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Abstract. The spread of MERS-Cov disease which was modelled by Susceptible Exposed Infected Recovered (SEIR) model has been solved by a reliable method so-called Homotopy Analysis Method (HAM). The solution using HAM is done by constructing the zero order deformation equation of SEIR model into a high order equation and selecting the convergence control ($\hbar$). The closeness of HAM and Fourth order Runge Kutta (RK4) solutions and also the existence of residual error showa benchmark of the success of the HAM. The result shows that the minimum errors of the closeness of HAM and fourth order Runge Kutta (RK4) solutions are 10^{-7}while the minimum residual error of HAM solutions are10^{-18}. Therefore, HAM has successfully obtained solution of SEIR model approximately. Overall, HAM can be an alternative method for solving more complex models.

1. Introduction

Middle East Respiratory Syndrome-Corona Virus (MERS-CoV) is a respiratory syndrome caused by a corona virus that attacks the respiratory tract from mild to severe [1]. Based on the World Health Organization (WHO) information, MERS-CoV disease firstly was identified in April 2012 at Saudi Arabia. From 2506 laboratories have reported MERS-CoV cases with a death toll of 862 or 34.4% from 27 nations [2].Due to the large number of deaths, WHO appealed to every country in the world to stay alert and ready for this disease.

The spread of MERS-CoV disease was modelled into systems of non-linear differential equations. For the first time, the MERS-CoV disease was modeled by Chowell et al. [3] with the Susceptible Exposed Asymptomatic Infected Hospitalized Recovered model (SEAIHR). Xia, et al. [4] built a Susceptible Exposed Asymptomatic Infected Hospitalized Recovered (SEAIHR) model for the spread of MERS-CoV disease in the Republic of Korea. The model indicated that the disease spread quickly due to insufficient control measures and other reasons. In the same year, Kim et al. [5] discussed the Susceptible Exposed Infected Recovered (SEIR) model of the spread of MERS-CoV in the Republic of Korea. Next, Tang et al. [6]considered the concentration of uninfected cells, Infected, Virus and the

represented the concentration of DPP4 variable on the surface of uninfected cells as so-called TIVD model for MERS-CoV disease. Tahir et al. [7] discussed the stability behavior of the Susceptible Infected Hospitalized model (SIH) of the spread of MERS-CoV, which assumes that the main transmitters of this virus are camels. Recently, research the MERS-CoV model is still being conducted. Manaqib et al[8] developed SEIR model by considering medical mask. Manaqib devided the individus into the following categories, namely Susceptible individual without the use of medical mask(S_1) and individual using medical mask(S_2), latent individual (E), infected individual without using medical mask(I_1), infected individual with medical mask(I_2), as given by

$$\begin{aligned}
\frac{dS_1}{dt} &= (1-\rho)\mu + u_2 S_2 - (\mu + u_1)S_1 - \beta S_1 I_1 \\
\frac{dS_2}{dt} &= u_1 S_1 - (\mu + u_2)S_2 \\
\frac{dE}{dt} &= \beta S_1 I_1 - (\mu + \delta)E \\
\frac{dI_1}{dt} &= \delta E + u_2 I_2 - (\mu + u_1 + \sigma)I_1 \\
\frac{dI_2}{dt} &= u_1 I_1 - (\mu + u_2 + \sigma)I_2 \\
\frac{dR}{dt} &= \sigma I_1 + \sigma I_2 + \rho\mu - \mu R
\end{aligned} \tag{1}$$

In the formation models, the population is assumed to be closed. The number of births and the death amount of each unit of time is assumed to equal to rate μ. The population is homogeneously mixed, meaning that each individual has the same opportunity to make contact with other individuals, individuals who are born and not vaccinated will enter into theS_1 compartment at rate $(1-\rho)\mu$, susceptible individuals will be given vaccinations with certain vaccination measures so that it can lead to individuals given vaccines immune to disease by rate ρ. Susceptible individuals with health masks cannot be infected by MERS-CoV virus with a rate of awareness of the use of masks u_1, individuals on the compartment S_2will be replaced toS_1if they stop using a health mask, so individuals are on infected compartment at rateu_2.Virus infections occur when contact with an infected individual in the infected compartment, either directly or indirectly at a rate β. Individuals infected with the virus experience a latent period of pace δ. Virus infected individuals can recover from disease by rate σ.Individuals who have recovered cannot return to being susceptible individuals. The death from illness is ignored, natural death only occurs in each subpopulation at a rate u_2.

Solving a system of differential equation especially nonlinear solutions is difficult to obtain analytical solutions. The novelty of this study is related to apply a power semi-analytic method that recently has been used to predict the number of spread of MERS-Cov in [8].Several studies focus on finding the solution of SEIR model, where some researchers doing by various semi-analytic methods as Modified Homotopy Pertubation Method (MHPM) [9], Variational Iteration Method (VIM) and Differential Transform Method (DTM) [10,11],Bernstein polynomial (BP) [12], etc. For the best knowledge, Homotopy Analysis Method (HAM)which was proposed by Liao [13] in his Ph.D. thesis has been successfully employed to solve many types of nonlinear problems in science and engineering.HAM provides us with a convenient way to control the convergence of approximation series and adjust convergence regions when necessary. All of these successful applications of the HAM verify its validity for nonlinear problems in science and engineering as in [14-16]Another method will be used is fourth order runge kutta method (RK4). Furthermore, it allows a continuous representation of the approximate solution, which gives better information on the solution over the time interval. In contrast, the Runge-Kutta method provides solutions in discretized form, only at two ends of the time interval, thereby complicating the achievement of a continuous representation [17].

In this paper, we employ HAM to obtain series solution of SEIR model for MERS-CoV disease. HAM solution will compare to solution of an accuracy numerical method, RK4. In the end, the absolute and residual errors of HAM solution will be presented.

2. Computational Method

2.1. HAM for system of Ordinary Differential Equations

In order that show the HAM fundamentals which is an effective and powerful mathematical method for finding the approximate solution of a system of nonlinear differential equations, we firstly consider the following differential equation**:**

$$N_i[x_i(t)] = 0, \tag{2}$$

whereN_j are nonlinear operators, $t$denote the independent variable, $x_i(t)$are unknown functions. Let $x_{i,0}(t)$denote the initial guesses of the exact solution $x_i(t)$, $\hbar_i \neq 0$ an control convergence parameters, $H_i(t) \neq 0$the auxiliary functions, and $L_i$areauxiliary linear operators. Then, using$q \in [0,1]$ as an embedding parameter, we construct such a function of homotopy

$$H_i(\phi_i(t;q), q, \hbar, H(t)) = (1-q)L_i\left[\phi_i(t;q) - x_{i,0}(t)\right] = q\hbar_i H_i(t) N_i\left(\phi_i(t;q)\right). \tag{3}$$

It should be emphasized that the above homotopy contains the so-called auxiliary parameters$\hbar_i$and the auxiliary functions$\boldsymbol{H_i(t)}$. To the best of the knowledge, the nonzero auxiliary parameters and auxiliary functions play important roles within the frame of the HAM. It should be emphasized that we have great freedom to choose the initial guesses$\boldsymbol{x_{i,0}(t)}$, the auxiliary linear operators$\boldsymbol{L_i}$, the nonzero auxiliary parameters$\hbar_i$ and the auxiliary functions$\boldsymbol{H_i(t)}$.Let $\boldsymbol{q \in [0,1]}$ denotes an embedding parameter. Next, enforcing the homotopy in Eq. (3) to be zero as

$$H_i(\phi_i(t;q), q, \hbar, H(t)) = 0. \tag{4}$$

We have the so-called zero-order deformation equation as

$$(1-q)L_i\left[\phi_i(t;q) - x_{i,0}(t)\right] = q\hbar_i H_i(t) N_i\left(\phi_i(t;q)\right). \tag{5}$$

When $q = 0$and $q = 1$, both

$$\phi_i(t;0) = x_{i,0}(t) \text{and} \phi_i(t;1) = x_i(t) \tag{6}$$

hold. Thus, as q increases from 0 to 1, the solution $\phi_i(t;0)$ vary from the intial guesses$x_{i,0}(t)$ to the solutions$x_i(t)$. Expanding $\phi_i(t;q)$in Taylor series with respect to$q$, one has

$$\phi_i(t;q) = x_{i,0}(x) + \sum_{j=1}^{\infty} x_{i,j}(t) q^j, \tag{7}$$

where

$$x_j = \frac{1}{j!}\frac{d^j \phi_i(t;q)}{dq^j}\bigg|_{q=0}. \tag{8}$$

If the auxiliary linear operators, the auxilirary parameters$\hbar_i$, and the auxiliary functions are so properly chosen, then series (5) converges at $q = 1$ and

$$\phi_i(t;q) = x_{i,0}(x) + \sum_{j=1}^{\infty} x_{i,j}(t), \tag{9}$$

which must be one of the solution of the original nonlinear equation. According to (9), the governing equatons can be deduced from the zeroth-order deformation equation (5). Define the vectors

$$\vec{x}_i = \left(x_{i,0}, x_{i,0}, \cdots, x_{i,0}\right) \tag{10}$$

Differentiating (5) $j$times with respect to the embedding parameter$q$, then setting$q = 1$, and finally dividing them by $j!$, we have the so-called jth-order deformation equation

$$L_i\left[x_{i,j}(t) - \chi_j x_{i,j-1}(t)\right] = \hbar_i H_i(t) R_{i,j}\left(\vec{x}_{i,j}\right), \tag{11}$$

where

$$R_{i,j}\left(\vec{x}_{i,j}\right) = \frac{1}{(j-1)!}\frac{\partial^j N_i[\phi_i(t;q)]}{\partial q^j}\bigg|_{q=0} \tag{12}$$

and

$$\chi_j = \begin{cases} 0, j \leq 1, \\ 1, j > 1. \end{cases} \tag{13}$$

2.2. HAM for SEIR model

The system (1) is formed in a non-dimensional model to simplify the system. The proportion of the number of individual compartments can be expressed as follows [8]:

$$s_1 = \frac{S_1}{N}, s_2 = \frac{S_2}{N}, e = \frac{E}{N}, i_1 = \frac{I_1}{N}, i_1 = \frac{I_1}{N}, r = \frac{R}{N}. \tag{14}$$

From equation (*), we obtain

$$s_1 + s_2 + e + i_1 + i_1 + r = \frac{S_1}{N} + \frac{S_2}{N} + \frac{E}{N} + \frac{I_1}{N} + \frac{I_2}{N} + \frac{R}{N} = 1.$$

According to [8], in the system (1), variable $r$does not appeared in other equations. This suggested that the number of individuals in the $r$compartment did not affect the rate of change in the number of individuals in the other compartment, then the equation $r$for a while can be ignored from the system. So that the equation system (1) can be formed into non-dimensional models to:

$$\begin{aligned}
\frac{ds_1}{dt} &= (1-\rho)\mu + u_2 s_2 - (\mu + u_1)s_1 - \beta s_1 i_1,\\
\frac{ds_2}{dt} &= u_1 s_1 - (\mu + u_2)s_2,\\
\frac{de}{dt} &= \beta s_1 i_1 - (\mu + \delta)e,\\
\frac{di_1}{dt} &= \delta E + u_2 i_2 - (\mu + u_1 + \sigma)i_1,\\
\frac{di_2}{dt} &= u_1 i_1 - (\mu + u_2 + \sigma)i_2.
\end{aligned} \tag{15}$$

According to HAM to solve (15), we choose the linear operator as

$$L_i[\phi_i(t;q)] = \frac{d\phi_i(t;q)}{dt}, \quad i = 1,2,..,6, \tag{16}$$

where$L_i$is linear operator, with the property$L_i[0] = 0$, and $N_i[\phi_i(t;q)]$ the nonlinear operators

$$\begin{aligned}
N_1[\phi_1(t;q)] &= \frac{d\phi_1(t;q)}{dt} - (1-\rho)\mu - u_2\phi_2(t;q) + (\mu + u_1)\phi_1(t;q)\\
&\quad + \beta\phi_1(t;q)\phi_4(t;q),\\
N_2[\phi_2(t;q)] &= \frac{d\phi_2(t;q)}{dt} - u_1\phi_1(t;q) + (\mu + u_2)\phi_2(t;q),\\
N_3[\phi_3(t;q)] &= \frac{d\phi_3(t;q)}{dt} - \beta\phi_1(t;q)\phi_4(t;q) + (\mu + \delta)\phi_3(t;q),\\
N_4[\phi_4(t;q)] &= \frac{d\phi_4(t;q)}{dt} - \delta\phi_3(t;q) - u_2\phi_5(t;q) + (\mu + u_1 + \sigma)\phi_4(t;q),\\
N_5[\phi_5(t;q)] &= \frac{d\phi_5(t;q)}{dt} - u_1\phi_4(t;q) + +(\mu + u_2 + \sigma)\phi_5(t;q),
\end{aligned} \tag{17}$$

Again, using the above definition, we construct the zeroth-order deformation equation as in (5),

$$\begin{aligned}
(1-q)L_1\big[\phi_1(t;q) - s_{1,0}(t)\big] &= q\hbar H_1(t)N_1[\phi_1(t;q)],\\
(1-q)L_2\big[\phi_2(t;q) - s_{2,0}(t)\big] &= q\hbar H_2(t)N_2[\phi_2(t;q)],\\
(1-q)L_3[\phi_3(t;q) - e_0(t)] &= q\hbar H_3(t)N_3[\phi_3(t;q)],\\
(1-q)L_4\big[\phi_4(t;q) - i_{1,0}(t)\big] &= q\hbar H_4(t)N_4[\phi_4(t;q)],\\
(1-q)L_5\big[\phi_5(t;q) - i_{2,0}(t)\big] &= q\hbar H_5(t)N_5[\phi_5(t;q)].
\end{aligned} \tag{18}$$

For $q = 0$ dan $q = 1$, the above zeroth-order equations(18) have the solutions

$\phi_1(t;0) = s_{1,0}(t)$, $\phi_2(t;0) = s_{2,0}(t)$, $\phi_3(t;0) = e_0(t)$, $\phi_4(t;0) = i_{1,0}(t)$, and $\phi_5(t;0) = i_{2,0}(t)$

and

$\phi_1(t;1) = s_1(t)$, $\phi_2(t;1) = s_2(t)$, $\phi_3(t;1) = e(t)$, $\phi_4(t;1) = i_1(t)$ and $\phi_5(t;1) = i_2(t)$

When q increases from 0 to 1, then $s_{1,0}(t), s_{2,0}(t), e_0(t), i_{1,0}(t)$, and $i_{2,0}(t)$ vary to$s_1(t), s_2(t), e(t), i_1(t)$,and, $i_2(t)$, respectively. Expanding $s_1(t), s_2(t), e(t), i_1(t)$, and $i_2(t)$ in Taylor series with respect to q, we have

$$\begin{aligned}
\phi_1(t;q) &= \phi_1(t;0) + \sum_{j=1}^{+\infty} \frac{1}{j!} \frac{d^j \phi_1(t;q)}{dq^j}\bigg|_{q=0} q^j, \\
\phi_2(t;q) &= \phi_2(t;0) + \sum_{j=1}^{+\infty} \frac{1}{j!} \frac{d^j \phi_2(t;q)}{dq^j}\bigg|_{q=0} q^j, \\
\phi_3(t;q) &= \phi_3(t;0) + \sum_{j=1}^{+\infty} \frac{1}{j!} \frac{d^j \phi_3(t;q)}{dq^j}\bigg|_{q=0} q^j, \\
\phi_4(t;q) &= \phi_4(t;0) + \sum_{j=1}^{+\infty} \frac{1}{j!} \frac{d^j \phi_4(t;q)}{dq^j}\bigg|_{q=0} q^j, \\
\phi_5(t;q) &= \phi_5(t;0) + \sum_{j=1}^{+\infty} \frac{1}{j!} \frac{d^j \phi_5(t;q)}{dq^j}\bigg|_{q=0} q^j,
\end{aligned} \tag{19}$$

Differentiating Equation (18)$j$times with respect to embedding parameter q and setting $q = 0$ and finally dividing them by$j$!, we have the so-called jth-order deformation equation

$$\begin{aligned}
L_1\left[s_{1,j}(t) - \chi_j s_{1,j-1}(t)\right] &= \hbar H_1(t) R_{1,j}\left(\vec{s}_{1,j-1}(t)\right), \\
L_2\left[s_{2,j}(t) - \chi_j s_{2,j-1}(t)\right] &= \hbar H_2(t) R_{2,j}\left(\vec{s}_{2,j-1}(t)\right), \\
L_3\left[e_j(t) - \chi_j e_{j-1}(t)\right] &= \hbar H_3(t) R_{3,j}\left(\vec{e}_{j-1}(t)\right), \\
L_4\left[i_{1,j}(t) - \chi_j i_{1,j-1}(t)\right] &= \hbar H_4(t) R_{4,j}\left(\vec{i}_{1,j-1}(t)\right), \\
L_5\left[i_{2,j}(t) - \chi_j i_{2,j-1}(t)\right] &= \hbar H_5(t) R_{5,j}\left(\vec{i}_{2,j-1}(t)\right),
\end{aligned} \tag{20}$$

with the following intial conditions:

$$s_1(0) = s_{1,0}(t),\ s_2(0) = s_{2,0}(t),\ e(0) = e_0(t),\ i_1(0) = i_{1,0}(t), \text{ and } i_2(0) = i_{2,0}(t), \tag{21}$$

where

$$\begin{aligned}
R_{1,j}\left[\vec{s}_{1,j-1}\right] &= \frac{ds_{1,j-1}}{dt} - (1-\chi_j)(1-\rho)\mu + u_2 s_{2,j-1} + (\mu + u_1) s_{1,j-1} \\
&\quad + \beta \sum_{n=0}^{j-1} s_{1,n} i_{1,j-1-n}, \\
R_{2,j}\left[\vec{s}_{2,j-1}\right] &= \frac{ds_{2,j-1}}{dt} - u_1 s_{1,j-1} + (\mu + u_2) s_{2,j-1}. \\
R_{3,j}\left[\vec{s}_{3,j-1}\right] &= \frac{de_{j-1}}{dt} - \beta \sum_{n=0}^{j-1} s_{1,n} i_{1,j-1-n} + (\mu + \delta) e_{j-1}, \\
R_{4,j}\left[\vec{s}_{4,j-1}\right] &= \frac{di_{1,j-1}}{dt} - \delta e_{j-1} - u_2 i_{2,j-1} + (\mu + u_1 + \sigma) i_{1,j-1}, \\
R_{5,j}\left[\vec{s}_{5,j-1}\right] &= \frac{di_{2,j-1}}{dt} - u_1 i_{1,j-1} + (\mu + u_2 + \sigma) i_{2,j-1},
\end{aligned} \tag{22}$$

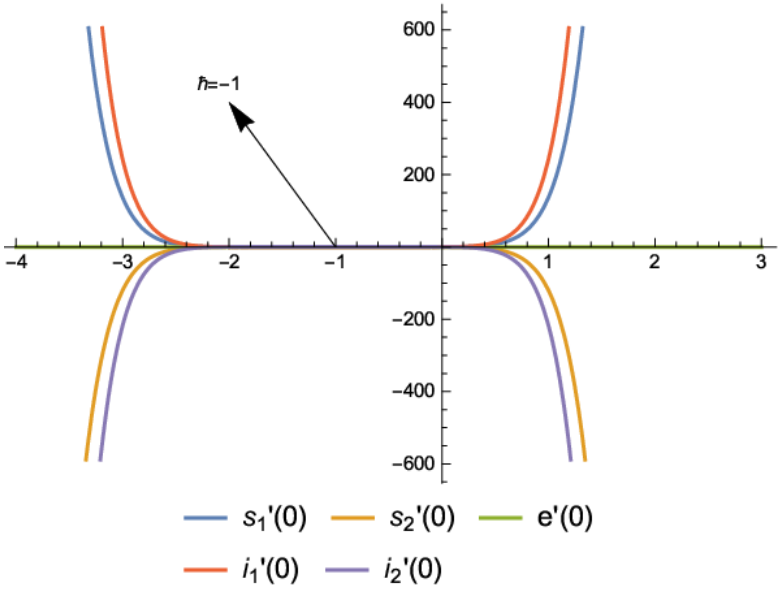
and

$$\chi_j = \begin{cases} 0, j \le 1, \\ 1, j > 1. \end{cases}$$

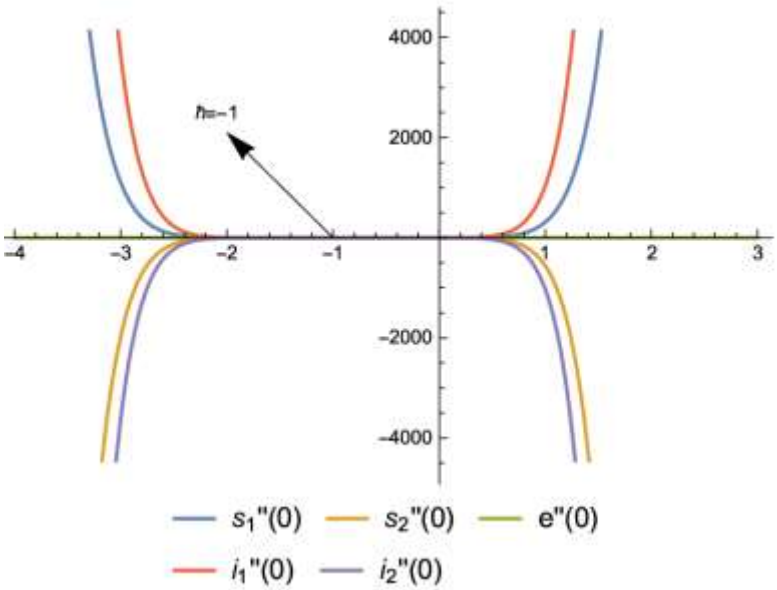
Then the HAM series solutions are in this form:

$$\begin{aligned} s_1 &= s_{1,0} + \sum_{j=1}^{30} s_{1,j}, \\ s_2 &= s_{2,0} + \sum_{j=1}^{30} s_{2,j}, \\ e &= e_0 + \sum_{j=1}^{30} e_j, \\ i_1 &= i_{1,0} + \sum_{j=1}^{30} i_{1,j}, \\ i_2 &= i_{2,0} + \sum_{j=1}^{30} i_{2,j}. \end{aligned} \tag{23}$$

To determine the value of $\hbar_i$ we plot the$\hbar_i$-curve for first and second derivative of each solution of Eq. (4) in Figure 1



(a)



(b)

Figure 1. $\hbar_i$-curves of 10 terms HAM for endemic case for: (a) first derivative, (b) second derivative

From this Figure 1, it is noted that the valid regions of $(\hbar_i,\ i = 1,\dots,5)$ correspond to the line segments nearly parallel to the horizontal axis, e.i.$\hbar_i = -1, i = 1,2,3,4,5$.

In this paper, all parameters$\mu = 0.07305936073$, ρ =0.8, u_1=0.7, u_2= 0.3, β =0.1, δ = 0.07142857143, $\sigma = 0.03333333333$, $N = 2000$and initial conditions ofendemic case, the initial approximationscan be chosen as$s_{1,0}(t) = 0.177434; s_{2,0}(t) = 0.0182347; e_0(t) = 0.188449; i_{1,0}(t) = 0.3222343294; i_{2,0}(t) = 0.0320187469$ and $r_0(t) = 0.261628$are taken from [8]. Overall calculations were done by Mathematic a software 11.2 version. The number of spread of the S_1, S_2, E, I_1, $I_2$and R for endemic case affected by preliminary data that population number (N) is 2000 [8]. By 120 terms HAM, The number of spread can be seen as follow

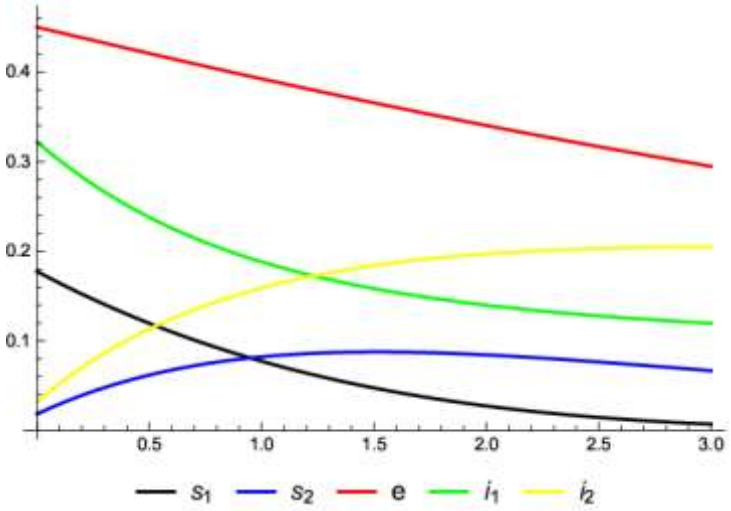


Figure 2. Approximate Solution of SEIR variablesversus t in Span Time [0,3] for $\Delta t = 0.001$

Figure 2 presents the approximate solution of SEIR model using 120 terms HAM in span time [0,3]. As presented Figure 2, black, blue, red, green,yellow linesasS_1, S_2, E, I_1, and I_2, respectively. FromFigure 2,the probability of susceptible individu who used mask, the probability of infected individual who used mask, and the probability of exposed individu decrease dramatically, while the propability of infected individu that didn't use mask increases contrastly. Furthermore, there are the effect of wearing a mask. It is shown that probability of susceptible individu deceases significantly that it reachsto 0.The following table presents the absolute error of RK4 and 120 terms HAM for $\Delta t = 0.001$ as

Table 1.Absolute Error of HAM and RK4 $\Delta t = 0.001$

t	s_1	s_2	e	i_1	i_2
0	0	0	0.	3.294E-07	2.531E-07
0.5	6.518E-03	1.049E-03	4.045E-05	5.741E-06	1.625E-05
1	1.253E-02	3.998E-03	1.352E-04	2.873E-06	2.174E-05
1.5	1.594E-02	7.965E-03	2.455E-04	4.362E-06	2.369E-05
2	1.617E-02	1.182E-02	3.450E-04	1.357E-05	2.549E-05
2.5	1.347E-02	1.460E-02	4.176E-04	2.315E-05	2.855E-05
3	8.441E-03	1.564E-02	4.546E-04	3.196E-05	3.315E-05

Table 1 presents the absolute errors of RK4 and HAM for $\Delta t = 0.001$ in span time [0,3]. From the table 1, the closeness of HAM and RK4 solutions are reached to minimum error on10^{-5}.

Another ways to demonstrate the power of HAM solutions are by determining the residual error of Eq. (15). We define the residual error for HAM solutions as

$$\begin{aligned} RE\tilde{s}_1 &= \frac{d\tilde{s}_1}{dt} - (1-\rho)\mu - u_2\tilde{s}_2 + (\mu+u_1)\tilde{s}_1 + \beta\tilde{s}_1\tilde{\imath}_1 \\ RE\tilde{s}_2 &= \frac{d\tilde{s}_2}{dt} - u_1\tilde{s}_1 + (\mu+u_2)\tilde{s}_2 \\ RE\tilde{e} &= \frac{d\tilde{e}}{dt} = \beta\tilde{s}_1\tilde{\imath}_1 - (\mu+\delta)\tilde{e} \\ RE\tilde{\imath}_1 &= \frac{d\tilde{\imath}_1}{dt} = \delta\tilde{e} + u_2\tilde{\imath}_2 - (\mu+u_1+\sigma)\tilde{\imath}_1 \\ RE\tilde{\imath}_2 &= \frac{d\tilde{\imath}_2}{dt} = u_1\tilde{\imath}_1 - (\mu+u_2+\sigma)\tilde{\imath}_2 \end{aligned} \tag{24}$$

where$\tilde{s}_1, \tilde{s}_2, \tilde{e}, \tilde{\imath}_1, \tilde{\imath}_2$and $\tilde{r}$are the HAM solutions for the Eq. (24). For the result, Table 2 present the residual Error of HAM in span time [0,3].

Table 2. Residual Error of Eq (14) with $\Delta t = 0.001$

t	Es_1	Es_2	Ee	Ei_1	Ei_2
0	1.963E-01	0	0	2.340E-01	0
0.5	2.225E-01	0	1.388E-17	1.005E-01	2.776E-17
1	2.346E-01	0	6.939E-18	2.355E-02	4.163E-17
1.5	2.379E-01	5.963E-18	1.388E-17	2.077E-02	4.857E-17
2	2.359E-01	2.949E-17	4.163E-17	4.619E-02	1.422E-16
2.5	2.312E-01	7.633E-17	4.163E-17	6.063E-02	3.140E-16
3	2.254E-01	3.816E-17	9.714E-17	6.866E-02	5.537E-16

From table2, the residual errors of Eq (15) reach minimum value are 10^{-18}**.** Since the HAM solution is analytic at each time step, it is easy to obtain the residual error at each time step.

3. Conclusions

In this present work, the Homotopy analysis method (HAM) was applied to solve the MERS-CoV disease via SEIR model. Comparisons between the HAM and the RK4 numerical solutions were made. We found that the 120-terms HAM solutions in span time [0,3] achieved comparable accuracy compared with the RK4 solutions. The HAM solutions were very close to RK4 solution. Moreover, Residual error for the HAM solution was obtained very small, specially, for susceptible and infected individuals what wear a mask as well Exposed individual. It demonstrated the accuracy of the HAM for the SIER model.Overall, HAM can be an alternative method for solving more complex models.

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