof. For infinity time as t $\rightarrow \infty$, the resultant of the system (5–6) as follows:

$$\lim_{t \to \infty} sup N(t) \leq \frac{a}{\mu}$$

Therefore, the set Γ is positive invariant.

We now present the following lemma as discussed in [46] to conclude this section.

Lemma 3: Consider the initial conditions as given in Eq. (4). Then the solutions (S, I, R) of the system (1)–(3) are positive for all time t > 0.

Proof: Let us suppose that, $S(0) \geq 0$, $I(0) \geq 0$, $R(0) \geq 0$.

Then from Eq. (1). we have

$$S^{'} = a - cSI(1 + \gamma) - \mu S + \alpha R$$

$$S^{'} \geq -[cI(1 + \gamma I) + \mu]S$$

$$\Rightarrow lnS = -[cI(1 + \gamma I) + \mu]t + c$$

$$\Rightarrow S = e^{c} \times e^{-[cI(1+\gamma I)+\mu]t}$$

$$\Rightarrow S(t) = S(0) \times e^{-[cI(1+\gamma I)+\mu]t} \geq 0$$

As $S(0) \geq 0$, therefore 'S' is the product of positive terms, is always positive for any time $t > 0$.

Similarly, we can have the following relations from Eqs. (2) & (3).

$$I(t) \geq I(0) \times e^{-[\beta+\mu+\delta-b]t} \geq 0$$

$$R(t) \geq R(0) \times e^{-[\alpha+\mu]t} \geq 0$$

Hence the model solutions S, I, R satisfying initial conditions, $S(0) \geq 0$, $I(0) \geq 0$, $R(0) \geq 0$ are positive any time $t > 0$.

2.2. Model equilibria

The system (1–3) admits the following equilibria as:

Trivial equilibrium (TE) $= E_0 = (S^0, I^0, R^0) = (0, 0, 0)$

Corona free equilibria (CFE) $= E_1 = (S^1, I^1, R^1) = (\frac{a}{\mu}, 0, 0)$

Corona existing equilibria (CEE) $= E_2 = (S^*, I^*, R^*)$

$$S^* = \frac{(a - \beta - \mu - \delta + b) + \alpha\beta I^*}{\mu(\alpha + \mu)},$$

$$I^* = \frac{-(cB + c\gamma A) + \sqrt{(cB + c\gamma A)^2 - 4(c\gamma B)(\mu - c_1)}}{2c\gamma B},$$

$$R^* = \frac{\beta I^*}{\alpha + \mu}$$

where $A = \frac{(a-\beta-\mu-\delta+b)}{\mu}$, $B = \frac{\alpha\beta}{\mu(\alpha+\mu)}$, $c_1 = (\beta + \mu + \delta - b)$.

The next-generation matrix method is presented in [34] for calculating the reproduction number. The said method is given an idea for transmission and transition matrices. We took two compartments like infectious presented by $I(t)$ and recovered presented by $R(t)$ rest of the susceptible compartments is ignored under assumptions of the method. The reproduction number R_O is the largest eigenvalue of FV^{-1}, where F and V are the transmission and transition matrices respectively, obtained from the system (1) to (3) by substituting the corona free equilibria of the model as follows:

$$F = \begin{bmatrix} \frac{ca}{\mu} & 0 \\ 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \beta + \mu + \delta - b & 0 \\ 0 & \alpha + \mu \end{bmatrix}$$

More exactly, notice that

$$R_0 = \frac{ac}{\mu(\mu + \beta + \delta - b)}$$

3. Transition probabilities of the model

Let us consider the vector $\mathrm{U(t)} = [S(t), \mathrm{I}(t), \mathrm{R}(t)]^{\mathrm{T}}$,and the number of chances of an event is presented in Table 2:

For the drift and diffusion coefficients of the system (1–3), we shall calculate the expectation and variance as follows:

$$\mathrm{E}^*[\Delta \mathrm{U}] = \sum_{\mathrm{i}=1}^{7} \mathrm{P_i T_i} = \begin{bmatrix} \mathrm{a} - cSI(1 + \gamma I) - \mu S + \alpha R \\ cIS(1 + \gamma I) - (\beta + \mu + \delta - b)I \\ \beta \mathrm{I} - (\alpha + \mu)R \end{bmatrix} \Delta t$$

$$\mathrm{Var} = \mathrm{E}^*\left[\Delta \mathrm{U} \Delta \mathrm{U}^{\mathrm{T}}\right] = \sum_{\mathrm{i}=1}^{7} \mathrm{P_i}[\mathrm{T_i}][\mathrm{T_i}]^{\mathrm{T}}$$

$$= \begin{bmatrix} P_1 + P_2 + P_3 + P_4 & -P_2 & -P_4 \\ -P_2 & P_2 + P_5 + P_6 & -P_6 \\ -P_4 & -P_6 & P_6 + P_7 \end{bmatrix} \Delta t$$

$\mathrm{drift} = \mathrm{H(U(t), t)} = \frac{\mathrm{E}^*[\Delta \mathrm{U}]}{\Delta \mathrm{t}}$, $\mathrm{diffusion} = \mathrm{K(U(t), t)} = \sqrt{\frac{\mathrm{E}^*[\Delta \mathrm{U} \Delta \mathrm{U}^{\mathrm{T}}]}{\Delta \mathrm{t}}}$, so

Table 2 Transition Probabilities of the model.

T_i = Transition	$\mathbf{P}_i$ = Probabilities
$\mathbf{T}_1 = [1 \quad 0 \quad 0]^{\mathbf{T}}$	$\mathrm{P}_1 = \mathrm{a}\Delta\mathrm{t}$
$\mathbf{T}_2 = [-1 \quad 1 \quad 0]^{\mathbf{T}}$	$\mathrm{P}_2 = c\mathrm{SI}(1 + \gamma\mathrm{I})\Delta\mathrm{t}$
$\mathbf{T}_3 = [-1 \quad 0 \quad 0]^{\mathbf{T}}$	$\mathrm{P}_3 = \mu\mathrm{S}\Delta\mathrm{t}$
$\mathbf{T}_4 = [1 \quad 0 \quad -1]^{\mathbf{T}}$	$\mathrm{P}_4 = \alpha R\Delta\mathrm{t}$
$\mathbf{T}_5 = [0 \quad -1 \quad 0]^{\mathbf{T}}$	$\mathrm{P}_5 = (\mu + \delta - \mathrm{b})\mathrm{I}\Delta\mathrm{t}$
$\mathbf{T}_6 = [0 \quad -1 \quad 1]^{\mathbf{T}}$	$\mathrm{P}_6 = \beta I\Delta\mathrm{t}$
$\mathbf{T}_7 = [0, 0, -1]^{\boldsymbol{T}}$	$\mathrm{P}_7 = \mu R\Delta\mathrm{t}$

$$dU(t) = H(U(t), t)dt + K(U(t), t)dW(t) \tag{7}$$

The Eq. (7), is called the stochastic differential equation with W(t) is the Brownian.

3.1. Euler Maruyama method

The following section will discuss a standard numerical methodology for approximating a stochastic model's solution (7). In this respect, we are going to agree $I_m = \{0, 1, 2, 3, \cdots, m\}$ for each m $\in \mathbb{N}$. Let $N \in \mathbb{N}$, and consider a uniform partition of the temporal interval [0, T] with partition norm equal to τ = T/N. The nodes of that partition are represented by

$$0 = t_o < t_1 < t_2 < \cdots < t_N = T \tag{7.1}$$

for each n $\in I_N$. Needless to mention that $t_n = \tau$n, for each n $\in I_N$. Moreover, we will agree that $U^n = U(t_n)$, whenever n $\in I_N$ and U = S, I, R. Also, we set

$$\Delta W_n = \mathrm{W}(t_n + 1) - \mathrm{W}(t_n), \forall \mathrm{n} \in I_N - 1 \tag{8}$$

Clearly, each ΔW_n has a normal distribution with a mean of zero and a variance of one [28].

3.2. Stochastic model

Let us consider the small noise as $cdt = cdt + \sigma dW(t)$ with parametric perturbation technique for the system (1–3) as follows [29]:

$$\begin{aligned} dS(t) = {} & [\mathrm{a} - cS(t)I(t)(1 + \gamma I(t)) - \mu S(t) + \alpha R(t)]dt \\ & - \sigma c[S(t)I(t)(1 + \gamma I(t))]dW(t), \forall t \geq 0, \end{aligned} \tag{9}$$

$$\begin{aligned} dI(t) = {} & [cI(t)S(t)(1 + \gamma I(t)) - (\beta + \mu + \delta - b)I(t)]dt \\ & + \sigma \mathrm{c} S(t)I(t)(1 + \gamma I(t))dW(t) \forall t \geq 0, \end{aligned} \tag{10}$$

$$dR(t) = [\beta \mathrm{I}(t) - (\alpha + \mu)R(t)]dt, \forall t \geq 0, \tag{11}$$

The Brownian motion is denoted by $W(t)$, σ is the randomness of Eqs. (9–11). The Eqs. (9–11) is non-integrable because of the Brownian motion.

3.2.1. Positivity and boundedness

Consider, a complete probability space which is denoted by (Ω, F, P) and with the filtration represented by $\{F_t\}_{t\epsilon R}$. While $F_o$contains all P-null sets that satisfying the following conditions: like right continuous and increasing [35]. Symbolize

$$U(t) = (S(t), I(t), R(t)) \tag{12}$$

And the norm $|U(t)| = \sqrt{S^2(t) + I^2(t) + R^2(t)}$. And denote $C^{2,1}(R^3 \times (0, \infty); R_+)$ as the family of all non-negative functions $V(U, t)$ defined on $R^3 \times (0, \infty)$ such that they are continuously twice differentiable in U and once in t.

We define the differential operator Lassociated with three-dimensional stochastic differential equation.

$$dU(t) = H(U, t)dt + K(U, t)dW(t) \tag{12.1}$$

As,$L = \frac{\partial}{\partial t} + \sum_{i=1}^{3} H_i(U, t)\frac{\partial}{\partial u_i} + \frac{1}{2}\sum_{i,j=1}^{3}\left(K^T(U, t)K(U, t)\right)_{i,j} \times \frac{\partial^2}{\partial U_i \partial U_j}$

If L acts on a function $V \in C^{2,1}(R^3 \times (0, \infty); R_+)$ then we denote

$$\begin{aligned} LV(U, t) = {} & V_t(U, t) + V_U(U, t)H(U, t) \\ & + \frac{1}{2} Trace\left(K^T(U, t)V_{UU}(U, t)K(U, t)\right), \end{aligned}$$

where T means transportation.

Theorem. *For model* (9–11) *and any given initial value* $(S(0), I(0), R(0)) \in R^3_+$, *there is a unique solution* $(S(t), I(t), R(t))$ *on* $t \geq 0$ *and will remain in* R^3_+ *with probability one.*

Proof. By Ito's formula, the model (9–11) admits positive solution in sense of unique [localon0, τ_e] and explosion time is denoted byτ_e. Because local Lipschitz condition is satisfied by all the coefficients of the aforesaid model.

Next, let us show that the given model (9–11) admits this solution in sense of global; that is, $\tau_e = \infty$ almost sure.

Let $m_o = 0$ be sufficiently large for $S(0), I(0)$ and $R(0)$ lying with the interval $[\frac{1}{m_o}, m_o]$. For each integer $m \geq m_o$, define a sequence that is so called stopping times as

$$\begin{aligned} & \tau_m = \\ & \inf\left\{t\epsilon[0, \tau_e] : S(t) \notin \left(\frac{1}{m}, m\right) or I(t) \notin \left(\frac{1}{m}, m\right) or R(t) \notin \left(\frac{1}{m}, m\right)\right\} \end{aligned} \tag{13}$$

where we set $inf\phi = \infty(\phi$represents theemptyset). Since τ_m is non-decreasing as $m \to \infty$,

$$\tau_\infty = \lim_{m\to\infty} \tau_m \tag{14}$$

Then $\tau_\infty \leq \tau_e$ almost sure. Now, we need to show $\tau_\infty = \infty$ almost sure.

If this statement is violated, then there exist $T > 0$ and $\varepsilon\epsilon(0, 1)$ such that

$$P\{\tau_\infty \leq T\} > \varepsilon \tag{15}$$

this, there is an integer $m_1 > m_0$ such that

$$P\{\tau_m \leq T\} \geq \varepsilon \forall m \geq m_1 \tag{16}$$

Define a C^3-function $V : R^3_+ \to R_+$ by

$$\begin{aligned} V(S, I, R) = {} & (S - 1 - \ln S) + (I - 1 - \ln I) \\ & + (R - 1 - \ln R) \end{aligned} \tag{17}$$

By using Ito's formula, we calculate

$$dV(S, I, R) = \left(1 - \frac{1}{S}\right)dS + \left(1 - \frac{1}{I}\right)dI + \left(1 - \frac{1}{R}\right)dR + \frac{\sigma^2}{2}dt$$

$$\begin{aligned} dV(S, I, R) = {} & \left(1 - \frac{1}{S}\right)([a - CSI(1 + \gamma I) - \mu S + \alpha R]dt - \sigma CSI(1 + \gamma I)dW(t)) \\ & + \left(1 - \frac{1}{I}\right)([CSI(1 + \gamma I) - (\beta + \mu + \delta - b)I]dt + \sigma CSI(1 + \gamma I)dW(t)) \\ & + \left(1 - \frac{1}{R}\right)[\beta I - (\alpha + \mu)R]dt + \frac{\sigma^2}{2}dt \end{aligned}$$

$$\begin{aligned} dV(S, I, R) \leq {} & \left[a + 2\mu + \beta + \delta + b + \frac{\sigma^2}{2}\right]dt \\ & + \sigma C(S - I)(1 + \gamma I)dW(t) \end{aligned} \tag{18}$$

For simplification, we assume

$N = \alpha + 2\mu + \beta + \delta + b + \frac{\sigma^2}{2}$, Then Eq. (18) could be written as:

$$dV(S, I, R) \leq Ndt + \sigma C(S - I)(1 + \gamma I)dW(t) \tag{19}$$

where N is a positive constant, After that integrating from 0 to $\tau_m \wedge \tau$, we get

$$\int_0^{\tau_m \wedge \tau} dV(S(s), I(s), R(s)) \leq \int_0^{\tau_m \wedge \tau} Nds + \int_0^{\tau_m \wedge \tau} \sigma C(S - I)(1 + \gamma I)dW(s) \tag{20}$$

where $\tau_m \wedge \tau = \min(\tau_m, T)$, the taking the expectations lead to

$$EV(S(\tau_m \wedge \tau), I(\tau_m \wedge \tau), R(\tau_m \wedge \tau)) \leq V(S(0), I(0), R(0)) + NT \tag{21}$$

Set $\Omega_m = \{\tau_m \leq T\}$ for $m > m_1$ and from (16), we have $P(\Omega_m \geq \varepsilon)$. For every $v \in \Omega_m$ there are some i such that $u_i(\tau_m, v)$ equals either m or $\frac{1}{m}$ for $i = 1, 2, 3$;

Hence, $V(S(\tau_m, v), I(\tau_m, v), R(\tau_m, v))$ is less than $\min\{m - 1 - \ln m, \frac{1}{m} - 1 - \ln\frac{1}{m}\}$.

Then we obtain,

$$V(S(0), I(0), R(0)) + NT \geq E\big(I_{\Omega_m(v)} V(S(\tau_m), I(\tau_m), R(\tau_m))\big) \geq \left\{\min\left(m - 1 - \ln m, \frac{1}{m} - 1 - \ln\frac{1}{m}\right)\right\} \tag{22}$$

The indicator function is represented by $I_{\Omega_m(v)}$ of Ω_m. Letting $m \to \infty$ leads to the contradiction$\infty = V(S(0), I(0), R(0)) + NT < \infty$

as desired.

3.2.2. Extinction and persistence

Definition: Let $W(t)$ be a Brownian motion and $I(t)$ be an Ito drift–diffusion process that satisfies the stochastic differential equation:

$$dI(t) = \mu(I(t), t)dt + \sigma(I(t), t)dW(t)$$

If $f(I, t) \in C^2(\mathscr{R}^2, \mathscr{R})$ then $f(I(t), t)$ is also an Ito drift–diffusion process, which satisfies as follows:

$$d(f(I(t), t)) = \frac{\partial f}{\partial t}(I(t), t)dt + f'((I(t), t))dW(t) + \frac{1}{2}f''((I(t), t))dW(t)^2.$$

Let us introduce $\mathrm{R_o^S} = \mathrm{R_o^d} - \frac{\sigma^2}{2(\beta+\mu+\delta-b)}$.

Lemma: The unique solution of the system (9–11) exist and lie in the regionΓ if it satisfies $(\mathrm{S}(0), \mathrm{I}(0), \mathrm{R}(0)) \in \mathrm{R_+}^3$.

Definition. The infected individuals will be extinct in the system (9–11), if $\lim_{t\to\infty} I(t) = 0$, $\forall t \geq 0$.

Theorem. If $\mathrm{R_o^S} < 1$ and $\sigma^2 < \frac{ca}{\mu(\beta+\mu+\delta-b)}$, then the infected individuals of the system (9–11) exponentially tend to zero.

Proof. let us consider the initial data $(\mathrm{S}(0), \mathrm{I}(0), \mathrm{R}(0)) \in \mathrm{R_+}^3$ and the system (9–11) admits the solution as $(\mathrm{S}(t), I(t), \mathrm{R}(t))$, with σ and c are the randomness and drift respectively, if it satisfies the stochastic differential equation

$$dI = [cIS(1 + \gamma I) - (\beta + \mu + \delta - b)I]dt + \sigma \mathrm{c}SI(1 + \gamma I)dW$$

By using the Itô's lemma with $\mathrm{f}(I) = \ln(\mathrm{I})$, we have

$$\mathrm{d}\ln(I) = \mathrm{f}'(\mathrm{I})\mathrm{dI} + \frac{1}{2}\mathrm{f}''(\mathrm{I})\mathrm{I}^2\sigma^2\mathrm{dt}$$

$$\mathrm{d}\ln(I) = \frac{1}{\mathrm{I}}\mathrm{dI} + \frac{1}{2}(-\frac{1}{\mathrm{I}^2})\mathrm{I}^2\sigma^2\mathrm{dt}$$

$$\mathrm{d}\ln(I) = (cS(1 + \gamma I) - (\beta + \mu + \delta - b) - \frac{1}{2}\sigma^2)\mathrm{dt} + \sigma \mathrm{c}\mathrm{S}(1 + \gamma I)\mathrm{dW}$$

$$\ln(I) = \ln \mathrm{I}(0) + \int_0^{\mathrm{t}} (cS(1 + \gamma I) - (\beta + \mu + \delta - b) - \frac{1}{2}\sigma^2)\mathrm{dt} + \int_0^{\mathrm{t}} \sigma \mathrm{c}\mathrm{S}(1 + \gamma I)\mathrm{dW},$$

Notice that, $\mathrm{M(t)} = \int_0^{\mathrm{t}} \sigma \mathrm{c}\mathrm{S}(1 + \gamma I)\mathrm{dW}$ with $\mathrm{M}(0) = 0$.

If $\sigma^2 > \frac{ca}{\mu(\beta+\mu+\delta-b)}$,

$$\ln(I) > (\frac{ca}{\mu(\beta + \mu + \delta - b)} - (\beta + \mu + \delta - b) - \frac{1}{2}\frac{ca}{\mu(\beta + \mu + \delta - b)})\mathrm{t} + \mathrm{M(t)} + \ln I(0)$$

$$\frac{\ln(I)}{\mathrm{t}} > \left(\frac{ca}{2\mu(\beta + \mu + \delta - b)} - (\beta + \mu + \delta - b)\right) + \frac{\mathrm{M(t)}}{\mathrm{t}} + \frac{\ln I(0)}{\mathrm{t}}$$

$\lim_{\mathrm{t}\to\infty} \frac{\ln(I)}{\mathrm{t}} > \left(\frac{ca}{2\mu(\beta+\mu+\delta-b)} - (\beta + \mu + \delta - b)\right) > 0$, with $\lim_{\mathrm{t}\to\infty} \frac{\mathrm{M(t)}}{\mathrm{t}} = 0$,

If $\sigma^2 < \frac{ca}{\mu(\beta+\mu+\delta-b)}$, then

$$\ln(I(\mathrm{t})) < \left(\frac{ca}{\mu(\beta + \mu + \delta - b)} - (\beta + \mu + \delta - b) - \frac{1}{2}\sigma^2\right)\mathrm{t} + \mathrm{M(t)} + \ln I(0),$$

$$\frac{\ln(I)}{\mathrm{t}} < (\beta + \mu + \delta - b)\left(\frac{ca}{\mu(\beta + \mu + \delta - b)^2} - \frac{\sigma^2}{2(\beta + \mu + \delta - b)} - 1\right) + \frac{\mathrm{M(t)}}{\mathrm{t}} + \frac{\ln I(0)}{\mathrm{t}},$$

$\limsup_{\mathrm{t}\to\infty} \frac{\ln(I)}{\mathrm{t}} < (\beta + \mu + \delta - b)\big(\mathrm{R_0}^{\mathrm{S}} - 1\big)$, when $\mathrm{R_0}^{\mathrm{S}} < 1$, we get $\limsup_{\mathrm{t}\to\infty} \frac{\ln(I)}{\mathrm{t}} \leq 0$,

$\lim_{\mathrm{t}\to\infty} I(\mathrm{t}) = 0$, as desired.

$$\mathrm{R_o^S} = \mathrm{R_o^d} - \frac{\sigma^2}{2(\beta + \mu + \delta - b)} < 1$$

4. Numerical methodology

For each $N \epsilon \mathbb{N}$, define the set $I_N = \{0, 1, 2 \cdots, N\}$. In this section we will present and analyse a system discretization (9–11). To that end, we consider the temporal period $T > 0$. Fix

a uniform partition of the temporal interval $[0, T]$ consisting of N subintervals, and let $k = \frac{T}{N}$. Define $t_m = mk$, for each $m \epsilon I_N$, the numerical approximation to the values of the functions S, I, and R are represented by S^n, I^n and R^n, respectively. The discrete initial data (S_0, I_0, R_0), where $S_0 = S(0), I_0 = I(0), R_0 = R(0)$, as desired.

4.1. Stochastic Euler method

This scheme could be practical to Eqs. (9–(11) as follows:

$$S^{m+1} = S^m + k[\mathrm{a} - cS^m I^m(1+\gamma I^m) - \mu S^m + \alpha R^m - \sigma c S^m I^m(1+\gamma I^m)\Delta W_m] \tag{23}$$

$$I^{m+1} = I^m + k[cI^m S^m(1+\gamma I^m) - (\beta+\mu+\delta-b)I^m + \sigma \mathrm{c} S^m I^m(1+\gamma I^m)\Delta W_m] \tag{24}$$

$$R^{m+1} = R^m + k[\beta I^m - (\alpha+\mu)R^m] \tag{25}$$

where $m = 0, 1, 2, \cdots$ and $\Delta \mathrm{W_m} = \Delta \mathrm{W}_{t_{m+1}} - \Delta \mathrm{W}_{t_m}$ is standard normal distribution. i.e. $\Delta \mathrm{W_m}$ $\mathrm{N}(0, 1)$.

4.2. Stochastic Runge-Kutta method

This scheme could be practical to Eqs. (9–11) as follows:

Stage1

$$X_1 = k[\mathrm{a} - cS^m I^m(1+\gamma I^m) - \mu S^m + \alpha R^m - \sigma c S^m I^m(1+\gamma I^m)\Delta W_m]$$

$$Y_1 = k[cI^m S^m(1+\gamma I^m) - (\beta+\mu+\delta-b)I^m + \sigma \mathrm{c} S^m I^m(1+\gamma I^m)\Delta W_m]$$

$$Z_1 = k[\beta I^m - (\alpha+\mu)R^m]$$

Stage2

$$X_2 = k[\mathrm{a} - c\left(S^m + \frac{X_1}{2}\right)(I^m + \frac{Y_1}{2})\left(1+\gamma(I^m+\frac{Y_1}{2})\right) - \mu(S^m + \frac{X_1}{2}) + \alpha(R^m + \frac{Z_1}{2}) - \sigma c(S^m + \frac{X_1}{2})(I^m + \frac{Y_1}{2})\left(1+\gamma(I^m+\frac{Y_1}{2})\right)\Delta W_m]$$

$$Y_2 = k[c(I^m + \frac{Y_1}{2})(S^m + \frac{X_1}{2})\left(1+\gamma(I^m+\frac{Y_1}{2})\right) - (\beta+\mu+\delta-b)(I^m + \frac{Y_1}{2}) + \sigma \mathrm{c}(S^m + \frac{X_1}{2})(I^m + \frac{Y_1}{2})\left(1+\gamma(I^m+\frac{Y_1}{2})\right)\Delta W_m]$$

$$Z_2 = k[\beta(I^m + \frac{Y_1}{2}) - (\alpha+\mu)(R^m + \frac{Z_1}{2})]$$

Stage3

$$X_3 = k[\mathrm{a} - c(S^m + \frac{X_2}{2})(I^m + \frac{Y_2}{2})\left(1+\gamma(I^m+\frac{Y_2}{2})\right) - \mu(S^m + \frac{X_2}{2}) + \alpha(R^m + \frac{Z_2}{2}) - \sigma c(S^m + \frac{X_2}{2})(I^m + \frac{Y_2}{2})\left(1+\gamma(I^m+\frac{Y_2}{2})\right)\Delta W_m]$$

$$Y_3 = k[c(I^m + \frac{Y_2}{2})(S^m + \frac{X_2}{2})\left(1+\gamma(I^m+\frac{Y_2}{2})\right) - (\beta+\mu+\delta-b)(I^m + \frac{Y_2}{2}) + \sigma \mathrm{c}(S^m + \frac{X_2}{2})(I^m + \frac{Y_2}{2})\left(1+\gamma(I^m+\frac{Y_2}{2})\right)\Delta W_m]$$

$$Z_3 = k[\beta(I^m + \frac{Y_2}{2}) - (\alpha+\mu)(R^m + \frac{Z_2}{2})]$$

Stage4

$$X_4 = k[\mathrm{a} - c(S^m + X_3)(I^m + Y_3)(1+\gamma(I^m+Y_3)) - \mu(S^m + X_3) + \alpha(R^m + Z_3) - \sigma c(S^m + X_3)(I^m + Y_3)(1+\gamma(I^m+Y_3))\Delta W_m]$$

$$Y_4 = k[c(I^m + Y_3)(S^m + X_3)(1+\gamma(I^m+Y_3)) - (\beta+\mu+\delta-b)(I^m + Y_3) + \sigma \mathrm{c}(S^m + X_3)(I^m + Y_3)(1+\gamma(I^m+Y_3))\Delta W_m]$$

$$Z_4 = k[\beta(I^m + Y_3) - (\alpha+\mu)(R^m + Z_3)].$$

Final stage

$$\left.\begin{aligned} \mathrm{S^{m+1}} &= \mathrm{S^m} + \tfrac{1}{6}[\mathrm{X_1} + 2\mathrm{X_2} + 2\mathrm{X_3} + \mathrm{X_4}] \\ \mathrm{I^{m+1}} &= \mathrm{I^m} + \tfrac{1}{6}[\mathrm{Y_1} + 2\mathrm{Y_2} + 2\mathrm{Y_3} + \mathrm{Y_4}] \\ \mathrm{R^{m+1}} &= \mathrm{R^m} + \tfrac{1}{6}[\mathrm{Z_1} + 2\mathrm{Z_2} + 2\mathrm{Z_3} + \mathrm{Z_4}] \end{aligned}\right\} \tag{26}$$

where $m = 0, 1, 2, \cdots$ and $\Delta \mathrm{W_m} = \Delta \mathrm{W}_{t_{m+1}} - \Delta \mathrm{W}_{t_m}$ is standard normal distribution. i.e. $\Delta \mathrm{W_m}$ $\mathrm{N}(0, 1)$.

4.3. Stochastic nonstandard computational method

The first equation of our parametric perturbation model (9) can be expressed in the non-standard computational method; namely, that stochastic non-standard finite difference method could be used for Eqs. (9–11):

$$\frac{dS}{dt} = [\mathrm{a} - cS(t)I(t)(1+\gamma I(t)) - \mu S(t) + \alpha R(t)] - \sigma c[S(t)I(t)(1+\gamma I(t))]\frac{dW(t)}{dt} \tag{27}$$

The decomposition of the Eq. (27), in the stochastic NSFD method, as follows:

$$\frac{S^{m+1} - S^m}{k} = \left[\mathrm{a} - cS^{m+1}I^m(1+\gamma I^m) - \mu S^{m+1} + \alpha R^m\right]dt - \sigma c\left[S^{m+1}I^m(1+\gamma I^m)\right]\Delta W_m \tag{28}$$

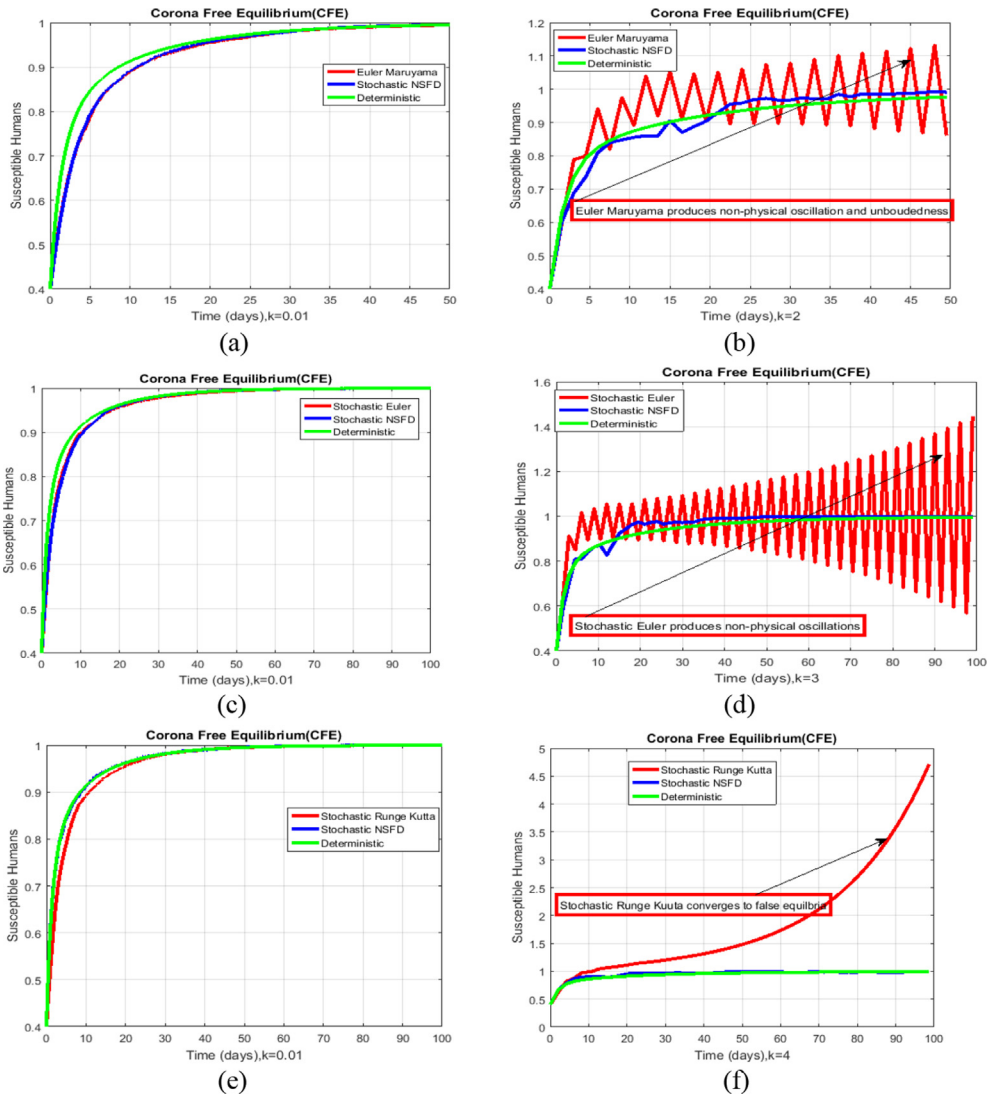

Fig. 2 Comparison graph of computational methods at the corona-free equilibria of the model.

Like (28), in the stochastic NSFD process, we can decompose the system (9–11) and then write the entire system accordingly:

$$S^{m+1} = \frac{S^m + ka + k\alpha R^m}{1 + kcI^m(1+\gamma I^m) + k\mu + kcI^m\sigma(1+\gamma I^m)\Delta W_m} \tag{29}$$

$$I^{m+1} = \frac{I^m + kcI^m S^m(1+\gamma I^m) + kbI^m + k\sigma cI^m S^m(1+\gamma I^m)\Delta w_m}{1 + k(\beta + \mu + \delta)} \tag{30}$$

$$R^{m+1} = \frac{R^m + k\beta I^m}{1 + k(\alpha + \mu)} \tag{31}$$

where $m = 0, 1, 2, \cdots$ and $\Delta W_m = \Delta W_{t_{m+1}} - \Delta W_{t_m}$ is standard normal distribution. i.e. ΔW_m $N(0, 1)$.

4.3.1. Convergence analysis

For the convergence analysis, the following theorems are presented.

Theorem. *For any given initial value* $(S^m(0), I^m(0), R^m(0)) \in R^3_+$, *Eqs. (29)–(31) has a unique positive solution* $(S^m, I^m, T^m, R^m) \in R^4_+$ *on* $m \geq 0$.

Proof. The proof is straightforward. Because the constraint of biological problems is non-negative.

Theorem. *The region* $\Gamma = \{(S^m, I^m, R^m) \in R^3_+ : S^m \geq 0, I^m \geq 0, R^m \geq 0, S^m + I^m + R^m \leq \frac{a}{\mu}\}$ *For all,* $m \geq 0$ *is a positive invariant feasible region for Eqs.* (29–31).

Proof. The system (29) to (31), could be decomposed as follows:

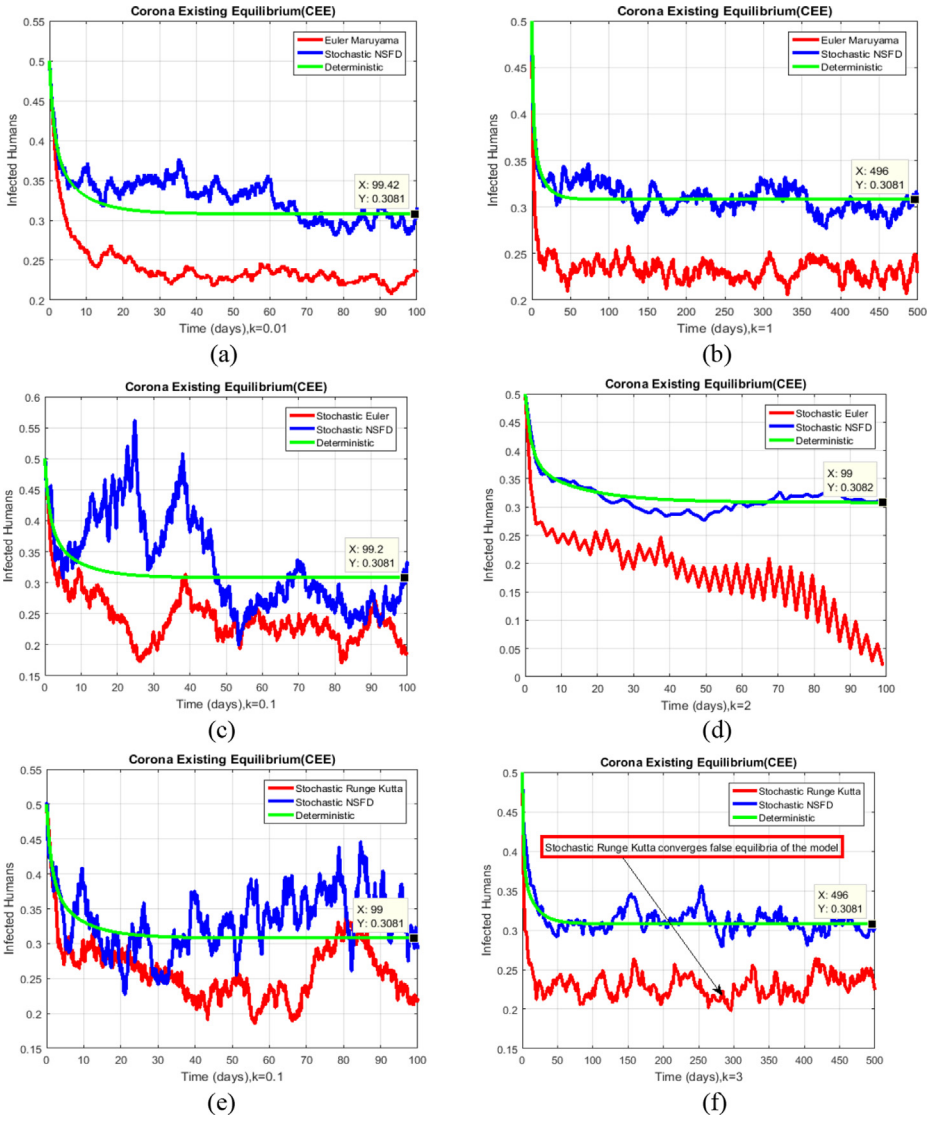

Fig. 3 Comparison graph at the existence of coronavirus.

$$\frac{\mathrm{S}^{\mathrm{m+1}}-\mathrm{S}^{\mathrm{m}}}{\mathrm{k}}=(\mathrm{a}-cS^mI^m(1+\gamma I^m)-\mu S^m+\alpha R^m - \sigma cS^mI^m(1+\gamma I^m)\Delta W_m)$$

$$\frac{\mathrm{I}^{\mathrm{m+1}}-\mathrm{I}^{\mathrm{m}}}{\mathrm{k}}=(cI^mS^m(1+\gamma I^m)-(\beta+\mu+\delta-b)I^m + \sigma \mathrm{c}S^mI^m(1+\gamma I^m)\Delta W_m)$$

$$\frac{\mathrm{R}^{\mathrm{m+1}}-\mathrm{R}^{\mathrm{m}}}{\mathrm{k}}=(\beta I^m-(\alpha+\mu)R^m)$$

After adding the above rewrite system, we have

$$\frac{(\mathrm{S}^{\mathrm{m+1}}+\mathrm{I}^{\mathrm{m+1}}+\mathrm{R}^{\mathrm{m+1}})-(\mathrm{S}^{\mathrm{m}}+\mathrm{I}^{\mathrm{m}}+\mathrm{R}^{\mathrm{m}})}{\mathrm{k}} = \mathrm{a}-\mu(\mathrm{S}^{\mathrm{m}}+\mathrm{I}^{\mathrm{m}}+\mathrm{R}^{\mathrm{m}})-(\delta-b)I^m$$

$$\frac{(\mathrm{S}^{\mathrm{m+1}}+\mathrm{I}^{\mathrm{m+1}}+\mathrm{R}^{\mathrm{m+1}})-(\mathrm{S}^{\mathrm{m}}+\mathrm{I}^{\mathrm{m}}+\mathrm{R}^{\mathrm{m}})}{\mathrm{k}} \leq \mathrm{a}-\mu(\mathrm{S}^{\mathrm{m}}+\mathrm{I}^{\mathrm{m}}+\mathrm{R}^{\mathrm{m}}).$$

$$(\mathrm{S}^{\mathrm{m+1}}+\mathrm{I}^{\mathrm{m+1}}+\mathrm{R}^{\mathrm{m+1}}) \leq (\mathrm{S}^{\mathrm{m}}+\mathrm{I}^{\mathrm{m}}+\mathrm{R}^{\mathrm{m}})+\mathrm{ka} - \mathrm{k}\mu(\mathrm{S}^{\mathrm{m}}+\mathrm{I}^{\mathrm{m}}+\mathrm{R}^{\mathrm{m}}).$$

$$(\mathrm{S}^{\mathrm{m+1}}+\mathrm{I}^{\mathrm{m+1}}+\mathrm{R}^{\mathrm{m+1}}) \leq \frac{\mathrm{a}}{\mu}+\mathrm{ka}-\mathrm{k}\mu\left(\frac{\mathrm{a}}{\mu}\right)$$

$$(\mathrm{S}^{\mathrm{m+1}}+\mathrm{I}^{\mathrm{m+1}}+\mathrm{R}^{\mathrm{m+1}}) \leq \frac{\mathrm{a}}{\mu}$$

Thus, our proposed non-standard computational method is bounded for all $\mathrm{m} \geq 0$.

Theorem. *For any $m \geq 0$, the equilibria are same in both sense of discrete and continuous dynamical systems.*

Proof. For solving the Eqs. (29–31), by assuming the perturbation is zero in the discrete model as follows:

$$\text{Trivial equilibrium (TE)} = (S^m, I^m, R^m) = (0, 0, 0)$$

$$(\text{Corona free equilibria CFE}) = (S^m, I^m, R^m) = \left(\frac{a}{\mu}, 0, 0\right).$$

$$(\text{Corona Existing equilibria CEE}) = (S^m, I^m, R^m)$$

$$S^m = \frac{(a-\beta-\mu-\delta+b)+\alpha\beta I^m}{\mu(\alpha+\mu)},$$

$$I^m = \frac{-(cB+c\gamma A)+\sqrt{(cB+c\gamma A)^2-4(c\gamma B)(\mu-c_1)}}{2c\gamma B},$$

$$R^m = \frac{\beta I^m}{\alpha+\mu}$$

where $A = \frac{(a-\beta-\mu-\delta+b)}{\mu}, B = \frac{\alpha\beta}{\mu(\alpha+\mu)}, c_1 = (\beta+\mu+\delta-b)$

Theorem. *For any $m \geq 0$, if the eigenvalue lies in the unit circle, then the proposed computational method is stable* [30–31].

Proof. Consider the right-hand sides of the equations in (29–31) as functions F, G and H by assuming the perturbation is zero as follows:

$$F = \frac{S+ka+k\alpha R}{1+kcI(1+\gamma I)}, G = \frac{I+kcSI(1+\gamma I)+kbI}{1+k(\mu+\beta+\delta)},$$
$$H = \frac{R+k\beta I}{1+k(\alpha+\mu)}$$

It is well known that a system of the form (29), (30), and (31) converges to the equilibria of the model if and only if the spectral radius, $\rho(J)$, of the Jacobean

$$\mathrm{J} = \begin{bmatrix} \frac{\partial F}{\partial S} & \frac{\partial F}{\partial I} & \frac{\partial F}{\partial R} \\ \frac{\partial G}{\partial S} & \frac{\partial G}{\partial I} & \frac{\partial G}{\partial R} \\ \frac{\partial H}{\partial S} & \frac{\partial H}{\partial I} & \frac{\partial H}{\partial R} \end{bmatrix} \tag{32}$$

evaluated at the equilibria satisfies the condition

$$\rho(J) < 1 \tag{33}$$

The equilibria of the model are stable or attractive if Eq. (33) is satisfied, is unstable or repelling if $\rho(J) > 1$ and it is neutrally stable if $\rho(J) = 1$.

The elements of the Jacobean associated with the method are given by

$$\frac{\partial F}{\partial S} = \frac{1}{1+kcI(1+\gamma I)+k\mu},$$
$$\frac{\partial F}{\partial I} = \frac{-(S+ka+k\alpha R)[kc+2kc\gamma I]}{[1+kcI(1+\gamma I)]^2}, \frac{\partial F}{\partial R} = \frac{h\alpha}{1+kcI(1+\gamma I)}$$

$$\frac{\partial G}{\partial S} = \frac{kcI(1+\gamma I)}{1+k(\beta+\mu+\delta)}, \frac{\partial G}{\partial I} = \frac{1+kcS+2kcSI}{1+k(\beta+\mu+\delta)}, \frac{\partial G}{\partial R} = 0$$

$$\frac{\partial H}{\partial S} = 0, \frac{\partial H}{\partial I} = \frac{k\beta}{1+k(\alpha+\mu)}, \frac{\partial H}{\partial R} = \frac{1}{k(\alpha+\beta)}$$

At the trivial equilibrium (TE) $= E_0 =$ (0,0,0). The given Jacobean is

$$J(E_0) = \begin{bmatrix} \frac{1}{1+k\mu} & -k^2ac & h\alpha \\ 0 & \frac{1+kb}{1+k(\beta+\mu+b)} & 0 \\ 0 & \frac{k\beta}{1+k(\alpha+\mu)} & \frac{1}{1+k(\alpha+\mu)} \end{bmatrix}$$

The eigenvalues of Jacobean matrix is

$\lambda_1 = \frac{1}{1+k\mu} < 1, \lambda_2 = \frac{1+kb}{1+k(\beta+\mu+b)} < 1$, provided that $R_0 = 1$, and $\lambda_3 = \frac{1}{1+k(\alpha+\mu)} < 1$.

At the corona free equilibria (CFE) $= E_1 = (\frac{a}{\mu}, 0, 0)$. The given Jacobean is

$$J(E_1) = \begin{bmatrix} \frac{1}{1+k\mu} & -(\frac{a}{\mu}+ka)kc & h\alpha \\ 0 & \frac{1+\frac{kac}{\mu}+kb}{1+k(\beta+\mu+\delta)} & 0 \\ 0 & \frac{k\beta}{1+k(\alpha+\mu)} & \frac{1}{1+k(\alpha+\mu)} \end{bmatrix}$$

So, the eigenvalues of the $J(E_1)$ as follows:

$\lambda_1 = \frac{1}{1+k\mu} < 1$, $\lambda_2 = \frac{\mu+kac\mu+k\mu b}{\mu[1+k(\beta+\mu+\delta)]} < 1$, provided that $R_0 < 1$ and $\lambda_3 = \frac{1}{1+k(\alpha+\mu)} < 1$.

At the corona existing equilibria (CEE) $= E_2 = (S^*, I^*, R^*)$. The given Jacobean is

$$J(E_2) = \begin{bmatrix} \frac{1}{1+kcI^*(1+\gamma I^*)+k\mu} & \frac{-(S^*+ka+h\alpha R^*)(kc+2kc\gamma I^*)}{[1+kcI^*(1+\gamma I^*)]^2} & \frac{h\alpha}{1+kcI^*(1+\gamma I^*)} \\ \frac{1+kcI^*(1+\gamma I^*)+k\mu}{1+k(\beta+\mu+\delta)} & \frac{1+kcS^*+2kcS^*I^*}{1+k(\beta+\mu+\delta)} & 0 \\ 0 & \frac{k\beta}{1+k(\alpha+\mu)} & \frac{1}{1+k(\alpha+\mu)} \end{bmatrix}$$

For the equilibria E_2, we have plotted the largest eigenvalues by using the MATLAB database and the values of parameters presented in [27], as desired.

4.4. Computational results

In this section, the comparative analysis of the existing numerical methods with the non-standard computational method [27], a = 0.5, $\beta = 0.09871$, $\alpha = 0.854302$, $\delta = 0.05, \mu = 0.5$, $\gamma = 0.0003, b = 0.205, c = 0.380, \sigma = 0.2$, for $R_0^S < 1$. For $R_0^S > 1$, a = 0.5, $\beta = 0.09871$, $\alpha = 0.854302$, $\delta = 0.05, \mu = 0.5$, $\gamma = 0.0003, b = 0.205, c = 0.580, \sigma = 0.2$. Moreover, we used $S_0(0) = 0.4, I_0(0) = 0.5, R_0(0) = 0.1$.

Example 1 (*(Simulation for corona-free equilibria)*). For small time step size, we could be observed in Fig. 2(a), Fig. 2(c), and Fig. 2(e), the solution of the system converges to true equilibria

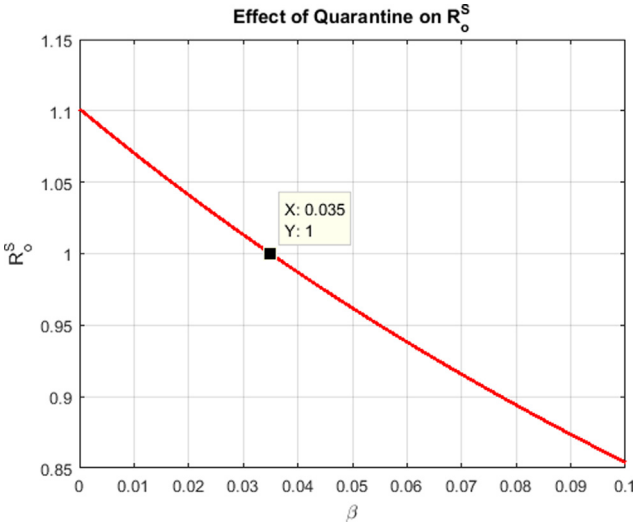

Fig. 4 Time-Plot with the comparison of reproduction number and parameter of quarantine.

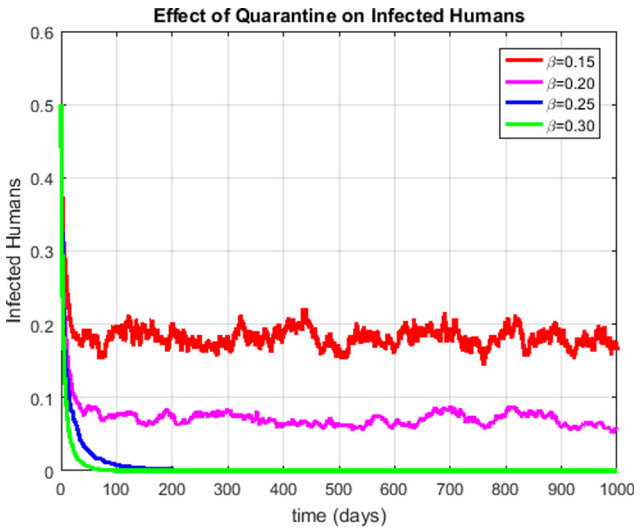

Fig. 5 Time-plot of the effect of quarantine on infected individuals.

$E_1 = \left(\frac{a}{\mu}, 0, 0\right)$, and $R_0^S = 0.8536 < 1$. In the same way, in Fig. 2(b), Fig. 2(d), and Fig. 2(f), the dynamical properties of the system have despoiled in the tiny change in the time step size. The proposed method could restore the dynamical properties, as desired.

Example 2 (*(Replication for the existence of coronavirus)*). For small time step size, we could be observed in Fig. 3(a), Fig. 3(c), and Fig. 3(e), the solution of the system converges to true equilibria $E_2 = (0.7648,\ 0.3081,\ 0.02247)$, and $R_0^S = 1.3043 > 1$. In the same way, in Fig. 3(b), Fig. 3(d), and Fig. 2(f), the dynamical properties of the system have desecrated in the tiny change in the time step size. The dynamical possessions such as non-negativity, boundedness, and dynamical consistency are the main key points of the proposed method, as desired.

Example 3 (*(The effect of quarantine with reproduction number)*). Let $\beta = 0.035$. Notice that the model dynamics move from virus existence to free equilibria with the decrease in the value of reproduction number. However, Fig. 4 shows that the strain of coronavirus could control the increases in quarantine strategies such as travel restrictions, hospitalization, social distancing, or vaccination, as needed.

Example 4 (*(Effect of quarantine on the infected humans)*). For different values of β (quarantine rate), Notice that in Fig. 5, we concluded that the infected humans converge to zero. It means that the reported ways of coronavirus has controlled in all aspect of scenarios, as desired.

5. Conclusion

Through the study, deterministic and stochastic susceptible-infected-recovered models are investigated, which provides a simplified description of coronavirus dynamics in the human population. Additionally, we examined the dynamics of the stochastic system using a variety of standard and non-standard computational methods. Compared to other well-known stochastic methods, the proposed non-standard computational method is unconditionally convergent. The dynamical possessions of the models, such as consistency, stability, positivity, and boundedness, are preserved using our proposed method [32]. Additionally, this study demonstrates how critical confinement rules resolve the situation in a reasonable amount of time. If the rate of contact between people decreases, class stabilization can occur much more quickly.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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