

**Infective Susceptible Phase Plane Analysis in the Extended SIR Model-I**

N Suresh Rao

Department of Computer Centre /
 Computer Science and IT Block
 University of Jammu Jammu- J & K State, India
 suresh_jmu@yahoo.co.in

Abstract: In the present investigation an attempt is made to understand the I-S phase plane. Trajectories, using the solutions of the second order differential equation, describing the virus growth in the extended model of SIR covering immigration studies, are presented. The value of the ratio of product of immigrant rate and birth rate of virus to square of death rate of virus, greater than or equal to value four, plays a dominant role in deciding the nature of I-S trajectories. For same values of immigration rate, birth and death rates of virus the trajectories reach asymptotically the stable equilibrium point (ratio of death and birth rate of virus, ratio of immigration and death rate of virus) which is termed as a nodal sink. Effect of low and high values of death rate, birth rate and threshold value along with different population sizes is also illustrated therein.

Keywords: Immigration, SIR model, I-S phase plane, Virus Growth, Birth and death Rates, 2nd Order Differential equations.

I. INTRODUCTION

The concept of immigrants plays an important role in the field of demographic studies. The inflow of population has a tremendous impact on the socio-economic-environmental values on the existing conditions in a given population. Similarly in the study of epidemics, immigrants play a vital role. This can be understood by transmission of virus leading to new class of diseases e.g., HIV leading to AIDS [1]. It is needless to emphasize in the field of computers also, in view of similarities between computers and biological viruses, the immigrants (the influx of computers) play an important role on the growth and spread of virus. To carry out such studies, SIR (susceptible- infected-removed) model [2] is convenient when extended to the inclusion of immigrants at a constant rate in the prevailing system of computers. Such studies have been made in [3], [4]. In these studies the attention was paid mostly for the general understanding of spread and growth of virus in computers.

The particular study of infected susceptible phase plane analysis throws lot of light on the relative removal rate, basic reproduction rate, birth and cure rates of computer virus [5]. The theoretical implications of the analysis was explained in Appendix-I [6]. A simple and elegant method of solving the second order differential equation for the virus growth was given by extended model of SIR [7], where in one of the solutions leading to complex roots for the virus growth was dealt. Out of the other two solutions, where the roots are (i), real and distinct and (ii), real and equal, the situation (i) real and distinct roots is presented in this publication while the situation (ii) real and equal roots is going to appear in a forth coming publication. The subject matter is arranged as follows. In section II the methodology is described. In section III the results and discussions are presented where as in section IV, the conclusions are high lighted. Finally, references are given in section V.

II. METHODOLOGY

The basic SIR model involves three classes of systems namely susceptibles(S), infectives (I) and removed(R). Some susceptibles (immigrants) at a constant rate (k) into the system are introduced. Thus, the effect of immigrants on the spread and growth of virus was discussed in detail by [7]. The prominent equations governing the virus growth are given by:-

$$\frac{ds}{dt} = k - \beta SI; \frac{dI}{dt} = \beta SI - \gamma I; \frac{dR}{dt} = \gamma I \quad (1)$$

With the condition,

$$S + I + R = S_0 + I_0 + kt = N + kt \quad (2)$$

Where k stands for immigrant rate, β for birth rate, γ for death rate, S_0 , I_0 are initial values of S and I. N stands for population size. It may be noted that all the three derivatives in "(1)" cannot vanish simultaneously. We confine our discussion to the first two derivatives. Let S_E and I_E correspond to equilibrium solution. By setting the first two derivatives in "(1)" = 0 one can obtain the steady state/equilibrium solutions S_E and I_E . In general the values of S and I can be expressed in terms of S_E and I_E by introducing small departures ϵ and v respectively. The values of ϵ and v are so small so that their squares, higher powers, and product terms can be neglected. On substituting in "(1)" and simplifying, one can obtain relations amongst ϵ , v , $\frac{d\epsilon}{dt}$, and

$\frac{dv}{dt}$. In these relations with suitable substitution and

simplification one can eliminate ϵ . This exercise will result in a second order differential equation in v as

$$v'' + (k\beta/\gamma)v' + (k\beta)v = 0 \quad (3)$$

This can be solved by standard method. In doing so one comes across a discriminator

$$\omega = \sqrt{1/4 * (k\beta/\gamma)^2 - k\beta} \quad (4)$$

Details of the above procedure are given by [7].

The value of ω may be +ve, zero or -ve according to $(k\beta/\gamma^2) >, =, < 4$ respectively. Accordingly the roots are (i) real and distinct, (ii) real and equal, (iii) complex and unequal.

A. Roots are real and distinct:

In general the solution is given by

$$v = c_1 e^{m_1 t} + c_2 e^{m_2 t} \tag{5}$$

Where

$$m_1 = (-1/2) * (k\beta/\gamma) + \omega$$

$$\& m_2 = (-1/2) * k\beta/\gamma - \omega \tag{6}$$

c_1, c_2 are arbitrary constants which can be derived from initial conditions. Values of v and v' from “(5)” along with expression for $\frac{dI}{dt}$ in “(1)”, expression, $I = I_E(1+v)$, where

$I_E = k/\gamma$, and the equilibrium value of I at $t = 0$ are used to determine the arbitrary constants c_1 and c_2 . Hence v and thereby I are found as a function of time. Similarly the expressions, $\varepsilon = (1/\gamma)*v, S = S_E(1+\varepsilon)$ where $S_E = \gamma/\beta$, the equilibrium value of S , are used to determine the values of ε and thereby S as a function of time. One can also plot I vs S for different combinations of K, β and γ preserving the condition that $k\beta/\gamma^2 > 4$.

III. RESULTS AND DISCUSSIONS

In the present investigation the main interest is focused on the $I-S$ phase plane analysis. Thus out of the three coupled differential equations used, the first two are sufficient for discussion. Unlike SIR model, the $\frac{dS}{dt}$ equation is not a

continuously decreasing function. It has no lower bound limit. On the contrary it has i) a term, $-\beta SI$, representing the number of susceptibles getting converted into infectives and ii) a term, K , representing an inflow of immigrants at a constant rate. So depending on the initial values of S, I, β and K , there will be a competition between the said two terms. As a result $\frac{dS}{dt}$ will be increasing / decreasing. In the

second equation, $\frac{dI}{dt}$ will be +ve, 0, -ve as $S >, =, < \gamma/\beta$. The value of γ/β is termed as threshold value or effective removal rate (ρ). Thus increase/decrease of I with time depends on whether $S > \rho$ or $S < \rho$. It may be noted that at equilibrium state the two differential equations, $\frac{dS}{dt}$ and $\frac{dI}{dt}$ will be zero. Hence at equilibrium, the values for S & I will be equal to $S_E = \gamma/\beta$ and $I_E = k/\gamma$ respectively.

B. Roots are real and distinct:

According to the above prescriptions of the model different values of parameters, N, I_0, K, γ, β of the virus are chosen so that conditions needed for Sec: II-A are satisfied. Further two sets of values for (i) high γ, β and low ρ and

(ii) low γ, β and high ρ are considered. Obtain S and I , as a function of time. With appropriate choice of input parameters the effect of different values of γ (0.2 to 0.05) and β (0.04 to 0.0025) or in other words different values of ρ (5 to 20) and various population sizes ($N=51$ to 20,001) is studied, with respect to the virus growth and time taken to reach S_E & I_E , through numerical simulations. Out of the figures drawn and studied exhaustively, for I vs S ; S vs t and I vs t , two typical sets of data (A and B) as mentioned are considered. The relevant data is shown in Table 1 and the results are described below.

Table 1: Input parameters data

Set	Population Size (N)	γ	β	k	I_0
A	51,81,121,151,301,501,551,1001,2001.	0.2	0.04	5	1
B	51,101,501,1001,2001,3001,5001,7001,10001,15001,20001.	0.05	0.0025	5	1

While studying the, I vs S trajectories some distinct features are noted irrespective of γ and β , accordingly, they are classified into three different phases.

Phase I: In this phase the values of S increase from S_0 up to a maximum value. The trajectory takes a reversal i.e. S decreases and finally reaches the value S_E asymptotically. The value of S is $> S_E$. Thus I will be increasing from I_0 to I_E asymptotically.

Phase II: In this case S will be decreasing from the beginning i.e. S_0 and asymptotically attains the value S_E . Here again the value of S is $> S_E$ i.e. ρ . Thus I will be increasing from I_0 to I_E asymptotically.

Phase III: In this phase also S will be decreasing from S_0 , passes through S_E and enters -ve region for a while and then with a reversal enters +ve region and finally attains S_E and continues to remain there for all the times. It may be noted that the value of S , till it passes the ordinate at S_E , will be $> S_E$ and later on the value will be $< S_E$ till it sinks to the value S_E . For this region S will be $< \rho$. Thus I will increase to a maximum value and then will decrease exponentially and asymptotically attains the equilibrium value I_E . This feature is in accordance with the second differential equation of (1).

For clarity in resolution, the I vs S trajectories are shown in “Figs.1.1.1, 1.1.2 and 1.1.3” for $N=51, 81,121; 151,301,501; 551, 1001, 2001$ respectively in set A. These three diagrams represent the three phases of I vs S trajectories as explained already. Similarly I vs t is shown in “Fig 1.2” for selected values of $N =81, 301, 551, 1001$. The variation of S vs t for $N=81,301$ is shown in “Fig. 1.3.1” and for $N=551, 1001$ is shown in “Fig. 1.3.2”. The features exhibited in all the graphs are in accordance with the prescription of the model.

From the numerical values obtained for I and S as a function of time, it is noted that the time taken to attain I_E and S_E values is close to 50 unit time steps. Further the value of I_E is reached earlier compared to the value S_E . In order to have a feeling about the effect of low γ and β values, ρ is increased by a factor of 4 i.e. ρ is changed from 5 to 20. The values given in Table 1, for set A and set B may be compared.

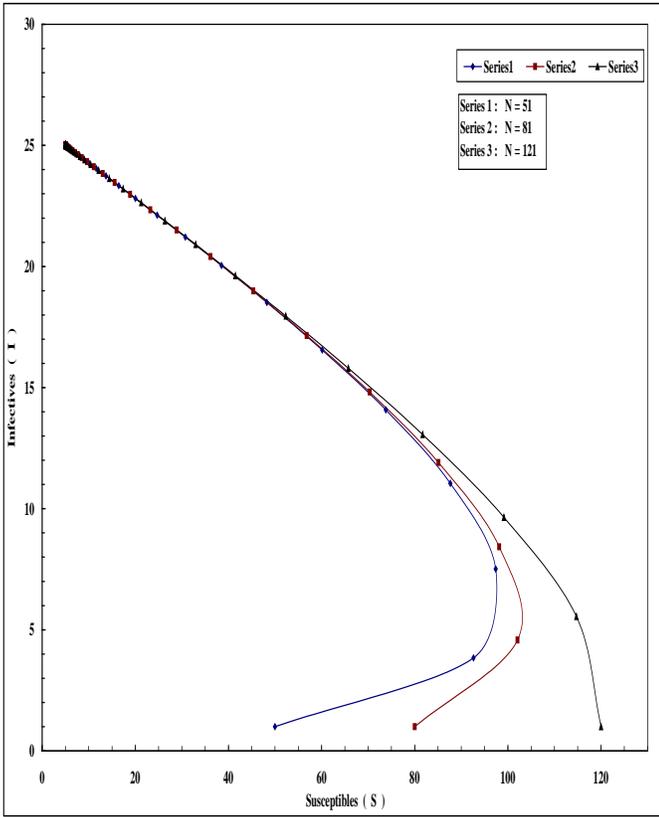


Figure 1.1.1: Infectives vs Susceptibles ($\omega > \text{zero}$)

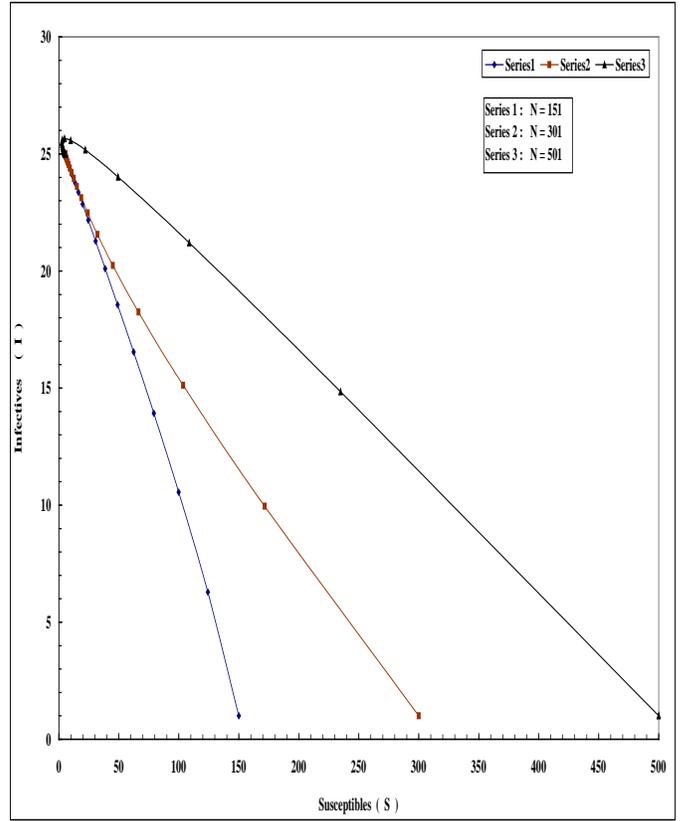


Figure 1.1.2: Infectives vs Susceptibles ($\omega > \text{zero}$)

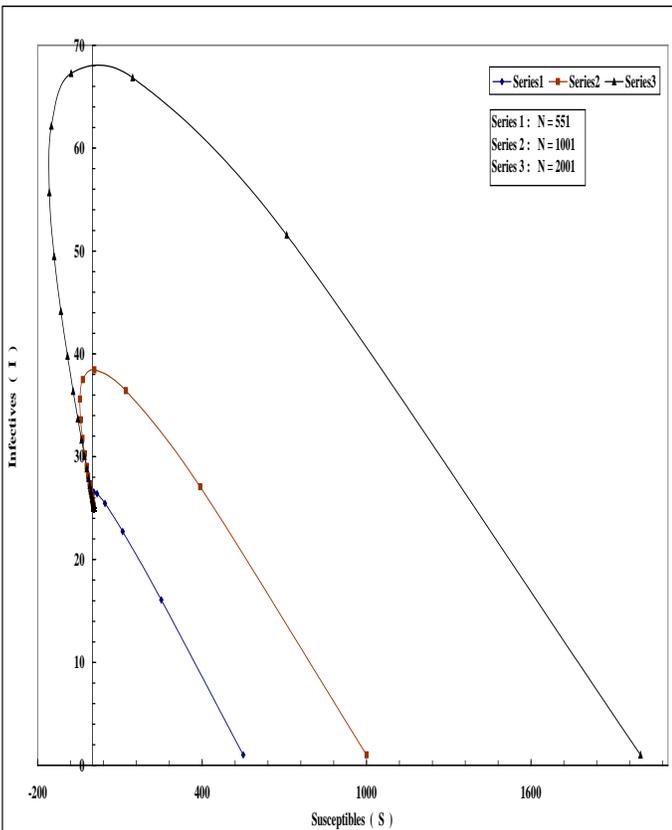


Figure 1.1.3: Infectives vs Susceptibles ($\omega > \text{zero}$)

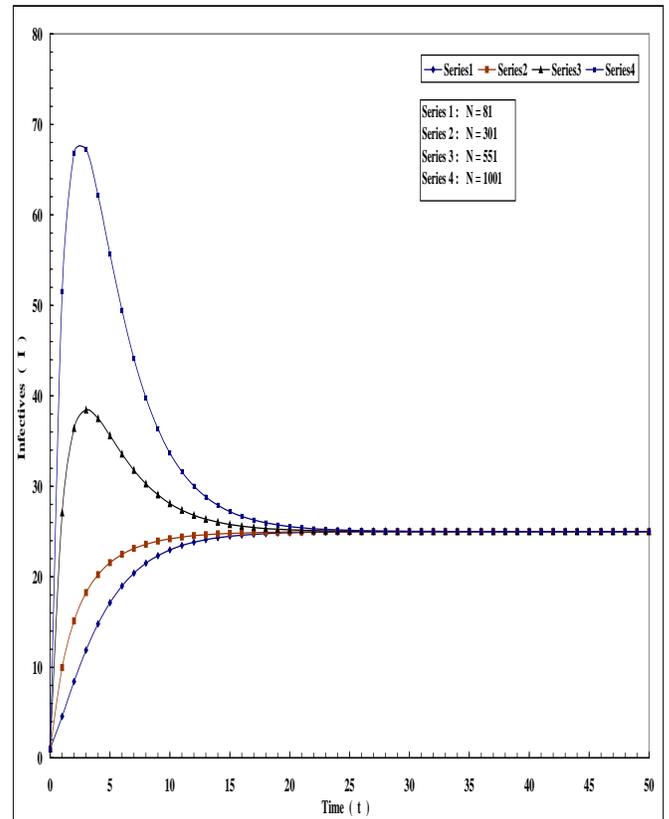


Figure 1.2: Infectives vs Time ($\omega > \text{zero}$)

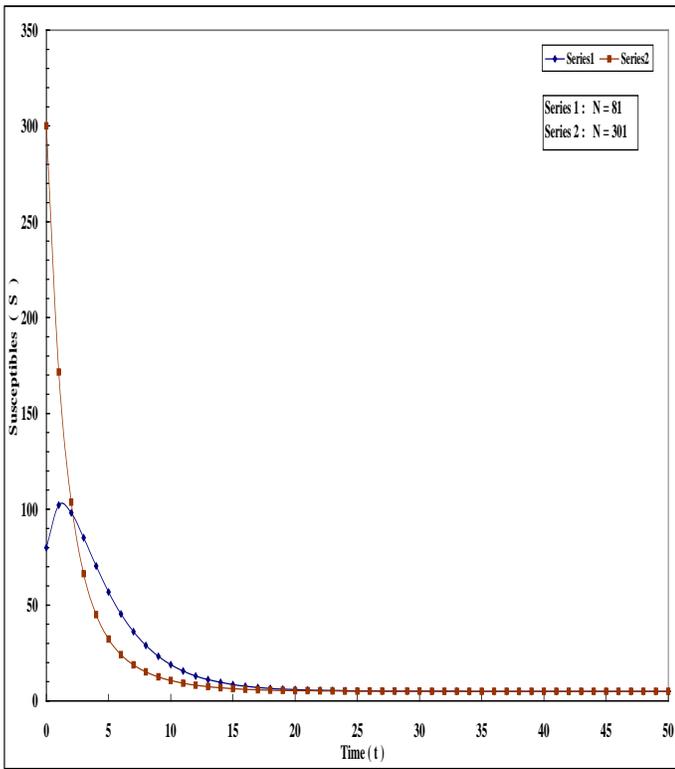


Figure 1.3.1: Susceptibles vs Time ($\omega > \text{zero}$)

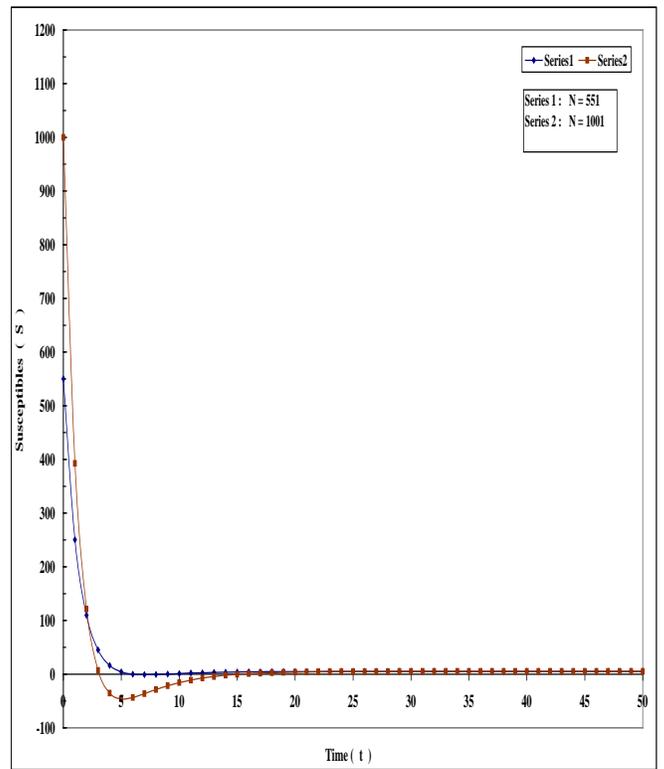


Figure 1.3.2: Susceptibles vs Time ($\omega > \text{zero}$)

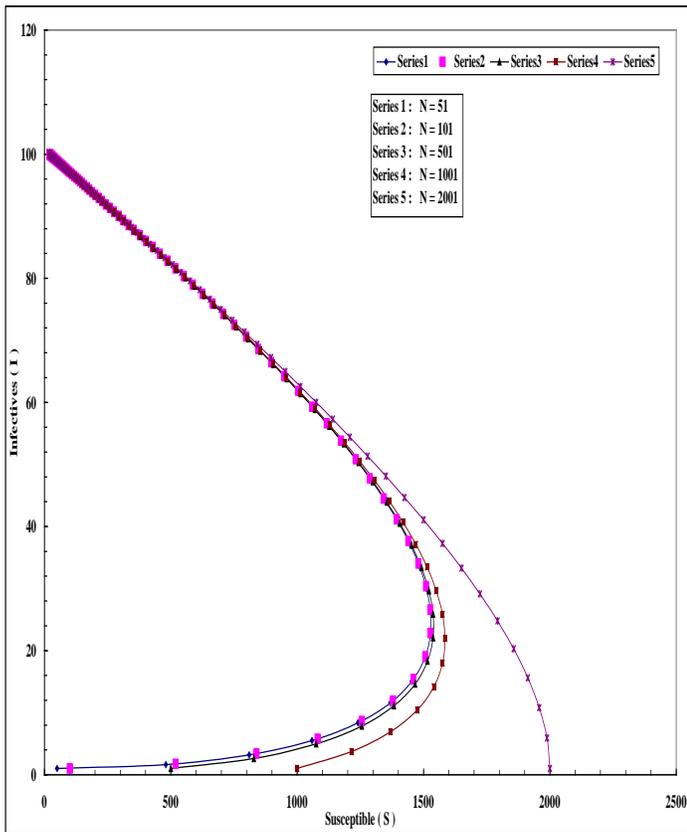


Figure 2.1.1: Infectives vs Susceptibles ($\omega > \text{zero}$)

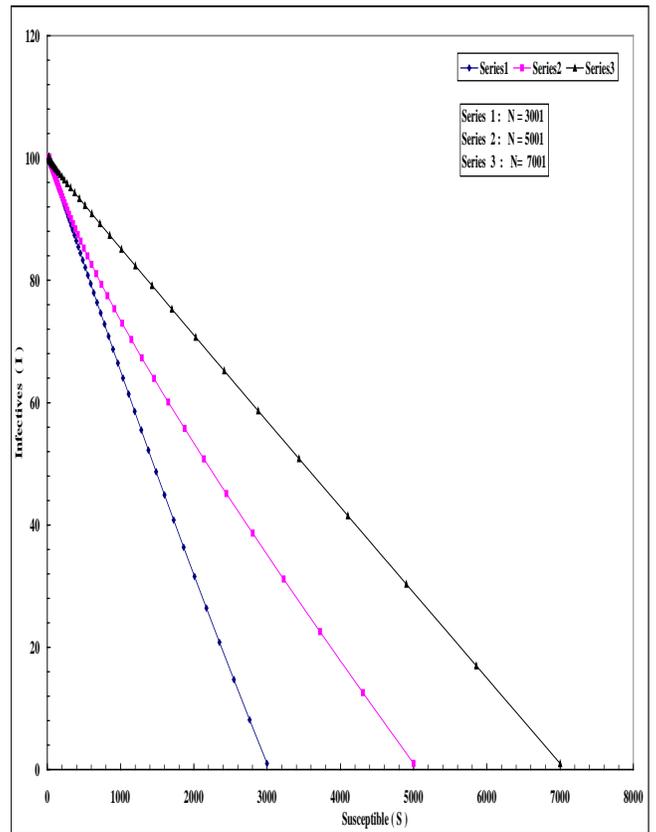


Figure 2.1.2: Infectives vs Susceptibles ($\omega > \text{zero}$)

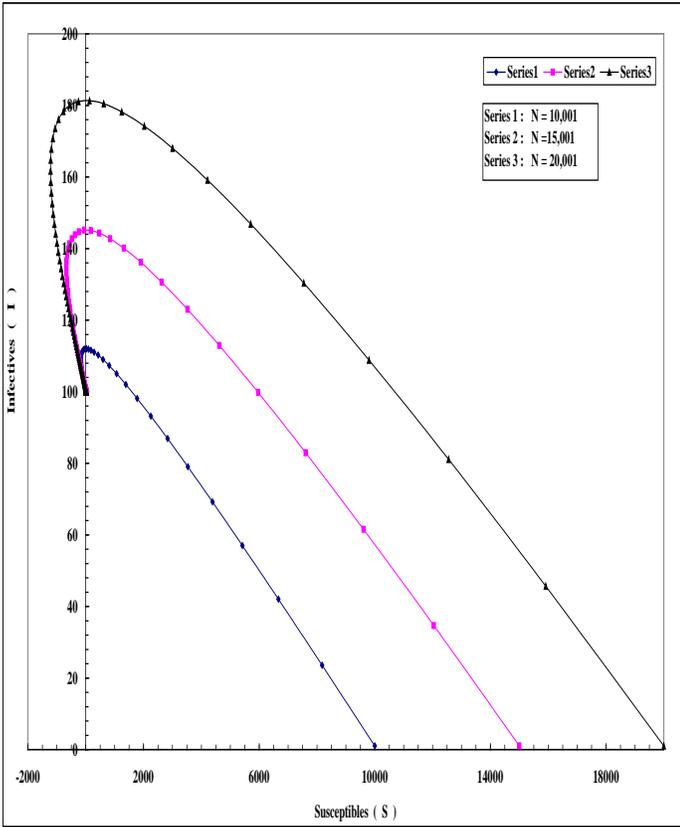


Figure 2.1.3: Infectives vs Susceptibles ($\omega > \text{zero}$)

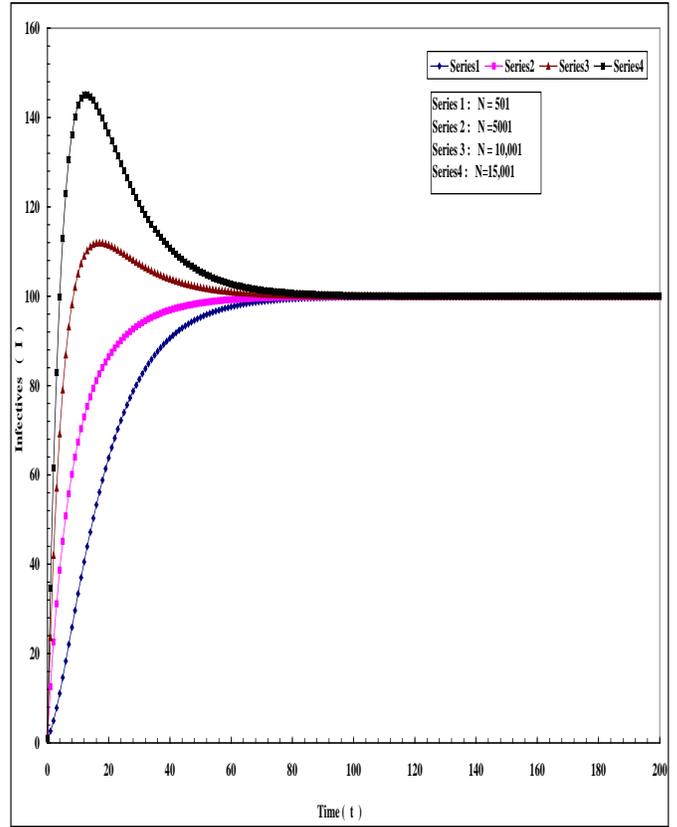


Figure 2.2: Infectives vs Time ($\omega > \text{zero}$)

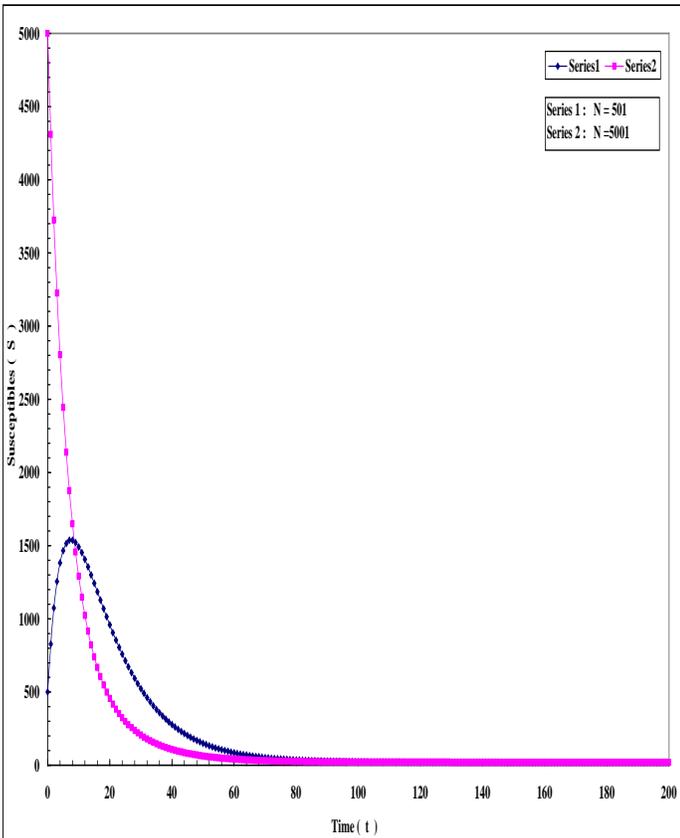


Figure 2.3.1: Susceptibles vs Time ($\omega > \text{zero}$)

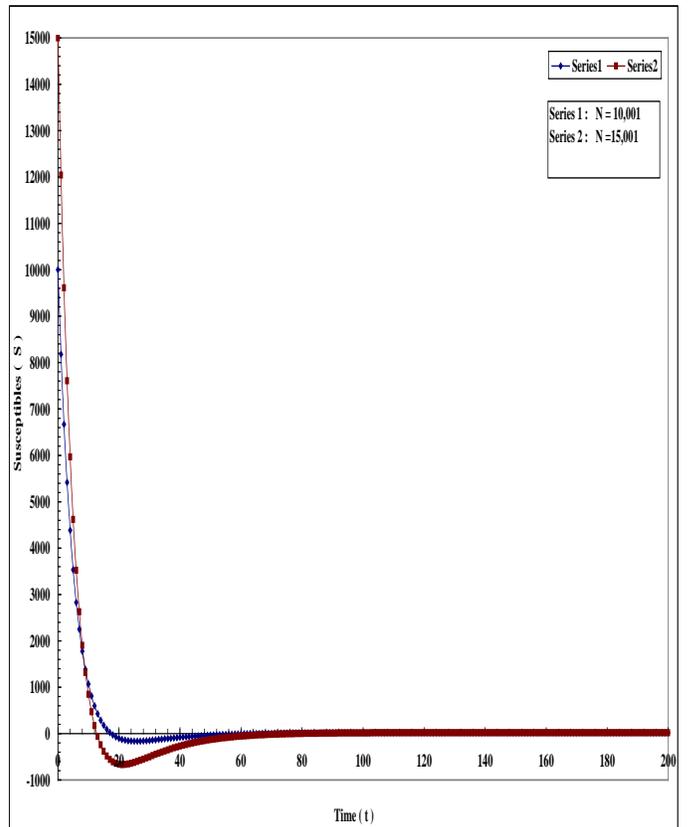


Figure 2.3.2: Susceptibles vs Time ($\omega > \text{zero}$)

Accordingly all the drawings for I vs S for N=51,101,501,1001,2001;3001,5001,7001;,10,001,15,001,20,001, I vs t for N=501,5001,10,001,15,001 and S vs t for N=501,5001;10,001,15,001 for set B are shown in “Figs.2.1.1, 2.1.2, 2.1.3; 2.2 and 2.3.1, 2.3.2” respectively. All the features as exhibited in “Fig.1” series are noted in “Figs. 2” series also. The corresponding population sizes at the transition of phases are enhanced e.g. for set A, the value of N is less than 121 for phase-I, lies between 151 to 501 for phase-II and greater than 551 for phase-III. Where as for the set B, the corresponding values are less than 2001 for Phase-I: for Phase-II limits are 3001 to 7001 and for phase-III the value is greater than 7001. Similarly the time taken to attain the equilibrium values for I and S is also enhanced to nearly 200 unit time steps. Again it is observed, that I attains the equilibrium value prior to that of S. Thus on comparing the results from set A to set B i.e. ρ from lower to higher value, one comes across higher values for population sizes and also time taken to reach equilibrium values for I and S. It can be verified that when ρ is increased by a factor of 4, the saturation times also increased by a similar factor. Thus it may be noted that higher the value of ρ slower is the growth of virus.

IV. CONCLUSIONS

In this investigation the term $k\beta/\gamma^2$ plays an important role in describing the nature of infection growth. Unlike SIR model there is no lower bound to S but it attains a stable equilibrium value, $S_E = \rho$, which is the threshold value. The Increasing / decreasing trend of S depends on the relative strengths of the terms, $-\beta SI$, k. The I value will not tend to zero but attains a stable equilibrium value for $I_E = k/\gamma$.

Variation of I depends on whether $S > \rho$ or $S \leq \rho$. For same values of k, γ and β , all trajectories in I-S phase plane reach the stable equilibrium point at (S_E, I_E) which is termed as nodal sink. It is observed that as the threshold value is increased, the time taken to reach equilibrium point (S_E, I_E) also increases indicating there by the slow rate for growth of virus.

V. REFERENCES

- [1]. H. J. Kim, “The continuous model for the transmission of HIV”, Research Project, Univ of Washington.2008.
- [2]. N. Suresh Rao, Devanand, P.S. Avadhani, “Propagation behavior of computer virus in the frame work of SIR model”, Journal of Comp.Sc, ICFAI, Vol .III, No 4, pp 1-11.,2009.
- [3]. E. Shim, “An epidemic model with immigration of infectives and vaccination”, M.S.Thesis, Univ of British Columbia.,2002.
- [4]. T.W.Huang, “A Mathematical model for infectious diseases-an extended SIR model”, Research Project, National Univ. Kaohsiung, Taiwan-811, R.O.C.,2008.
- [5]. E.A Allaman and J.A. Rhodes., “Mathematical models in Biology: An Introduction”, Cambridge Univ Press, 2004.
- [6]. J.D. Murray., “Mathematical Biology”, Springer-Verlag,3rd Edn, New York.,2002.
- [7]. N.Suresh Rao, “Influence of Immigration parameter for understanding growth of Computer Virus in SIR Model”, Journal of Computer science, ICFAI, Vol. VI, No.2, pp. 58-65, 2012.