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Mathematical Treatment of Nonlinear Pine Wilt Disease Model: An Evolutionary Approach

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Abstract.: In human life, the forest plays an important role in safeguarding trees against disease infection. The pine wilt disease is one of the big threats for the forest and the environment. Optimum control theory is about discovering a complex system control rule over a period of time. In this paper Evolutionary Padé Approximation (EPA) scheme has been implemented for the treatment of non-linear pine wilt disease model. Evolutionary Padé Approximation scheme transforms the nonlinear pine wilt disease model into optimization problem. Initial conditions are converted into problem constraints and then constraint problem is converted into unconstraint problem by using penalty function. Sufficient parameter settings for EPA have been implemented. The simulations are numerical solutions of the model of pine wilt disease by solving the proven problem of optimization. It is also determined the threshold value for the fundamental reproductive number and the endemic disease balance point of the model. Evolutionary Padé Approximation has provided convergence solution regarding relationship among the different population compartments for diseases equilibrium, it has been observed that the results EPA scheme are more reliable and significant when a comparison is drawn with

Non-Standard Finite Difference (NSFD) numerical scheme. Finally, EPA scheme reduces the infected rates very fast. Further, in a strong contrast to NFSD, this technique has eliminated the need to provide step size.

AMS (MOS) Subject Classification Codes: 35S29; 40S70; 25U09
Key Words: Optimization; Pine Wilt Disease; Pad$\acute{e}$ approximation; Differential Evolution.

1. INTRODUCTION

We can easily measure the flow of work, process, predictions and results from mathematical concepts and theory. Biologists therefore rely heavily on mathematics and use mathematics to model biological sciences [1, 2]. 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 [3]. Few decades ago, by using classical derivative many biological models are studied in detail [4, 5]. The trees are not only the source of greenery for the atmosphere, however moreover offer the human society with a pleasant atmosphere. Pine wilt disease, a drastic illness that kills pine trees in a short period of time, is one of the greatest threats to forestry and biodiversity. Dark reddish leaves are the main symptom of this disease. The disease of pine wilt was witnessed in the early 20th century in Japan and has now become the pine forest's main ecological disaster. This disease is continuous to spread despite the concerned actions of government agencies. A new strategy which is related to the national program for controlling of pinewood nematode introduced in 2006. Finally, nematode eradication was announced in Portugal [6]. Three species of this disease are a pinewood nematode, a gyms host and an insect vector [7]. In the meantime, mature beetles use twanged tree safe. They just emphasize the copulation and oviposition of the infested plants. Pine wilt infection has now become a serious risk for ecological planting over the course of several weeks [8]. The principal cause of trees ' deaths is Microscopic pine wood nematodes (Bursaphelenchus Xylophilus). There are many cures to the disease. The nematode murdered the infected trees by feeding on cells around the resin ducts [9]. Mature sawyers are fascinated by the dead or falling trees during the ovulation (egg laying). And the age of the tree also affects the pine wilt danger. The most affected are 10-year-old trees where beetles infest trees with nematodes and then transfer to another vulnerable region. The occurrence is due to nematodes not based on contact, water or root grafting [10]. Some mathematical models were based on PWD's dynamics. An optimal control strategy was carried out for the study of the impact of pine wild disease, pine trees having two categories: susceptible and infected pine trees, where beetles are infected; vector population was subdivided into two categories. [11]. These epidemiological models are important procedures, especially in cases where no empirical solution is available to analyze and gain better knowledge about development through mathematical tools based on arithmetic and numerical analysis, impact and derivative mechanisms. Reflective knowledge and experience on these models help to take preventive measures and to measure their efficacy and success in preventing these infections. The numerical analyzes of these epidemiological

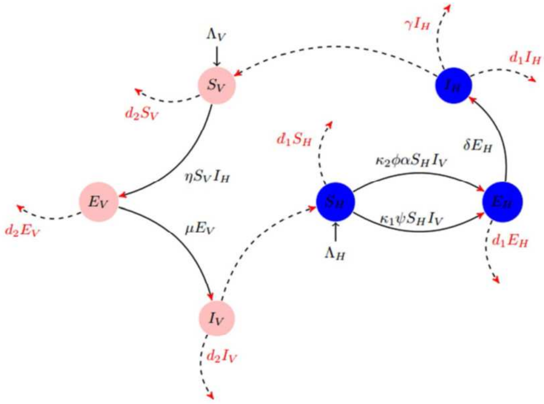

FIGURE 1. Pictorial representation of Pine wilt disease for transmission [9]

models based on a mathematical method are an important element of research in order to better understand their growth, impact and derivative mechanisms, especially where the analytical solution is not available. A thorough considerate of the model helps to lay down protections and assess their efficacy in avoiding infection networks [12, 13], but here is a problem that the applications of these Meta-heuristics to widespread and epidemic models are really hard to see. Solutions to differential equations in the class of non-standard mesh free methods are based on meta-heuristics. A creative approach [14] , based on the Differential Evolution Algorithm, is developed to manage numerical treatments of this type. This research provides an innovative approach. This suggested computational framework includes the following characteristics: 1) by creating an equivalent problem of optimization by manipulating the Pad$\acute{e}$ approximation extrapolation and interpolation techniques, 2) to maintain positivity through original boundaries and initial conditions, 3) penalty function approach has been developed for objective function, 4) optimize the fitness function has been calculated by using differential evolution. For these purposes, this entire paper has been prepared. Section 2 has the comprehensive detail of nonlinear epidemiological PWD model. Section 3 based on the fundamentals of Pad$\acute{e}$ approximation, differential evolution and penalty function developed in structure of EPA scheme to solve the numerical treatment of nonlinear PWD model. While in section 4, revolves around the analysis and simulations of the results which have been presented. Finally, in last section concluding remarks and findings for future directions have been given.

2. MATHEMATICAL MODEL OF DYNAMICAL TRANSMISSION OF PINE WILT DISEASE

The model proposed by Khan et al in [9] for the pine wilt disease has been described in Fig. 1.

The variables of the model at any time t are defined as:
$N(t)$: Total population of pine wood trees;
$S_H(t)$: Susceptible pine trees;
$E_H(t)$: Exposed pine trees;
$I_H(t)$: Infected pine trees

$N_H(t) = S_H(t) + E_H(t) + I_H(t)$
$N_V(t)$: Total population of vector (beetles);
$S_V(t)$: Susceptible vector beetles;
$E_V(t)$: The exposed vector beetles;
$I_V(t)$: Infected vector beetles
$N_V(t) = S_V(t) + E_V(t) + I_V(t)$
The model parameters are: $\wedge_H$: Susceptible pine tree's recruitment rate
$\wedge_V$: Vector pine beetle emergence rate
k_1: Maturation contact rate
k_2: Nematode probability (transmitted through oviposition by an infected beetle)
ψ: Maturation average number
d_1: Death rate of pine trees
d_2: Natural death rate
α: Probability that susceptible pine trees
γ: Disease induced death rate
φ: Average number of contacts per day
η: Measuring rate of adult beetles
μ: The transfer rate from E_V to I_V
δ: Rate of progression
$k_1\psi S_H I_V$: The incidence rates.
$k_2\varphi\alpha$: Transmission through oviposition
$k_2\varphi\alpha S_H I_v$: Number of new infections.
$\eta S_V I_H$: The transmission escaping from dead trees
The model with system of governing equations is given as:

$$
\begin{aligned}
S_H^{'}(t) &= \Lambda_H - k_1\psi S_H(t)I_V(t) - k_2\varphi\alpha S_H(t)I_V(t) - d_1 S_H(t) \\
E_H^{'}(t) &= k_1\psi S_H(t)I_V(t) - k_2\varphi\alpha S_H(t)I_V(t) - (d_1+\delta)E_H(t) \\
I_H^{'}(t) &= \delta E_H(t) - (d_1+\gamma)I_H(t) \\
S_V^{'}(t) &= \Lambda_V - \eta S_V(t)I_H(t) - d_2 S_V(t) \\
E_V^{'}(t) &= \eta S_V(t)I_H(t) - (d_2+\mu)E_V(t) \\
I_V^{'}(t) &= \mu E_V(t) - d_2 I_V(t)
\end{aligned}
$$

Followings are the initial conditions

$$
\begin{gathered}
S_H(0) = S_H^0 \geq 0, E_H(0) = E_H^0 \geq 0, I_H(0) = I_H^0 \geq 0 \\
S_V(0) = S_V^0 \geq 0, E_V(0) = E_V^0 \geq 0, I_V(0) = I_V^0 \geq
\end{gathered}
$$

The PWD model may be rewrite as

$$
\begin{aligned}
S_H^{'}(t) &= X_1(t) = \Lambda_H - k_1\psi S_H(t)I_V(t) - k_2\varphi\alpha S_H(t)I_V(t) - d_1 S_H(t) \\
E_H^{'}(t) &= X_2(t) = k_1\psi S_H(t)I_V(t) - k_2\varphi\alpha S_H(t)I_V(t) - (d_1+\delta)E_H(t) \\
I_H^{'}(t) &= X_3(t) = \delta E_H(t) - (d_1+\gamma)I_H(t) \\
S_V^{'}(t) &= X_4(t) = \Lambda_V - \eta S_V(t)I_H(t) - d_2 S_V(t) \\
E_V^{'}(t) &= X_5(t) = \eta S_V(t)I_H(t) - (d_2+\mu)E_V(t)
\end{aligned}
$$

TABLE 1. Values of physical parameters of the PWD model

Notation	Value	References
Λ_H	0.002021	[9]
d_1	0.0000301	[15]
k_1	0.00166	[16]
γ	0.00220	[9]
ψ	0.20	[17]
Λ_v	0.0132652	[9]
k_2	0.0004	[16]
η	0.00305	[18]
φ	0.0023	[9]
μ	0.01	[9]
α	0.0032	[9]
d_2	0.011764	[19]
δ	0.0133	[9]

$$I_V^{'}(t) = X_6(t) = \mu E_V(t) - d_2 I_V(t)$$

production number R_0 for model (1)

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

When $R_0 > 1$ unique endemic equilibrium exists, which is denoted by $E_1 = (S_H^*, E_H^*, I_H^*, S_V^*, E_V^*, I_V^*)$

$$S_H^* = \frac{d_2(d_2 + \mu)(d_2(\gamma + d_1)(\delta + d_1) + \delta\eta\Lambda_H)}{\delta\eta(d_1 d_2(d_2 + \mu) + \mu\Lambda_V(k_1\psi + k_2\varphi\alpha))}$$

$$E_H^* = \frac{d_1 d_2^2(\gamma + d_1)(\delta + d_1)(d_2 + \mu)(R_0 - 1)}{\delta\eta(\delta + d_1)(d_1 d_2(d_2 + \mu) + \mu\Lambda_V(k_1\psi + k_2\varphi\alpha))}/$$

$$I_H^* = \frac{d_1 d_2^2(\gamma + d_1)(\delta + d_1)(d_2 + \mu)(R_0 - 1)}{\eta(\gamma + d_1)(\delta + d_1)(d_1 d_2(d_2 + \mu) + \mu\Lambda_V(k_1\psi + k_2\varphi\alpha))}$$

$$S_V^* = \frac{(\gamma + d_1)(\delta + d_1)(d_1 d_2(d_2 + \mu) + \mu\Lambda_V(k_1\psi + k_2\varphi\alpha))}{\mu(k_1\psi + k_2\varphi\alpha)(d_2(\gamma + d_1)(\delta + d_1) + \delta\eta\Lambda_H)}$$

$$E_V^* = \frac{d_1 d_2^2(\gamma + d_1)(\delta + d_1)(d_2 + \mu)(R_0 - 1)}{(d_2 + \mu)\mu(k_1\psi + k_2\varphi\alpha)(d_2(\gamma + d_1)(\delta + d_1) + \delta\eta\Lambda_H)}$$

$$I_V^* = \frac{d_1 d_2^2(\gamma + d_1)(\delta + d_1)(d_2 + \mu)(R_0 - 1)}{d_2(d_2 + \mu)(k_1\psi + k_2\varphi\alpha)(d_2(\gamma + d_1)(\delta + d_1) + \delta\eta\Lambda_H)}$$

Disease free equilibrium is given by: $E_0 = (S_H^0, 0, 0, S_V^0, 0, 0)$ Numerical values of parameter are exhibited in Table 1.

3.Evolutionary Padé Approximation scheme

Evolutionary Padé Approximation scheme was developed and implemented for the numerical treatment of computer networks nonlinear model of virus propagation [20]. The design of developed scheme is established on Pad$\acute{e}$-approximation [21], Differential Evolution [22],[23] and penalty function [24]. Evolutionary Pad$\acute{e}$ Approximation scheme has been applied on a nonlinear epidemiology PWD model which involves the following steps.

3.1.Pad$\acute{e}$ approximation At the end of the 19th century, a classic theory of continuing fractions introduced the concept of a Pad-approximation. The reasonable (N,M) order function of the approximation of Pad$\acute{e}$ referred in [21].

$$P_{N,M}(t) = \frac{\Sigma_{i=0}^{N} a_i t^i}{\Sigma_{j=0}^{M} b_j t^j}$$

The polynomials $\Sigma_{i=0}^{N} a_i t^i$ and $\Sigma_{j=0}^{M} b_j t^j$ are known as Pad$\acute{e}$ approximants. By putting $b_0 \neq 0$ normalizing the above expression and attain the following form:

$$P_{N,M}(t) = \frac{\Sigma_{i=0}^{N} a_i t^i}{1 + \Sigma_{j=1}^{M} b_j t^j}$$

The above expression contains $(N + M + 1)$ undetermined coefficients, applying the Maclaurin series expansions of $P_{N,M}(t)$ to get the target referred in [14].
Suppose that $S_H(t), E_H(t), I_H(t), S_V(t), E_V(t)$ and $I_V(t)$ are approximated by Pad$\acute{e}$ rational functions as

$$S_H(t) = \frac{\Sigma_{i=0}^{N} a_i t^i}{1 + \Sigma_{j=1}^{M} b_j t^j}, E_H(t) = \frac{\Sigma_{i=0}^{N} c_i t^i}{1 + \Sigma_{j=1}^{M} d_j t^j}, I_H(t) = \frac{\Sigma_{i=0}^{N} e_i t^i}{1 + \Sigma_{j=1}^{M} f_j t^j}$$

$$S_V(t) = \frac{\Sigma_{i=0}^{N} g_i t^i}{1 + \Sigma_{j=1}^{M} h_j t^j}, E_V(t) = \frac{\Sigma_{i=0}^{N} k_i t^i}{1 + \Sigma_{j=1}^{M} l_j t^j}, I_V(t) = \frac{\Sigma_{i=0}^{N} o_i t^i}{1 + \Sigma_{j=1}^{M} p_j t^j}$$

Imposing initial conditions from equation (2) we obtain

$$a_0 = S_H^0, c_0 = E_H^0, e_0 = I_H^0, g_0 = S_V^0, k_0 = E_V^0, o_0 = I_V^0 (4)$$

The discrete time steps are $t_q = t_0 + qh; q = 0, 1, 2, 3, ..., q_m ax$, and the above system of equations (3) reduces as:

$$\varepsilon_1(t_q) = \varepsilon_2(t_q) = \varepsilon_3(t_q) = \varepsilon_4(t_q) = \varepsilon_5(t_q) = \varepsilon_6(t_q) = 0(5)$$

Here $\varepsilon_1, \varepsilon_2, \varepsilon_3, \varepsilon_4, \varepsilon_5$ and ε_6 are the residuals defined by

$$\varepsilon_1(t_q) = (1+\Sigma_{j=1}^{M} b_j t_q^j)(\Sigma_{i=0}^{N} i a_i t_q^{i-1}) - (\Sigma_{i=0}^{N} a_i t_q^i)(\Sigma_{j=1}^{M} j b_j t_q^{j-1}) - X_1(t_q)(1+\Sigma_{j=1}^{M} b_j t_q^j)(6)$$

$$\varepsilon_2(t_q) = (1+\Sigma_{j=1}^{M} d_j t_q^j)(\Sigma_{i=0}^{N} i c_i t_q^{i-1}) - (\Sigma_{i=0}^{N} c_i t_q^i)(\Sigma_{j=1}^{M} j d_j t_q^{j-1}) - X_1(t_q)(1+\Sigma_{j=1}^{M} d_j t_q^j)(7)$$

$$\varepsilon_3(t_q) = (1+\Sigma_{j=1}^{M} f_j t_q^j)(\Sigma_{i=0}^{N} i e_i t_q^{i-1}) - (\Sigma_{i=0}^{N} e_i t_q^i)(\Sigma_{j=1}^{M} j f_j t_q^{j-1}) - X_1(t_q)(1+\Sigma_{j=1}^{M} f_j t_q^j)(8)$$

$$\varepsilon_4(t_q) = (1+\Sigma_{j=1}^{M} h_j t_q^j)(\Sigma_{i=0}^{N} i g_i t_q^{i-1}) - (\Sigma_{i=0}^{N} g_i t_q^i)(\Sigma_{j=1}^{M} j h_j t_q^{j-1}) - X_1(t_q)(1+\Sigma_{j=1}^{M} h_j t_q^j)(9)$$

$$\varepsilon_5(t_q) = (1+\Sigma_{j=1}^{M} l_j t_q^j)(\Sigma_{i=0}^{N} i k_i t_q^{i-1}) - (\Sigma_{i=0}^{N} k_i t_q^i)(\Sigma_{j=1}^{M} j l_j t_q^{j-1}) - X_1(t_q)(1+\Sigma_{j=1}^{M} l_j t_q^j)(10)$$

$\varepsilon_6(t_q) = (1+\Sigma_{j=1}^{M} p_j t_q^j)(\Sigma_{i=0}^{N} i o_i t_q^{i-1}) - (\Sigma_{i=0}^{N} o_i t_q^i)(\Sigma_{j=1}^{M} j p_j t_q^{j-1}) - X_1(t_q)(1+\Sigma_{j=1}^{M} p_j t_q^j)(11)$

After the solution of equation (5), 6 $q_m ax$ equations have been generated to find the $6(M+N)$ coefficients of Pad$\acute{e}$-approximants.

3.2. Objective Function

Suppose that

$x = (a_1, a_2, ..., a_M, b_1, b_2, ..., b_N, c_1, c_2, ..., c_M, d_1, d_2, ..., d_N, e_1, e_2, ..., e_M, f_1, f_2, ..., f_N, g_1, g_2, ..., g_M, h_1, h_2, ...,$

By converting the system (5) into minimization problem as:

$$Minimize \phi(x) = \frac{1}{6} \sum_{z=1}^{6} \sum_{q=0}^{q_{max}} [\varepsilon_z(t_q)](12)$$

3.3. Problem Constraints

The equality constraints of the model are considered as stated in system (4):

$$h_1(t) = S_H(t) - S_H^0 = 0(13)$$

$$h_2(t) = E_H(t) - E_H^0 = 0(14)$$

$$h_3(t) = I_H(t) - I_H^0 = 0(15)$$

$$h_4(t) = S_V(t) - S_V^0 = 0(16)$$

$$h_5(t) = E_V(t) - E_V^0 = 0(17)$$

$$h_6(t) = I_V(t) - I_V^0 = 0(18)$$

Following are the positivity inequality constraints

$$g_{1q} = \frac{\Sigma_{i=0}^{N} a_i t_q^i}{1+\sum_{j=1}^{M} b_j t_q^j}(19)$$

$$g_{2q} = \frac{\Sigma_{i=0}^{N} c_i t_q^i}{1+\sum_{j=1}^{M} d_j t_q^j}(20)$$

$$g_{3q} = \frac{\Sigma_{i=0}^{N} e_i t_q^i}{1+\sum_{j=1}^{M} f_j t_q^j}(21)$$

$$g_{4q} = \frac{\Sigma_{i=0}^{N} g_i t_q^i}{1+\sum_{j=1}^{M} h_j t_q^j}(22)$$

$$g_{5q} = \frac{\Sigma_{i=0}^{N} k_i t_q^i}{1+\sum_{j=1}^{M} l_j t_q^j}(23)$$

$$g_{6q} = \frac{\Sigma_{i=0}^{N} o_i t_q^i}{1+\sum_{j=1}^{M} p_j t_q^j}(24)$$

whereas (25) incorporates the bounded-ness of the numerical solution.

$$g_{1q} + g_{2q} + g_{3q} \leq \frac{\Lambda_H}{d_1}$$

$$g_{4q} + g_{5q} + g_{6q} \leq \frac{\Lambda_V}{d_2}(25)$$

3.4. Penalty Function

By using the following penalty function methodology unconstrained optimization model is obtained:

$$\zeta(x) = \Sigma_{q=1}^{q_max} P_q \times max\{0, (h_1)^2, (h_2)^2, (h_3)^2, (h_4)^2, (h_5)^2, (h_6)^2, -g_{1q}, -g_{2q}, -g_{3q}, -g_{4q}, -g_{5q}, -g_{6q}, \Sigma_{s=1}^{6} g_{sq} -$$

Here scalar P_q is a large positive real number of q^{th} discrete time step acting as a penalty factor then the unconstrained objective function is

$$Minimize \varpi(x) = \phi(x) + \zeta(x)(26)$$

3.5. Optimization process with differential evolution

The following steps are involved to optimize objective function (26) through EPA scheme as: Evolutionary Pad$\acute{e}$ Approximation Algorithm
Step 1. Generate population randomly,population of K solutions $x_j \varepsilon R^6(M+N); 1 \leq j \leq K$.
Step 2. Evaluate the value $\varpi_j = \varpi(x_j)$ of each solution. Collect the best solution of objective function. Initially set $T = 0$.
Step 3. Set $T = T + 1$.
Step 4. Choose three distinct solutions $x_A, x_B and x_C$ from the population excluding x_j for each of $j = 1, 2, 3, ..., K, Set y = x_j$.
Step 5. For each of the dimensions $i = 1, 2, 3, ..., 6(M+N)$, alter the ith coordinate according to

$$y_i = (x_A i + F(x_B i - x_C i) if rand_i j[0,1] < CR@x_j i otherwise$$

Step 6. If $\varpi(y) < \varpi_j$ then $x_j \leftarrow y$,otherwise discard y.
Step 7. Best solution must be update.
Step 8. If T ¿ number of iterations,then terminate,by maintaining the best solution, otherwise repeat all the process from step 3.

3. NUMERICAL RESULTS

For numerical illustrations set parameters of DE algorithm: $N = 50; F = 0.55; CR = 0.91$ and maximum iterations = 2000. Pad$\acute{e}$ approximation order is set as $(N, M) = (2, 2)$. The parameter q_{max} is set as 2000. Penalty factor is set to be $L_q = 10^10$ for all q. The optimized parameters of PWD model is given in Table 1. The mathematical analysis of epidemic PWD model with non-linear occurrence has been offered. To notice the sound effects of the EPA algorithm on susceptible pine trees, exposed pine trees and infected pine trees population comparison with NSFD having the property of uniqueness and positivity represent in figures 2-4. Also notice the sound effects of the EPA algorithm on susceptible vector beetles, exposed vector beetles and infected vector beetle's population comparison with NSFD having the property of uniqueness and positivity represent in figures 5-7. Figure

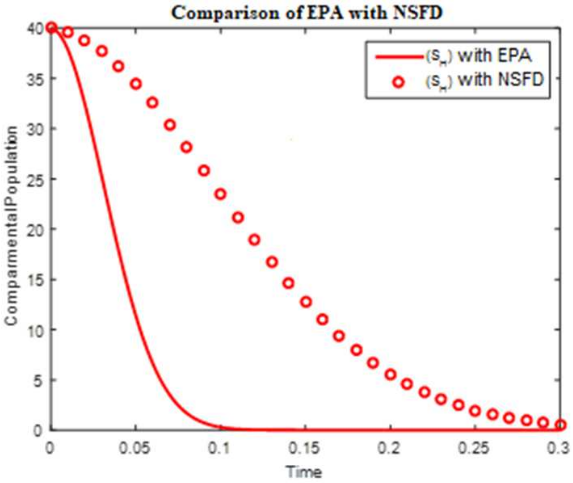

FIGURE 2. Simulations for susceptible population $S_H(t)$ in a time t with EPA and NSFD

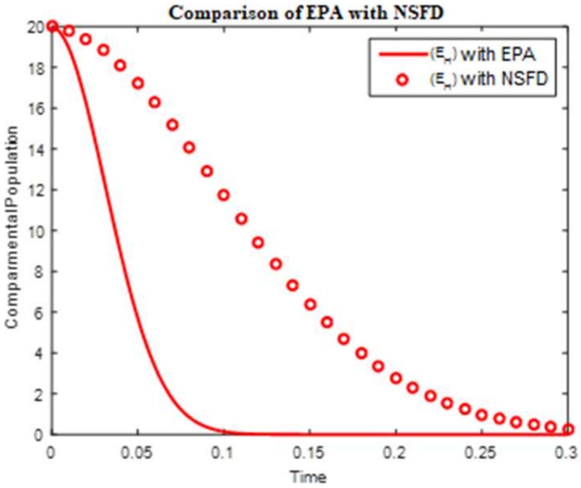

FIGURE 3. Simulations for exposed population $E_H(t)$ in a time t with EPA and NSFD

8 show convergence solution with relationship between the different population compartments for diseases free equilibrium by using EPA algorithm and NSFD scheme, here it can be easily observed that the results EPA algorithm are more reliable and better convergence as with numerical scheme. In figure 9 represents the relationship between variable in model, here impact of EPA approximation can be easily seen which provide more reliable and efficient analysis to control the disease in plans or plans for precaution to overcome the

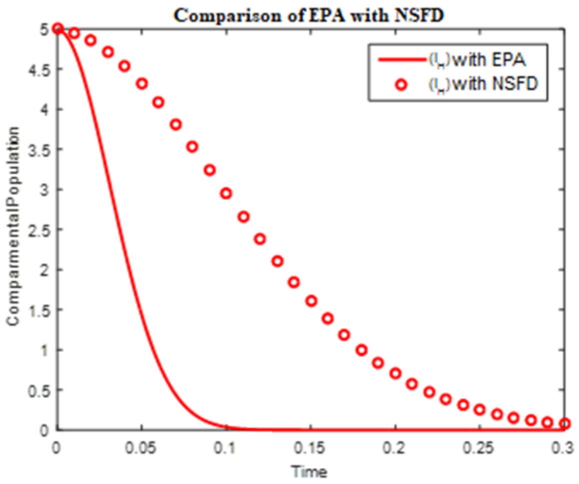

FIGURE 4. Simulations for infected population $I_H(t)$ in a time t with EPA and NSFD

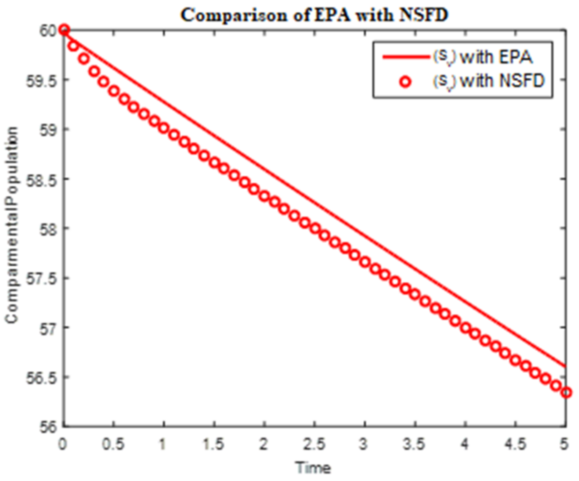

FIGURE 5. Simulations for susceptible population $S_V(t)$ in a time t with EPA and NSFD

disease impact. The describe results in Khan et al. [9] 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,

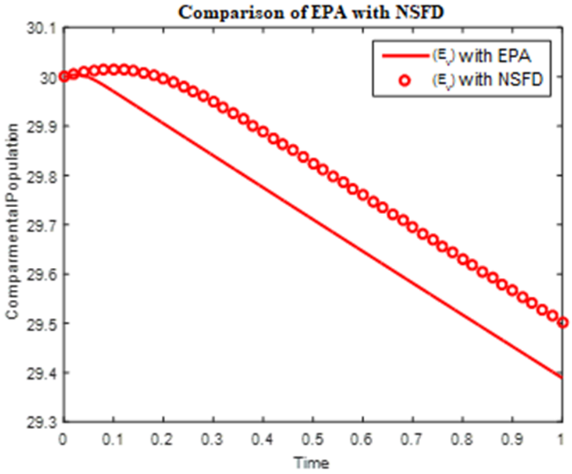

FIGURE 6. Simulations for exposed population $E_V(t)$ in a time t with EPA and NSFD

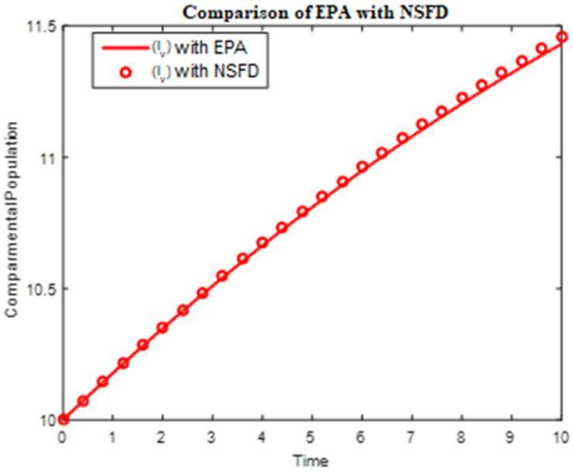

FIGURE 7. Simulations for infected population $I_V(t)$ in a time t with EPA and NSFD

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.

4. CONCLUSION

This work proposes an evolutionary Pad$\acute{e}$ approximation scheme for the solution of nonlinear epidemiological PWD model. The EPA scheme efficiently applies to the highly nonlinear epidemiological PWD model, this scheme produces excellent approximations of

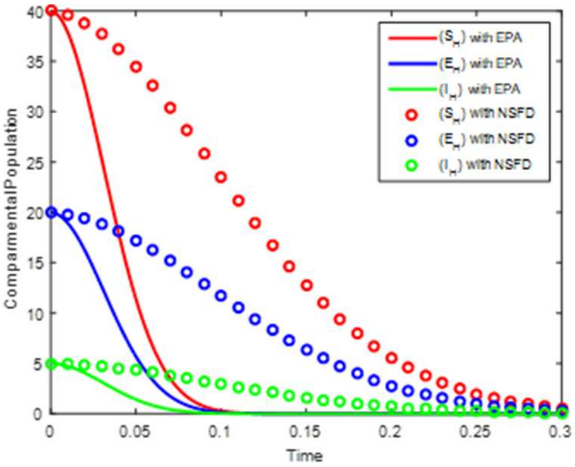

FIGURE 8. Disease free equilibrium for $S_H(t), E_H(t), I_H(t)$ populations in a time t with EPA and NSFD

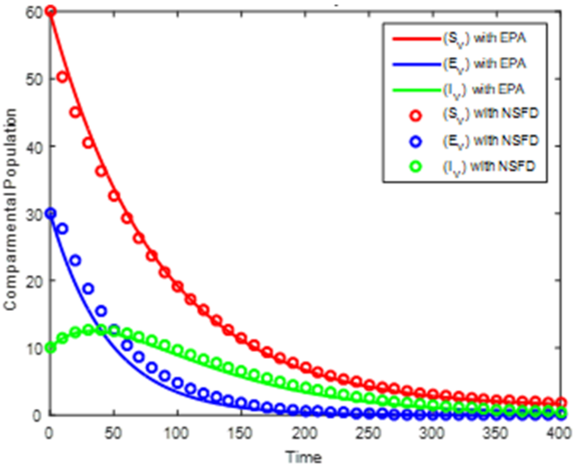

FIGURE 9. Disease free equilibrium for $S_V(t), E_V(t), I_V(t)$ populations in a time t with EPA and NSFD

state variables that are highly accurate to the governing equations. Initial conditions are converted into problem constraints and then constraint problem is converted into unconstraint problem by using penalty function. The EPA scheme has provided convergence solution regarding relationship among the different population compartments for diseases free equilibrium, it has been observed that the results EPA scheme are more reliable and significant when a comparison is drawn with NSFD numerical scheme. Further, we presented the numerical simulation and verified all the analytical results numerically by using EPA to reduce the infected rates very fast for disease equilibria. Finally, in a strong contrast to NFSD, this technique has eliminated the need to provide step size, and we are able to control the spreading of PWD in forest.

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