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Author (s):	Zafar Ullah Khan[1], Muhammad Rafiq[2] , Fazal Dayan[3]
Affiliation (s):	[1] Rashid Latif Medical College Lahore, Pakistan. [2]University of Central Punjab, Lahore, Pakistan. [3]University of Management and Technology, Lahore, Pakistan.
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Numerical Analysis of *Varicella Zoster* Virus and its Vaccination

Zafar Ullah Khan[1], Muhammad Rafiq[2*], Fazal Dayan[3]

[1]Department of Dermatology, Rashid Latif Medical College Lahore, Pakistan
[2]Department of Mathematics, Faculty of Sciences & Technology, University of Central Punjab, Lahore, Pakistan
[3]Department of Mathematics, School of Science, University of Management and Technology, Lahore, Pakistan.

*m.rafiq@ucp.edu.pk

ABSTRACT

Chickenpox is caused by Varicella-Zoster-Virus (VZV). VZV is a DNA virus of the group of herpes that is transferred by direct contact with infected individuals. A VZV model is studied in this article with reference to chickenpox disease. An NSFD scheme was used to obtain the numerical solution of the studied model. The current study discussed the stability and consistency of the proposed scheme. The result of the simulation is presented after conducting a consistency analysis. The proposed scheme gives reliable estimations in order to describe the studied model of VZV.

***Keywords*:** chickenpox, consistency, NSFD scheme, stability, varicella-zoster-virus

INTRODUCTION

Chickenpox caused by the varicella-zoster virus (VZV) is a highly contagious disease. Only a single VZV serotype is known and the only reservoir is human- beings. Transmission of VZV happens by drops, vapor sprayers, or direct contact with respiratory discharges that quite often cause clinical ailments in susceptible people. After contamination, the infection stays lethargic in the brain ganglia, and in 10-20% of cases, it reactivates and causes shingles or herpes zoster, in people who are immunocompromised. In spite of the fact that chickenpox is generally a gentle illness of young age, in general, it could get more serious in adult age. It tends to be deadly, particularly in newborn children and immunocompromised individuals.

In mild environments, maximum cases show up before 10 years of age. Chickenpox is portrayed as a bothersome rash that normally starts on the scalp and face and is at first joined by fever and disquietude. The rash progressively spreads to the storage compartment and limits. The rankles

step by step dry out and hull over, then, at that point, vanish within one to fourteen days [1].

Garnett and Grenfell studied a mathematical model of VZV [2]. Various hypotheses about the VZV virus were discussed and a mathematical model was derived. Edmunds and Brisson studied the effects of vaccination on the VZV [3]. Brisson et al. constructed a mathematical model to predict the various strategies for the vaccination of VZV transmission [4]. Forde and Meeker studied the VZV through mathematical modeling [5]. Edward et al. developed a model of VZV with its vaccination [6]. The reproductive number and equilibrium points were derived for the model. The stability of the equilibria was discussed. Sensitivity analyses and numerical simulations were also performed for the studied model. Rafiq et al. developed a non-standard finite difference scheme to describe the dynamics of transmission of VZV [7]. Numerical simulations were presented to verify the theoretical results. Elisha et al. studied a VZV model and solved it through the Adomian Decomposition method and RK methods of orders 4 and 5 [8]. The obtained results were compared. It was concluded in this study that vaccination and treatment are the most effective strategies to combat this disease. Qureshi et al. propped the fractional model VZV model using Caputo, Caputo–Fabrizio, and the Atangana Baleanu Caputo derivatives respectively [9]. Pillsbur et al. fitted various models to clinical trial data on emerging infections and assessed their suitability [10].

Reliable estimations are required as far as human health is concerned. The NSFD schemes were introduced by Mickens [11]. Many researchers studied epidemiological models using NSFD theory. Cresson and Pierret developed an NSFD scheme and studied its convergence [12]. Several standard numerical schemes like were also studied for the comparative study. Naveed et al. studied a COVID-19 model with a delayed effect. Reproduction number, local and global stability of the studied model were discussed for the analysis. Delayed strategies were also presented in the current study [13]. Shatanawi et al. presented a stochastic corona virus model and developed numerical Euler, RK-4, and NSFD schemes for its solutions [14]. Baleanu et al. presented and analyzed a fractional chaotic system. NSFD scheme was used to study the chaotic behavior of the model [15]. Hoang studied a model of the hepatitis B virus using the NSFD approach. A comparison with standard finite difference schemes was also made in the current research [16]. Hoang presented and analyzed a virus

patch dynamic model. Global stability of the presented model was studied. Convergence and error bounds were also discussed [17]. Ratnam et al. studied a Cooperative Supportive Neural Network using NSFD scheme. Equilibria, local and global stability for the model were discussed [18]. Calatayud and Jornet presented a two-population model using NSFD theory [19]. Tijani and Appadu developed an NSFD scheme in order to study a biofilm formation model [20]. Consistency and convergence of the studied model were performed. The obtained numerical results were compared with existing numerical schemes. Nawaz et al. proposed a fractional order diffusive epidemic model to study COVID-19 [21]. Ahmad et al. investigated a tumor-immune model using some fractal fractional operators. The existence of the solution and stability of the model was studied using fixed point theory and Ulam-Hyres respectively. Simulation results were also presented to support the numerical results [22]. Fractional operators were used for the numerical solution of the one-dimensional sine-Gordon equation, telegraph differential equations, Fornberg–Whitham type equations, and Thomas–Fermi equation [23-26]. The NSFD method was studied in stochastic senses by many researchers. Arif et al. proposed a stochastic model for the numerical investigation of the computer virus [27]. Shatanawi et al. studied a Dengue model in stochastic senses using NSFD scheme [28]. Noor et al. presented a stochastic model of COVID-19 and studied it using the NSFD scheme [29]. Arif et al. studied a structure-preserving stochastic SIR epidemic model [30]. Researchers studied fractional stochastic models, for example [31, 32]. NSFD schemes were also developed to obtain the numerical solutions of fractional stochastic models [33-36].

Vaccination plays an important role in the prevention of chickenpox. Millions of cases, thousands of hospitalizations, and many deaths are prevented by the vaccination worldwide. There are two chickenpox vaccines, namely Varivax and ProQuad. Normally, two doses of vaccine are recommended for children and adults who never had chickenpox and were never vaccinated. The current study investigates the effects of vaccinations using the NSFD scheme. The novelty of the current work is the construction and mathematical analysis of the NSFD numerical scheme of the studied VZV. The consistency analysis of the NSFD approach for the studied model was also not researched before.

2. MATHEMATICAL MODEL

We considered the following SVEIR model [37].

$$\begin{cases} \frac{dS}{dt} = (1-\emptyset)N\kappa + (1-\zeta)\mathrm{A} + (1-f)\alpha V - (\omega+\sigma+\theta_1)S, \\ \frac{dV}{dt} = \rho\Lambda + \phi\kappa + \theta_1 S - \big((1-f)\alpha + f\theta_2 + \sigma\big)V, \\ \frac{dE}{dt} = \omega S - (\delta+\sigma)E, \\ \frac{dI}{dt} = \delta E - (\xi+\sigma)I, \\ \frac{dR}{dt} = \xi I + \theta_2 f V - \sigma R. \end{cases} \quad (1)$$

Where, $\omega = \frac{c\beta I}{N}$. The normalization of the above system gives us the following system;

$$\begin{cases} \frac{ds}{dt} = (1-\emptyset)\kappa + (1-\zeta)a + (1-f)\alpha v - (\omega+\sigma+\theta_1)s, \\ \frac{dv}{dt} = \rho a + \phi\kappa + \theta_1 s - \big((1-f)\alpha + f\theta_2 + \sigma\big)v, \\ \frac{de}{dt} = \omega s - (\sigma+\delta)e, \\ \frac{di}{dt} = \delta e - (\sigma+\xi)i, \\ \frac{dr}{dt} = \xi i + f\theta_2 v - \sigma r. \end{cases} \quad (2)$$

The variable $S, V, E, I,$ and R represents the susceptible, vaccinated, exposed, infected, and recovered subpopulations respectively. Detail of the parameter used are given below:

a = Arrival rate.

θ_1= individuals get first dose and get recovered.

θ_2= individuals get second dose and get recovered.

c = Per capita contact rate.

σ= death rate.

κ= birth rate.

φ= newborns vaccinated.

f = individuals get second dose.

α = rate of lessening the vaccine.

δ= rate of progress of infection from latent

ζ = immigrants vaccinated.

ξ = Rat of recovery

The disease-free equilibrium (DFE) of the above model is $E_0 = (s_0, v_0, 0, 0, r_0)$ is given by

$$s_0 = \frac{\alpha(1-f)(a+\kappa) + (f\theta_2 + a + \kappa)\{(1-\phi)\kappa + (1-\zeta)a\}}{\theta_1(f\theta_2 + a + \kappa) + (\lambda + a + \kappa)\{\alpha(1-f) + f\theta_2 + a + \kappa\}},$$

$$v_0 = \frac{(\zeta a + \phi\kappa + \theta_1)(a+\kappa)}{[\alpha(1-f) + f\theta_2 + a + \kappa](a+\kappa) + \theta_1(f\theta_2 + a + \kappa)},$$

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

3. NUMERICAL MODELLING

NSFD scheme for the system (2) can be written as;

$$\begin{cases} s^{n+1} = \frac{s^n + h[(1-\emptyset)\kappa + (1-\zeta)a + (1-f)\alpha v^n]}{1 + h(\omega + \sigma + \theta_1)}, \\ v^{n+1} = \frac{v^n + h[\emptyset\kappa + \zeta a + \theta_1 s^n]}{1 + h\big((1-f)\alpha + f\theta_2 + \sigma\big)}, \\ e^{n+1} = \frac{e^n + h\lambda s^n}{1 + h(\delta + \sigma)}, \\ i^{n+1} = \frac{i^n + h\delta e^n}{1 + h(\xi + \sigma)}, \\ r^{n+1} = \frac{r^n + h(\xi i^n + f\theta_2 v^n)}{1 + h\sigma}. \end{cases} \quad (3)$$

3.1 Consistency Analysis

To check the consistency of the proposed scheme, we applied the Taylor's series. From first Eq. of the system (3),

$$S^{n+1}[1 + h(\omega + \sigma + \theta_1)] = s^n + h[(1-\emptyset)\kappa + (1-\zeta)a + (1-f)\alpha v^n].$$

For the consistency, following procedure was adopted, considering the Taylor's series expansion

$$S^{n+1} = S^n + h\frac{dS}{dt} + \frac{h^2}{2!}\frac{d^2S}{dt^2} + \frac{h^3}{3!}\frac{d^3S}{dt^3} + \cdots,$$

Substituting the value of S^{n+1} in the above equation and after some simplifications, we obtain

$$\left(S^n + h\frac{dS}{dt} + \frac{h^2}{2!}\frac{d^2S}{dt^2} + \frac{h^3}{3!}\frac{d^3S}{dt^3} + \cdots,\right) + h(\omega + \sigma + \theta_1)\left(S^n + h\frac{dS}{dt} + \frac{h^2}{2!}\frac{d^2S}{dt^2} + \frac{h^3}{3!}\frac{d^3S}{dt^3} + \cdots,\right) = S^n + h[(1-\emptyset)\kappa + (1-\zeta)a + (1-f)\alpha V^n],$$

Taking, $h \to 0$, we obtain

$$\frac{dS}{dt} + (\omega + \sigma + \theta_1)S^n = (1-\emptyset)\kappa + (1-\zeta)a + (1-f)\alpha V^n,$$

or

$$\frac{dS}{dt} = (1-\emptyset)\kappa + (1-\zeta)a + (1-f)\alpha V - (\omega + \sigma + \theta_1)S.$$

From the second equation of the system (3), we have

$$V^{n+1}\left[1 + h\left((1-f)\alpha + f\theta_2 + \sigma\right)\right] = V^n + h[\emptyset\kappa + \zeta a + \theta_1 S^n].$$

The Taylor's series expansion of the compartment V^{n+1} is

$$V^{n+1} = V^n + h\frac{dV}{dt} + \frac{h^2}{2!}\frac{d^2V}{dt^2} + \frac{h^3}{3!}\frac{d^3V}{dt^3} + \cdots,$$

Substituting the value of V^{n+1} in the above equation and after some simplifications, we obtain

$$\left(V^n + h\frac{dV}{dt} + \frac{h^2}{2!}\frac{d^2V}{dt^2} + \frac{h^3}{3!}\frac{d^3V}{dt^3} + \cdots,\right) + h\left((1-f)\alpha + f\theta_2 + \mu\right)\left(V^n + h\frac{dV}{dt} + \frac{h^2}{2!}\frac{d^2V}{dt^2} + \frac{h^3}{3!}\frac{d^3V}{dt^3} + \cdots,\right) = V^n + h[\emptyset\kappa + \zeta a + \theta_1 S^n],$$

Taking, $h \to 0$, we obtain

$$\frac{dV}{dt} + \left((1-f)\alpha + f\theta_2 + \sigma\right)V^n + \beta_2 I^n {S_2}^n = \emptyset\kappa + \zeta a + \theta_1 S^n,$$

or

$$\frac{dV}{dt} = \zeta a + \phi\kappa + \theta_1 S - \big((1-f)\alpha + f\theta_2 + \sigma\big)V.$$

From the third equation of the system (3), we have

$$E^{n+1}[1 + h(\delta + \sigma)] = E^n + h\lambda S^n$$

The Taylor's series expansion of the compartment E is

$$E^{n+1} = E^n + h\frac{dE}{dt} + \frac{h^2}{2!}\frac{d^2E}{dt^2} + \frac{h^3}{3!}\frac{d^3E}{dt^3} + \cdots,$$

Substituting the value of E^{n+1} in the above equation and after some simplifications, we obtain

$$\left(E^n + h\frac{dE}{dt} + \frac{h^2}{2!}\frac{d^2E}{dt^2} + \frac{h^3}{3!}\frac{d^3E}{dt^3} + \cdots,\right) + h(\delta + \sigma)\left(E^n + h\frac{dE}{dt} + \frac{h^2}{2!}\frac{d^2E}{dt^2} + \frac{h^3}{3!}\frac{d^3E}{dt^3} + \cdots,\right) = E^n + h\lambda S^n,$$

Taking, $h \to 0$, we get

$$\frac{dE}{dt} + (\delta + \sigma)E^n = E^n + h\lambda S^n,$$

or

$$\frac{dE}{dt} = \omega S - (\sigma + \delta)E.$$

Similarly, we can obtain

$$\frac{dI}{dt} = \delta E - (\sigma + \xi)I$$

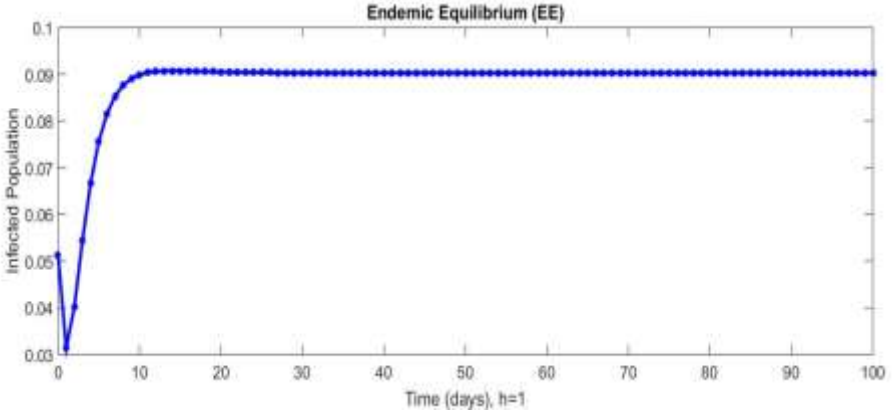
and

$$\frac{dR}{dt} = \xi i + f\theta_2 V - \mu R$$

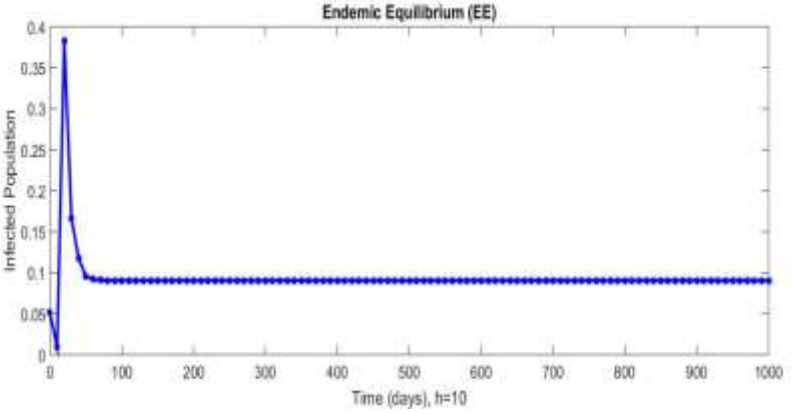
by applying Taylor's series to the remaining equations of the system (3). It is concluded that our proposed scheme is consistent with order 1.

4. NUMERICAL SIMULATIONS

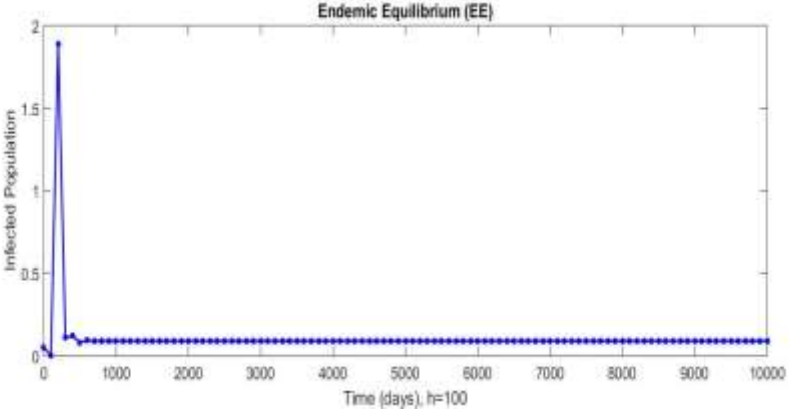
In this section we analyzed the simulation results of the developed schemes for the underlying model.



(a)



(b)



(c)

Figure 1. Infected population at (a) $h = 1$ (b) $h = 10$,and (c) $h = 100$.

In Fig.1, the compartment of the infected population is represented at different step size values. The proposed method showed positivity and convergence at all values of the step size. Positivity is one of the main characteristic of the epidemiological model as negative values of the subpopulation are meaningless. Convergence is another major property of these models. Our proposed model holds both of these properties which many standard finite difference schemes do not hold. We concluded from this behavior that the proposed method was capable to describe the disease dynamics of the studied model.

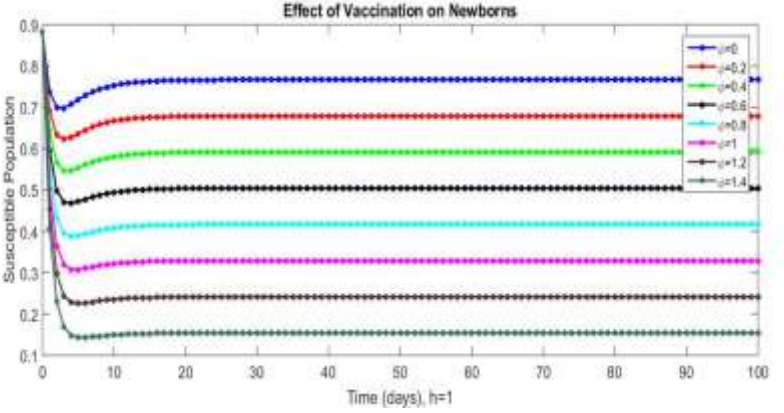


Figure 2. Effect of vaccination on susceptible population

The effects of vaccinations on the susceptible compartment are shown in Fig. 2 using our proposed scheme. The graph shows that the susceptible individuals are decreasing as the number of vaccinated people increases.

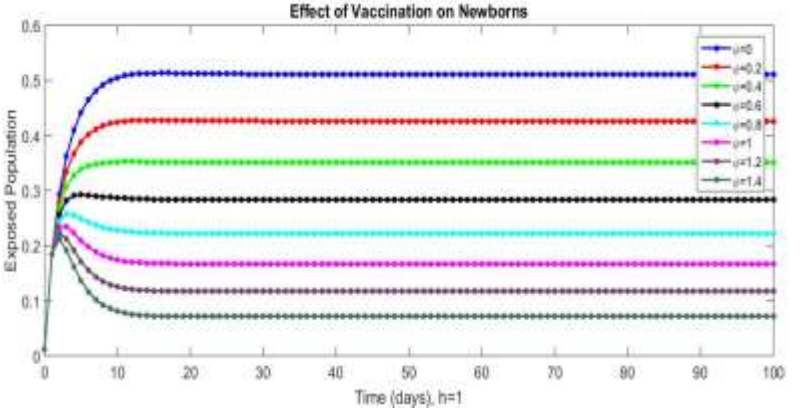


Figure 3. Effect of vaccination on Exposed Population

The effects of vaccinations on the exposed compartment are depicted in Fig. 3. There is an inverse relation between the number of exposed individuals and the number of vaccinated ones. The exposed proportion decrease with the increase in the vaccinated people.

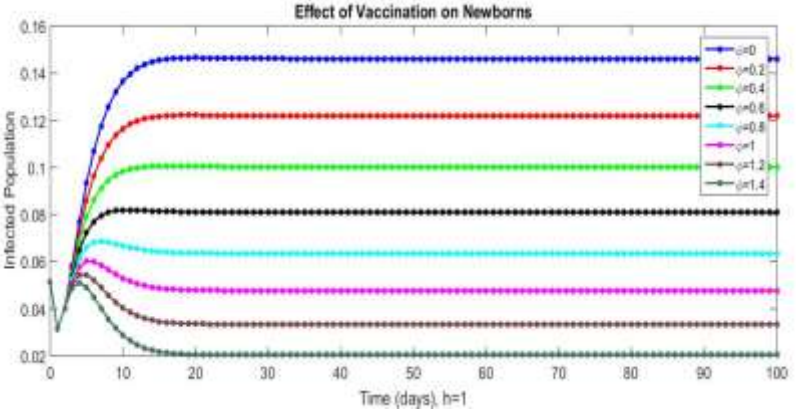


Figure 4. Effect of vaccination on infected population

The effects of vaccinations on the newborns of the infected compartment are given in Fig. 4. The number of infected persons decreased with the increased number of vaccinated people.

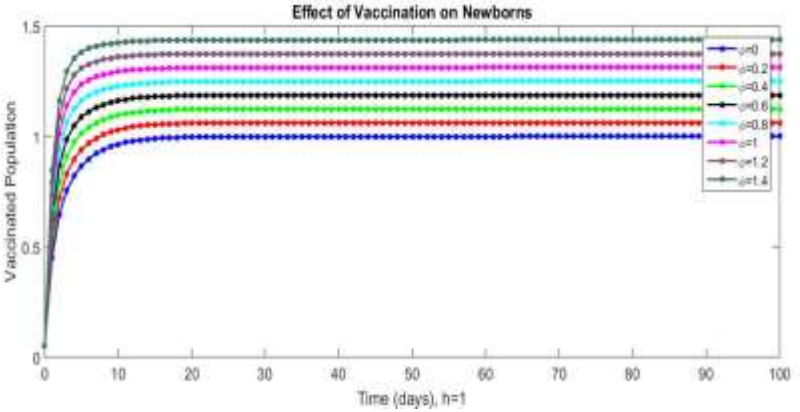


Figure 5. Effect of vaccination on vaccinated population

Fig. 5 and Fig. 6 show the effects of vaccinations on the remaining compartments of the studied model. The portion of the recovered population increases with an increase in the vaccination and there is a direct proportion between the vaccination and the recovered population.

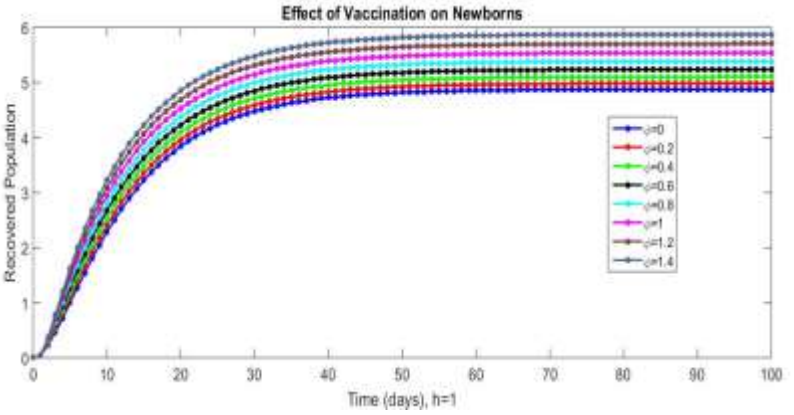


Figure 6. Effect of vaccination on recovered population

5. CONCLUSION

In this article, a reliable NSFD technique was developed to numerically approach the transmission dynamics of the varicella epidemic model. standard finite difference schemes produced numerical approximations that were negative and unstable, oscillating around the equilibrium position and diverging. These schemes did not preserve some important structural properties like positivity, boundedness, and dynamical consistency for certain choices of parameters [7]. The proposed Non-standard finite difference scheme remained consistent and preserved all the essential structures of continuous dynamical system in all scenarios. The major strength of the proposed NSFD scheme is that it behaved well for all parameters, initial conditions, and values of the step sizes which can also be seen in the graphs discussed in results and discussion section. The consistency and error analysis of the NSFD was also studied using Taylor series.

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