Approximate Solution of SIR Infectious Disease Model Using Homotopy Perturbation Method (HPM).

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ABSTRACT

In this paper we proposed a SIR model for general infectious disease dynamics. The analytical solution is obtained using the Homotopy Perturbation Method (HPM). We used the MATLAB computer software package to obtain the graphical profiles of the three compartments while varying some salient parameters. The analysis revealed that the efforts at eradication or reduction of disease prevalence must always match or even supersede the infection rate.

(Keywords: SIR infectious disease, Homotopy Perturbation Method, HPM)

INTRODUCTION

Standard convention labels the three compartments; S (for susceptible), I (for infectious) and R (for recovered). Therefore, the model is called the SIR model.

The letters also represent the number of people in each compartment at a particular time. To indicate that the numbers might vary over time (even if the total population size remains constant), we make the precise numbers a function of *t* (time): S(*t*), I(*t*) and R(*t*). For a specific disease in a specific population, these functions may be estimated in order to predict possible outbreaks and bring them under control.

Kermack and McKendrick, (1927), proposed a model in which they considered a fixed population with only three compartments, susceptible: S(t), infected, I(t), and recovered, R(t).The compartments used for this model consist of three classes:

S(t) is used to represent the number of individuals not yet infected with the disease at time t, or those susceptible to the disease; I(t) denotes the number of individuals who have been infected with the disease and are capable of spreading the disease to those in the susceptible category; R(t) is the compartment used for those individuals who have been infected and then recovered from the disease. Those in this category are not able to be infected again or to transmit the infection to others.

As implied by the variable function of *t*, the model is dynamic in that the numbers in each compartment may fluctuate over time. The importance of this dynamic aspect is most obvious in an endemic disease with a short infectious period, such as measles. Such diseases tend to occur in cycles of outbreaks due to the variation in number of susceptibles (S(*t*)) over time. During an epidemic, the number of susceptible individuals falls rapidly as more of them are infected and thus enter the infectious and recovered compartments. The disease cannot break out again until the number of susceptible has built back up as a result of babies being born into the susceptible compartment.

Each member of the population typically progresses from susceptible to infectious to recovered. This can be shown as a flow diagram in which the boxes represent the different compartments and the arrows the transition between compartments.

Biazar and Aminikhah (2009) Solving nonlinear differential equations is an important issue in sciences because many physical phenomena are modeled using such equations. One of the most powerful methods to approximately solve

nonlinear differential equations is the homotopy perturbation method (HPM). The HPM method is based in the use of a power series, which transforms the original nonlinear differential equation into a series of linear differential equations. Two continuous functions from one topological space to another are called homotopic if one can be “continuously deformed" into the other, such a deformation being called a homotopy between the two functions. The Homotopy Perturbation Method (HPM), which provides analytical approximate solution, is applied to various linear and non-linear equations. He (1999). The homotopy perturbation method (HPM) is a series expansion method used in the solution of nonlinear partial differential equations. Jiya (2010). The method employs a homotopy transform to generate a convergent series solution of differential equations.

MATERIALS AND METHODS

The SIR Model

$$\frac{\mathrm{dS}}{\mathrm{dt}} = \beta N - \alpha SI - \mu \mathrm{S} \qquad (1.0)$$

$$\frac{dI}{dt} = \alpha SI - (\gamma + \delta + \mu)I \qquad (1.1)$$

$$\frac{dR}{dt} = \gamma I - \mu R \qquad (1.2)$$

Where
β= Natural Birth rate
α= contact rate
μ = Natural death rate
S = Susceptible Compartment
γ = Recovery rate
I = Infected Compartment
δ = Death rate due to disease
R = Immune/ Recovered Compartment

$$N = \mathrm{S} + \mathrm{I} + \mathrm{R}$$

In this work we set, N=1 , i.e. assuming a closed population for a given period of time.

Approximate Solution of the Model

Consider the system:

$$\frac{\mathrm{dS}}{\mathrm{dt}} + \alpha SI + \mu S - \beta = 0 \qquad (1.3)$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} - \alpha SI + (\gamma + \delta + \mu)I = 0 \qquad (1.4)$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} + \mu R - \gamma I = 0 \qquad (1.5)$$

With the initial conditions S(0) = S_0 , I(0) = I_0 and R(0) = R_0

Let

$$S = x_0 + px_1 + p^2 x_2 + \ldots \qquad (1.6a)$$

$$I = y_0 + py_1 + p^2 y_2 + \ldots \qquad (1.6b)$$

$$R = z_0 + pz_1 + p^2 z_2 + \ldots \qquad (1.6c)$$

Applying HPM to (1.3) we have:

$$(1-p)\frac{dS}{dt} + p\left[\frac{dS}{dt} + \alpha SI + \mu S - \beta\right] = 0 \qquad (1.7)$$

Substituting (1.6a) and (1.6b) into (1.7) and expanding we have:

$$\begin{aligned}&(1-p)\left(x_0' + px_1' + p^2 x_2' + \ldots\right)\\ &+ p\left\{\begin{aligned}&x_0' + px_1' + p^2 x_2' + \ldots\\ &+ \alpha\left(x_0 + px_1 + p^2 x_2 + \ldots\right)\left(y_0 + py_1 + p^2 y_2 + \ldots\right)\\ &+ \mu\left(x_0 + px_1 + p^2 x_2 + \ldots\right) - \beta\end{aligned}\right\} = 0\end{aligned}$$

Collecting the coefficients of powers of p we have

$$p^{\circ} : x_0' = 0 \qquad (1.8)$$

$$p^1 : x_1' + \alpha x_0 y_0 + \mu x_0 - \beta = 0 \qquad (1.9)$$

$$p^2 : x_2' + \alpha(x_0 y_1 + x_1 y_0) + \mu x_1 = 0 \quad (1.10)$$

Applying HPM to (1.4) we have:

$$(1-p)\frac{dI}{dt} + p\left[\frac{dI}{dt} - \alpha SI + (\gamma + \delta + \mu)I\right] = 0 \quad (1.11)$$

Substituting (1.6a) and (1.6b) into (1.11) and expanding we have:

$$\begin{aligned}&(1-p)(y_0' + py_1' + p^2 y_2' + \ldots)\\ &+ p\begin{bmatrix} y_0' + py_1' + p^2 y_2' + \ldots \\ -\alpha(x_0 + px_1 + p^2 x_2 + \ldots) \\ (y_0 + py_1 + p^2 y_2 + \ldots)\end{bmatrix}\\ &+ (\gamma + \delta + \mu)(y_0 + py_1 + p^2 y_2 + \ldots)\Big] = 0\end{aligned}$$

Collecting the coefficients of powers of p we have:

$$p^0 : y_0' = 0 \quad (1.12)$$

$$p^1 : y_1' - \alpha x_0 y_0 + (\gamma + \delta + \mu)y_0 = 0 \quad (1.13)$$

$$\begin{aligned}&p^2 : y_2' - \alpha(x_0 y_1 + x_1 y_0)\\ &+ (\gamma + \delta + \mu)y_1 = 0 \quad (1.14)\end{aligned}$$

Applying HPM to (1.5) we have:

$$(1-p)\frac{dR}{dt} + p\left[\frac{dR}{dt} + \mu R - \gamma I\right] = 0 \quad (1.15)$$

Substituting (1.6b) and (1.6c) into (1.15) and expanding we have:

$$\begin{aligned}&(1-p)(z_0' + pz_1' + p^2 z_2' + ..)\\ &+ p\begin{bmatrix} z_0' + pz_1' + p^2 z_2' + \ldots \\ +\mu(z_0 + pz_1 + p^2 z_2 + \ldots) \\ -\gamma(y_0 + py_1 + p^2 y_2 + ..)\end{bmatrix} = 0\end{aligned}$$

Collecting the coefficients of powers of p we have:

$$p^0 : z_0' = 0 \quad (1.16)$$

$$p^1 : z_1' + \mu z_0 - \gamma y_0 = 0 \quad (1.17)$$

$$p^2 : z_2' + \mu z_1 - \gamma y_1 = 0 \quad (1.18)$$

Solving (1.8), (1.9) and (1.10) we have:

$$\begin{aligned}S(t) &= S_0 + [(\beta - \alpha S_0 I_0 - \mu S_0)t]\\ &- \left\{\begin{matrix}\alpha S_0 I_0[\alpha S_0 - (\gamma + \delta + \mu)]\\ +(\beta - \alpha S_0 I_0 - \mu S_0)(\alpha I_0 + \mu)\end{matrix}\right\}\frac{t^2}{2} \quad (1.19)\end{aligned}$$

Solving (1.12), (1.13) and (1.14) we have:

$$\begin{aligned}I(t) &= I_0 + [\alpha S_0 - (\gamma + \delta + \mu)]I_0 t\\ &+ \left\{\begin{matrix}I_0[\alpha S_0 - (\gamma + \delta + \mu)]^2\\ +\alpha I_0(\beta - \alpha S_0 I_0 - \mu S_0)\end{matrix}\right\}\frac{t^2}{2} \quad (1.20)\end{aligned}$$

Solving (1.16), (1.17) and (1.18) we have:

$$\begin{aligned}R(t) &= R_0 + [(\gamma I_0 - \mu R_0)t]\\ &+ \left\{\gamma I_0\begin{bmatrix}\alpha S_0\\ -(\gamma + \delta + \mu)\end{bmatrix} - \mu(\gamma I_0 - \mu R_0)\right\}\frac{t^2}{2} \quad (1.21)\end{aligned}$$

Equations (1.19), (1.20) and (1.21) are the general solutions of (1.0), (1.1) and (1.2) respectively.

$$\begin{aligned}S(t) &= S_0 + [(\beta - \alpha S_0 I_0 - \mu S_0)t]\\ &- \left\{\begin{matrix}\alpha S_0 I_0[\alpha S_0 - (\gamma + \delta + \mu)]\\ +(\beta - \alpha S_0 I_0 - \mu S_0)(\alpha I_0 + \mu)\end{matrix}\right\}\frac{t^2}{2}\\ I(t) &= I_0 + [\alpha S_0 - (\gamma + \delta + \mu)]I_0 t\\ &+ \left\{\begin{matrix}I_0[\alpha S_0 - (\gamma + \delta + \mu)]^2\\ +\alpha I_0(\beta - \alpha S_0 I_0 - \mu S_0)\end{matrix}\right\}\frac{t^2}{2}\\ R(t) &= R_0 + [(\gamma I_0 - \mu R_0)t]\\ &+ \{\gamma I_0[\alpha S_0 - (\gamma + \delta + \mu)] - \mu(\gamma I_0 - \mu R_0)\}\frac{t^2}{2}\end{aligned}$$

RESULTS AND DISCUSSION

Tabular and Graphical Presentation of the Model Using MATLAB

This section shows the tables and graphs generated from the general solution of our Model (i.e. equation (1.19), (1.20) and (1.21) using the MATLAB software.

We use hypothetical values to generate the tables and graphs for low contracting rate and high contracting rate, respectively.

Table 1: Low Contracting Rate and High Recovery Rate (α= 0.001 and γ = 0.15).

t	S(t)	I(t)	R(t)
0	60.0000	25.0000	15.0000
1	57.9303	22.2628	18.2829
2	56.1212	19.8012	21.0816
3	54.5727	17.6152	23.3961
4	53.2848	15.7048	25.2264
5	52.2575	14.0700	26.5725
6	51.4908	12.7108	27.4344
7	50.9847	11.6272	27.8121
8	50.7392	10.8192	27.7056
9	50.7543	10.2868	27.1149
10	51.0300	10.0300	26.0400

Simulated result for β= 0.2, α= 0.001, δ= 0.01, μ= 0.015, γ = 0.15, S_0= 60, I_0= 25, R_0 = 15.

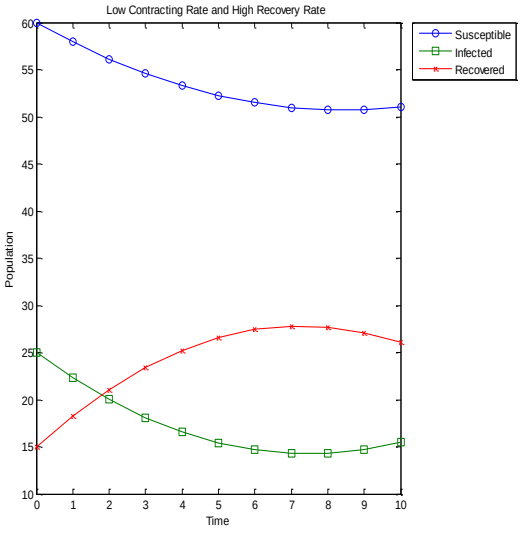

Figure 1: Graphical Profile for Low Contracting Rate and High Recovery Rate (α= 0.001 and γ = 0.15).

Table 2: High Contracting Rate and High Recovery Rate (α= 0.002 and γ = 0.15).

t	S(t)	I(t)	R(t)
0	60.0000	25.0000	15.0000
1	56.5028	23.5964	18.3954
2	53.4112	22.1357	21.5316
3	50.7252	20.6179	24.4086
4	48.4448	19.0429	27.0264
5	46.5700	17.4108	29.3850
6	45.1008	15.7215	31.4844
7	44.0372	13.9751	33.3246
8	43.3792	12.1715	34.9056
9	43.1268	10.3108	36.2274
10	43.2800	8.3930	37.2900

Simulated result for β= 0.2, α= 0.002, δ= 0.01, μ= 0.015, γ = 0.15, S_0= 60, I_0= 25, R_0 = 15.

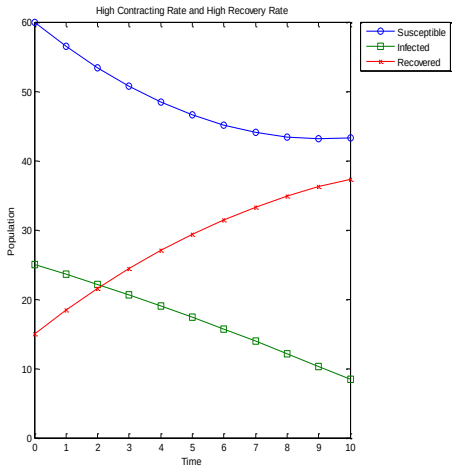

Figure 2: Graphical Profile for High Contracting Rate and High Recovery Rate (α= 0.002 and γ = 0.15).

DISCUSSION OF RESULTS

Table 1 and Figure 1 are for low contracting rate, α= 0.001 and high recovery rate, γ = 0.15.This shows that the population of susceptible and infected were decreasing, while the population of recovered was increasing, and this shows that as disease break out efforts are made to tackle the epidemics and over time the infected class will move to recovered class.

Table 3: Low Contracting Rate and Low Recovery Rate (α= 0.001 and γ = 0.1).

t	S(t)	I(t)	R(t)
0	60.0000	25.0000	15.0000
1	57.8927	23.4003	17.1767
2	55.9710	21.8512	19.1568
3	54.2347	20.3528	20.9402
4	52.6840	18.9050	22.5270
5	51.3188	17.5078	23.9172
6	50.1390	16.1612	25.1108
7	49.1448	14.8652	26.1078
8	48.3360	13.6198	26.9082
9	47.7128	12.4251	27.5119
10	47.2750	11.2810	27.9190

Simulated result for β= 0.2, α= 0.001, δ= 0.01, μ= 0.015, γ = 0.1, S_0= 60, I_0= 25, R_0 = 15.

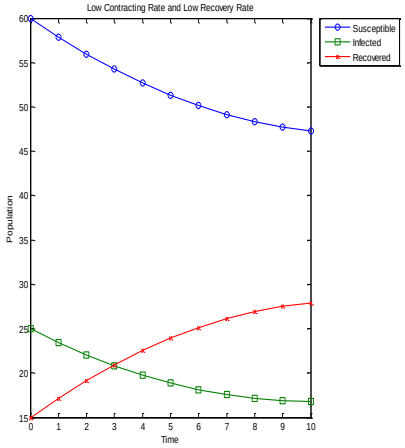

Figure 3: Graphical Profile for Low Contracting Rate and Low Recovery Rate (α= 0.001 and γ = 0.1).

Table 2 and Figure 2 are for the high contracting rate, α= 0.002 and high recovery rate, γ = 0.15. We can see from the graph that the susceptible and the infected population decreased more than when the contracting rate was low, but the population of recovered increased. The more people are infected the lesser the susceptible population and the more effort are required to eradicate the disease from the population.

Table 4: High Contracting Rate and Low Recovery Rate (α= 0.002 and γ = 0.1)

t	S(t)	I(t)	R(t)
0	60.0000	25.0000	15.0000
1	56.4278	24.8661	17.2517
2	53.1112	24.7142	19.4568
3	50.0502	24.5446	21.6152
4	47.2448	24.3570	23.7270
5	44.6950	24.1516	25.7922
6	42.4008	23.9282	27.8108
7	40.3622	23.6870	29.7828
8	38.5792	23.4280	31.7082
9	37.0518	23.1510	33.5869
10	35.7800	22.8562	35.4190

Simulated result for β= 0.2, α= 0.002, δ= 0.01, μ= 0.015, γ = 0.1, S_0= 60, I_0= 25, R_0 = 15.

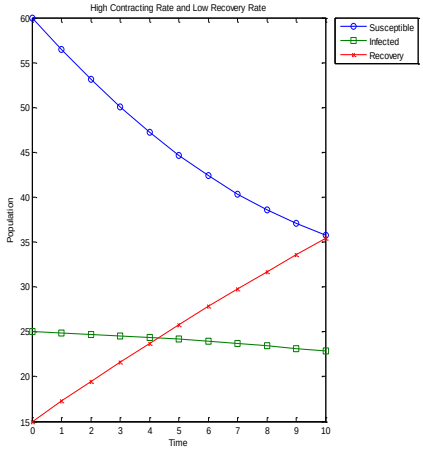

Figure 4: Graphical Profile for High Contracting Rate and Low Recovery rate (α= 0.002 and γ = 0.1).

Table 3 and Figure 3 are for the low contracting rate, α= 0.001 and low recovery rate, γ = 0.1. The graph show us that the population of recovered is not as high as when the contracting rate is high. This shows that when the disease is not much in population people are relaxed to combat the epidemics.

Table 4 and Figure 4 are for the high contracting rate, α= 0.002 and low recovery rate, γ = 0.1. The decrease in infected population was gradual compare to other results. This means people will suffer the disease for a long time before they are recovered.

CONCLUSION

The use of Homotopy Perturbation Method (HPM) had enabled us to get the approximate solution of the each compartment of the Model. The approximate solution was use to present the Model graphically, which gives us the better understanding of the infectious disease dynamics. It is obvious from our result that whether high or low contracting rate, the recovered population increases; though it increase more with high recovery rate. The number of recovered population depends on the contracting rate. It is clear that once the disease breakout, efforts are made to eradicate the disease from the society.

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