A Numerical & Analytical Study of Sirc Epidemic Model Using HPM

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ABSTRACT
This paper examines the SIRC epidemic model. The suggested model's analytical solution is found using the Homotopy Perturbation Method (HPM). By employing these methods, we first solve the problem analytically then utilising the Runge-Kutta method (RK4) to compare the numerical results. The findings demonstrate how well HPM works as a solution to these concerns, and it is anticipated that HPM will be used in a variety of new problems.

Keywords: SIRC model, Homotopy Perturbation Method, Numerical simulation.

1. INTRODUCTION

By applying mathematical modelling to analyse the transmission and management of infectious diseases has become more important. In McKendrick and Kermack [1], was presented to predict how a disease will spread. The total population is separated into three classes in this model: susceptible, infectious, and recovered, with the assumption being that it will remain stable over time. These models are hence known as SIR models. Cross-immune individuals (C) in the population have just recently been introduced in [2]; they exist in a state that is between totally protected and unprotected (R). Because of this, the derived SIRC model considers transient partial immunity and might effectively characterise, say, influenza A. This study introduces and develops the homotopy analysis approach for approximately solving the SIRC model. The model is

$$\begin{aligned}
\dot{S} &= \eta(1-S) - \xi SI + \beta C \\
\dot{I} &= \xi SI + \sigma\xi CI - (\eta+\alpha)I \\
\dot{R} &= (1-\sigma)\xi CI + \alpha I - (\eta+\gamma)R \\
\dot{C} &= -\xi CI - (\beta+\eta)C + \gamma R
\end{aligned} \qquad (1)$$

Rihan et al. [3] studied the fractional SIRC model with salmonella bacterial infection. Amjad Ali et al. [4] studied the numerical simulation and qualitative theory of the SIRC model, which corresponds to the nonlocal fractional order derivative. Naik et al.[5] expressed the Approximate solution of the SIR epidemic model using the homotopy analysis approach, stability analysis, and Crowley-Martin type and Holling type II treatment rate.The authors was published stability and hopf bifurcation analysis of a delayed SIRC epidemic model for Covid19, and semi-analytical solutions of mathematical models in EIAV (Equine Infectious Anemia Virus) infection using HAM in [6,7]. Also the authors was established an approximate solutions and dynamical analysis of an EIAV infection [8, 9 & 10]. Anwar et al. [11] studied the approximation and analytical solution for SIRC model using multi step differential transform method.In recent years, the Homotopy Perturbation Method has been successfully applied for solving various nonlinear problems in many branches of mathematics and engineering[12-16].

As most biological issues take the shape of epidemic models, they are by nature nonlinear. Consequently, it is seldom easy to find the precise answers that perfectly capture the entirety of a biological phenomenon.Hence, in order to determine both the exact and approximate solutions to these non-linear problems, scientists are searching for such numerical approaches or perturbations methods. Stability and convergence are important factors in numerical methods to take into account to prevent divergence or incorrect findings.However, we must exert the tiny parameter in the equation when using the analytical perturbation approach. Thus, the challenges of this approach are locating the small parameter and applying it to the equation.1.As a result, numerous potent mathematical techniques, like the artificial parameter method, have lately been presented to eliminate the tiny parameters [17& 18]. One of the well-known techniques for solving nonlinear equations is the Homotopy Analysis Method (HAM). Over the past decade, perturbation and homotopy have been integrated. He and Liao completed the essential task. This approach uses a free parameter, whose appropriate selection leads to quick convergence. He [19, 20 &21] was the first to introduce the Homotopy Perturbation Method (HPM) and its use in a number of issues. These techniques encompass all the benefits of the perturbation method and do not depend on the small parameter assumption.

2. The Homotopy Perturbation Method

The HPM integrates principles from both perturbation techniques and homotopy techniques. To elucidate the fundamental concept of employing the homotopy perturbation method to solve the following equation:

$$A(\bar{u}) - f(\bar{r}) = 0,\ \bar{r} \in \Omega, \tag{2}$$

$$\bar{B}_1(\bar{u}, \partial\bar{u}/\partial n) = 0,\ \bar{r} \in \Gamma, \tag{3}$$

Where,

A = differential operator,

$\bar{B}_1$ = boundary operator,

$f(\bar{r})$ = analytical function,

∂ / ∂ n = differentiation along the normal drawn from X.

In broad terms, one can decompose the operator A into two distinct components: a linear portion denoted as L and a nonlinear component represented as N. This is expressed in Equation (2):

$$L(\bar{v}) + N(\bar{v}) - f(\bar{r}) = 0 \tag{4}$$

$$H(\bar{v}, p) = p[A(\bar{v}) - f(\bar{r})] + (1-p)[L(\bar{v}) - L(\bar{u}_0)] = 0,\ p \in [0,1], \bar{r} \in \Omega \tag{5}$$

$$H(\bar{v}, p) = pL(\bar{u}_0) + p[N(\bar{v}) - f(\bar{r})] + L(\bar{v}) - L(\bar{u}_0) = 0 \tag{6}$$

The parameter p, which lies in the interval [0,1], while u0 stands for an initial approximate estimation of equation (2),which satisfies the boundary conditions .It follows from (5)and(6)that

$$H(\bar{v}, 0) = L(\bar{v}) - L(\bar{u}_0) = 0, H(\bar{v}, 1) = A(\bar{v}) - f(\bar{r}) = 0 \tag{7}$$

In this instance, the embedding parameter is seamlessly introduced, devoid of any artificial influences. Moreover, it can be regarded as a diminutive parameter within the range of 0 to 1. Consequently, it is highly reasonable that the solution to equations (6) and (5) is represented as

$$\bar{v} = \bar{v}_0 + p\bar{v}_1 + p^2\bar{v}_2 + \ldots (8)$$

The solution of Eq.(2),therefore, we have:

$$\bar{u} = \lim_{p \to 1} \bar{v} = \bar{v}_0 + \bar{v}_1 + \bar{v}_2 + \bar{v}_3 + \ldots \tag{9}$$

v

3. General procedure for approximate solution

Following the principles of the HPM for (1) can be formulated in the following manner:

$$\begin{aligned}
&(1-p)(\dot{v}_1 - \dot{x}_0) + p(\dot{S} - \eta(1-S) + \xi SI - \beta C) = 0 \\
&(1-p)(\dot{v}_2 - \dot{y}_0) + p(\dot{I} - \xi SI - \sigma\xi CI + (\eta + \alpha)I) = 0 \\
&(1-p)(\dot{v}_3 - \dot{z}_0) + p(\dot{R} - (1-\sigma)\xi CI - \alpha I + (\eta + \gamma)R) = 0 \\
&(1-p)(\dot{v}_4 - \dot{w}_0) + p(\dot{C} + \xi CI - \gamma R + (\eta + \beta)C) = 0
\end{aligned} \tag{10}$$

Consider,

$$\begin{aligned}
v_{1,0}(t) &= x_0(t) = x(0) = N_1 \\
v_{2,0}(t) &= y_0(t) = y(0) = N_2
\end{aligned} \tag{11}$$

$$v_{3,0}(t) = z_0(t) = z(0) = N_3$$
$$v_{4,0}(t) = w_0(t) = w(0) = N_4$$

And

$$v_1 = v_{1,0} + pv_{1,1} + p^2 v_{1,2} + \dots$$
$$v_2 = v_{2,0} + pv_{2,1} + p^2 v_{2,2} + \dots$$
$$v_3 = v_{3,0} + pv_{3,1} + p^2 v_{3,2} + \dots$$
$$v_4 = v_{4,0} + pv_{4,1} + p^2 v_{4,2} + \dots \quad (12)$$

Substituting Eqs. (11) and (12) into Eq. (10), we have

$$\begin{aligned}
&p(\dot{v}_{1,1} - \eta + \eta v_{1,0} + \xi v_{1,0} v_{2,0} - \beta v_{4,0}) + p^2(\dot{v}_{1,2} + \eta v_{1,1} + \xi v_{1,1} v_{2,0} + \xi v_{1,0} v_{2,1}) + \\
&p^3(\dot{v}_{1,3} + \eta v_{1,2} + \xi v_{1,1} v_{2,1} + \xi v_{1,2} v_{2,0} + \xi v_{1,0} v_{2,2}) + \dots = 0 \\
&p(\dot{v}_{2,1} - \xi v_{1,0} v_{2,0} - \sigma\xi v_{2,0} v_{4,0} + (\eta + \alpha) v_{2,0}) + \\
&p^2(\dot{v}_{2,2} - \xi v_{1,0} v_{2,1} + \xi v_{1,1} v_{2,0} - \sigma\xi v_{2,0} v_{4,1} - \sigma\xi v_{2,1} v_{4,0} + (\eta + \alpha) v_{2,1}) + \\
&p^3(\dot{v}_{2,3} - \xi v_{1,1} v_{2,1} - \xi v_{1,2} v_{2,0} - \sigma\xi v_{2,0} v_{4,2} - \sigma\xi v_{2,2} v_{4,0} - \xi v_{1,0} v_{2,2} \\
&-\sigma\xi v_{2,1} v_{4,1} + (\eta + \alpha) v_{2,2}) + \dots = 0 \quad (13) \\
&p(\dot{v}_{3,1} - (1-\sigma)\xi v_{2,0} v_{4,0} - \alpha v_{2,0} + (\eta + \gamma) v_{3,0}) + \\
&p^2(\dot{v}_{3,2} - (1-\sigma)\xi v_{2,1} v_{4,0} - (1-\sigma)\xi v_{2,0} v_{4,1} - \alpha v_{2,1} + (\eta + \gamma) v_{3,1}) + \\
&p^3(\dot{v}_{3,3} - (1-\sigma)\xi v_{2,2} v_{4,0} - (1-\sigma)\xi v_{2,0} v_{4,2} \\
&-(1-\sigma)\xi v_{2,1} v_{4,1} - \alpha v_{2,2} + (\eta + \gamma) v_{3,2}) + \dots = 0 \\
&p(\dot{v}_{4,1} - \gamma v_{3,0} + \xi v_{4,0} v_{2,0} + (\eta + \beta) v_{4,0}) + \\
&p^2(\dot{v}_{4,2} - \gamma v_{3,1} + \xi v_{4,0} v_{2,1} + \xi v_{4,1} v_{2,0} + (\eta + \beta) v_{4,1}) + \\
&p^3(\dot{v}_{4,3} - \gamma v_{3,2} + \xi v_{4,0} v_{2,2} + \xi v_{4,2} v_{2,0} + \xi v_{2,1} v_{4,1} + (\eta + \beta) v_{4,2}) + \dots = 0
\end{aligned}$$

Therefore,

$$\begin{aligned}
S(t) &= N_1 + t(\eta - \eta N_1 - \xi N_1 N_2 + \beta N_4) + \\
&\quad [-(\eta - \eta N_1 - \xi N_1 N_2 + \beta N_4)(\eta + \xi N_2) - \xi N_1(\xi N_2 N_1 + \xi N_2 N_4 \sigma - (\eta + \alpha) N_2)] \frac{t^2}{2} + \dots \\
I(t) &= N_2 + t(\sigma\xi N_2 N_4 + (-(\eta + \alpha) + \xi N_1) N_2) + \\
&\quad \frac{t^2}{2}[\xi N_2(\eta - \eta N_1 - \xi N_1 N_2 + \beta N_4) + \sigma\xi N_2(\gamma N_3 - \xi N_4 N_2 - (\eta + \beta) N_4) \\
&\quad + \sigma\xi N_4(\xi N_1 N_2 + \sigma\xi N_4 N_2 - (\eta + \alpha) N_2)(\xi N_1 - (\eta + \alpha))(\xi N_1 N_2 + \sigma\xi N_4 N_2 - (\eta + \alpha) N_2)] + \dots \\
R(t) &= N_3 + t((1-\sigma)\xi N_4 N_2 + \alpha N_2 - (\eta + \gamma) N_3) + \\
&\quad \frac{t^2}{2}[((1-\sigma)\xi N_4 + \alpha)(\xi N_1 N_2 + \sigma\xi N_4 N_2 - (\eta + \alpha) N_2) + \\
&\quad (1-\sigma)\xi N_2(\gamma N_3 - \xi N_4 N_2 - (\eta + \beta) N_4) - (\eta + \gamma)((1-\sigma)\xi N_4 N_2 + \alpha N_2 - (\eta + \gamma) N_3)] + \dots
\end{aligned}$$

$$C(t) = N_4 + t(\gamma N_3 - \xi N_4 N_2 - (\eta + \beta)N_4) +$$
$$\frac{t^2}{2}[(\gamma(1-\sigma)\xi N_2 N_4 + \alpha N_2 - (\eta + \gamma)N_3) - \xi N_4(\xi N_1 N_2 + \sigma\xi N_4 N_2 - (\eta + \alpha)N_2) - (\xi N_2 + \eta + \beta)$$
$$(\gamma N_3 - \xi N_4 N_2 - (\eta + \beta)N_4)] + \ldots$$

4. Numerical Simulations

We present numerical simulation results for system (1) using Matlab. We select the set of parameters are presented in Table 1.

Table 1. Definition of Variables / Parameters

Parameter and Variables	**values**
η =Death rate in every compartment assumed to be equal to the rate of new born in the population	0.5 [3]
β = Amount of re-susceptibility of the cross-immune population	0.5
ξ = Rate of contact	5.4
σ = Average probability of reinfection of cross-immune individuals	0.9[3]
α = Regaining amount of the infected population	2.5[3]
γ = Amount at which the regaining population to the cross-immune population and from fully immunized to partial immunity	0.5[3]
S(0)= Susceptible	0.1
I(0)= Infected	0.01
R(0)= Recovered	1
C(0)= Cross-immune	0.01

The results of the HPM match the solutions of the classical RK4 quite well, as can be seen from the graphical results in Figs. 1-4. This suggests that the presented method is capable of accurately predicting the behaviour of the variables S,I, R & C. The S(t),I(t),R(t), and C(t) error graphs are shown in Figs. 5-8 and the errors are presented in Tables 2,3,4 &5.

Table 2. Comparisons of the values of S(t) by Homotopy Perturbation Method& RK4

t	HPM	RK4	Error
0	0.1000	0.1000	0
0.2	0.1143	0.1144	0.0001
0.4	0.1281	0.1284	0.0003
0.6	0.1414	0.1421	0.0007
0.8	0.1541	0.1553	0.0012
1	0.1663	0.1682	0.0019

Table 3. Comparisons of the values of I(t) by Homotopy Perturbation Method& RK4

t	HPM	RK4	Error
0	2.0000	1.5000	0.5
0.2	1.6475	1.2719	0.3755
0.4	1.3790	1.0751	0.3039
0.6	1.1947	0.9064	0.2883
0.8	1.0944	0.7626	0.3318
1	1.0783	0.6405	0.4377
1	0.1663	0.1682	0.0019

Table 4. Comparisons of the values of R(t) by Homotopy Perturbation Method& RK4

t	HPM	RK4	Error
0	1.0000	1.0000	1
0.2	0.7556	0.7297	0.7556
0.4	0.5466	0.5318	0.5466

0.6	0.3728	0.3879	0.3728
0.8	0.2343	0.2834	0.2343
1	0.1311	0.2074	0.1311

Table 5. Comparisons of the values of C(t) by Homotopy Perturbation Method& RK4

t	HPM	RK4	Error
0	0.4	1.7	1.3
0.2	1.3088	2.5049	1.1961
0.4	2.0290	2.7992	0.7703
0.6	2.5605	2.9121	0.3516
0.8	2.9033	2.9596	0.0562
1	3.0576	2.9825	0.0751

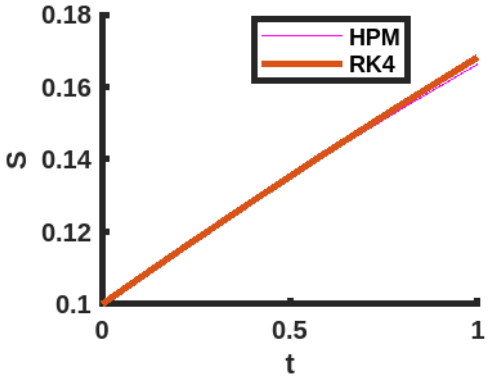

Fig 1. Shows the comparison of susceptible individuals with RK4.

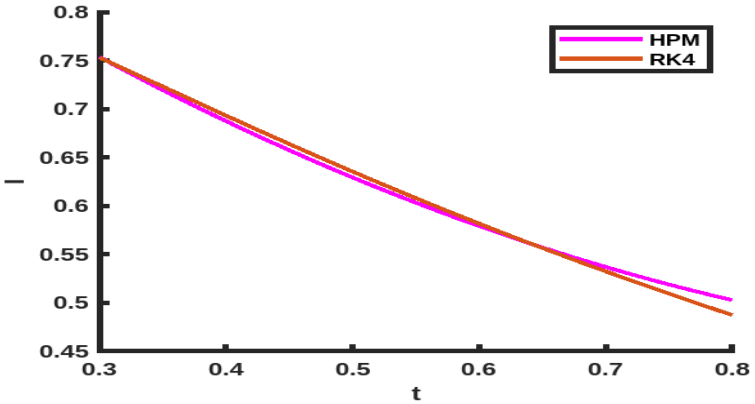

Fig 2. Shows the comparison of infected individuals with RK4.

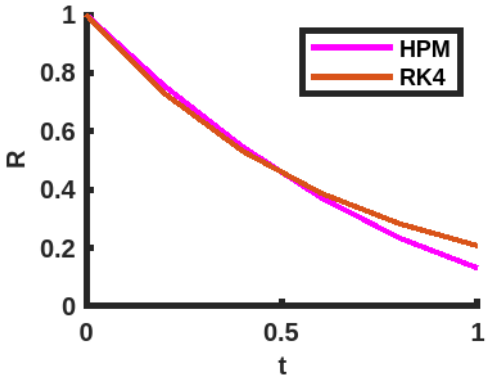

Fig 3. Shows the comparison of recovered individuals with RK4.

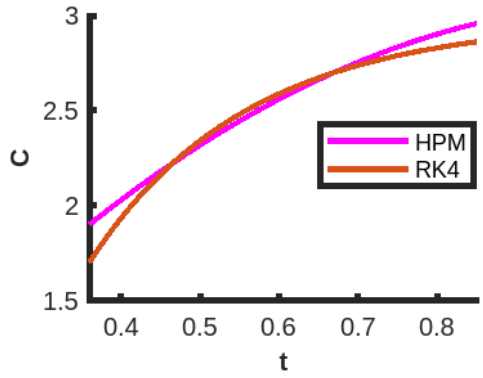

Fig 4. Shows the comparison of cross-immune individuals with RK4.

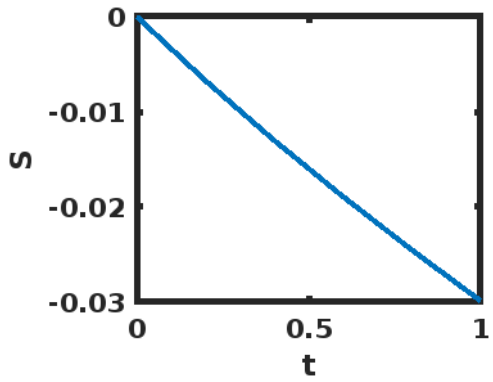

Fig 5. Shows the Error of S(t) individuals.

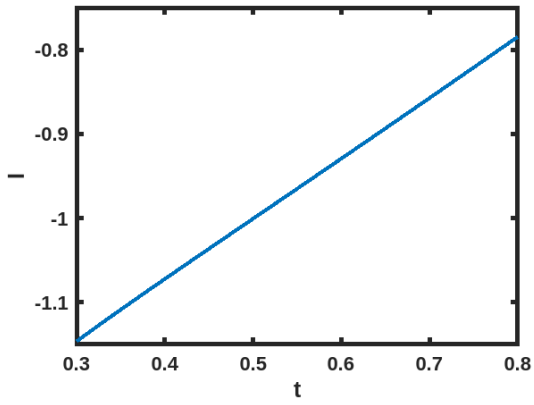

Fig 6. Shows the Error of I(t) individuals.

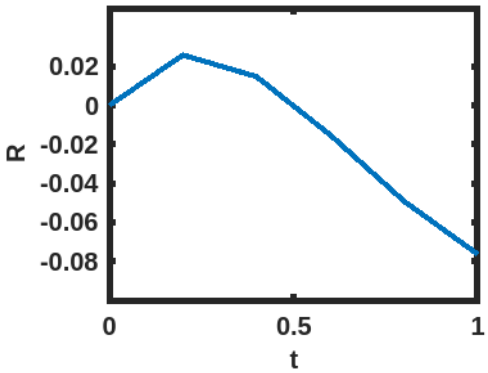

Fig 7. Shows the Error of R(t) individuals.

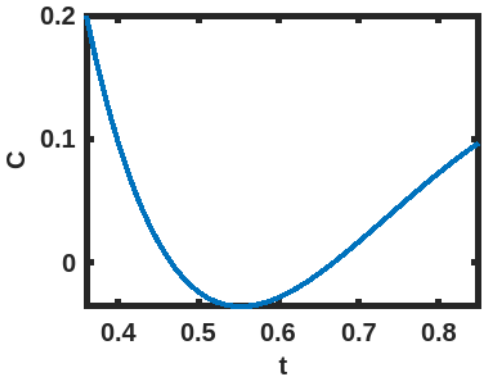

Fig 8. Shows the Error of C(t) individuals.

5. CONCLUSION

We have suggested an approximation method in this study for solving biological equations. In conclusion, we demonstrated the applicability and accuracy of our technique to the differential equation solution system for models of influenza and HIV.

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