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# A Reliable Numerical Analysis of Transmission Dynamics of Chicken Pox (Varicella Zoster Virus)

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## Abstract

*Solutions generated through numerical techniques are great in solving real-world problems. This manuscript deals with the numerical approximation of the epidemic system, describing the transmission dynamics of the Vercilla Zoster Virus (VZV) through the impact of vaccination. To discretize the continuous dynamical system, we proposed a novel numerical technique that preserves the true dynamics of the VZV epidemic model. The proposed technique is established in such a manner that it sustains all necessary physical traits depicted by the epidemic model under study. The designed technique is named a nonstandard finite difference (NSFD) scheme. Theoretical analysis of the designed NSFD technique is presented which describes its strength over the standard numerical procedures which are already being used for such purposes. The graphical solutions of all the numerical techniques are presented which verify the efficacy of the proposed NSFDS technique.*

***Keywords:*** convergence, epidemiology, mathematical modeling, Non-Standard Finite Difference (NSFD) method, sensitivity, treatment, vaccination, Varicella Zoster

## Introduction

Human alphaherpesvirus 3 is a contagious virus also known as Varicella-Zoster Virus (VZV). It is a member of a family of 9 herpesviruses known to spread infection in the human population. It causes a skin infection called chickenpox, which most commonly affects children, teens, and young adults. Another name of chickenpox

is Varicella, a disease that is easily transmitted to others through the virus Varicella Zoster Virus [1]. The symptoms of the disease are skin rash, blisters, itching and scabbing. Initially, it affects the face, then the chest and finally the whole body. The infected person may also feel tiredness, fever, vomiting and loss of hunger which often remain for five to ten days [2]. If the disease complicates then the inflammation of the brain and an infection on the skin is also caused by bacteria [3]. Chickenpox is an airborne disease that is very easily transmitted by the infected person. With the invention of the VZV vaccine, the harm of the disease has been reduced [4]. Using the vaccine, about 70 to 90 percent of the patients have recovered [5]. A person is usually attacked once by the chickenpox virus in a lifetime [6]. If the kids have a good immune system they can cover within three days [7]. Cure of Varicella is through antiviral medicines, paracetamol, and calamine lotion [6]. In 1990, globally, 8900 peoples died due to Varicella but in 2013 the number reduced to 7000, which occurred at a rate of 1 death per 60,000 cases [8].

Mathematical models of infectious diseases are hard to analyze due to their highly non-linear behavior. Most of the standard numerical techniques to handle these problems are inadequate and do not depict a true picture of the epidemic spread. Public health professionals and policymakers, however, are keen on getting reliable results produced by mathematical modeling of infectious diseases. Yet, they also require results that are very close to real-world scenarios of disease dynamics. In this work, a reliable numerical analysis of the VZV epidemic is proposed. The proposed work gives some useful conclusions regarding the epidemic spread. Moreover, this work overcomes the discrepancies caused by existing techniques and remains consistent with the biological nature of a continuous dynamical system. The works presented in [13-15] have also been examined to validate and authenticate the results proposed in this work.

## 2. Mathematical Model

### 2.1. Assumptions

- A constant population of humans.
- All newborns are susceptible.
- All newborns should take two doses of vaccine to get full immunity.

There are four compartments of the underlying epidemic model named susceptible population, infected population, vaccinated population and recovered population. The population which can get an infection but is not yet infected is still susceptible. The population which gets the infection is termed infected. The population which recovers from the infection is termed recovered. Vaccinated individuals have received the dose of the vaccine. The human population is divided into four compartments susceptible, infected, recovered and vaccinated.

## 2.2 Parameters involved in the epidemic system

$S$= Population size of susceptible
$V$ = Population size of vaccinated
$E$ = Population size of exposed
$I$ = Population size of infected
$R$ = Population size of recovered
$N$= Total population size
$r$= Parameter which describes the recovery rate
$a$ = Rate of arrival
$c$ =Rate of contact per capita
$\theta_1$= The proportion of the susceptible population who get the first vaccine dose
$\theta_2$=The proportion of individuals who get vaccine dose and recovered
$\mu$= Per capita rate of natural death
$\pi$= Rate of birth per capita
$\eta$= Rate of the population who recovered from infection after getting treatment
$\Lambda$= The rate of recruitment
$f$= Proportion of individuals who get second dose Vaccine
$\alpha$ = Lessening rate of vaccine
$\beta$= The rate at which exposed population become infectious
$\delta$= Conversion rate from latent to infectious
$\phi$=Vaccinated newborns population
$\rho$=Vaccinated immigrants' individuals

The compartmental diagram of transmission of Varicella Zoster Virus is shown in the following flow chart:
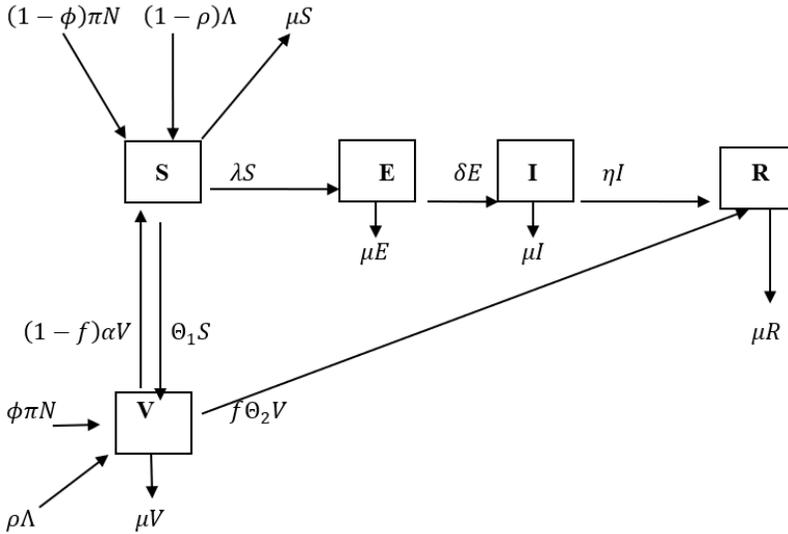
**Figure 1.** Flow chart of Varicella Zoster Virus in population

## 2.3. Transmission Model of Varicella Zoster Virus

We presume that chickenpox disease is transferred to the human population through infection. We defined the following system of differential equations developed with the help of the flow chart diagram given in Figure 1 [9].

$$\frac{dS}{dt} = (1 - \emptyset)\pi N + (1 - \rho)\Lambda + (1 - f)\alpha V$$
$$- (\lambda + \mu + \theta_1)S$$

$$\frac{dV}{dt} = \rho\Lambda + \phi\pi N + \theta_1 S - ((1 - f)\alpha + f\theta_2 + \mu)V$$

$$\frac{dE}{dt} = \lambda S - (\mu + \delta)E$$

$$\frac{dI}{dt} = \delta E - (\eta + \mu)I$$

$$\frac{dR}{dt} = \eta I + f\theta_2 V - \mu R$$

Where $\lambda = \frac{\beta c I}{N}$ and the total population size is

$$N(t) = S(t) + V(t) + E(t) + I(t) + R(t)$$

Besides the above equations,

$$\frac{dN}{dt} = \Lambda + (\pi - \mu)$$

When normalizing the system, we have

$$v = \frac{V}{N} \,, s = \frac{S}{N} \qquad , e = \frac{E}{N} \,, i = \frac{I}{N} \,, \qquad r = \frac{R}{N}$$

After normalization, the system becomes

$$\frac{ds}{dt} = (1 - \emptyset)\pi + (1 - \rho)a + (1 - f)\alpha v - (\lambda + \theta_1 + a + \pi)s \quad (1)$$

$$\frac{dv}{dt} = \rho a + \phi\pi + \theta_1 s - \left((1 - f)\alpha + f\theta_2 + a + \pi\right)v \qquad (2)$$

$$\frac{de}{dt} = \lambda s - (a + \pi + \delta)e \qquad (3)$$

$$\frac{di}{dt} = \delta e - (\eta + a + \pi)i \qquad (4)$$

$$\frac{dr}{dt} = \eta i + f\theta_2 v - (a + \pi)r \qquad (5)$$

Where $\mu = a + \lambda$ and $a = \frac{\lambda}{N}$,

# 3. Analysis of the Mathematical Model

## 3.1. Fixed Points of the Model without EIP

The equilibrium points/fixed points can be found by setting the above system equal to zero.

Now, for disease-free equilibrium (DFE) we put

$$\frac{ds}{dt} = \frac{dv}{dt} = \frac{de}{dt} = \frac{di}{dt} = \frac{dr}{dt} = 0$$

$E_0 = (s_0, 0,0,0, r_0)$ is the disease-free equilibrium point, where

$$s_0 = \frac{\alpha(a + \pi)(1 - f) + \{f\theta_2 + a + \pi\}\{(1 - \phi)\pi + (1 - \rho)a\}}{\theta_1(f\theta_2 + a + \pi) + (\lambda + a + \pi)\{\alpha(1 - f) + f\theta_2 + a + \pi\}}$$

$$r_0 = \frac{f\theta_2(\theta_1 + \phi\pi + a\rho)}{[\theta_1(f\theta_2 + a + \pi) + (a + \pi)\{\alpha(1 - f) + f\theta_2 + a + \pi\}]}$$

Where $R_e$ is the basic reproductive number of the disease given by

$$R_e = \frac{\beta c \delta}{(\delta + a + \pi)(\eta + a + \pi)}$$

## 3.2. Numerical Method

In this section, we will design numerical techniques for the epidemic model under study.

For discretization, time $(t \geq 0)$ with $t_m = mh$ for $m = 0, 1, 2, 3, \ldots\ldots$ and the step size of time is considered as $h$. The nodal

points of $S, V, E, I$ and R at $t_m$ are $S(t_m), V(t_m), E(t_m), I(t_m), R(t_m)$ which will be denoted by $S^m, V^m, E^m, I^m$ and $R^m$ respectively.

The proposed NSFDS technique is the discrete portrayal of differential equations which are summed up based on the rules given by R.E. Mickens. These rules benefit in designing the dynamically consistent numerical schemes which hold the stability of equilibria and positive solution of the underlying system [10-12].

The proposed NSFDS method emerged as an effective numerical scheme for the solution of various physical problems involving ordinary and partial differential equations.

First, we make an approximation to $\frac{dS}{dt}, \frac{dV}{dt}, \frac{dE}{dt}, \frac{dI}{dt}$ and $\frac{dR}{dt}$ using first-order forward differences.

$$\frac{dS}{dt} = \frac{s^{n+1} - s^n}{h}$$
$$\frac{dV}{dt} = \frac{v^{n+1} - v^n}{h}$$
$$\frac{dE}{dt} = \frac{e^{n+1} - e^n}{h}$$
$$\frac{dI}{dt} = \frac{i^{n+1} - i^n}{h}$$
$$\frac{dR}{dt} = \frac{r^{n+1} - r^n}{h}$$

Solving the above equations for $s^{n+1}, v^{n+1}, e^{n+1}, i^{m+1}$ and $r^{n+1}$ we have

$$s^{n+1} = \frac{s^n + h[(1-\emptyset)\pi + (1-\rho)a + (1-f)\alpha v^n]}{(1 + h(\lambda + \theta_1 + a + \pi))} \tag{6}$$

$$v^{n+1} = \frac{v^n + h[\emptyset\pi + \rho a + \theta_1 s^{n+1}]}{\left(1 + h((1-f)\alpha + f\theta_2 + a + \pi)\right)} \tag{7}$$

$$e^{n+1} = \frac{e^n + h\lambda s^{n+1}}{\left(1 + h(\delta + a + \pi)\right)} \tag{8}$$

$$i^{n+1} = \frac{i^n + h\delta e^{n+1}}{\left(1 + h(\eta + a + \pi)\right)} \tag{9}$$

$$r^{n+1} = \frac{r^n + h(\eta i^{n+1} + f\theta_2 v^{n+1})}{\left(1 + h(a + \pi)\right)} \tag{10}$$

The discrete system is given by equations (5)-(9) is the proposed Non-Standard Finite Difference (NSFD) scheme for the continuous model (2).

## 3.3. Convergence Analysis

This section is devoted to the convergence analysis of the designed NSFDS technique. For this, let us suppose

$$F_1 = \frac{S + h[(1 - \emptyset)\pi + (1 - \rho)a + (1 - f)\alpha v]}{(1 + h(\lambda + \theta_1 + a + \pi))}$$

$$F_2 = \frac{v + h[\emptyset\pi + \rho a + \theta_1 s]}{\left(1 + h\big((1 - f)\alpha + f\theta_2 + a + \pi\big)\right)}$$

$$F_3 = \frac{e + h\lambda s}{\left(1 + h(\delta + a + \pi)\right)}$$

$$F_4 = \frac{i + h\delta e}{\left(1 + h(\eta + a + \pi)\right)}$$

$$F_5 = \frac{r + h(\eta i + f\theta_2 v)}{(1 + h(a + \pi))}$$

The Jacobian for this system is:

$$J(s,v,i,e,r) = \begin{bmatrix} \frac{\partial F_1}{\partial s} & \frac{\partial F_1}{\partial v} & \frac{\partial F_1}{\partial i} & \frac{\partial F_1}{\partial e} & \frac{\partial F_1}{\partial r} \\ \frac{\partial F_2}{\partial s} & \frac{\partial F_2}{\partial v} & \frac{\partial F_2}{\partial i} & \frac{\partial F_2}{\partial e} & \frac{\partial F_2}{\partial r} \\ \frac{\partial F_3}{\partial s} & \frac{\partial F_3}{\partial v} & \frac{\partial F_3}{\partial i} & \frac{\partial F_3}{\partial e} & \frac{\partial F_3}{\partial r} \\ \frac{\partial F_4}{\partial s} & \frac{\partial F_4}{\partial v} & \frac{\partial F_4}{\partial i} & \frac{\partial F_4}{\partial e} & \frac{\partial F_4}{\partial r} \\ \frac{\partial F_5}{\partial s} & \frac{\partial F_5}{\partial v} & \frac{\partial F_5}{\partial i} & \frac{\partial F_5}{\partial e} & \frac{\partial F_5}{\partial r} \end{bmatrix}$$

The numerical scheme (6)-(10) will be unconditionally convergent if the absolute eigenvalue of the Jacobian matrix is less than unity i.e., $|\lambda_i| < 1, \ i = 1,2,3,4,5.$

The Jacobian matrix at disease-free point of equilibrium $(s, v, i, e, r) = (s_0, 0,0,0, r_0)$ is given by:

$$J(s, v, 0, 0, r) = \begin{bmatrix} j_{11} & j_{12} & j_{13} & 0 & 0 \\ j_{21} & j_{22} & 0 & 0 & 0 \\ 0 & 0 & j_{33} & j_{34} & 0 \\ 0 & 0 & j_{43} & j_{44} & 0 \\ 0 & j_{52} & j_{53} & 0 & j_{55} \end{bmatrix}$$

Where

$$j_{11} = \frac{1}{1 + h(\theta_1 + a + \pi)}$$

$$j_{12} = \frac{h(1 - f)\alpha}{1 + h(\theta_1 + a + \pi)}$$

$$j_{13} = \frac{-h\beta c\{s + h[(1 - \emptyset)\pi + (1 - \rho)a + (1 - f)\alpha v]\}}{[1 + h(\beta c i + \theta_1 + a + \pi)]^2}$$

$$j_{21} = \frac{h\theta_1}{1 + h((1 - f)\alpha + f\theta_2 + a + \pi)}$$

$$j_{22} = \frac{1}{1 + h((1 - f)\alpha + f\theta_2 + a + \pi)}$$

$$j_{33} = \frac{h\beta cs}{1 + h(\delta + a + \pi)}$$

$$j_{34} = \frac{1}{1 + h(\delta + a + \pi)}$$

$$j_{43} = \frac{1}{1 + h(\eta + a + \pi)}$$

$$j_{44} = \frac{h\delta}{1 + h(\eta + a + \pi)}$$

$$j_{52} = \frac{hf\theta_2}{1 + h(a + \pi)}$$

$$j_{53} = \frac{\eta h}{1 + h(a + \pi)}$$

$$j_{55} = \frac{1}{1 + h(a + \pi)}$$

$\lambda_1 = \frac{1}{1 + h(a + \pi)} < 1$. The remaining eigenvalues are given by the matrix:

$$J^* = \begin{bmatrix} j_{11} & j_{12} & j_{13} & 0 \\ j_{21} & j_{22} & 0 & 0 \\ 0 & 0 & j_{33} & j_{34} \\ 0 & 0 & j_{43} & j_{44} \end{bmatrix}$$

To calculate the eigenvalues of $J^*$, we will use the following lemma:

***Lemma 1[16]: For the quadratic equation $\lambda^2 - \lambda A + B = 0$, both roots satisfy $|\lambda_i| < 1, i = 2,3$ if and only if the following conditions are satisfied:***

1. $1 - A + B > 0$
2. $1 + A + B > 0$
3. $B < 1$

$$for\ j^{**} = \begin{bmatrix} j_{11} & j_{12} \\ j_{21} & j_{22} \end{bmatrix}$$

Let us define $A = TraceJ^{**}$ and $B = DetJ^{**}$. Therefore,

$$A = \frac{1+h[(1-f)\alpha+f\theta_2+a+\pi]+1+h(\theta_1+a+\pi)}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}} > 0$$

$$B = \frac{1}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}} -$$

$$\frac{h^2\alpha\theta_1(1-f)}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}}$$

$$B = \frac{1-h^2\alpha\theta_1(1-f)}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}} < 1$$

if $R_0 < 1$

$\Rightarrow B < 1$

$$1 + A + B = 1 + \frac{1+h[(1-f)\alpha+f\theta_2+a+\pi]+1+h(\theta_1+a+\pi)}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}} +$$

$$\frac{1-h^2\alpha\theta_1(1-f)}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}}$$

$\Rightarrow 1 + A + B > 0$

Now, for

$$1 - A + B = 1 - \frac{1+h[(1-f)\alpha+f\theta_2+a+\pi]+1+h(\theta_1+a+\pi)}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}} +$$

$$\frac{1-h^2\alpha\theta_1(1-f)}{\{1+h(\theta_1+a+\pi)\}\{1+h[(1-f)\alpha+f\theta_2+a+\pi]\}}$$

$\Rightarrow 1 - A + B > 0$

Now, $for\ j^{***} = \begin{bmatrix} j_{33} & j_{34} \\ j_{43} & j_{44} \end{bmatrix}$

Let us define $A = TraceJ^{***}$ and $B = DetJ^{***}$. Therefore,

$$A = \frac{h\beta cs\{1+h(\eta+a+\pi)\}+h\delta\{1+h(\delta+a+\pi)\}}{\{1+h(\eta+a+\pi)\}\{1+h(\delta+a+\pi)\}}$$

$B = \dfrac{h^2\beta cs - 1}{\{1+h(\delta+a+\pi)\}\{1+h(\eta+a+\pi)\}}$

Now, consider

$1 + A + B > 0$

$1 + \dfrac{h\beta cs\{1+h(\eta+a+\pi)\}+h\delta\{1+h(\delta+a+\pi)\}}{\{1+h(\eta+a+\pi)\}\{1+h(\delta+a+\pi)\}} + \dfrac{h^2\beta cs - 1}{\{1+h(\delta+a+\pi)\}\{1+h(\eta+a+\pi)\}} > 0$

Now, consider $1 - A + B > 0$

$1 + B > A$

$1 + \dfrac{h^2\beta cs - 1}{\{1+h(\delta+a+\pi)\}\{1+h(\eta+a+\pi)\}} > \dfrac{h\beta cs\{1+h(\eta+a+\pi)\}+h\delta\{1+h(\delta+a+\pi)\}}{\{1+h(\eta+a+\pi)\}\{1+h(\delta+a+\pi)\}}$

Since $R_e < 1$, and $s < 1$,
So, the above inequality holds.
Now, considering the $B < 1$

$$\frac{h^2\beta cs - 1}{\{1 + h(\delta + a + \pi)\}\{1 + h(\eta + a + \pi)\}} < 1$$

Since $R_e < 1$ and $s < 1$, the inequality holds.

Now, it can be seen from the above that the lemma 1 holds. For each step size of value $h$, both eigenvalues of a matrix $J^*$ are less than 1 if $R_e < 1$.

Thus, it proves that the proposed NSFDS method is unconditionally convergent for all values of $h$.

**Table 1.** Values of the Parameters

| Parameters | Values |
|:---:|:---:|
| $\eta$ | 0.6 |
| $\rho$ | 0.7 |
| $\theta_1$ | 0.7 |
| $\theta_2$ | 0.8 |
| $A$ | 0.2 |
| $C$ | 10 |
| $\phi$ | 0.5 |
| $\delta$ | 1 |
| $\beta$ | 0.1 |
| $\alpha$ | 0.36 |
| $F$ | 0.5 |
| $\pi$ | 0.45 |

## 3.4. Graphs for Transmission of Varicella Zoster Virus
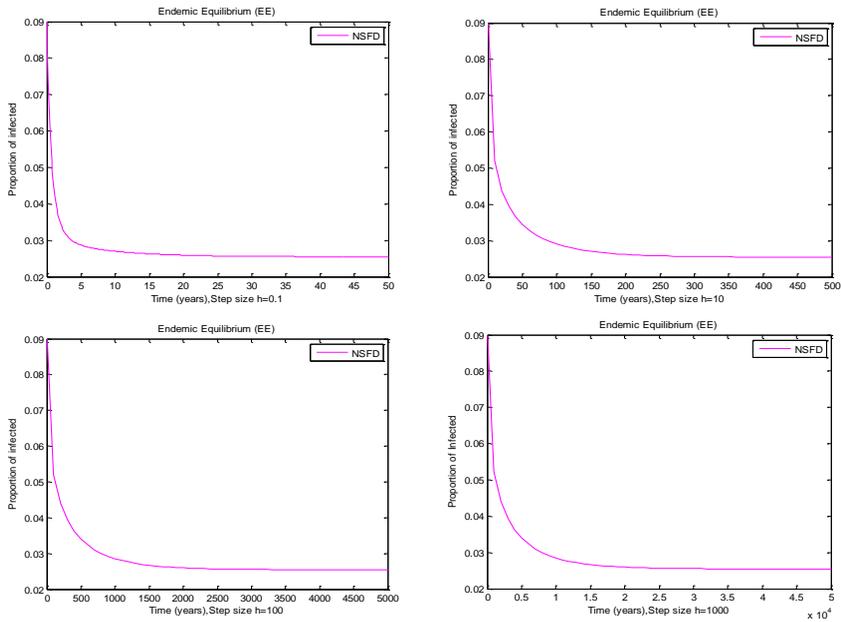


**Figure 2.** Numerical solutions of the infected population of the system (6-10)
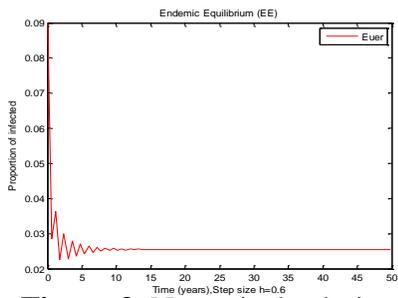


**Figure 3.** Numerical solutions of the infected population
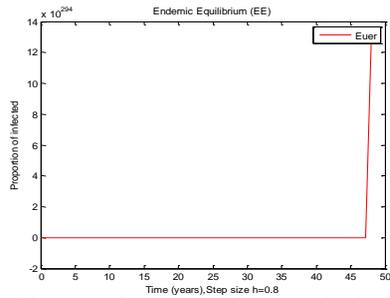


**Figure 4.** Numerical solutions of the infected population
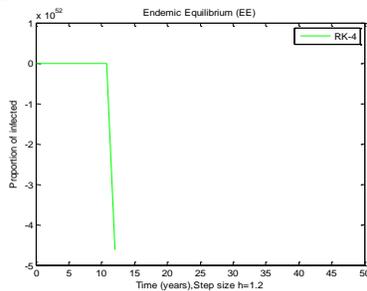


**Figure 5.** Numerical solutions of the infected population

## 4. Results and Discussion

In this paper, we have examined the behavior of chickenpox disease through a dynamical analysis of the Varicella Zoster Virus model. As it is clear from the graphs that both the models show dissimilar behaviors although they converge to the same equilibrium points in Figure 2. But for the same system when we are solving it with the help of the 'EULER' method which is given in Fig 3, it shows that the solution of the same system is not stable and demonstrates unsteady oscillations. Fig 4 shows that for a little higher value of the step size the graphical solution presented with the help of the 'EULER' method depicts divergence. When we solved the same system with the help of the 'RK-4' method, the solution of the system also diverges as shown in figure Fig 5. Next, we implemented the NSFDS method to solve the system of ordinary differential equations numerically and graphical behavior is presented for various values of '$h$' in Fig 2. The results are compared with the existing and classical numerical schemes, i.e., Euler and RK-4. It is verified from the graphical behavior that the underlying existing techniques give convergence solutions for very small values of '$h$' but fails for a large '$h$'. On the other hand, the proposed NSFDS scheme behaves well and gives convergent solutions for very large values of step size '$h$', i.e., h=1000. For more clarification, table 2 is presented below which demonstrates the effect of various time steps $h$ for all the underlying methods at disease-free and endemic equilibrium points.

**Table 2.** Comparison of Schemes

| $h$ | Euler | RK-4 | NSFD scheme |
|------|-------------|-------------|-------------|
| 0.1  | Convergence | Convergence | Convergence |
| 0.6  | Divergence  | Convergence | Convergence |
| 1.2  | Divergence  | Divergence  | Convergence |
| 100  | Divergence  | Divergence  | Convergence |
| 1000 | Divergence  | Divergence  | Convergence |

## 5. Conclusion

In this article, a reliable technique called NSFDS is designed for the numerical approximation of the transmission dynamics of the chickenpox epidemic model of Vercilla Zoster Virus. This technique depicts the solution required in the underlying epidemic model, as the state variables involved in it represent the population densities. The

developed NSFDS technique describes the convergence solution at each time step size. While the classical Euler and RK-4 show unbounded solutions for even very small time steps. The NSFDS technique is an explicit numerical scheme, therefore, easy to implement, shows stable behavior numerically and demonstrates a good agreement with analytic results possessed by the continuous model. It describes that NSFDS is more reliable as compared to the other two techniques.

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