Research Article

Analysis and numerical solution of epidemic models by using nonstandard finite difference scheme

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Abstract

In this work, nonlinear epidemic models for measles, dengue fever, smoking, and SVIR are considered in order to understand the outbreaks of this epidemic disease. Developed unconditionally convergent nonstandard finite difference scheme by applying Mickens approach with $\phi(h) = h + O(h^2)$ as this will provide a feasible solution to overcome its disease risk as these are the main requirement for the dynamical systems in real-life solution. This method proved to be a very efficient technique for solving epidemic models to control infection diseases. Numerical simulations are carried out to support the analytic results.

Keywords: Epidemic model; Non-standard finite difference scheme; Qualitative analysis; Stability analysis

Introduction

In the human population, epidemiology studies play an important role to understand the disease in the human population. Often the work of mathematical epidemiology consists of model building, estimation of parameters and investigation of the sensitivity of models to change in the parameters and numerical simulations. Epidemiologists use mathematical models to understand previous outbreaks of diseases and to better understand the dynamics of how infections spread through populations [1]. The research of this kind helps to understand the ratio of disease spread in the population and to control their parameters [2, 3]. These

types of diseased models are often called infectious diseases (i.e. the disease which transferred from one person to another person). Measles, rubella, chickenpox, mumps, aids and gonorrhea syphilis are examples of infectious disease [4, 5].

The Nonstandard Finite Difference (NSFD) schemes preserve the main properties of the differential counterparts, such as positivity, monotonicity, periodicity, stability, and some other invariant including energy and geometrical shapes. It should be emphasized that NSFD schemes can preserve all properties of continuous models for any discretization parameters. The discrete

models with these properties are called dynamically consistent [6-9].

SIR Model

Kermack and McKendrick are those persons who are the inventor of the disease models and they played an important role in Mathematical epidemiology. In the purposed model, the population is divided into three groups which denoted by S (susceptible), I (infected) and R (recovered). The class S of

susceptible is increased by birth at a rate πN where both rate π and death rate μ are the same in [7], so susceptible is increased by μN . It is decreased by infection following contacts with infected individuals I at rate α . This class is decreased by recovery from infection at a rate γ and dimensioned by natural death rate μ . This generates a class R of individuals who have complete protection against disease and can be seen in (Figure 1).

Figure 1. Flow chart of SIR model

Followings are the equations of the model

$$\frac{dS}{dt} = \mu N - \alpha SI - \mu S \quad (1)$$

$$\frac{dI}{dt} = \alpha SI - (\gamma + \mu)I \quad (2)$$

$$\frac{dR}{dt} = \gamma I - \mu R \quad (3)$$

Where μ, α and γ represents the per capita removal rate, transitivity rate and per capita recovery rate respectively and $N = S + I +$

R , with initial conditions $S(0) = 990, I(0) = 10, R(0) = 0$

Qualitative analysis of the model

By simplifying the above equations we get disease-free equilibrium denoted by E_0 i.e. $E_0 = (N, 0, 0)$ and the endemic equilibrium point denoted by E_1 i.e.

$$E_1 = \left(\frac{(\gamma + \mu)}{\alpha}, \frac{\alpha \mu N - \mu(\gamma + \mu)}{\alpha(\gamma + \mu)}, \frac{\alpha \gamma \mu N - \mu \gamma(\gamma + \mu)}{\alpha \mu(\gamma + \mu)} \right) \text{ and the reproductive number is } R_0 = \frac{\alpha N}{(\gamma + \mu)} > 1$$

Nonstandard finite difference (NSFD) scheme

In recent years, NSFD discrete models have been constructed and or tested for a wide range of nonlinear dynamical systems. In this section, we design the NSFD scheme that replicates the dynamics of a continuous model (1-3). Let $Y_k = (S_k, I_k, R_k)^t$ denoted

the approximation of $X(t_k)$ where $t_k = k\Delta t$, with $k \in \mathbb{N}, h = \Delta t > 0$ be a step size then:

$$\frac{S^{k+1} - S^k}{\phi} = \mu N - \alpha S^{k+1} I^k - \mu S^{k+1}$$

$$\frac{I^{k+1} - I^k}{\phi} = \alpha S^{k+1} I^k - (\gamma + \mu) I^{k+1}$$

$$\frac{R^{k+1}-R^k}{\phi} = \gamma I^{k+1} - \mu R^{k+1}$$

$$S^{k+1} = \frac{\mu N \phi + S^k}{1 + \phi \alpha I^k + \phi \mu} \quad (4)$$

$$I^{k+1} = \frac{(\alpha \phi S^{k+1} I^k + I^k)}{1 + \phi(\gamma + \mu)} \quad (5)$$

$$R^{k+1} = \frac{\gamma \phi I^{k+1} + R^k}{1 + \phi \mu} \quad (6)$$

Which is the purposed NSFD scheme for the given model, where

$$\phi = \phi(h) = \frac{1 - e^{-(\gamma + \mu)h}}{(\gamma + \mu)}$$

Numerical simulations

The mathematical analysis of the epidemic measles SIR model with non-linear incidence

has been presented. To observe the effects of the parameters using in this dynamics measles SIR model (1-3), conclude several numerical simulations with parameters values $\alpha = 0.003, \mu = 0.05, \gamma = 1, N = 1000$ are given in [7]. In (Figure 2) shows that the model presented gradually approaches the steady states for different values of h . It is clearly shows that infected individuals at the latent period are diagnosed and treated, the number of susceptible individuals decreases significantly, the infected decreases steadily while the recovered increased steadily.

Figure 2. Numerical solutions for susceptible, infected individual, recovered population in a time t for $\phi = \phi(h)$, where $h = 10$

Dengue model

Esteva and Vargas [11] settled this model with the assumption that if a person gets the immunity against the disease, then the individuals will not be reinserted by this disease. In this model host population assuming constantly that means natural death rate and birth rate are equal. The differential equation of the dengue model as follows.

$$\frac{dS_h}{dt} = A - \frac{\beta_h b}{N_h} S_h I_v - \mu_h S_h \quad (7)$$

$$\frac{dI_h}{dt} = \frac{\beta_h b}{N_h} S_h I_v - (\mu_h + \gamma) I_h \quad (8)$$

$$\frac{dR_h}{dt} = \gamma I_h - \mu_h R_h \quad (10)$$

$$\frac{dS_v}{dt} = B - \frac{\beta_v b}{N_h} S_v I_h - \mu_v S_v \quad (11)$$

$$\frac{dI_v}{dt} = \frac{\beta_v b}{N_h} S_v I_h - \mu_v I_v \quad (12)$$

Where

$S_h, I_h, R_h, N_v, S_v, I_v, \mu_v, \beta_h, \beta_v, \gamma, b, A, B$ are host population of susceptible individuals, host population of infected individuals, host population of permanent immune individuals, vector population, vector population of susceptible individuals, vector population of infected individuals, death rate of vector population, transmission probability from vector to host, transmission probability from host to vector, rate of recovery from host population, biting rate of vector, recruitment rate of host population, Recruitment rate of host population respectively.

Nonstandard finite difference (NSFD) scheme of the model

In this section, we design the NSFD [8-10] scheme that replicates the dynamics of a continuous model (1)-(5). Let $Y_k = ((S_h)_k, (I_h)_k, (R_h)_k, (S_v)_k, (I_v)_k)^t$ denoted the approximation of $X(t_k)$ where $t_k = k\Delta t$, with $k \in \mathbb{N}$, $h = \Delta t > 0$ be a step size then;

$$\begin{aligned} \frac{S_h^{k+1} - S_h^k}{\phi} &= A - \frac{\beta_h}{N_h} b S_h^{k+1} I_v^k - \mu_h S_h^{k+1} \\ \frac{I_h^{k+1} - I_h^k}{\phi} &= \frac{\beta_h}{N_h} b S_h^{k+1} I_v^k - (\gamma + \mu_h) I_h^{k+1} \\ \frac{R_h^{k+1} - R_h^k}{\phi} &= \gamma I_h^{k+1} - \mu_h R_h^{k+1} \\ \frac{S_v^{k+1} - S_v^k}{\phi} &= B - \frac{\beta_v}{N_h} b S_v^{k+1} I_h^k - \mu_v S_v^{k+1} \\ \frac{I_v^{k+1} - I_v^k}{\phi} &= \frac{\beta_v}{N_h} b S_v^{k+1} I_h^k - \mu_v I_v^{k+1} \\ S_h^{k+1} &= \frac{A\phi + S_h^k}{1 + \frac{\beta_h}{N_h} b\phi I_v^k + \phi\mu_h} \end{aligned} \quad (13)$$

$$I_h^{k+1} = \frac{\frac{\beta_h}{N_h} b\phi S_h^{k+1} I_v^k + I_h^k}{1 + \phi(\gamma + \mu_h)} \quad (14)$$

$$R_h^{k+1} = \frac{\gamma\phi I_h^{k+1} + R_h^k}{1 + \phi\mu_h} \quad (15)$$

$$S_v^{k+1} = \frac{B\phi}{1 + \frac{\beta_v}{N_h} b\phi I_h^k + \phi\mu_v} \quad (16)$$

$$I_v^{k+1} = \frac{\frac{\beta_v}{N_h} b\phi S_v^{k+1} I_h^k + I_v^k}{1 + \phi\mu_v} \quad (17)$$

Which is the purposed NSFD scheme for the given model, where

$$\phi = \phi(h) = \frac{1 - e^{-(\gamma + \mu_h)h}}{(\gamma + \mu_h)}$$

The discrete method (13-17) is certainly defined by using Mickens's rules.

Numerical simulation

The mathematical analysis of the vector-borne disease dengue fever model with non-linear incidence has been presented. To observe the effects of the parameters using in this dynamics Dengue epidemic model (7-12), conclude several numerical simulations with parameters values $A = 0.457, B = 400, \beta_h = 0.75, b = 0.5, \mu_h = 0.0000457, \gamma = 0.1428, N_h = 1000, \beta_v = 1, \mu_v = 0.25$ are given in [11]. In (Figure3) shows the convergence solution using the NSFD scheme at $h = 1$ for the true equilibrium point. It can be easily seen from (Figure3) which shows fast convergence for each compartment. It clearly shows that infected individuals at the latent period are diagnosed and treated, the number of susceptible individuals decreases significantly, the infected decreases steadily.

Smoking Model

Smoking model is divided into five sub-compartment like potential smokers $P(t)$, occasional smokers $L(t)$, heavy smoker's $S(t)$ temporary quitters $Q(t)$ and smokers who quit permanently $R(t)$ specified by $T(t) = P(t) + L(t) + S(t) + Q(t) + R(t)$. The proposed smoking [12] in the form of the system of the nonlinear differential equation is given as:

$$\frac{dP}{dt} = a(1 - P) - bPS \quad (18)$$

$$\frac{dL}{dt} = -aL + bPS - cLS \quad (19)$$

$$\frac{dS}{dt} = -(a + d)S + cLS + fQ \quad (20)$$

$$\frac{dQ}{dt} = -(a + f)Q + d(1 - e)S \quad (21)$$

$$\frac{dR}{dt} = -aR + edS \quad (22)$$

Here b indicates the contact rate between potential smokers and smokers who smoke occasionally, c represents the contact rate

between temporary quitters and smokers who smoke occasionally, d represents the rate of giving up smoking, $(1 - e)$ stances for the fraction of smokers who temporarily give up smoking at a rate d , f indicate the contact rate between smokers and temporary quitters who return back to smoking, a denotes the rate of natural death, e denotes the remaining fraction of smokers who give up smoking permanently (at a rate d).

Nonstandard finite difference (NSFD) scheme of the model

Let $Y_k = (P_k, L_k, S_k, Q_k, R_k)^T$ denoted an approximation of $X(t_k)$ where $t_k = k\Delta t$ with $k \in N, h = \Delta t > 0$ be a step size, then

$$\begin{aligned} \frac{P^{k+1} - P^k}{\phi} &= a - aP^{k+1} - bP^{k+1}S^k \\ \frac{L^{k+1} - L^k}{\phi} &= -aL^{k+1} + bP^{k+1}S^k - cL^{k+1}S^k \\ \frac{S^{k+1} - S^k}{\phi} &= -(a + d)S^{k+1} + cL^{k+1}S^k + fQ^k \\ \frac{Q^{k+1} - Q^k}{\phi} &= -(a + f)Q^{k+1} + d(1 - e)S^{k+1} \\ \frac{R^{k+1} - R^k}{\phi} &= -aR^{k+1} + edS^{k+1} \end{aligned}$$

$$P^{k+1} = \frac{a\phi + P^k}{1 + a\phi + b\phi S^k} \quad (23)$$

$$L^{k+1} = \frac{b\phi P^{k+1}S^k + L^k}{1 + a\phi + c\phi S^k} \quad (24)$$

$$S^{k+1} = \frac{\phi cL^{k+1}S^k + \phi fQ^k + S^k}{1 + (a + d)\phi} \quad (25)$$

$$Q^{k+1} = \frac{\phi d(1 - e)S^{k+1} + Q^k}{1 + \phi(a + f)} \quad (26)$$

$$R^{k+1} = \frac{R^k + \phi edS^{k+1}}{1 + a\phi} \quad (27)$$

Which is the proposed NSFD Scheme for the given model, where

$$\phi = \phi(h) = \frac{1 - e^{-d(1 - e)h}}{d(1 - e)} \quad (28)$$

Numerical simulation

The technique creates a better impact to control the smoking, it reduces the infected rate and increases the potential smokers during disease Free State. In (Figure 4) by decreasing the value of h potential smokers (P) increases with time. In (Figure 5) by decreasing the value of h occasional smokers (L) decreases rapidly with time. In (Figure 6) by decreasing the value of h heavy smokers (S) decreases rapidly with time. In (Figure 7), by decreasing the value of h temporary quitters (Q) increases initially, but after some time decreases rapidly with time. In (Figure 8) by decreasing the value of h permanent quitters (R) increases initially, but after some time decreases rapidly with time. It can be easily seen that by reducing the step size the system (18-22) converge rapidly to the steady-state point [13].

Figure 3. Host Population of Susceptible individual, Host Population of Infected Individual, Host Population of Permanent Immune individual, Vector Population of Susceptible, Vector Population of Infected

Figure 4. Numerical solutions for potential smokers in a time t with step size $h = 1$, $h = 5$ and $h = 10$ for disease free equilibrium points

Figure 5. Numerical solutions for occasional smokers in a time t with step size $h = 1$, $h = 5$ and $h = 10$ for disease free equilibrium points

Figure 6. Numerical solutions for heavy smokers in a time t with step size $h = 1$, $h = 5$ and $h = 10$ for disease free equilibrium points

Figure 7. Numerical solutions for temporary quitters in a time t with step size $h = 1$, $h = 5$ and $h = 10$ for disease free equilibrium points

Figure 8. Numerical solutions for permanently quitters in a time t with step size $h = 1$, $h = 5$ and $h = 10$ for disease-free equilibrium points

SVIR model

$$\frac{dS}{dt} = \mu - \mu S - \beta SI - \alpha S \quad (29)$$

$$\frac{dV}{dt} = \alpha S - \beta_1 VI - \gamma_1 V - \mu V \quad (30)$$

$$\frac{dS}{dt} = \beta SI + \beta_1 VI - \gamma I - \mu I \quad (31)$$

$$\frac{dS}{dt} = \gamma_1 V + \gamma I - \mu R \quad (32)$$

Here $S(t)$, $I(t)$ and $R(t)$ denote the densities of susceptible, infected and recovered individuals, respectively. $V(t)$ denotes the density of vaccines who have begun the vaccination process. In the above model, all parameters are positive and have the following features: μ is the recruitment rate and natural death rate of the population; β

denotes the transmission coefficient between compartments S and I ; α is the rate at which susceptible individuals are moved into the vaccination process; β_1 denotes the disease transmission rate when the vaccines contact with infected individuals before obtaining immunity; γ_1 is the average rate for the vaccines move into recovered population; γ is the recovery rate of infected individuals [14].

$$S_E(S, I, V, R) = S_E\left(\frac{\mu}{\alpha + \mu}, 0, \frac{\alpha\mu}{(\alpha + \mu)(\mu + \gamma_1)}, \frac{\alpha\gamma_1}{(\alpha + \mu)(\mu + \gamma_1)}\right)$$

Nonstandard finite difference (NSFD) scheme of the model

Followings are the scheme

$$S^{k+1} = \frac{h\mu + S^k}{1 + h\mu + h\beta_1 I^k + h\alpha} \quad (33)$$

$$V^{k+1} = \frac{(h\alpha S^{k+1} + V^k)}{1 + h\beta_1 I^k + h\gamma_1 + h\mu} \quad (34)$$

$$I^{k+1} = \frac{h\beta S^{k+1} I^k + h\beta V^{k+1} I^k}{1 + h\gamma + h\mu} \quad (35)$$

$$R^{k+1} = \frac{h\gamma_1 V^{k+1} + R^k}{1 + h\mu} \quad (36)$$

The mathematical analysis of the epidemic SVIR (Susceptible Vaccination Infected

Qualitative analysis

For the equilibrium points, we take $\frac{dS}{dt} =$

$$0, \frac{dV}{dt} = 0, \frac{dI}{dt} = 0, \frac{dR}{dt} = 0 \text{ then we get}$$

$$0 = \mu - \mu S - \beta SI - \alpha S$$

$$0 = \alpha S - \beta_1 VI - \gamma_1 V - \mu V$$

$$0 = \beta SI + \beta_1 VI - \gamma I - \mu I$$

$$0 = \gamma_1 V + \gamma I - \mu R$$

By solving the above model we get

Recovered) model with non-linear incidence has been presented. To observe the effects of the parameters using in this dynamics SVIR model, conclude several numerical simulations with the given parameter values. In (Figure 9) shows that the model presented gradually approaches the steady states and infected individuals at the latent period are diagnosed and treated after vaccination, the number of susceptible individual's decreases significantly; the infected decreases steadily while the recovered increased rapidly.

Figure 9. Numerical solutions for susceptible, vaccination, infected individual and recovered population in a time t for $\phi = \phi(h)$

Conclusion

Numerical simulations are performed and all the analytical results are verified numerically by using the Non-Standard Finite Difference Scheme to reduce the infected rate in different epidemic models. This leads to the practical implications for the control of measles infections, dengue fever, smoking and SVIR by these models. It can easily be seen from the developed scheme and their graphical representations that NSFD preserves all the mandatory properties of continuous models like positivity, boundedness etc. for epidemic models, while all other numerical techniques fail to maintain the properties of continuous models for the larger step sizes. NSFD Scheme also always converges to their steady-state points while other numerical techniques like Adomian Decomposition Method (ADM), Differential Transform Method (DTM), Runge Kutta Method and Euler's Methods etc. fails to do so. This can help to control the spreading of infectious diseases in the community.

Authors' contributions

Conceived and designed the experiments: M Farman & A Ahmad, Performed the experiments: MU Saleem & M Farman, Analyzed the data: A Ahmad & MO Ahmad, Contributed materials/ analysis/ tools: MU Saleem & MO Ahmad, Wrote the paper: M Farman & A Ahmad.

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