# Transmission Dynamics of a SIR Infectious Disease Model using Multi-Step Homotopy Analysis Method

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## ABSTRACT

We propose and analyze in a varying population a compartmental mathematical model for an infectious disease. The model is studied qualitatively using the concept of stability theory of differential equations and the basic reproductive number that represents the epidemic indicator is obtained. Further, we solve the model equation by Multi-step Homotopy Analysis Method (MHAM) and compute the approximate solution of the model. The fractional derivatives are described in the Caputo sense. We illustrate the profiles of the solutions of each of the compartments. Figurative comparisons between the MHAM and the classical fourth-order reveal that this method is very effective.

(Keywords: mathematical biology, disease model, stability theory, differential equations, epidemic indicator, MHAM, multi-step homotopy analysis method)

## INTRODUCTION

According to World Health Organization (WHO) as quoted in (Tilahun, et. al. 2017), "infectious diseases are disorders instigated by bacteria, viruses, and parasites like worms or protozoans that have every tendency to invade the population. Infectious diseases, in many quarters, are referred to as communicable or transmissible diseases because of their potential to transmit from one individual to another via replicating agents (Djordjevic, et. al. 2018).

The transmission of communicable diseases can be linked to a particular or various pathways as in interaction with infectious individuals (Sharomi, and Malik, 2017). The agents of communicable diseases can also be contracted through airborne inhalation, food, body fluids, and contaminated objects or through vector-borne transmission (Peter, et al., 2020, Peter, et al., 2021).

The nature of infectious diseases has posed serious fear to man since the start of human evolution (Asor and Ugwu, 2011). The global panic accompanied the eruption of SARS and avian flu in Asia and Ebola in Africa are evidence that our sense of horror escalates with our understanding of the epidemics (Lhous, et al., 2019). One of the interests of epidemic modelling is investigating the spread of infections in hosts' populations, both in time and space.

The first infectious model was invented by Daniel Bernoulli in 1760 (Mhlanga, 2019), which was designed to examine the impact of inoculation on the life expectancy of man (Carvalho, et al., 2019). Nevertheless, there exists inadequacy in epidemic modelling until the ground-breaking work of Hammer on both malaria and measles at the beginning of the 20th century (Shulgin,1998).

Bartlett (Bartlett, 1960) who studied the conditions that activate the persistence of diseases in populations through close examinations of models and data. Perhaps, the first innovating book on modelling regarding the systems of epidemiology was advanced by Bailey (Keeling, and Grenfell, 2002) who facilitated the awareness of the importance of modelling in public health as regards decision making.

Given the array of infectious diseases investigated since 1950s, a notable set of infectious models has been developed. In this study, we employ the Multi-step Homotopy Analysis Method (MHAM) to the system of differential equations proposed by Gebremeskel and Krogstad (2015), which describe our model

and approximating the solutions in a sequence of time intervals. In other to illustrate the accuracy of the MHAM, the obtained results are compared with fourth-order Runge-Kutta Method.

Other semi-analytical methods to determine the solutions of nonlinear system includes: Homotopy Perturbation Method (HPM), Reduced Differential Transform Method (RDTM), Variational Iterational Method (VIM), Differential Transform Method. The methods mentioned above have been used as a tools to approximate linear and non-linear problems in Physics and Engineering, respectively (Abbasbandy and Shivanian, 2009; Peter and Akinduko, 2018; Peter and Ibrahim, 2017; Peter et al., 2018).

## FORMULATION OF THE MODEL

The Susceptible subpopulation is generated from daily recruitment of birth at rate $\theta$. It is decreased by natural death at the rate $\mu$. Furthermore, they acquired infection and move to the infected class I(t) via interaction of the infected and the susceptible at the rate $\beta$. The infected class are generated from susceptible individual that acquired infection. The subpopulation reduced through recovery from infection, disease induced death at the rate $\gamma$ and $\alpha$, respectively.

Furthermore, the Recovery subclass are generated from the recovered infected individuals. They are reduced due to loss of immunity from recovery and natural death at the rate $\varepsilon$ and $\mu$ respectively. To indicate this mathematically, we have:

$$\begin{aligned}\frac{dS_h}{dt} &= \theta - \beta S_h I_h + \varepsilon R - \mu S_h \\ \frac{dI_h}{dt} &= \beta S_h I_h - (\mu + \gamma + \alpha) I_h \\ \frac{dR_h}{dt} &= \gamma I - (\mu + \varepsilon) R_h \end{aligned} \qquad \textbf{(1)}$$

## THE ANALYSIS OF THE MODEL

### Invariant Region

The invariant region where the solutions of the model are bounded is obtained. The sum of the population (N) is:

$N=S_h+I_h+R_h$ **(2)**

and, the differential coefficient of both sides of (2) with respect to t yields:

$$\frac{dN}{dt} = \frac{dS_h}{dt} + \frac{dI_h}{dt} + \frac{dR_h}{dt}. \qquad \textbf{(3)}$$

Combining the equations in the system (1) together with (3) leads to:

$$\frac{dN}{dt} = \theta - \mu N - \alpha I_h. \qquad \textbf{(4)}$$

In the absence of infection:

$$\frac{dN}{dt} \le \theta - \mu N. \Rightarrow \qquad \textbf{(5)}$$

$$\int \frac{dN}{\theta - \mu N} \le dt. \Rightarrow \qquad \textbf{(6)}$$

$$-\frac{1}{\mu}\ln(\theta - \mu N) \le t + c, \Rightarrow$$

$$\theta - \mu N \ge p e^{-\mu t} \qquad \textbf{(7)}$$

At $N(0)=N_0$ in (7), $p = \theta - \mu N_0$ and by substituting in (6) leads to:

$$\theta - \mu N \ge (\theta - \mu N_0) e^{-\mu t} \qquad \textbf{(8)}$$

and, by rearranging (8):

$$N \le \frac{\theta}{\mu} - \left[\frac{\theta - \mu N_0}{\mu}\right] e^{-\mu t}. \Rightarrow \qquad \textbf{(9)}$$

As $t \to \infty$ in (10), $N \to \frac{\theta}{\mu} \Rightarrow$

$$0 \le N \le \frac{\theta}{\mu}.$$

Hence, the solutions of the model remain in:

$$\Omega = \left\{ \left(S_h, I_h, R_h\right) \in \Re_+^3 : N = \frac{\theta}{\mu} \right\} \qquad \textbf{(10)}$$

**Positivity of Solution**

Assuming the model has nonnegative initial conditions. The solutions of the model can be shown to be nonnegative as well.

Theorem 1. Let:

$\left\{ \left(S_h, I_h, R_h\right) \in \Re_+^3 : Sh_0 > 0, Ih_0 > 0, Rh_0 > 0 \right\}$: then $\left\{S_h, I_h, R_h\right\}$ contains positive solutions for $t \ge 0$.

Proof. From (1)

$$\frac{dS_h}{dt} = \theta - \beta S_h I_h + \varepsilon R_h - \mu S_h \Rightarrow$$
$$\frac{dS_h(t)}{dt} \ge -(\beta I_h + \mu) S_h \Rightarrow$$
$$\frac{dS_h(t)}{S_h(t)} \ge -(\beta I_h + \mu) t \Rightarrow$$
$$\int \frac{dS_h(t)}{S_h(t)} \ge -\int (\beta S_h + \mu) dt \Rightarrow$$
$$S_h(t) \ge S_{h0} e^{-(\beta I_h + \mu)t} \ge 0 \qquad \textbf{(11)}$$

Similarly,

$$I_h(t) \ge I_{h0} e^{-(\mu+\gamma+\alpha)t} \ge 0 \qquad \textbf{(12)}$$

$$R_h(t) \ge R_0 e^{-(\mu+\varepsilon)t} \ge 0 \qquad \textbf{(13)}$$

(11)-(13) show that the solutions to the model are positive.

**The Disease-Free Equilibrium (DFE)**

When there is no infection in the population:

$$\text{DFE, } E_0 = (S_{h0}, I_{h0}, R_{h0}) = \left\{ \frac{\theta}{\mu}, 0, 0 \right\} \qquad \textbf{(14)}$$

**The Endemic Equilibrium (EE)**

When the infection persists in the population:

$$E^* = (S_h{}^*, I_h{}^*, R_h{}^*) = \left\{ \frac{k_1}{\beta}, \frac{k_2(\beta\theta - k_1\mu)}{k_1 k_2 - \varepsilon\gamma}, \frac{\gamma(\beta\theta - k_1\mu)}{k_1 k_2 - \varepsilon\gamma} \right\} \qquad \textbf{(15)}$$

where

$$k_1 = \mu + \alpha + \gamma, \quad k_2 = \mu + \varepsilon.$$

**The Basic Reproduction Number ($R_0$)**

There is need to derive a threshold for disease outbreak or inhibition. The parameter that serves the purpose is known as the reproduction number. The parameter shall be derived for our model at the steady state of the second equation in the system (1):

$$\beta S_h I_h - (\mu + \gamma + \alpha) I_h = 0$$
$$I_h \left[ \frac{\theta}{\mu} \beta - \left(\mu + \gamma + \alpha\right) \right] = 0 \Rightarrow$$
$$R_0 = \frac{\theta\beta}{\mu(\mu + \alpha + \gamma)} \qquad \textbf{(16)}$$

**Local Stability of Disease-Free Equilibrium Proposition 2**

The disease-free equilibrium point is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof. The Jacobian matrix of the system (1) at the DFE, $E_0$ is derived as follows:

$$J(E_0)=\begin{pmatrix} -\mu & \frac{-\theta\beta}{\mu} & \varepsilon \\ 0 & -(\mu+\gamma+\alpha) & 0 \\ 0 & \gamma & -(\mu+\varepsilon) \end{pmatrix} \quad \textbf{(17)}$$

From (17), $|J(E_0)-\lambda I|=0 \Rightarrow$
$(\mu+\lambda)(\mu+\gamma+\alpha+\lambda)(\mu+\varepsilon+\lambda)=0$,

from which,
$\lambda_1=-\mu,\ \lambda_2=-(\mu+\alpha+\gamma), \qquad \lambda_3=-(\mu+\varepsilon)$

Since all the roots are negative then $R_0<1$ and the disease-free equilibrium is locally asymptotically stable.

**Basic Definitions and Notation**

Lemma 1
[Generalized Mean Value Theorem (Lin, 2007)]
Let $q(x)\in C[e,f]$ and $D^{\alpha}\,q(x)\in C[e,f]$ for $0<\alpha\leq 1$, then we have:

$$q(x)=q(e)+\frac{1}{\Gamma(\alpha)}D^{\alpha}q(\varepsilon)(x-e)^{\alpha}$$

$$0\leq\varepsilon<x\,\forall\,x\in[e,f]$$

Remark.

Suppose $q(x)\in C[e,f]$ and $D^{\alpha}q(x)\in C[e,f]$ for $0<\alpha\leq 1$. It is obvious from Lemma 1 that if $D^{\alpha}\,q(x)\geq 0,\forall x\in(0,f)$ then the function $q$ is non-deceasing and if $D^{\alpha}\,q(x)\leq 0,\forall x\in(0,f)$ then the function $p$ is non-increasing.

Definition 1

A function $f(x)$ having a position value of $x$ is defined in the space $D_{\alpha}\,(\alpha\in\mathbb{R})$ if it is expressed in the form $f(x)=x^{a}f(x)$ and for some $a>\alpha$ where $f(x)$ is continuous in $[0,\infty]$ and it is identified to be in the space $D_{\alpha}^{n}$ if $f^{(n)}\in Dn\in\mathbb{N}$

Definition 2

The Riemann Liouvoille integral Operator of a given order $\alpha>0$ with $b\geq 0$ is expressed as:

$$(J_a^{\alpha}f)(x)=\frac{1}{\Gamma(\alpha)}\int_a^x(x-t)^{n-1}\,f(t)dt,x>\alpha$$
$$(J_b^0f)(x)=f(x).$$

We require only the following for:

$$f\in\beta_n,\alpha>0,\beta>0,c\in\mathbb{R}\text{ and }\ \gamma>-1,$$

we get

$$J_b^{\alpha}x^{\gamma}=\frac{x^{\gamma+\alpha}}{\Gamma(b)}\beta(x-b)(\alpha,\gamma+1)$$

Where $\beta_{\omega}\,(\alpha,\gamma+1)$ characterized the incomplete beta function stated as:

$$D_{\omega}(\alpha,\gamma+1)=\int_0^{\omega}t^{\alpha_1}(1-t)^{\gamma}dt,$$
$$J_b^{\alpha}f^{(x)}=f^{(x)}(x-b)^{\alpha}\sum_{k=0}^{\infty}\frac{[c(c-b)]^k}{\Gamma(\alpha+k+1)}$$

The Riemann Liouville derivative possesses some setbacks when applying to a real-life situation with fractional differential equations. Thus, we employ a modified version of fractional differential operator $D_b^{\alpha}$ which has been employed in the Caputo work on the theory of viscoelasticity.

Definition 3
The Caputo fractional derivative of $p(x)$ order $\alpha>0$ with $a\geq 0$ is given as:

$$(D_b^{\alpha}f)(x)=(J_b^{m-\alpha})(x)$$
$$=\frac{1}{\Gamma(m-\alpha)}\int_b^x\frac{f^{(m)}(t)}{(x-t)^{\alpha+1-m}}dt$$

For,

$$m-1<\alpha\leq m, m\in\mathbb{N}, x\geq bf(x)\in D_{-1}^{m}$$

## ANALYSIS METHOD

The homotopy analysis method's principles are outlined in (Ibrahim, et al., 2017; Liao, 1992). In terms of convergent sequences, HAM is used to provide approximate solutions for a broad variety of non-linear problems. Many researchers have extended the HAM to solve linear and nonlinear problems in terms of convergent series with easily computed components, but it has some drawbacks: the series solution often converges in a small region, has a slow convergent rate, or is completely divergent in the larger region (Alomari, et al., 2009; Zurigat, et al., 2010). It's just a simple modification of HAM, but it ensures the approximant solution's validity over a long interval. To address HAM's shortcoming, we present (MHAM), a program we created for numerically solving a system of fractional differential equations.

$$D^{\alpha_1}S(t) = \theta-\beta SI+\varepsilon R-\mu S$$

$$D^{\alpha_2}I(t) = \beta SI-(\mu+\gamma+\alpha)I$$

$$D^{\alpha_3}R(t) = \gamma I-(\mu+\varepsilon)R$$

To expand the solution over the interval $[0,t]$, we subdivide the interval $[0,t]$ into $n$ subintervals of equal length:

$$\Delta t, [t_0,t_1),[t_1,t_2],[t_2,t_3),[t_3,t_4)\ldots\ldots\ldots\ldots\ldots\ldots[t_{n-1},t_n)$$

with $t_0=0$, and $t_n=t$

We let $t^*$ be the initial value for each subinterval $[t_{j-1},t_j]$; $j=1,2,\cdots n$ with initial guesses:

$$S_1(t^*)=3, S_{(h,j)(t^*)}=S_{h,j}(t_{j-1}) = S_{hj-1}(t_{j-1})$$

$$I_2(t^*)=1, I_{h,j}(t^*)=i_{h,j}(t_{j-1}) = i_{hj-1}(t_j-1)$$

$$R_{3(t^*)}=1, R_{h,j}(t^*)=r,j(t_{j-1})=r_{j-1}(t_{j-1})$$

Now, we constructed the Zeroth order transformation of the model equation (1):

$$(1-p)\left[\phi_{1,j}(t;p)-S_j(t^*)\right]=ph\,[D^{\alpha_1}\phi_{1_j}(t;p)-\theta+\beta\phi_{1,j}(t;p)\phi_{5,j}(t,p)-\varepsilon\phi_{1,j}(t;p)+\mu\phi_{1,j}(t;p)\quad]$$

$$(1-p)\left[\phi_{2,j}(t;p)-I_j(t^*)\right] = \rho h\left[D^{\alpha_2}\phi_{2,j}\right)(t;p) - \beta_h\phi_{1,j}(t;p)(t;p)\phi_{5,j}(t,p) +(\mu+\gamma+\alpha)\phi_{2,j}(t,p)]$$

$$(1-p)L\left[\phi_{3,j}(t;p)-R_h(t^*)\right] = ph[D^{\alpha_3}\phi_{3,j}(t;p) - \gamma\phi_{2,j}(t,p)+(\mu+\varepsilon)(t,p)]$$

Where $p\in[0,1]$ is an embedding parameter, $L$ is an auxiliary linear operator, $h\neq 0$, is an auxiliary parameter and $\phi_{i,j}(t,p), i=1,2,3, j=1,2,3,\cdots n$ are unidentified function. When $p=0$, we have:

$$\phi_{1,1}(t;0)=3,\phi_{1,j}(t;0)=S_{h_{j-1}}(t_{j-1}),$$

$$\phi_{2,1}(t;0)=1,\phi_{2,j}(t;0)=I_{h_{j-1}}(t_{j-1}),$$

$$\phi_{3,1}(t;0)=1,\phi_{3,j}(t;0)=R_{h_{j-1}}(t_{j-1}),\ j=1,2,\cdots n$$

**(18)**

And when $p=1$, we obtain:

$$\phi_{1,j}(t;0)=S_{h_j}(t_j),$$

$$\phi_{2,j}(t;0)=I_{h_j}(t_j),$$

$$\phi_{3,j}(t;0)=R_{h_j}(t_j),$$

Expanding $\phi_{i,j}(t;p),\ i=1,2,3$ and $j=1,2,3,\cdots n$ using Taylor's series expansion with respect to $p$, we obtain:

$$\phi_{1,j}(t;p)=S_{h_j}(t^*)+\sum_{m=1}^{\infty}S_{h_{j,m}}(t)P^m$$

$$\phi_{2,j}(t;p) = I_{h_j}(t^*) + \sum_{m=1}^{\infty} I_{h_{j,m}}(t)P^m$$

$$\phi_{3,j}(t;p) = R_{h_j}(t^*) + \sum_{m=1}^{\infty} R_{h_{j,m}}(t)P^m$$

**(19)**

Where

$$S_{h_{j,m}(t)} = \frac{1}{m!}\frac{\partial^m \phi_{1,j}(t,p)}{\partial p^m}|p = 0 \quad j = 1,2,\cdots n$$

$$I_{h_{j,m}(t)} = \frac{1}{m!}\frac{\partial^m \phi_{2,j}(t,p)}{\partial p^m}|p = 0$$

$$R_{h_{j,m}(t)} = \frac{1}{m!}\frac{\partial^m \phi_{3,j}(t,p)}{\partial p^m}|p = 0$$

**(20)**

If the auxiliary linear operator $L$ together with the initial guesses $S_{h_j}(t^*), I_{h_j}(t^*), R_{h_j}$ and the nonzero auxiliary parameter $h$ are power series selected in order that the power series (1) converges at $p = 1$, we obtain:

$$S_{h_j}(t) = \phi_{1,j}(t;1) = S_{h_j}(t^*) + \sum_{m=1}^{\infty} S_{h_{j,m}}(t)$$

$$I_{h_j}(t) = \phi_{2,j}(t;1) = I_{h_j}(t^*) + \sum_{m=1}^{\infty} I_{h_{j,m}}(t)$$

$$R_{h_j}(t) = \phi_{3,j}(t;1) = R_{h_j}(t^*) + \sum_{m=1}^{\infty} R_{h_{j,m}}(t)$$

**(21)**

Define the vectors:

$$\vec{S}_{h_{j,m}}(t) = \left\{S_{h_{j,o}}(t), S_{h_{j,1}}(t)\cdots S_{h_{j,m}}(t)\right\}$$

$$\vec{I}_{h_{j,m}}(t) = \left\{I_{h_{j,o}}(t), I_{h_{j,1}}(t)\cdots I_{h_{j,m}}(t)\right\}$$

$$\vec{R}_{h_{j,m}}(t) = \left\{R_{h_{j,o}}(t), R_{h_{j,1}}(t)\cdots R_{h_{j,m}}(t)\right\}$$

**(22)**

Differentiating the zero-order definition m times with regard to $p$ then putting $p = 0$ and partitioning them by $m!$. Finally, we obtain the higher order definition equations:

$$L\left[S_{h_{j,m}}(t) - X_m S_{h_{j,m-1}}(t)\right] = h\,\mathbb{R}'_{j,m}(\vec{S}_{h_{j,m-1}}(t))$$

,

$$L\left[I_{h_{j,m}}(t) - X_m I_{h_{j,m-1}}(t)\right] = h\,\mathbb{R}^2_{j,m}(\vec{I}_{h_{j,m-1}}(t))$$

,

$$L\left[R_{h_{j,m}}(t) - X_m R_{h_{j,m-1}}(t)\right] = h\,\mathbb{R}^3_{j,m}(\vec{R}_{h_{j,m-1}}(t))$$

,

**(23)**

Subject to the initial condition:

$$S_{h_{j,m}}(0) = I_{h_{j,m}}(0) = R_{h_{j,m}}(0) \quad \textbf{(24)}$$

$$j = 1,2,\cdots n, \quad m = 1,2,\cdots n \quad \textbf{(25)}$$

Where

$$X_m = \begin{cases} 0 & m \le 1 \\ 1 & m > 1 \end{cases}$$

Selecting the linear operator $L = D^{\alpha_i}, i = 1,2,3,\cdots n$ then, the $m^{th}$ - order deformation can be written in the form:

$$S_{h_{j,m}}(t) = X_m S_{h_{j,m-1}}(t) + hJ^{\alpha_1}\left[\mathbb{R}^1_{j,m}\left(\vec{S}_{h_{j,m-1}}\right)\right],$$

$$I_{h_{j,m}}(t) = X_m I_{h_{j,m-1}}(It) + hJ^{\alpha_2}\left[\mathbb{R}^2_{j,m}\left(\vec{I}_{h_{j,m-1}}\right)\right],$$

$$R_{h_{j,m}}(t) = X_m R_{h_{j,m-1}}(t) + hJ^{\alpha_3}\left[\mathbb{R}^3_{j,m}\left(\vec{R}_{h_{j,m-1}}\right)\right],$$

**(26)**

The solutions of system (2) in every subinterval $[t_{j-1}, t_j], j = 1,2,3,\cdots n$ has the structure:

$$s_{h_j}(t) = \sum_{m=0}^{\infty} S_{h_{j,m}}(t - t_{j-1})$$

$$i_{h_j}(t) = \sum_{m=0}^{\infty} I_{h_{j,m}}(t - t_{j-1}) j = 1,2,\cdots n$$

$$r_{h_j}(t) = \sum_{m=0}^{\infty} R_{h_{j,m}}(t - t_{j-1})$$

**(27)**

and the solution of the system (6) for $[0, T]$ as:

$$S_{h_j}(t) = \sum_{m=0}^{\infty} s_{h_{j,m}}(t - t_{j-1})$$

$$I_{h_j}(t) = \sum_{m=0}^{\infty} i_{h_{j,m}}(t - t_{j-1}) \quad j = 1,2,\cdots n$$

$$R_{h_j}(t) = \sum_{m=0}^{\infty} r_{h_{j,m}}(t - t_{j-1})$$

Where

$$X_p = \begin{cases} 0, & t \in [t_{j-1}, t_j] \\ 1, & t \notin [t_{j-1}, t_j] \end{cases}$$

## RESULTS AND DISCUSSION

### Numerical Simulation and Graphical Illustration of the Model

We present the numerical simulation which demonstrate the analytical results for the model. This is achieved by using some set of parameter values. The MHAM provides approximate solutions to linear as well as nonlinear differential equations. We choose the auxiliary parameter h= -1 and partition the interval [0, 25] into subintervals with step size $\Delta t = 0.1$ and thereafter we obtain HAM series solutions of order k=5 at every subinterval.

We also employ MHAM algorithm constructed on the interval [0, 30]. The MHAM is demonstrated against Maple in-built fourth order Runge-Kutta procedure for the solution of the model. Figures 1 to 3 show the combined plots of the solutions of Sh, Ih, Rh, MHAM, and RK4.

**Table 1:** Parameters of the Model and Values.

| Parameter | Value | Source |
|---|---|---|
| $\theta$ | 0.03 | Peter et al. 2019 |
| $\beta$ | 0.02 | Assumed |
| $\mu$ | 0.002 | Peter et al. 2019 |
| $\varepsilon$ | 0.001 | Peter et al. 2019 |
| $\gamma$ | 1.2 | Assumed |
| $\alpha$ | 0.01 | Peter et al. 2019 |

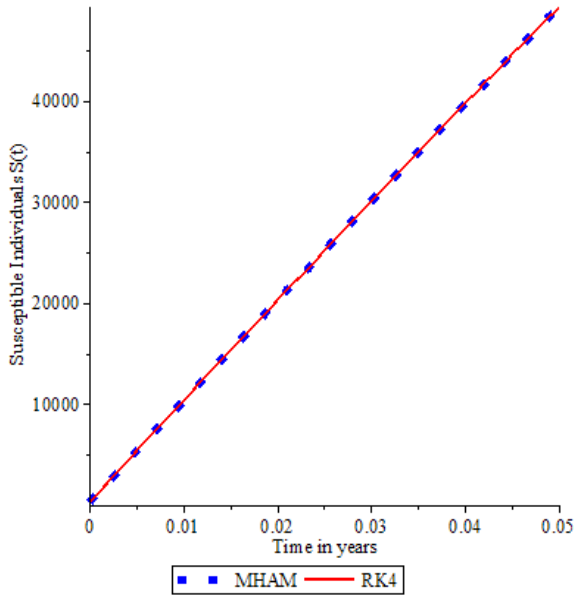


**Figure 1:** Solution of Susceptible Human Population by MHAM and RK4.

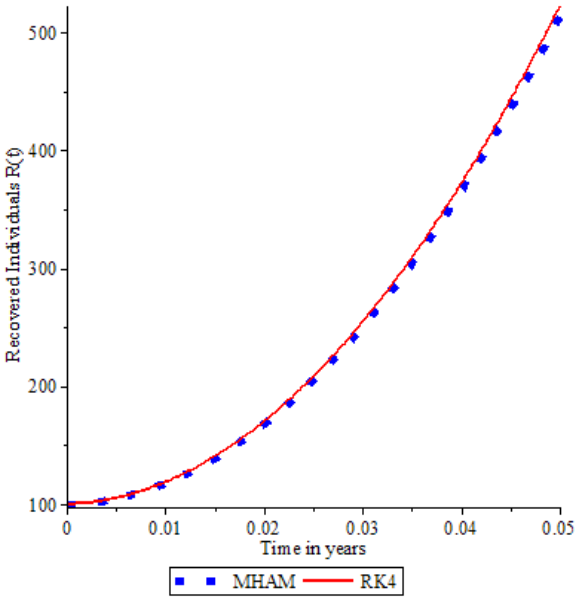


**Figure 3:** Solution of Recovered Human Population by MHAM and RK4.

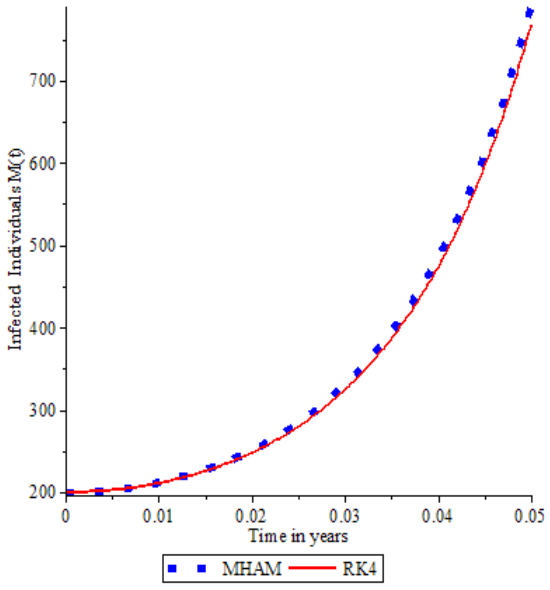


**Figure 2:** Solution of Infected Human Population by MHAM and RK4.

## CONCLUSION

In this paper, a fractional order differential Sh, Ih, Rh, model is studied, and its approximate solution is presented using a MHAM. The approximate solutions obtained by MHAM are highly accurate and valid for a long time. The reliability of the method and the reduction in the size of computational domain gives impetus of broad applicability. The comparison between MHAM and Runge-Kutta (RK4) were performed which were found to be efficient, accurate, and rapidly convergence

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