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Theoretical Analysis of A SIR Epidemic Model With Constant Vaccination Strategy

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ABSTRACT

A *SIR (Susceptible-Infected-Removed) model that monitors the temporal dynamics of a childhood disease in the presence of preventive vaccine is discussed. The aim of epidemic modeling is to understand and if possible control the spread of disease. To do this, it tries to relate disease dynamics at the population level to basic properties of the host and pathogen populations and of the infection process. Epidemic models thus express scientific hypotheses. In this paper, a powerful analytical method, called Homotopy analysis method (HAM) is used to solve the system of nonlinear differential equations. Furthermore, in this work the numerical simulation of the problem is also reported using Scilab/Matlab program. Our analytical results are compared with simulation results. A good agreement between analytical and numerical results is noted.*

Keywords: *Epidemic models; Vaccination; Homotopy analysis method, Mathematical modeling; Non-linear equations.*

1. INTRODUCTION

Important control problems nowadays related to life sciences are the control of ecological models like, for instance, those of population via the online adjustment of the species environment carrying capacity, that of the population growth or that of the regulated harvesting quota as well as the disease propagation via vaccination control. In a set of papers, several variants and generalizations of the Beverton-Holt model (standard time–invariant, time-varying parameterized, generalized model or modified generalized model) have been investigated at the levels of stability, cycle- oscillatory behavior, permanence and control through the manipulation of the carrying capacity [1-5]. The sets of models include the most basic ones, as follows: (i) SI- models where not removed- by – immunity group is assumed. In other word, only susceptible and infected groups are assumed;(ii) SIR models, which include susceptible plus infected plus removed- by –immunity groups; (iii) SEIR models where the infected group is split into two ones. Those models have also two major variants, namely, the so-called “pseudo-mass action models”, where the total population is not taken into account as a relevant disease contagious factor and the so-called “true-mass action models”, where the total population is more realistically considered as an inverse factor of the disease transmission rates [6].

In particular, the SIR model is a standard compartmental model that has been used to describe many epidemiological diseases [7-10]. In this model the population divided into three groups: the susceptible (S), infective (I), and the recovered (R). The susceptible groups are those who are not infected and not immune, the infective groups are those who are infected and can transmit the disease, and the recovered are those who have been infected and are immune (recovered or dead). This model assumes that the efficacy of the vaccine is 100% and the natural death rates μ in the classes remain unequal to births, so that the population size N is realistically not constant [11].

Makinde has derived an approximation to the solution of the non-linear system of differential equations governing the problem using Adomian decomposition method. In this paper we have derived an analytical expression for the concentrations of susceptible group *(S)*, infected group *(I)*, and removed group *(R)* for all values of parameters using Homotopy analysis method.

2. MATHEMATICAL FORMULATION AND ANALYSIS OF THE PROBLEM

2.1 Mathematical formulation

The differential equations for the SIR model are [11]

$$\frac{dS}{dt} = (1-P)\pi N - \beta\frac{SI}{N} - \mu S, \tag{1}$$

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$$\frac{dI}{dt} = \beta \frac{SI}{N} - (\gamma + \mu)I, \tag{2}$$

$$\frac{dR}{dt} = P\pi N + \gamma I - \mu R. \tag{3}$$

$$\frac{dN}{dt} = (\pi - \mu)N. \tag{4}$$

We also have the relationship $N=S+I+R$ and assume $\mu, \pi, \beta, \gamma, \mu$ are constant parameters. A summary of the process is drawn in a flow chart in Fig.1.

2.2 Normalized form

By introducing the following set of non-dimensional variables, $s = \frac{S}{N}, i = \frac{I}{N}, r = \frac{R}{N}$ where $N=S+I+R$. We obtain the following system of non- linear equations

$$\frac{ds}{dt} = (1-P)\pi - \beta si - \pi s \tag{5}$$

$$\frac{di}{dt} = \beta si - (\gamma + \pi)i \tag{6}$$

$$\frac{dr}{dt} = P\pi + \gamma i - \pi r \tag{7}$$

where *s*-normalized susceptible group, *i*-normalized infected group, *r*-normalized removed group.

The transformed boundary conditions are

$s=a, i=b, r=c$ when $t=0$ (8)

where *a*, *b* and *c* are the normalized parameters.

3. HOMOTOPY ANALYSIS METHOD APPROACH TO A SIR EPIDEMIC MODEL WITH CONSTANT VACCINATION STRATEGY

3.1. Homotopy analysis method

Homotopy analysis method (HAM) [12-13] is a general analytic method to get series solutions of various types of non-linear equations, including ordinary differential equations, partial differential equations and coupled nonlinear equations. Unlike perturbation methods, the HAM is independent of small/large physical parameters. More importantly, different from all perturbation and traditional non-perturbation methods, the HAM provides us a simple way to ensure the convergence of solution series. Besides, different from all perturbation and previous non-perturbation methods, the HAM provides us with great freedom to choose proper base functions to approximate a nonlinear problem [14, 15]. Now, more and more researchers have been successfully applying this method to various nonlinear problems in science and engineering. In this paper we employ HAM to solve the nonlinear differential equations (Eqs. (5) – (7)). The basic concept of Homotopy analysis method is given in Appendix A.

3.2. Solution of boundary value problem using the Homotopy analysis method

Using HAM method (Appendix B), we obtained the analytical expression corresponding to the concentrations of susceptible group, infectious group and removed groups as follows:

$$s(t) = (1-P) + (a-(1-P))e^{-\pi t} + \frac{h\beta(1-P)b\left(e^{-\pi t} - e^{-(\gamma+\pi)t}\right)}{\gamma} + \frac{h\beta b(a-(1-P))\left(e^{-\pi t} - e^{-(\gamma+2\pi)t}\right)}{\gamma+\pi} \tag{9}$$

$$i(t) = be^{-(\gamma+\pi)t} - h\beta b(1-P)te^{-(\gamma+\pi)t} + \frac{h\beta b(a-(1-P))(e^{-(\gamma+2\pi)t} - e^{-(\gamma+\pi)t})}{\pi} \tag{10}$$

$$r(t) = P - be^{-(\gamma+\pi)t} + ce^{-\pi t} - Pe^{-\pi t} + be^{-\pi t} - \frac{h\beta b\gamma(a-(1-P))(e^{-\gamma t} - e^{-\pi t})}{(\gamma+\pi)\pi} + h\beta bt(1-P)e^{-(\gamma+\pi)t}$$
$$+ \frac{h\beta b(1-P)(e^{-(\gamma+\pi)t} - e^{-\pi t})}{\gamma} + \frac{h\beta b(a-(1-P))(e^{-(\gamma+\pi t)} - e^{-\pi t})}{\pi} + P(1-e^{-\pi t})(1+h) \quad (11)$$

3.3. Previous work of Mankinde [11]

Mankinde has derived the analytical expressions of concentrations of *s*(t), *i*(t) and *r*(t) by using the following cases

Case 1:

$$s(t) = 1.0 - 0.36t + 0.72\times10^{-1}t^2 - 0.96\times10^{-2}t^3 + 0.96\times10^{-3}t^4 - 0.768\times10^{-4}t^5 - 0.5688888892\times10^{-6}t^6.$$
$$i(t) = 0.$$
$$r(t) = 0.36t - 0.72\times10^{-1}t^2 + 0.96\times10^{-2}t^3 - 0.96\times10^{-3}t^4 + 0.768\times10^{-4}t^5 - 0.512\times10^{-5}t^6.$$

Case 2:

$$s(t) = 0.8 - 0.408t + 0.1008*t^2 - 0.8223999996\times10^{-2}t^3 - 0.1811776\times10^{-2}t^4 + 0.2838500158\times10^{-3}t^5$$
$$- 0.4866281149\times10^{-4}t^6 - 0.1973168518\times10^{-5}t^7 + 0.1567280763\times10^{-7}t^8$$
$$+ 0.4557699387\times10^{-9}t^9 - 0.1747626667\times10^{-11}t^{10}.$$

$$i(t) = 0.2 + 0.42\times10^{-1}t - 0.2823\times10^{-1}t^2 - 0.1169699999\times10^{-2}t^3 + 0.2759918751\times10^{-2}t^4$$
$$- 0.3762609484\times10^{-3}t^5 + 0.4741940899\times10^{-4}t^6 + 0.1990139977\times10^{-5}t^7 - 0.1540349563\times10^{-7}t^8$$
$$- 0.4575903832\times10^{-9}t^9 + 0.1747626667\times10^{-11}t^{10}.$$
$$r(t) = 0.366t - 0.7257\times10^{-1}t^2 + 0.93937\times10^{-2}t^3 - 0.94814275\times10^{-3}t^4 + 0.9241093251\times10^{-4}t^5$$
$$- 0.4445486401\times10^{-5}t^6 - 0.1697145904\times10^{-7}t^7 - 0.269312\times10^{-9}t^8 + 0.1820444445\times10^{-11}t^9.$$

4. RESULTS AND DISCUSSION

4.1. Numerical simulation

In order to investigate the effect of vaccination control strategy, the system of differential equations (Eqs. (5) - (7)) are also solved by numerical methods. The function ode45 in Scilab/Matlab software which is a function of solving ODE is used to solve these nonlinear equations. The Scilab/Matlab program is also given in Appendix C. Its numerical solution is compared with the solution obtained by using Homotopy analysis method and gives a satisfactory result .To show the efficiency of the vaccination control strategy, our results are compared with the numerical solution (Scilab/Matlab program) in Fig. (2)
and Fig. (3).

4.2. Effect of vaccination strategy

Eqs. (5) - (7) are the simple analytical expressions of normalized susceptible group *s*(*t*), normalized infected group *i*(*t*) and normalized removed group *r*(*t*) using Homotopy analysis technique for the boundary conditions (8). Fig.2 shows the power of high vaccination coverage on the disease free initial population groups. The susceptible group decreases when the time increases. and the removed group gradually increases due to inclusion of vaccinated susceptible group. Fig.3 illustrates the impact of high vaccination coverage on the initial population groups with low level of infective group. The population of the susceptible and infective groups decreases with time. The removed group increases when the time increases.

5. CONCLUSIONS

In this paper, SIR epidemic model with constant vaccination strategy are solved analytically using the HAM. This method is powerful tool which enables to find analytical solution in case of linear and non-linear systems of differential equations. we conclude when the high vaccination coverage on the concentrations of susceptible group (*S*), infected group (*I*), and removed group (*R*) are derived. It gives the good agreement with simulation and limiting case results.

Appendix A:

Basic idea of Liao's Homotopy analysis method

Consider the following differential equation [16]:

$$N[u(t)] = 0 \tag{A.1}$$

where, N is a nonlinear operator, t denotes an independent variable, $u(t)$ is an unknown function. For simplicity, we ignore all boundary or initial conditions, which can be treated in the similar way. By means of generalizing the conventional Homotopy method, Liao constructed the so-called zero-order deformation equation as:

$$(1-p)L[\varphi(t;p) - u_0(t)] = phH(t)N[\varphi(t;p)] \tag{A.2}$$

where $p \in [0,1]$ is the embedding parameter, $h \neq 0$ is a nonzero auxiliary parameter, $H(t) \neq 0$ is an auxiliary function, L is an auxiliary linear operator, $u_0(t)$ is an initial guess of $u(t)$ and $\varphi(t:p)$ is an unknown function. It is important, that one has great freedom to choose auxiliary unknowns in HAM. Obviously, when $p = 0$ and $p = 1$, it holds:

$$\varphi(t;0) = u_0(t) \text{ and } \varphi(t;1) = u(t) \tag{A.3}$$

respectively. Thus, as p increases from 0 to 1, the solution $\varphi(t;p)$ varies from the initial guess $u_0(t)$ to the solution $u(t)$. Expanding $\varphi(t;p)$ in Taylor series with respect to p, we have:

$$\varphi(t;p) = u_0(t) + \sum_{m=1}^{+\infty} u_m(t)\, p^m \tag{A.4}$$

where

$$u_m(t) = \left[\frac{1}{m!} \frac{\partial^m \varphi(t;p)}{\partial p^m} \right]_{p=0} \tag{A.5}$$

If the auxiliary linear operator, the initial guess, the auxiliary parameter h, and the auxiliary function are so properly chosen, the series (A.4) converges at p =1 then we have:

$$u(t) = u_0(t) + \sum_{m=1}^{+\infty} u_m(t). \tag{A.6}$$

Define the vector

$$\vec{u}_n = \{u_0, u_1, ..., u_n\} \tag{A.7}$$

Differentiating Eq. (A.2) for$m$ times with respect to the embedding parameter p, and then setting p = 0 and finally dividing them by m!, we will have the so-called m^{th}-order deformation equation as:

$$L[u_m - \chi_m u_{m-1}] = hH(t)\Re_m(\vec{u}_{m-1}) \tag{A.8}$$

where

$$\Re_m(\vec{u}_{m-1}) = \frac{1}{(m-1)!} \frac{\partial^{m-1} N[\varphi(t;p)]}{\partial p^{m-1}} \Big|_{p=0} \tag{A.9}$$

and

$$\chi_m = \begin{cases} 0, & m \leq 1, \\ 1, & m > 1. \end{cases} \tag{A.10}$$

Applying L^{-1} on both side of Eq. (A.8), we get

$$u_m(t) = \chi_m u_{m-1}(t) + hL^{-1}[H(t)\Re_m(\vec{u}_{m-1})] \tag{A.11}$$

In this way, it is easily to obtain u_m for $m \geq 1$, at M^{th} order, we have

$$u(t) = \sum_{m=0}^{M} u_m(t) \tag{A.12}$$

When $M \to +\infty$, we get an accurate approximation of the original Eq. (A.1). For the convergence of the above method we refer the reader to Liao [12]. If Eq. (A.1) admits unique solution, then this method will produce the unique solution. If Eq. (A.1) does not possess unique solution, the HAM will give a solution among many other (possible) solutions.

Appendix B:

Analytical solution of non-linear equations (5) to (7)

In order to solve equations (5) to (7) by means of the HAM, we first construct the equations as follows:

$$(1-p)\left[\frac{ds}{dt} - (1-P)\pi + \pi s\right] = ph\left[\frac{ds}{dt} - (1-P)\pi + \beta si + \pi s\right] \tag{B.1}$$

$$(1-p)\left[\frac{di}{dt} + (\gamma + \pi)i\right] = ph\left[\frac{di}{dt} - \beta si + (\gamma + \pi)i\right] \tag{B.2}$$

$$(1-p)\left[\frac{dr}{dt} - P\pi - \gamma i + \pi r\right] = ph\left[\frac{dr}{dt} - P\pi - \gamma i + \pi r\right] \tag{B.3}$$

The approximate solutions of Eqs. (B.1) - (B.3) are as follows

$$s(t) = s_0 + ps_1 + p^2 s_2 + \ldots \tag{B.4}$$

$$i(t) = i_0 + pi_1 + p^2 i_2 + \ldots \tag{B.5}$$

$$r(t) = r_0 + pr_1 + p^2 r_2 + \ldots \tag{B.6}$$

Substituting (B.4) in Eq. (B.1), (B.5) in Eq.(B.2) and (B.6)in Eq.(B.3) equating the like powers of p we get

$$p^0 : \frac{ds_0}{dt} - (1-P)\pi + \pi s_0 = 0 \tag{B.7}$$

$$p^1 : \frac{ds_1}{dt} + \pi s_1 - \frac{ds_0}{dt} + (1-P)\pi - \pi s_0 - h\frac{ds_0}{dt} + h(1-P)\pi - \beta h s_0 i_0 - h\pi s_0 = 0 \tag{B.8}$$

$$p^0 : \frac{di_0}{dt} + (\gamma + \pi)i_0 = 0 \tag{B.9}$$

$$p^1 : \frac{di_1}{dt} + (\gamma + \pi)i_1 - \frac{di_0}{dt} - (\gamma + \pi)i_0 - h\frac{di_0}{dt} + h\beta s_0 i_0 - h(\gamma + \pi)i_0 = 0 \tag{B.10}$$

$$p^0 : \frac{dr_0}{dt} - \gamma i_0 + \pi r_0 - P\pi = 0 \tag{B.11}$$

$$p^1 : \frac{dr_1}{dt} + \pi r_1 - \gamma i_1 - \frac{dr_0}{dt} + \gamma i_0 - \pi r_0 - h\frac{dr_0}{dt} + h\gamma i_0 - h\pi r_0 = 0 \tag{B.12}$$

The boundary conditions Eq. (8) becomes

$$s_0(t) = a, i_0(t) = b \text{ and } r_0(t) = c \text{ when } t=0 \tag{B.13}$$

$$s_1(t) = 0, i_1(t) = 0 \text{ and } r_1(t) = 0 \text{ when } t=0 \tag{B.14}$$

From Eqs. (B.7), (B.9) and (B.11) and from the boundary conditions (B.13) we get,

$$s_0(t) = (1-P) + (a-(1-P))e^{-\pi t} \tag{B.15}$$

$$i_0(t) = be^{-(\gamma+\pi)t} \tag{B.16}$$

$$r_0(t) = P - be^{-(\gamma+\pi)t} + ce^{-\pi t} - Pe^{-\pi t} + be^{-\pi t} \tag{B.17}$$

Substituting the values of s_0, i_0 and r_0 in Eq. (B.8), Eq. (B.10) and Eq. (B.12) and solving the equations using the boundary conditions (B.14) we obtain the following results:

$$s_1(t) = \frac{h\beta(1-P)b\left(e^{-\pi t} - e^{-(\gamma+\pi)t}\right)}{\gamma} + \frac{h\beta b(a-(1-P))\left(e^{-\pi t} - e^{-(\gamma+2\pi)t}\right)}{\gamma+\pi} \tag{B.18}$$

$$i_1(t) = -h\beta b(1-P)te^{-(\gamma+\pi)t} + \frac{h\beta b(a-(1-P))(e^{-(\gamma+2\pi)t} - e^{-(\gamma+\pi)t})}{\pi} \tag{B.19}$$

$$r_1(t) = -\frac{h\beta b\gamma(a-(1-P))(e^{-(\gamma t)} - e^{-(\pi t)})}{(\gamma+\pi)\pi} + h\beta bt(1-P)e^{-(\gamma+\pi)t} + \frac{h\beta b(1-P)(e^{-(\gamma+\pi)t} - e^{-(\pi)t})}{\gamma} + \frac{h\beta b(a-(1-P))(e^{-(\gamma+\pi)t} - e^{-\pi t})}{\pi} + P(1-e^{-\pi t})(1+h) \tag{B.20}$$

Adding Eqs. (B.15) and (B.18), we get Eq. (9) in the text. Similarly we get Eqs. (10) and (11) in the text.

Appendix C:

Scilab/Matlab program to find the numerical solution of nonlinear Eqs. (5)-(7):

```
function main
options= odeset('RelTol',1e-6,'Stats','on');
%initial conditions
x0 = [1;0;0];
tspan = [0 10];
tic
[t,x] = ode45 (@TestFunction, tspan,x0,options);
toc
figure
hold on
plot(t, x(:,1))
plot(t, x(:,2))
plot(t, x(:,3))
legend('x1','x2')
ylabel('x')
xlabel('t')
return
function [dx_dt]= TestFunction(t,x)
P=0.9;d=0.4;e=0.8;f=0.03;
dx_dt(1)=(1-P)*d-e*x(1)*x(2)-d*x(1);
dx_dt(2) =e*x(1)*x(2)-(f+d)*x(2);
```



```
dx_dt(3) =P*d+f*x(2)-d*x(3);
dx_dt = dx_dt';
return
```

Appendix D

Nomenclature

Symbols:

S	Susceptible group
I	Infected group
R	Removed group
N	Population size
μ	Natural death rates
π	Constant birth rate
P	Population fraction
β	Rate change of susceptible group to infective group
γ	Rate change of infective group to removed group
s	Normalized susceptible group
i	Normalized infected group
r	Normalized removed group
a, b, c	Saturation parameter
t	Time

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Figures:

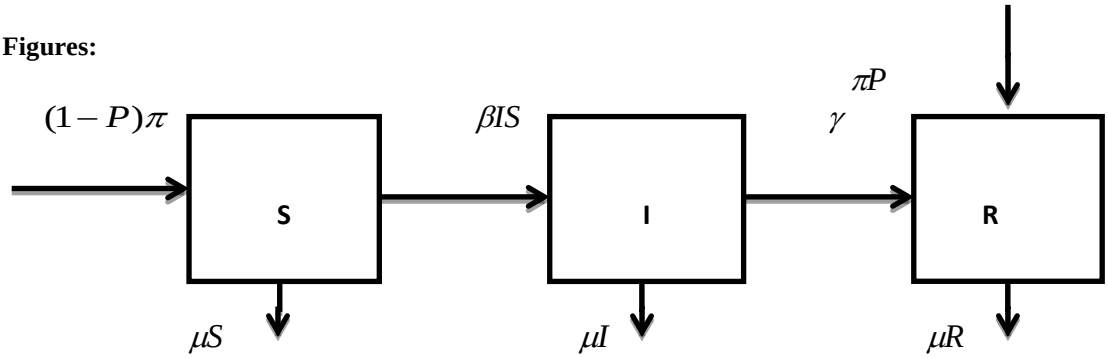

Fig. 1: Flow chart for the SIR model.

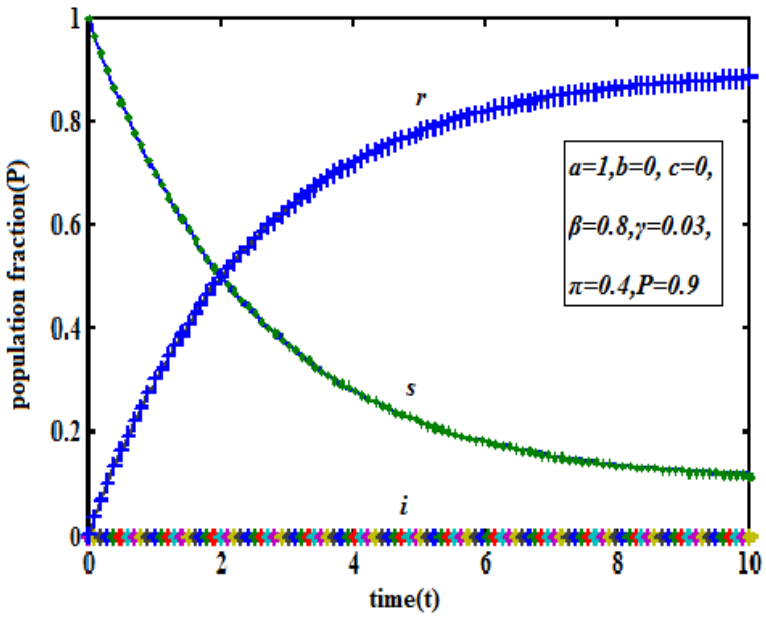

Fig.2: The effect of population fraction versus time for the various values of parameters. The key to the graph: (——) represents the analytical solution of the Eqs. (5)-(7). (…) represents the normalized susceptible group *s*; **(***)** represents the numerical result for normalized infected group *i*; and (+++) represents the numerical result for normalized removed group *r*.

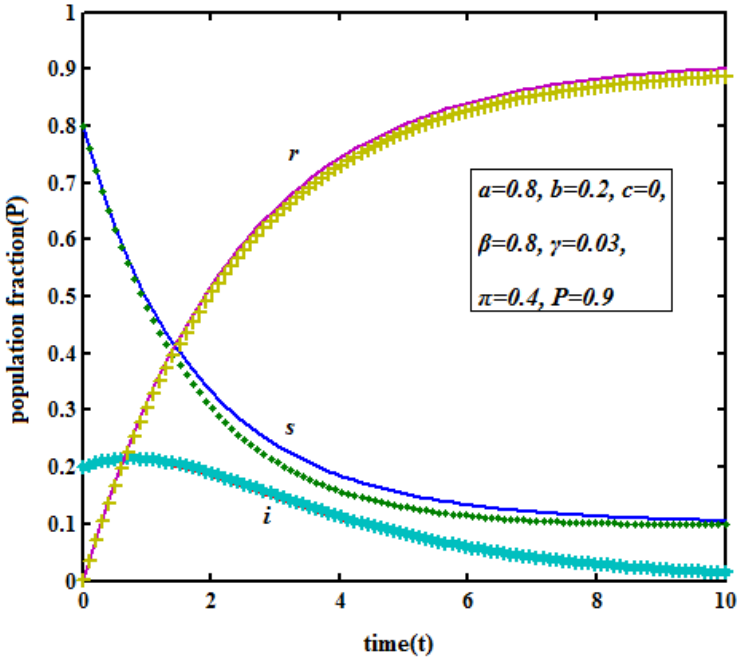

Fig.3: The effect of population fraction versus time for the various values of parameters. The key to the graph:(———) represents the analytical solution of the Eqs. (5)- (7). (…) represents the normalized susceptible group *s*; (***) represents the numerical result for normalized infected group *i*; and (+++) represents the numerical result for normalized removed group *r*.

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