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A dynamical transmission with nonstandard finite difference scheme for pine wilt disease

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ABSTRACT

In this article, we present and examine a mathematical system of equations which describes the dynamics of pine wilt disease. A non-linear mathematical model is employed to study and assess the dynamics of pine wilt disease in a wild life. We prove the essential properties, bounded, positivity and well-posed, also local and global stability analysis has been made for the epidemic model. The sensitivity analysis of the model is provided by threshold or reproductive number as well as analyzed qualitatively. To control the spread of the infection, we develop a control strategy by applying three control variables. An unconditionally convergent nonstandard finite difference scheme has been employed to solve model with different compartment. Finally, numerical results are depicted graphically and discussed quantitatively.

1. Introduction

Mathematical concepts and theory, we can easily measure the flow of work, process, predictions and outcomes. Therefore, biologists are highly dependent on mathematics and they applied mathematical for modeling on biological sciences (Biazar, 2006; Busenberg and Van den Driessche, 1990; El-Sayed et al., 2009). Biological system, integer order differential equations are involved in mathematical modeling and represent their change in structure which describes the dynamic and complex behavior of system. The behaviors of nonlinearity and multistage in mathematical modeling is describe the mutual relationship between parameter (Makinde, 2007). Few decades ago, by using classical derivative many biological models are studied in detail (Arafa et al., 2012; Kribs-Zaleta, 1999).

In human life, the forest has great importance. Therefore, it is compulsory to take necessary actions for the protection of the trees which are being infected by various diseases. Trees not only enhance the beauty of the environment but also provide august or blooming atmosphere for human community. For the forest and ecosystem the pine wilt disease (PWD) is the major threat. Within a very short period of time it kills pine trees and the red dish brown foliage is the symptom of this dangerous diseases (Buonomo and Lacitignola, 2008; Kiyohara and Tokushige, 1971).

In Japan, the pine wilt disease was noted in the beginning of the 2th century and now pine wilt disease had become the major ecological catastrophe of pine forest. For example in the 1980s, in Portugal, The pinewood nematode was first detected in 1990 (Ryss et al., 2011). This disease is continuous to spread despite the concerned actions of government agencies. A new strategy which is related to the national program for the control of pinewood nematode introduced in 2006. Finally, in Portugal the eradication of the nematode has been announced (Ryss et al., 2011; Mota and Vieira, 2008). A pinewood nematode, a gymnosperm host, and an insect vector are three organism of this disease (Shi and Song, 2013; Mamiya, 2002). For feeding purpose mature beetles use healthy tree twinges during breeding. For copulation and ovipositionl they focus only on the infected trees (Arakawa and Togashi, 2002). Today, all over the world pine wilt disease has become major threat to forests ecosystems (Togashi, 1991). A pine wilt disease is very dangerous and affects trees within weeks. The microscopic pine wood nematodes (Bursaphelenchus Xylophilus) are the major reason to the deaths of trees and disease is limited to prevention primarily. There are many cures for the disease. The nematode killed the infected trees by feeding on cells surrounding the resin ducts (Togashi, 1991; Khan et al., 2017).

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The Non Standard Finite Difference Method (NSFDM) has been used widely for systems of differential equations that are describing problems in mathematical biology and other different areas. The positivity of the state variables of the systems under study showed by these methods is preserved (when compared to other numerical methods) (Mickens, 1994; Lubuma and Patidar, 2007). Applications of this NSFD method for singularly perturbed problems. However, a comprehensive account of work that uses such methods is contribute in survey articles by patidar (Munyakazi and Patidar, 2010; Patidar, 2005; Patidar, 2016).

In this paper, we examine the stability and qualitative analysis of Pine wilt disease model. An unconditionally convergent nonstandard finite difference scheme has been given to obtain solution of model. Numerical results are conferred graphically to show the dynamics of the model.

2. Materials and method

The population of pinewood is denoted by $N_H(t)$. The susceptible, exposed and infected pine trees are represented as $S_H(t), E_H(t)$ and $I_H(t)$, where $N_H(t) = S_H(t) + E_H(t) + I_H(t)$. The population of vector (beetles), susceptible beetles, exposed vector and infected vector beetles is donated by $N_V(t)$, $S_V(t)$, $E_V(t)$ and $I_V(t)$ at any time t, with $N_V(t) = S_V(t) + E_V(t) + I_V(t)$ (Khan et al., 2017). Thus, the system of nonlinear differential equations are:

$$\frac{dS_H}{dt} = \Lambda_H - k_1\psi S_H I_V - k_2\phi\alpha S_H I_V - d_1 S_H \quad (1)$$
$$\frac{dE_H}{dt} = k_1\psi S_H I_V - k_2\phi\alpha S_H I_V - (d_1+\delta)E_H \quad (2)$$
$$\frac{dI_H}{dt} = \delta E_H - (d_1+\gamma)I_H \quad (3)$$
$$\frac{dS_V}{dt} = \Lambda_V - \eta S_V I_H - d_2 S_V \quad (4)$$
$$\frac{dE_V}{dt} = \eta S_V I_H - (d_2+\mu)E_V \quad (5)$$
$$\frac{dI_V}{dt} = \mu E_V - d_2 I_V. \quad (6)$$

The parameter Λ_V is susceptible recruitment rate, k_1 is the contact rate during maturation. $k_1\psi S_H I_V$ shows the incidence rate, k_2 represents the nematode transmitted probability through oviposit ion by an infected beetle and adult beetles represents ϕ with average number of contacts per d. The probability of susceptible cease oleoresin exudation without infected by nematode is represented by α. The new infection is represented by $k_2\phi\alpha S_H I_V$ and $k_2\phi\alpha$ is transmission through oviposit ion. δ and d_1 represents the progression rate and natural death rate of pine trees respectively. The transfer rate from E_V to I_V, natural death rate and disease induced death rate are respectively denoted by μ, d_2 and γ are given Khan et al. (2017). System (1-6) with initial conditions $S_H(0) = S_H^*, I_H(0) = I_H^*, E_H(0) = E_H^*, S_V(0) = S_V^*, I_V(0) = I_V^*, E_V(0) = E_V^*$, Adding Eqs. 1 to 3 from system, we obtain the conservation law

$$\frac{dH}{dt} = \Lambda_H + \Lambda_V - d_1 H_H - d_2 H_V - \gamma I_H, \quad (7)$$

here, $S_H + E_H + I_H = H_H$, $S_V + E_V + I_V = H_V$, is the total active population.

Theorem 1: Suppose that model in Eqs. 1 to 6 has a global solution corresponding to non-negative initial conditions. Then the solution is non-negative at all time.

Proof: Suppose that

$S_H(0) \geq 0,\ I_H(0) \geq 0,\ E_H(0) \geq 0,\ S_V(0) \geq 0,\ I_V(0) \geq 0,\ E_V(0) \geq 0,$

Eq. 1 of the given system is as follows:

$$\frac{dS_H}{dt} = \Lambda_H - A(t)\, S_H$$

where $A(t) = k_1\psi I_V - k_2\phi\alpha I_V - d_1$.

The solution of linear first order equation in S

$$S = S(0) \exp\left(\int_0^t -B(s)ds\right) + \exp\left(\int_0^t -B(s)ds\right) \times \left(\int_0^t \pi \exp\left(\int_0^u -B(w)dw\right) du \geq 0.\right.$$

Hence $S_H \geq 0, \forall t \geq 0$, About the non-negativity of the residual variables, we deliberate the subsystem

$$\frac{dE_H}{dt} = k_1\psi S_H I_V - k_2\phi\alpha S_H I_V - (d_1+\delta)E_H$$
$$\frac{dI_H}{dt} = \delta E_H - (d_1+\gamma)I_H$$
$$\frac{dS_V}{dt} = \Lambda_V - \eta S_V I_H - d_2 S_V$$
$$\frac{dE_V}{dt} = \eta S_V I_H - (d_2+\mu)E_V$$
$$\frac{dI_V}{dt} = \mu E_V - d_2 I_V. \quad (8)$$

This can be redrafted in the matrix system

$$\frac{dX(t)}{dt} = N\, Y(t) + C(t) \quad (9)$$

where,

$$X(t) = \begin{bmatrix} E_H \\ I_H \\ S_v \\ E_v \\ I_v \end{bmatrix}, N = \begin{bmatrix} -(d_1+\delta) & 0 & 0 & 0 & (K_1\psi - K_2\phi\alpha)S_H \\ \delta & -(d_1+\gamma) & 0 & 0 & 0 \\ 0 & -\eta S_v & \eta I_H - d_2 & 0 & 0 \\ 0 & \eta S_v & \eta I_H & -(d_2+\mu) & 0 \\ 0 & 0 & 0 & \mu & -d_2 \end{bmatrix}, B(t) = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ \gamma \end{bmatrix}$$

We take note of that N is a Metzler matrix (i.e., with non-negative off-diagonal elements) in assessment of the before now perceived non-negativity of S. Subsequently, Eq. 9 is a monotone framework. In this way, R_+^5 is invariant under the stream of framework (9). This finishes the evidence of the recommendation.

We would now be able to state and demonstrate the accompanying suggestion, which ensures the boundedness of the solution of framework (1-6).

Theorem 2: Suppose that the initial conditions for system given in Eqs. 1 to 6 satisfy

$H(0) \le H_n, I_H(0) \le I_{H(n)}, E_H(0) \le E_{H(n)}, S_V(0) \le S_{V(n)}, I_V(0) \le I_{V(n)}, E_V(0) \le E_{V(n)}$

$H_n = \frac{(\Lambda_H+\Lambda_V)}{\mu}, \quad E_H = \frac{(K_1\psi - K_2\phi\alpha)S_H(\Lambda_H+\Lambda_V)}{(d_{1+}\delta)\mu}, I_H = \frac{\delta E_H(\Lambda_H+\Lambda_V)}{(d_{1+}\gamma)\mu}, \quad E_V = \frac{\eta S_v(\Lambda_H+\Lambda_V)}{(d_2+\mu)\mu}, \quad I_V = \frac{\mu E_V(\Lambda_H+\Lambda_V)}{d_2\mu}.$

Then, if the solution exists on an interval J, it satisfies the following a priori bounds:

$H(t) \le H_n, \quad I_H(t) \le I_{H(n)}, E_H(t) \le E_{H(n)}, \quad I_V(t) \le I_{V(n)}, E_V(t) \le E_{V(n)}$

Proof: Subsequently $I_V(t) \ge 0$ we know as of Eq. 2 that

$$\frac{dH(t)}{dt} = \Lambda_H + \Lambda_V - d_1 H_H - d_2 H_V.$$

Submission of the Gronwall inequality yields

$$H(t) \le \frac{\Lambda_H+\Lambda_V}{\mu} + \left(H(0) - \frac{\Lambda_H+\Lambda_V}{\mu}\right)e^{-\mu t}$$

Since which

$$H(t) \le H_n,$$

whenever

$$H(0) \le H_n$$

Accordingly $I_V(t) \le H_n$. Substituting this in the 2nd Eqs. 1 to 6 provides

$$\frac{dE_H}{dt} \le (k_1\psi S_H - k_2\phi\alpha S_H)H_n - (d_1+\delta)E_H$$

As of someplace alternative presentation of the Gronwall inequality clues to

$$E_H(t) \le H_{(n)}$$

If

$$E_H(0) \le E_{H(n)}$$

The boundedness of I_H, E_V and I_V are demonstrated correspondingly.

Joining theorem 1 and 2 together with the unimportant presence and uniqueness of nearby roots for the Eqs. 1 to 6, we have built up the accompanying hypothesis which guarantees the numerical and organic well-posedness of framework (1-6).

Theorem 3: System (1 – 6) is a dynamical system on the compact set

$k = \{S_H(t), I_H(t), E_H(t), S_V(t), I_V(t), E_V(t) \in R^+; H(t) \le \frac{(\Lambda_H+\Lambda_V)}{\mu}, E_H \le \frac{(K_1\psi - K_2\phi\alpha)S_H(\Lambda_H+\Lambda_V)}{(d_{1+}\delta)\mu}, I_H \le \frac{\delta E_H(\Lambda_H+\Lambda_V)}{(d_{1+}\gamma)\mu}, E_V \le \frac{\eta S_v(\Lambda_H+\Lambda_V)}{(d_2+\mu)\mu}, \quad I_V \le \frac{\mu E_V(\Lambda_H+\Lambda_V)}{d_2\mu}\}$

3. Qualitative and sensitivity analysis

By substituting the values of parameters in given system of differential equations and the rate of change with respect to time is zero, we get.

By simplifying the above equations we get, disease-free equilibrium, denoted by E_0 i.e., $E_0 = (1,0,0,0,0)$. Reproductive number R_0 of the given system is as follows

$$R_0 = \sqrt{\frac{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}}$$

The sensitivity of $R_0 = \sqrt{\frac{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}}$, to each of its parameters is

$$\frac{\partial R_0}{\partial \eta} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial \Lambda_H} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_V(k_1\psi+k_2\phi\alpha)}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial \Lambda_V} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H(k_1\psi+k_2\phi\alpha)}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial \alpha} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V k_2\phi}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial \phi} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V k_2\alpha}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial \psi} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V k_1}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial k_1} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V\psi}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial k_2} = \frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V\phi\alpha}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}\right) \ge 0$$

$$\frac{\partial R_0}{\partial \mu}=\frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)d_2}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)^2}\right)\geq 0$$

$$\frac{\partial R_0}{\partial \delta}=\frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)d_1}{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)^2(d_2+\mu)}\right)\geq 0$$

$$\frac{\partial R_0}{\partial \gamma}=-\frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}{d_1{d_2}^2(\gamma+d_1)^2(\delta+d_1)(d_2+\mu)}\right)\leq 0$$

$$\frac{\partial R_0}{\partial d_1}=\frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)(d_1^2+\gamma\delta+2d_1\delta}{d_1^2d_2^2(\gamma+d_1)^2(\delta+d_1)^2(d_2+\mu)}\right)\geq 0$$

$$\frac{\partial R_0}{\partial d_2}=-\frac{1}{2}\sqrt{\frac{d_1{d_2}^2(\gamma+d_1)(\delta+d_1)(d_2+\mu)}{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)}}\left(\frac{\eta\mu\delta\Lambda_H\Lambda_V(k_1\psi+k_2\phi\alpha)(3d_2^2+\mu}{d_1(\gamma+d_1)(\delta+d_1)(d_2^3+\mu d_2)^2}\right)\leq 0$$

It can be seen that R_0 is most sensitive to change in parameter, here; R_0, is increasing with $\eta, \varphi, \phi, k_1, k_2, \delta, \mu, \alpha, d_1\Lambda_H, \Lambda_V$, and decreasing with d_2, γ.

4. Nonstandard finite difference (NSFD) scheme

In recent years, nonstandard finite difference (NSFD) scheme for discrete models have been constructed or tested for wide range of nonlinear systems of differential equations (Anguelov and Lubuma, 2001; Lubuma and Patidar, 2007; Roeger, 2014). The positivity of the state variables involved in the system is satisfied by prosed method. This property has key role when we solve mathematical models arising in biology because these state variables represent sub-populations which never take negative values.

In this section, we design an NSFDS scheme (Roeger, 2014). Let

$$Y=(S_H^k, E_H^k, I_H^k, S_V^k, E_V^k, I_V^k)^T$$

denoted an approximation of X (t_k). Where $t_k=\kappa\Delta t$, with $k\in N, h=\Delta t>0$ be a step size then

$$\frac{S_H^{k+1}-S_H^k}{T}=\Lambda_H-\kappa_1\psi S_H^{k+1}I_V^k-\kappa_2\phi\alpha S_H^{k+1}I_V^k-\mathrm{d}_1S_H^{k+1} \quad (7)$$

$$\frac{E_H^{k+1}-I_H^k}{T}=(\kappa_1\psi+\kappa_2\phi\alpha)S_H^{k+1}I_V^k-(\mathrm{d}_1+\delta)E_H^{k+1} \quad (8)$$

$$\frac{I_H^{k+1}-I_H^k}{T}=\delta E_H^{k+1}-(d_1+\gamma)I_H^{k+1} \quad (9)$$

$$\frac{S_V^{k+1}-I_V^k}{T}=\Lambda_V-\eta S_V^{k+1}I_H^{k+1}-d_2S_V^{k+1} \quad (10)$$

$$\frac{E_V^{k+1}-E_V^k}{T}=\eta S_V^{k+1}I_H^{k+1}-(d_2+\mu)E_V^{k+1} \quad (11)$$

$$\frac{I_V^{k+1}-I_V^k}{T}=\mu E_V^{k+1}-d_2I_V^{k+1} \quad (12)$$

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

$$T=T(h)=\frac{1-e^{(d_1+\gamma)h}}{d_1+\gamma} \quad (13)$$

5. Analysis of the scheme

The analysis of NSFD scheme for the given system on the biological feasible domain κ are given as follows.

$$S_H^{k+1}=\frac{x\Lambda_H+S_H^k}{1+x(k_1\psi+k_2\phi\alpha)I_V^k+xd_1}$$

$$E_H^{k+1}=\frac{[x(k_1\psi+k_2\phi\alpha)(x\Lambda_H+S_H^k)I_V^k+(1+x(k_1\psi+k_2\phi\alpha)I_V^k+xd_1)E_H^k}{[1+x(d_1+\delta)][1+x(k_1\psi+k_2\phi\alpha)I_V^k+xd_1]}$$

$$I_H^{k+1}=\frac{A^*+C^*}{B^*}$$

$$S_V^{k+1}=\frac{B^*(x\Lambda_V+S_V^k)}{B^*+x(\eta A^*+B^*d_2)}$$

$$E_V^{k+1}=\frac{A^*B^*x\eta(x\Lambda_V+S_V^k)+B^*[B^*+x(\eta A^*+B^*d_2)]}{B^*[1+x(d_2+\mu)][B^*+x(\eta A^*+B^*d_2)]}$$

$$I_V^{k+1}=\frac{x\mu[A^*B^*x\eta(x\Lambda_V+S_V^k)+B^*[B^*+x(\eta A^*+B^*d_2)]]+B^*[1+x(d_2+\mu)][B^*+x(\eta A^*+B^*d_2)]I_V^k}{B^*(1+xd_2)[1+x(d_2+\mu)][B^*+x(\eta A^*+B^*d_2)]}$$

where

$$A^*=x\delta[x(k_1\psi+k_2\phi\alpha)(x\Lambda_H+S_H^k)I_V^k+(1+x(k_1\psi+k_2\phi\alpha)I_V^k+xd_1)E_H^k$$
$$B^*=(1+x(d_1+\gamma))(1+x(d_1+\delta))(1+x(k_1\psi+k_2\phi\alpha)I_V^k+xd_1)$$
$$C^*=(1+x(d_1+\delta))(1+x(k_1\psi+k_2\phi\alpha)I_V^k+xd_1)I_H^k,$$

thus

$$S_H^{k+1}\geq 0, E_H^{k+1}\geq 0, I_H^{k+1}\geq 0, S_V^{k+1}\geq 0, E_V^{k+1}\geq 0, I_V^{k+1}\geq 0,$$

Adding the (7) and (8), we get

$$[1+Td_1]M^{k+1}=T\Lambda_H+M^k-[1+(d_1+\delta)T]E_H^{k+1}\leq T\Lambda_H+M^k$$
$$[1+Td_1]M^{k+1}\leq T\Lambda_H+M^k$$
$$\Rightarrow M^{k+1}\leq\frac{\Lambda_H}{d_1}$$

whenever

$$M^k\leq\frac{\Lambda_H}{d_1}$$

The priori bonds for I_2^{k+1} and R^{k+1} follow the radially from the fact that I_2^{k+1} and I_1^{k+1} and less then or equal H^{k+1}. Which proves the positivity and invariant κ.

6. Results and discussion

The mathematical analysis of Pine welt epidemic model with non-linear incidence has been presented. To observe the effects of the parameters using in this dynamics given in model in Eqs. 1 to 6, conclude several numerical simulations varying the value of parameters (Khan et al., 2017) for $R_0 < 1$. Figs. 1-6 shows the convergence solution for diseases free equilibrium by using NSFD scheme at different values of h for $\emptyset = \emptyset(h) + O(h^2)$. The technique create a better impact to control the Disease, It can be easily seen that by reducing the step size the system (1-6) converge rapidly to the steady state point. The describe results in Khan et al. (2017) are given with different initial conditions for each case and control strategy should try to approach the result for desired free equilibrium point which is taking time to control the diseases in plants or may be negative with large time interval. It is very time consuming for susceptible, exposed and infected in each case and results only shows by increasing behavior of susceptible and decreasing behavior of infected but not contained in the feasible domain according to steady state points. Our derived algorithm precise that the obtained results are in feasible domain for stability, uniqueness and preserve positivity for short as well as long time intervals and Pine welt diseases can be completely controlled in short period of time without effecting. The result can be easily observed in the Figs. 1-6 which meets the requirement.

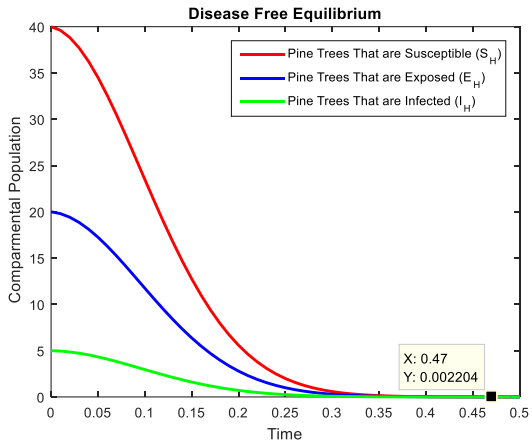

Fig. 1: Numerical solutions for Susceptible pine trees, Exposed pine trees and infected pine trees in a time t for disease free equilibrium points

Theorem 5: The endemic fixed-point of the NSFD scheme (7-12) for all the full model is GAS.

Proof: Let $Y_k \epsilon R_+^6$ is the bounded sequence defined by the NSFD scheme (7-12), Therefore, there exists $\theta > 0$ such that for an initial condition Y_0 satisfying

$$\| P^0 - P^* \| \leq \theta, \tag{14}$$

we have

$$\lim_{x \to +\infty} \| P^0 - P^* \| = 0$$

Let P^0 be an arbitrary initial condition. As

$$\lim_{x \to +\infty} P_{\eta\kappa} = P^*.$$

There exists a integer k_0 such that

$$\| P_{\eta k0} - P^* \| \leq \theta. \tag{15}$$

In view equation (14) and (15), we have

$$\lim_{x \to +\infty, \eta \geq 1} \| P_{\eta_\eta} - P^* \| = \lim_{x \to +\infty, \eta \geq \eta_{k_0}} \| P_{\eta_\eta} - P^* \| = 0 \tag{16}$$

This proves that P^* is GAS.

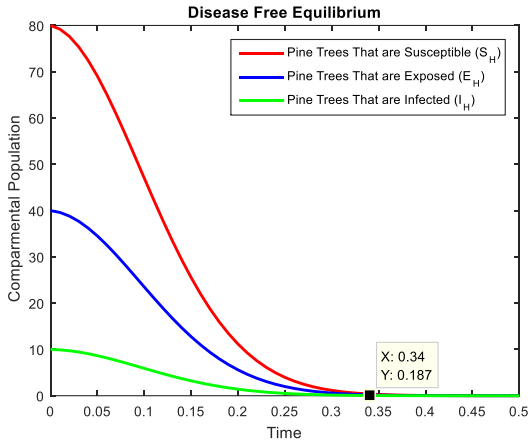

Fig. 2: Numerical solutions for Susceptible pine trees, Exposed pine trees and infected pine trees in a time t with different initial conditions for disease free equilibrium points

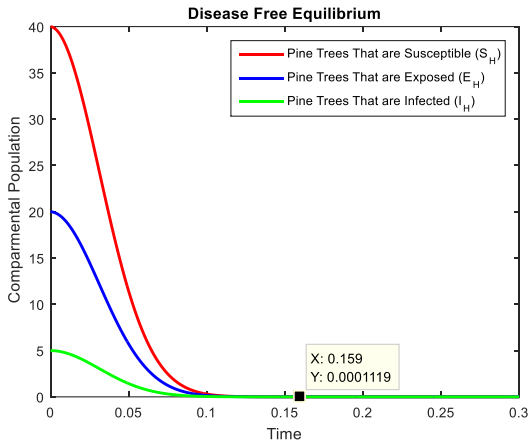

Fig. 3: Numerical solutions for Susceptible pine trees, Exposed pine trees and infected pine trees in a time t with different step size for disease free equilibrium points

7. Conclusion

Sufficient conditions for local stability of the DFE point E_0 are given by using the basic reproduction number R_0 of the model, where it is asymptotically stable and sensitivity analysis of the parameters involved in threshold parameter R_0, which shows the actual behavior of the dynamical model to reduce the effect of pine welt disease in the forest for society beneficial.

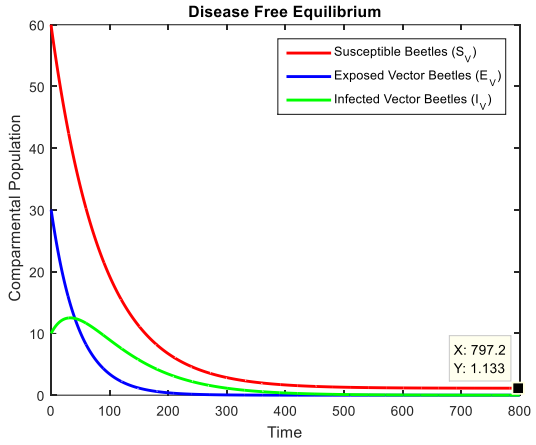

Fig. 4: Numerical solutions for Susceptible beetles, Exposed vector beetles and infected vector beetles in a time t for disease free equilibrium points

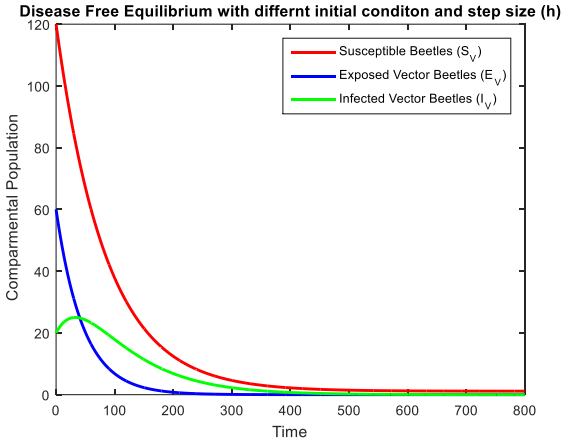

Fig. 5: Numerical solutions for Susceptible beetles, Exposed vector beetles and infected vector beetles in a time t with different initial conditions for disease free equilibrium points

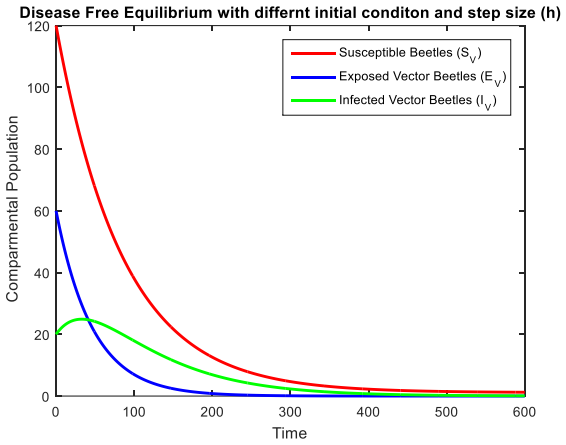

Fig. 6: Numerical solutions for Susceptible beetles, Exposed vector beetles and infected vector beetles in a time t with different step size for disease free equilibrium points

It is important to note that nonstandard finite difference scheme for mathematical models based on system of differential equations is more powerful approach to compute the convergent solutions for the disease models. Finally, we presented the numerical simulation and verified all the analytical results numerically by using nonstandard finite difference scheme to reduce the infected rates very fast for disease free equilibria by using different initial conditions, we are able to control the spreading of pine welt disease in the forest to make country neat and green.

Compliance with ethical standards

Conflict of interest

The authors declare that they have no conflict of interest.

References

Anguelov R and Lubuma JMS (2001). Contributions to the mathematics of the nonstandard finite difference method and applications. Numerical Methods for Partial Differential Equations: An International Journal, 17(5): 518-543. https://doi.org/10.1002/num.1025

Arafa AAM, Rida SZ, and Khalil M (2012). Fractional modeling dynamics of HIV and CD4+ T-cells during primary infection. Nonlinear Biomedical Physics, 6(1): 1-7. https://doi.org/10.1186/1753-4631-6-1 **PMid:22214194 PMCid:PMC3275462**

Arakawa Y and Togashi K (2002). Newly discovered transmission pathway of Bursaphelenchus xylophilus from males of the beetle Monochamus alternatus to Pinus densiflora trees via oviposition wounds. Journal of Nematology, 34(4): 396-404.

Biazar J (2006). Solution of the epidemic model by Adomian decomposition method. Applied Mathematics and Computation, 173(2): 1101-1106. https://doi.org/10.1016/j.amc.2005.04.036

Buonomo B and Lacitignola D (2008). On the dynamics of an SEIR epidemic model with a convex incidence rate. Ricerche Di Matematica, 57(2): 261-281. https://doi.org/10.1007/s11587-008-0039-4

Busenberg S and Van den Driessche P (1990). Analysis of a disease transmission model in a population with varying size. Journal of Mathematical Biology, 28(3): 257-270. https://doi.org/10.1007/BF00178776 **PMid:2332704**

El-Sayed AMA, Rida SZ, and Arafa AAM (2009). On the solutions of time-fractional bacterial chemotaxis in a diffusion gradient chamber. International Journal of Nonlinear Science, 7(4): 485-492.

Khan MA, Ali K, Bonyah E, Okosun KO, Islam S, and Khan A (2017). Mathematical modeling and stability analysis of pine wilt disease with optimal control. Scientific Reports, 7(1): 3115. https://doi.org/10.1038/s41598-017-03179-w **PMid:28596525 PMCid:PMC5465188**

Kiyohara T and Tokushige Y (1971). Inoculation experiments of a nematode, Bursaphelenchus sp., onto pine trees. Journal of the Japanese Forestry Society, 53(7): 210-218.

Kribs-Zaleta CM (1999). Structured models for heterosexual disease transmission. Mathematical Biosciences, 160(1): 83-108. https://doi.org/10.1016/S0025-5564(99)00026-7

Lubuma JMS and Patidar KC (2007). Non-standard methods for singularly perturbed problems possessing oscillatory/layer solutions. Applied Mathematics and Computation, 187(2): 1147-1160. https://doi.org/10.1016/j.amc.2006.09.011

Makinde OD (2007). Adomian decomposition approach to a SIR epidemic model with constant vaccination strategy. Applied Mathematics and Computation, 184(2): 842-848. https://doi.org/10.1016/j.amc.2006.06.074

Mamiya Y (2002). The pine wood nematode. In: Nickle WR (Ed.), Plant and insect nematodes: 589-626. Marcel Dekker, New York, USA.

Mickens RE (1994). Nonstandard finite difference models of differential equations. World Scientific, Singapore, Singapore. https://doi.org/10.1142/2081

Mota MM and Vieira P (2008). Pine wilt disease: A worldwide threat to forest ecosystems. Springer, Berlin, Germany. https://doi.org/10.1007/978-1-4020-8455-3

Munyakazi JB and Patidar KC (2010). Higher order numerical methods for singularly perturbed elliptic problems. Neural, Parallel, and Scientific Computations, 18(1): 75-88.

Patidar KC (2005). On the use of nonstandard finite difference methods. Journal of Difference Equations and Applications, 11(8): 735-758. https://doi.org/10.1080/10236190500127471

Patidar KC (2016). Nonstandard finite difference methods: Recent trends and further developments. Journal of Difference Equations and Applications, 22(6): 817-849. https://doi.org/10.1080/10236198.2016.1144748

Roeger LW (2014). Exact difference schemes. In Gumel AB (ed.), Mathematics of continuous and discrete dynamical systems: 147-161. American Mathematical Society, Providence, USA. https://doi.org/10.1090/conm/618/12349

Ryss AY, Kulinich OA, and Sutherland JR (2011). Pine wilt disease: A short review of worldwide research. Forestry Studies in China, 13(2): 132-138. https://doi.org/10.1007/s11632-011-0205-8

Shi X and Song G (2013). Analysis of the mathematical model for the spread of pine wilt disease. Journal of Applied Mathematics, 2013: Article ID 184054. https://doi.org/10.1155/2013/184054

Togashi K (1991). Spatial pattern of pine wilt disease caused by Bursaphelenchus xylophilus (Nematoda: Aphelenchoididae) within a Pinus thunbergii stand. Population Ecology, 33(2): 245-256. https://doi.org/10.1007/BF02513552