



ISSN 0972-0871



**Reprinted from the**

**Far East Journal of  
Mathematical Sciences (FJMS)  
Volume 84, Number 2, 2014, pp 187-198**

**HOMOTOPY PERTURBATION METHOD  
FOR A SEIR MODEL WITH VARYING  
TOTAL POPULATION SIZE**

*by*

Jaharuddin



**Pushpa Publishing House**

Vijaya Niwas, 198 Mumfordganj

Allahabad 211002, INDIA

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## HOMOTOPY PERTURBATION METHOD FOR A SEIR MODEL WITH VARYING TOTAL POPULATION SIZE

**Jaharuddin**

Department of Mathematics  
Bogor Agricultural University  
Jalan Meranti, Kampus IPB Dramaga  
Bogor 16680, Indonesia  
e-mail: jaharipb@yahoo.com

### Abstract

We consider a SEIR model with varying total population size. We find the analytical solution of the proposed model by homotopy perturbation method which is one of the best methods for finding the solution of the nonlinear problem. By using this method, we solve the problem analytically and then compare the numerical result with other standard methods. We also justify the numerical simulation and their results. The comparison reveals that our approximate solutions are in very good agreement with those by numerical method. Moreover, the results show that the proposed method is a more reliable, efficient and convenient one for solving the nonlinear differential equations.

### 1. Introduction

Mathematical modelling has become important tools in analyzing the spread and control of infectious diseases. The model helps us to understand different factors such as the transmission and recovery rates and to predict

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Received: November 20, 2013; Accepted: January 10, 2014

2010 Mathematics Subject Classification: 34A25, 34A34, 41A10, 92D25.

Keywords and phrases: epidemic models, homotopy perturbation method, system of nonlinear differential equation.

how the diseases will spread over a period of time [1]. In recent years, many attempts have been made to develop realistic mathematical models for investigating the transmission dynamic of infectious diseases. One of them is a model of epidemic which is usually given as a system of differential equations. To understand the behavior of epidemic model, we need to know the analysis of steady state and their stability [8]. Studies of epidemic models that incorporate disease caused death and varying total population have become one of the important areas in the mathematical theory of epidemiology. Most of the research literatures on these types of models assume that the disease incubation is negligible so that once infected, each susceptible individual instantaneously becomes infected and later recovered with a permanent or temporary acquired immunity. A compartmental model based on these assumptions is customarily called a *SIR model*. Models that are more general than the SIR types need to be studied to investigate the role of incubation in disease transmission [10]. Using a compartmental approach, one may assume that a susceptible individual first goes through a latent period after infection before becoming infected. The resulting models are of SEIR types depending on whether the acquired immunity is permanent or otherwise. In this article, the SEIR model with varying total population size will be discussed and this model is in the form of nonlinear.

We know that except a limited number of these problems, most of them do not have analytical solution. Therefore, these nonlinear equations should be solved using other methods. Some of them are solved using numerical techniques. In the numerical method, stability and convergence should be considered so as to avoid divergence or inappropriate result. In the analytical perturbation method, we should exert the small parameter in the equation. Therefore, finding the small parameter and exerting it into the equation are difficulties of this method. Many different mathematical methods have been recently introduced to eliminate the small parameter. In 1992, Liao [9] has proposed a new analytical method called the *homotopy analysis method*, which introduce an embedding parameter to construct a homotopy and then analyzes it by means of Taylor formula. Therefore, unlike the perturbation

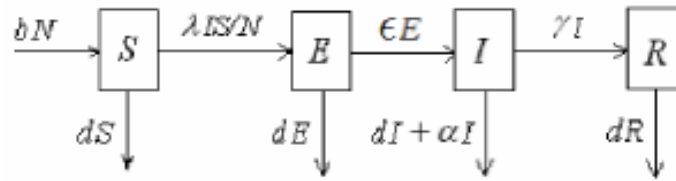
method, this method is independent of small parameters and can overcome the restrictions of the perturbation methods. The homotopy perturbation method provides a universal technique to introduce a perturbative parameter. This method has been introduced in 1999 by He [6] and was further developed and improved by him [4]. The method has been used by many authors [3] in a wide variety of scientific and engineering applications to solve different types of governing differential equations. In this paper, the basic idea of the homotopy perturbation method is introduced and then, the nonlinear equation of SEIR model is solved through the homotopy perturbation method. The purpose of this paper is to extend the homotopy perturbation method for computing the approximate analytical solution of a SEIR model with varying total population size and then see how these solutions compare with the solutions by numerical method.

This paper is organized as follows: Sections 2 and 3 are devoted to a short description of the SEIR models with varying total population size and the analysis of homotopy perturbation method, respectively. In Section 4, we present the analytical approximate solutions obtained by implementing the homotopy perturbation method to the SEIR model with varying total population size followed by comparison of results between the approximate solutions and the solutions obtained by numerical method. The last section is conclusion.

## 2. Mathematical Formulation

Formulation of SEIR model with varying total population size using by a compartmental approach is given by Li and Fang [7]. It is assumed that the local density of the total population is a constant. A population of size  $N(t)$  is partitioned into subclasses of individuals who are susceptible, exposed (infected but not yet infectious), infectious and recovered, with sizes denoted by  $S(t)$ ,  $E(t)$ ,  $I(t)$ , and  $R(t)$ , respectively. The sum  $E(t) + I(t)$  is the total infected population. Our assumptions on the dynamical transfer of the population are then demonstrated in the form of SEIR model as depicted by Figure 1.





**Figure 1.** A schematic representation of the flow of individuals between epidemiological classes.

The parameter  $b > 0$  is the constant rate for natural birth and  $d > 0$  is that of natural death. It is assumed that all newborns are susceptible and vertical transmission can be neglected. The parameter  $\alpha$  is the constant rate for disease-related death and  $\gamma$  is the rate for recovery. The rate of removal  $\varepsilon$  of individuals from the exposed class is assumed to be a constant so that  $1/\varepsilon$  can be regarded as the mean latent period. In the limiting case, when  $\varepsilon \rightarrow \infty$ , or equivalently, when the mean latent period  $1/\varepsilon \rightarrow 0$ , the SEIR model becomes a SIR model. The recovered individuals are assumed to acquire permanent immunity; there is no transfer from  $R$  class back to the  $S$  class. The per capita contact rate  $\lambda$ , which is the average number of effective contacts with other individual hosts per unit time, is then a constant. A fraction  $I(t)/N(t)$  of these contacts is with infectious individuals and thus the average number of relevant contacts of each individual with the infectious class is  $\lambda I(t)/N(t)$ . The total number of new infections at a time  $t$  is given by  $\lambda I(t)S(t)/N(t)$ . The following differential equations are derived based on the basic assumption and using the transfer diagram:

$$\begin{aligned}\frac{dS}{dt} &= bN - dS - \frac{\lambda IS}{N}, \\ \frac{dE}{dt} &= \frac{\lambda IS}{N} - (\varepsilon + d)E, \\ \frac{dI}{dt} &= \varepsilon E - (\gamma + \alpha + d)I, \\ \frac{dR}{dt} &= \gamma I - dR,\end{aligned}\tag{1}$$

subject to the initial conditions

$$S(0) \geq 0, E(0) \geq 0, I(0) \geq 0, R(0) \geq 0.$$

The total population size  $N(t)$  can be determined by  $N(t) = S(t) + E(t) + I(t) + R(t)$  or from the differential equation

$$\frac{dN}{dt} = (b - d)N - \alpha I, \quad (2)$$

which is derived by adding the equations in (1).

### 3. Analysis of Method

In this section, we illustrate the basic idea of the homotopy perturbation method for solving nonlinear differential equation in which we consider the following general nonlinear problem:

$$A(u(r)) = 0, \quad r \in \Omega, \quad (3)$$

where  $A$  is a nonlinear operator,  $u(r)$  is an unknown function,  $r$  is an independent variable, and  $\Omega$  is the domain. We construct a homotopy  $v(r, p) : \Omega \times [0, 1] \rightarrow \mathbb{R}$  which satisfies

$$H(v, p) = (1 - p)(L(v) - L(v_0)) + pA(v),$$

where  $p \in [0, 1]$  is an embedding parameter,  $L$  denotes an auxiliary linear operator and  $v_0$  is an initial approximation of the exact solution. By equating to zero the homotopy function, the zero-order deformation equation is constructed as

$$(1 - p)(L(v) - L(v_0)) + pA(v) = 0. \quad (4)$$

Setting  $p = 0$ , the zero-order deformation equation (4) becomes

$$L(v) - L(v_0) = 0. \quad (5)$$

Using (5), by linearity

$$v(r, 0) = v_0(r).$$

When  $p = 1$ , the zero-order deformation equation (4) is reduced to

$$A(v(r, 1)) = 0,$$

which is exactly the same as the nonlinear equation (3), provided  $v(r, 1) = u(r)$ .

According to the homotopy perturbation method, the solution of the equation (4) can be expressed as a series in  $p$  in the form:

$$v = v_0 + pv_1 + p^2v_2 + \dots \quad (6)$$

When  $p \rightarrow 1$ , equation (4) corresponds to the original equations (3) and (6) becomes the approximate solution of equation (3), i.e.,

$$u = \lim_{p \rightarrow 1} v = v_0 + v_1 + v_2 + \dots \quad (7)$$

The convergence of the series in equation (7) is discussed by He in [5].

#### 4. Application of Method

In this section, the homotopy perturbation method described in the previous section for solving a SEIR model with varying total population size is applied. Then comparison is made with the numerical method to assess the accuracy and the effectiveness of the homotopy perturbation method. The first step is to transform the variables.

Let  $s = S/N$ ,  $e = E/N$ ,  $i = I/N$ , and  $r = R/N$  denote the fractions of the classes  $S$ ,  $E$ ,  $I$ , and  $R$  in the population, respectively. It is easy to verify that  $s$ ,  $e$ ,  $i$ , and  $r$  satisfy the system of differential equations:

$$\frac{ds}{dt} = b - bs - \lambda is + \alpha is,$$

$$\frac{de}{dt} = \lambda is - (\varepsilon + b)e + \alpha ie,$$

$$\frac{di}{dt} = \varepsilon e - (\gamma + \alpha + b)i + \alpha i^2,$$

$$\frac{dr}{dt} = \gamma i - br + \alpha ir, \quad (8)$$

subject to the restriction  $s + e + i + r = 1$ . Note that the total population size  $N(t)$  does not appear in (8); this is a direct of the homogeneity of the system (8). Also observe that the variable  $r$  does not appear in the first three equations of (8). This allows us to attack (8) by studying the subsystem:

$$\begin{aligned} \frac{ds}{dt} &= b - bs - \lambda is + \alpha is, \\ \frac{de}{dt} &= \lambda is - (\varepsilon + b)e + \alpha ie, \\ \frac{di}{dt} &= \varepsilon e - (\gamma + \alpha + b)i + \alpha i^2, \end{aligned} \quad (9)$$

and determining  $r$  from  $r = 1 - s - e - i$  or

$$\frac{dr}{dt} = \gamma i - br + \alpha ir.$$

Subsystem (9) will be solved by generalizing the described homotopy perturbation method. The linear operators  $L_1$ ,  $L_2$ , and  $L_3$  can be defined as below:

$$L_1(s) = \frac{ds}{dt}, \quad L_2(e) = \frac{de}{dt}, \quad L_3(i) = \frac{di}{dt}.$$

From (9) nonlinear operators  $A_1$ ,  $A_2$ , and  $A_3$  can be defined as

$$A_1(s) = \frac{ds}{dt} - b + bs + \lambda is - \alpha is,$$

$$A_2(e) = \frac{de}{dt} - \lambda is + (\varepsilon + b)e - \alpha ie,$$

$$A_3(i) = \frac{di}{dt} - \varepsilon e + (\gamma + \alpha + b)i - \alpha i^2.$$

According to equation (4), we can obtain

$$\begin{aligned}
 (1-p)\left(\frac{ds}{dt} - \frac{ds_0}{dt}\right) + p\left(\frac{ds}{dt} - b + bs + \lambda is - \alpha is\right) &= 0, \\
 (1-p)\left(\frac{de}{dt} - \frac{de_0}{dt}\right) + p\left(\frac{de}{dt} - \lambda is + (\varepsilon + b)e - \alpha ie\right) &= 0, \\
 (1-p)\left(\frac{di}{dt} - \frac{di_0}{dt}\right) + p\left(\frac{di}{dt} - \varepsilon e + (\gamma + \alpha + b)i - \alpha i^2\right) &= 0, \quad (10)
 \end{aligned}$$

and the initial approximations are as follows:

$$s_0(t) = s(0), \quad e_0(t) = e(0), \quad i_0(t) = i(0).$$

In the following we assume the solution for system (10) in the form:

$$\begin{aligned}
 s &= s_0 + ps_1 + p^2s_2 + p^3s_3 + \dots, \\
 e &= e_0 + pe_1 + p^2e_2 + p^3e_3 + \dots, \\
 i &= i_0 + pi_1 + p^2i_2 + p^3i_3 + \dots. \quad (11)
 \end{aligned}$$

Substituting equation (11) into (10) and equating the term with identical powers of  $p$ , we obtain the set of initial value problems. Coefficient of  $p$  gives the following initial value problem:

$$\begin{aligned}
 \frac{ds_1}{dt} &= b - bs_0 - (\lambda - \alpha)i_0s_0, \\
 \frac{de_1}{dt} &= \alpha i_0e_0 + \lambda i_0s_0 - (\varepsilon + b)e_0, \\
 \frac{di_1}{dt} &= \varepsilon e_0 - (\gamma + \alpha + b)i_0 + \alpha i_0^2,
 \end{aligned}$$

with initial conditions:  $s_1(0) = 0$ ,  $e_1(0) = 0$ ,  $i_1(0) = 0$ . Solving the above equations, we obtain the following approximations:

$$s_1 = [b - bs_0 - (\lambda - \alpha)i_0s_0]t,$$

$$e_1 = [\alpha i_0 e_0 + \lambda i_0 s_0 - (\varepsilon + b)e_0]t,$$

$$i_1 = [\varepsilon e_0 - (\gamma + \alpha + b)i_0 + \alpha i_0^2]t.$$

Coefficient of  $p^2$  gives the following initial value problem:

$$\frac{ds_2}{dt} = -bs_1 - (\lambda - \alpha)(i_0 s_1 + i_1 s_0),$$

$$\frac{de_2}{dt} = \lambda(i_1 s_0 + i_0 s_1) + \alpha(i_0 e_1 + i_1 e_0) - (\varepsilon + b)e_1,$$

$$\frac{di_2}{dt} = \varepsilon e_1 + (\gamma + \alpha + b)i_1 + 2\alpha i_0 i_1,$$

with initial conditions:  $s_2(0) = 0$ ,  $e_2(0) = 0$ ,  $i_2(0) = 0$ . Solving the above equations, we obtain the following approximations:

$$\begin{aligned} s_2 = & -\frac{1}{2}b[b - bs_0 - (\lambda - \alpha)i_0 s_0]t^2 \\ & - (\lambda - \alpha)\left[\frac{1}{2}i_0(b - bs_0 - (\lambda - \alpha)i_0 s_0)t^2\right. \\ & \left. + \frac{1}{2}[\varepsilon e_0 - (\gamma + \alpha + b)i_0 + \alpha i_0^2]s_0 t^2\right], \\ e_2 = & \frac{1}{2}\lambda[\varepsilon e_0 - (\gamma + \alpha + b)i_0 + \alpha i_0^2]s_0 t^2 + \frac{1}{2}\lambda i_0[b - bs_0 - (\lambda - \alpha)i_0 s_0]t^2 \\ & + \frac{1}{2}\alpha i_0[\alpha i_0 e_0 + \lambda i_0 s_0 - (\varepsilon + b)e_0]t^2 \\ & + \frac{1}{2}\alpha[\varepsilon e_0 - (\gamma + \alpha + b)i_0 + \alpha i_0^2]e_0 t^2 \\ & - \frac{1}{2}(\varepsilon + b)[\alpha i_0 e_0 + \lambda i_0 s_0 - (\varepsilon + b)e_0]t^2, \\ i_2 = & \frac{1}{2}\varepsilon[\alpha i_0 e_0 + \lambda i_0 s_0 - (\varepsilon + b)e_0]t^2 \\ & + \frac{1}{2}(\gamma + \alpha + b)[\varepsilon e_0 - (\gamma + \alpha + b)i_0 + \alpha i_0^2]t^2 \\ & + \alpha i_0[\varepsilon e_0 - (\gamma + \alpha + b)i_0 + \alpha i_0^2]t^2, \end{aligned}$$

and so on, in the same manner the rest of the components can be obtained using the symbolic package. According to the homotopy perturbation method, we can obtain the solution in a series formed as follows:

$$\begin{aligned} s &= s_0 + s_1 + s_2 + \dots, \\ e &= e_0 + e_1 + e_2 + \dots, \\ i &= i_0 + i_1 + i_2 + \dots. \end{aligned} \tag{12}$$

Suppose given the following data: the initial number of susceptible individual in the location  $S(0) = 10$  thousand; the initial number of expose people  $E(0) = 1$  thousand; initial number of actively infected people  $I(0) = 0$ ; The parameter values used for numerical simulation is given in Table 1.

**Table 1.** Values used in the numerical simulation [2]

|               |  |         |
|---------------|--|---------|
| $\lambda$     | The parameter controlling how often a susceptible-infected contact results in a new exposure | 0.05    |
| $\gamma$      | The rate an infected recovers and moves into the resistant phase                             | 0.003   |
| $\varepsilon$ | The rate at which an exposed person becomes infective  | 0.05    |
| $b$           | The natural birth rate   | 0.00001 |
| $\alpha$      | The rate for diseases related death  | 0.002   |

Then following approximate solution is obtained as result of first 6 terms of the series decomposition (12). Results calculated by homotopy perturbation method are compared with numerical solution in Table 2. The explicit Runge-Kutta method in symbolic computation package has been used to find numerical solution of  $s(t)$ ,  $e(t)$ , and  $i(t)$ . As it can be seen in Table 2, there exists a very good agreement between homotopy perturbation method result and numerical solutions.

**Table 2.** Comparison between absolute error of homotopy perturbation method (HPM) and numerical method (NM)

| $t$ | $ s(t)_{HPM} - s(t)_{NM} $ | $ e(t)_{HPM} - e(t)_{NM} $ | $ i(t)_{HPM} - i(t)_{NM} $ |
|-----|----------------------------|----------------------------|----------------------------|
| 0   | 0                          | 0                          | 0                          |
| 0.1 | $3.0000 \times 10^{-10}$   | $3.6000 \times 10^{-10}$   | $2.2769 \times 10^{-7}$    |
| 0.2 | $2.7000 \times 10^{-9}$    | $2.7600 \times 10^{-9}$    | $9.1061 \times 10^{-7}$    |
| 0.3 | $8.9000 \times 10^{-9}$    | $9.3200 \times 10^{-9}$    | $2.0485 \times 10^{-6}$    |
| 0.4 | $2.1200 \times 10^{-8}$    | $2.2050 \times 10^{-8}$    | $3.6413 \times 10^{-6}$    |
| 0.5 | $4.1500 \times 10^{-8}$    | $4.3010 \times 10^{-8}$    | $5.6887 \times 10^{-6}$    |
| 0.6 | $7.1600 \times 10^{-8}$    | $7.4700 \times 10^{-8}$    | $8.1902 \times 10^{-6}$    |
| 0.7 | $1.1400 \times 10^{-7}$    | $1.1922 \times 10^{-7}$    | $1.1146 \times 10^{-5}$    |
| 0.8 | $1.7040 \times 10^{-7}$    | $1.7842 \times 10^{-7}$    | $1.4554 \times 10^{-5}$    |
| 0.9 | $2.4260 \times 10^{-7}$    | $2.5412 \times 10^{-7}$    | $1.8418 \times 10^{-5}$    |
| 1   | $3.3290 \times 10^{-7}$    | $3.4813 \times 10^{-7}$    | $2.2734 \times 10^{-5}$    |

## 5. Conclusions

In this paper, homotopy perturbation method has been successfully applied to find the solution of the SEIR model with varying total population size. The method is reliable and easy to use. The main advantage of the method is the fact that it provides its user with an analytical approximation, in many cases an exact solution, in a rapidly convergent sequence with elegantly computed term.

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