

## NUMERICAL TREATMENT OF PINE WILT DISEASE MODEL BY NON-STANDARD FINITE DIFFERENCE SCHEME

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**ABSTRACT.** In this work, we compute numerical solution to highly nonlinear mathematical model of pine wilt disease. For the required solution, we extend non-standard finite difference method (NSFDM). Further we also derive results regarding feasible regain and boundedness of solution in the proposed method.

### 1. INTRODUCTION

In plant pathology, pine wilt disease (PWD) is a vector-borne disease. Some significant tree wilting diseases, such as pine wilt disease and palm red ring disease, are caused by nematodes that have an unusual relationship with insect vectors ([1]). The pinewood nematode *Bursaphelenchus xylophilus* (Steiner and Buhrer) Nickle, whose synonym is *Bursaphelenchus lignicolus*, causes pine wilt ([2], [3]). Cerambycid beetles of the species *Monochamus*, which serve as vectors, transmit the nematode ([4], [5], [6]). The pinewood nematode has decimated pine forest ecosystems in the Far East (Japan, China, and Korea), North America (the United States and Canada), and Portugal ([7]). The most serious danger to pine forest systems today is pine wilt disease (PWD), which is caused by the pine wood worm. PWD was listed first on the European Plant Protection Organization's 1986 quarantine list; quarantining has resulted in international lumber trade disputes ([8]).

In late May to early July, the vector beetle, *M. Alternatus* emerges from dead pine trees carrying harmful nematodes and feeds on young twigs of healthy pines. Nematodes infest the host pine trees through the vector beetle's feeding wounds. As an early indication of disease, nematode infection causes oleoresin exudation to stop in 2-3 weeks, after which worm populations rapidly expand and spread through the wood tissue, causing the pine to wilt. The majority of affected trees die within a year of infection, with reddish-brown leaves, however a small proportion succumb to the disease early the next year ([9]). PWD control has been focused on eradicating pine sawyer larvae from wilt pine trees, either with winter fumigation or summer aerial insecticide spraying of adult sawyers. Despite rigorous attempts to remove dead pine trees from stands, new dead trees often develop around the stumps of

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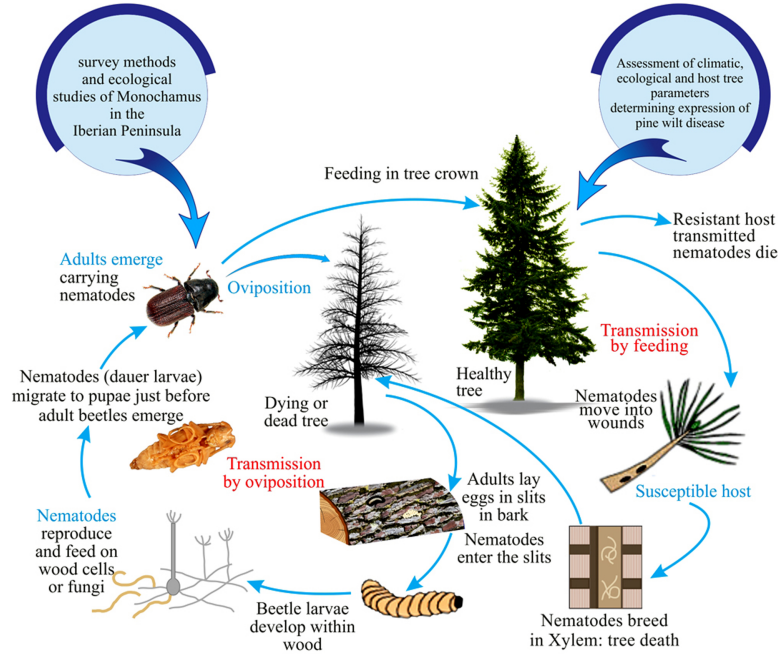


FIGURE 1. Pine Wilt Disease [22]

trees destroyed the previous year, and pine wilt disease recurs in the same pine stand year after year ([10], [11]).

A tree that houses *B. xylophilus* but shows no visible signs such as needle chlorosis or browning, and may or may not stop exuding oleoresin could be classified as an asymptomatic carrier tree. They could be important as attractants for *M. alternatus*, which could subsequently spread *B. xylophilus* to nearby trees. Many factors influence the spread and prevalence of PWD, including weather, vector beetle flight abilities, soil eutrophication, topographic circumstances, mycorrhizal associations, asymptomatic carrier trees, and human activities ([12], [13]). Recently, numerous mathematical models have been used to analyse the dynamics of pine wilt disease spread ([14], [15]). The authors of these works used an integro-difference equation with a dispersal kernel that describes beetle movement to model population dynamics of the vector beetle (*Monochamus alternatus*) and the pine tree to investigate disease expansion. Furthermore, several mathematical studies use ordinary differential equations to describe the host-vector interaction between pine trees and pine sawyer bugs ([16], [17], [18], [19]).

In biology, mathematical modelling is a significant tool for investigating epidemic diseases. If we revisit the history, we can observe that Bernoulli was the first to propose mathematical modelling in 1766 [20]. Mckendrick and Kermack [21] presented a formal mathematical model of deterministic kind in 1927. The proposed model was created to represent the link between three types of population compartments:

susceptible infectious, recovered, and non-susceptible infectious.

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta SI}{N}, & S(0) \geq 0, \\ \frac{dI}{dt} = \frac{\beta SI}{N} - \lambda I, & I(0) \geq 0, \\ \frac{dR}{dt} = -\lambda I, & R(0) \geq 0. \end{cases} \quad (1)$$

Now how to deal these nonlinear model in this regards large numbers of methods and schemes have been established. These scheme include RKM methods, decomposition method, perturbation method etc. All these methods have been applied properly. Further, the difference methods are powerful tools to handle many nonlinear problems. Therefore finite difference method have to used very well. One of the most powerful method that has been used in literature to large number of simple problems is known as NSFDM. Some qualitative results in relation to nonlinear differential equation of high order have been obtained in [23], [24], [25],[26], [27].

Therefore, in this work, we will utilize the side method to deal the following highly nonlinear pine wilt model as,

$$\begin{cases} \frac{dS_h}{dt} = \mu_1 \alpha_h - \frac{\alpha_1 S_h I_v}{1 + m I_v} - \frac{\alpha_2 \Phi S_h I_v}{1 + m I_v} - \mu_1 S_h, \\ \frac{dI_h}{dt} = \frac{\alpha_1 S_h I_v}{1 + m I_v} + \frac{\alpha_2 \Phi S_h I_v}{1 + m I_v} - \mu_1 I_h, \\ \frac{dS_v}{dt} = b_v - \frac{\beta I_h S_v}{1 + n I_h} - \mu_2 S_v, \\ \frac{dI_v}{dt} = \frac{\beta I_h S_v}{1 + n I_h} - \mu_2 I_v. \end{cases} \quad (2)$$

Symbols	Biological descriptions
$S_h$	Susceptible pine hosts at time t
$I_h$	Infected pine hosts at time t
$S_v$	Susceptible beetle vectors at time t
$I_v$	Infected beetle vectors at time t
$\mu_1, \mu_2$	the natural death rates of the host and vector populations
$\alpha_1$	Transmission rate per constant with infected vectors during maturation feeding.
$\alpha_2$	The rat at which infected vectors transmit the nematode via oviposition.
$\beta$	The rat at which adult beetles carry the pine wood nematode when they migrate from dead trees.
$\Phi$	The probability that susceptible host pine trees die of natural causes and cease oleoresin exudation with being infected by the nematode.
$m, n$	The level at which the infection saturates.

TABLE 1. Description of Variables and parameters of the Model (2).

We established feasible region and boundedness of solution to the proposed model.

1.1. **Theorem.** Feasible region and bounded of solution of model (2) is given by

$$\beta = \{(S_h, I_h, S_v, I_v) \in R_+^4 : 0 \leq N(t) \leq \frac{\mu_1 \alpha_h + b_v}{\mu_0}\},$$

where  $\mu_0 = \min\{\mu_1, \mu_2\}$ .

1.2. **Proof.** Let  $N$  be total population, then

$$\begin{aligned} N(t) &= S_h(t) + I_h(t) + S_v(t) + I_v(t), \\ \frac{dN}{dt} &= \frac{dS_h}{dt} + \frac{dI_h}{dt} + \frac{dS_v}{dt} + \frac{dI_v}{dt}, \\ \frac{dN}{dt} &= \mu_1 \alpha_h + b_v - \mu_1(S_h + I_h) - \mu_2(S_v + I_v) \end{aligned} \quad (3)$$

Let  $\min\{\mu_1, \mu_2\} = \mu_0$ . Then (3) implies

$$\frac{dN}{dt} + \mu_0 N \leq \mu_1 \alpha_h + b_v.$$

Hence

$$N(t) \leq \frac{\mu_1 \alpha_h + b_v + ce^{-\mu_0 t}}{\mu_0},$$

where  $c$  is constant of integration.

If  $t \rightarrow \infty$ , then

$$N(t) \rightarrow \frac{\mu_1 \alpha_h + b_v}{\mu_0}.$$

Hence  $N(t)$  is bounded.

Parameters	Value
$\mu_1$	0.0000301
$\mu_2$	0.011764
$\alpha_H$	305
$\beta$	0.0004
$\alpha_1$	0.00166
$\alpha_2$	0.00166
$\Phi$	0.0000301
$b_V$	0.75411.
$n$	0.01

TABLE 2. Values of parameter used in numerical simulation.

1.3. **Non-standard finite difference scheme.** Consider a general differential equation of the form

$$\begin{cases} \frac{dy}{dt} = f(t)y(t), \\ y(0) = y_0. \end{cases} \quad (4)$$

Written (4) in discretized form as  $\frac{y_{i+1}-y_i}{h} = f(t, y_i(t))$  which gives

$$y_{i+1} = y_i + hf(t, y_i(t)).$$

with the help of above method are considered system (2) can be written as

$$\begin{cases} S_h^{(i+1)} = S_h^{(i)} + h(\mu_1\alpha_h - \frac{\alpha_1 S_h^{(i)} I_v^{(i)}}{1 + m I_v^{(i)}} - \frac{\alpha_2 \Phi S_h^{(i)} I_v^{(i)}}{1 + m I_v^{(i)}} - \mu_1 S_h^{(i)}), \\ I_h^{(i+1)} = I_h^{(i)} + h(\frac{\alpha_1 S_h^{(i)} I_v^{(i)}}{1 + m I_v^{(i)}} + \frac{\alpha_2 \Phi S_h^{(i)} I_v^{(i)}}{1 + m I_v^{(i)}} - \mu_1 I_h^{(i)}), \\ S_v^{(i+1)} = S_v^{(i)} + h(b_v - \frac{\beta I_h^{(i)} S_v^{(i)}}{1 + n I_h^{(i)}} - \mu_2 S_v^{(i)}), \\ I_v^{(i+1)} = I_v^{(i)} + h(\frac{\beta I_h^{(i)} S_v^{(i)}}{1 + n I_h^{(i)}} - \mu_2 I_v^{(i)}). \end{cases} \quad (5)$$

1.4. **Numerical interpretation and discussion.** With the help of scheme (5) we have taken different values for  $m = 0.01, 0.03, 0.05, 0.07$  and  $n = 0.01, 0.03, 0.05, 0.07$  for the four classes of beetle population namely  $S_h, I_h, S_v, I_v$ . It can be observed from the simulation graphs that though the values of different classes vary slightly in the beginning but over the time they settle down to steady state behavior irrespective of the initial population. The classes  $S_h, I_h$  attain steady state in 80 days, where as the classes  $S_v, I_v$  attain steady state in 130 and 150 days respectively.

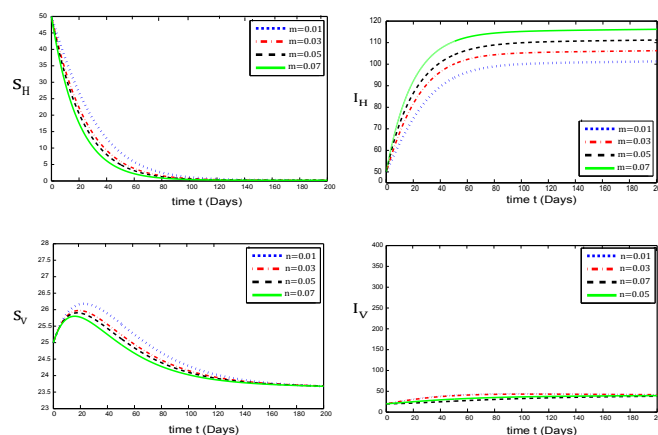


FIGURE 2. Plot of the compartments of pine trees  $S_h$ ,  $I_h$ ,  $S_v$ ,  $I_v$  in pine trees population at the given different initial values.

## 2. CONCLUSION

We have successfully developed a numerical scheme known as NSFDM for the considered model. Through the mentioned method, we have computed the solution of the proposed model for different values of  $n$ ,  $m$ . Hence NSFDM will excellently used in future for dealing non complicated problems.

**Authors contribution:** All authors contribute equally to the writing of this manuscript.

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