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APPROXIMATE SOLUTIONS OF MALARIA DISEASE TRANSMISSION MODEL: USING MULT-STEP DIFFERENTIAL TRANSFORM METHOD

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ABSTRACT

In this paper, numerical solutions to the SPEIR-SEI Malaria disease model were obtained using the Multi-Step Differential Transformation Method (MS-DTM). MS-DTM is a semi-analytical method for solving a system of a non-linear differential equation where its exact solution is difficult to obtain. The analytical solution of MS-DTM was compared with the solution of Maple21'sin-built classical fourth-order Runge-Kutta method. The results demonstrate the reliability and efficiency of the method and the graphs show that the solutions from both methods agreed well with each other.

Keywords: Malaria disease, Fourth order Runge-Kutta method, Multi-Step Differential Transform Methods, Maple21, SPEIR-SEI

INTRODUCTION

Mathematics is widely applied to so many real-life problems and these problems cannot be solved completely by analytical means and as a result, requires numerical methods to solve them. Most of these mathematical model varies from simple to complex depending on the nature of the research problems and it requires an analytical method to obtain their solution due to their non-linear nature.

Malaria is a vector-borne infectious disease that is predominantly present in poor tropical and subtropical areas of the world such as sub-Saharan Africa, Central, and South America, South East, Asia, and the Pacific Islands regions (Agada, et. al, 2021; Mandal, et. al, 2011). This infectious disease is life-threatening to humans and other animals and it is the leading cause of death and diseases in many developing countries. Malaria is caused by single-celled microorganisms (Protozoan) of the plasmodium group that causes the illness and it is characterized by vomiting, fever, chills, discomfort, and headaches (WHO,2011; Malaria fact sheet, 2014). The disease is most commonly spread by an infected female Anopheles mosquito, the mosquito bite introduces the plasmodium parasites from the mosquito's saliva into the Host (Human). In 2020, malaria caused an estimated 241 million clinical episodes, 627, 00 people died of malaria and they were mostly children in the sub-Saharan Africa region (CDC, 2021).

There are four different plasmodium species leading to malaria infection and disease among humans such as Plasmodium Falciparum (P. falciparum), Plasmodium vivax (P. vivax), Plasmodium Ovale (P. ovale), Plasmodium malaria (P. malaria) (Ortiz-Ruiz, et. al, 2018). Plasmodium falciparum is the most dangerous of all which causes malignant malaria also Plasmodium falciparum is responsible for about three-quarters of reported malaria cases (Agada, et. al, 2021).One of the problems arising in the field of epidemiology is the dynamics of malaria disease. The dynamics of Malaria disease is a complex system. To have a better understanding of the transmission of malaria disease dynamics and found appropriate control strategies, the use of a mathematical model has become very necessary.

Several research has been done in the area of mathematical modeling of malaria (Anderson and May, 1991; Bakare and Nwozo, 2015;Chitnis, et. al., 2006; Forouzannia, 2014; Hyun, 2000; Isoa, et. al., 2004; Jia, 2011; Killeen, et.al., 2000; Macdonald, 1957; Okosun 2010; Makinde and Okosun, 2011; Puntani and I-ming, (2010); Rafikov, et. al., 2011; Ross, et. al., 1910;).The differential Transform Method (DTM) is a semi-analytical method that has been applied to solve different non-linear model models (Abioye et. al., 2018; Adewale et. al., 2016;Akogwu, 2022; Ghazala and Shaista, 2019; Omoloye, et. al., 2022; Peter et. al., 2018).The series solution of DTM always converges in a very small region and it has a slow convergent rate in the wider region (Arikoglu and Ozkol, 2006; Bildik, et. al., 2006; Gokdogan et. al., 2012). To overcome the drawback of DTM, the Multi-Step Differential Transformation Method which is a semi-analytical method has been applied by several researchers to solve non-linear differential equations (Astuti, et. al., 2019;EL-Zahar, 2015; Merdan, et.al., 2013; Odibat*et al.* 2010; Yildirim, et. al., 2012).

Notwithstanding the several analytical methods applied to solve the dynamic of the malaria disease model, none has used the MS-DTM to solve the model. This work aims to apply the Multi-Step Differential Transformation Method (MS-DTM) to find the approximate series solution for the SPEIR-SEI Malaria model as proposed by Usman, et al., (2020) and to validate the efficiency of MS-DTM solutions with Maple21's in-built Runge-Kutta method of order four.

MATERIALS AND METHODS

Seir-Sei Model

This paper considered the SPEIR-SEI model proposed by Usman, et al., (2020). The SPEIR-SEI model is a system of eight (8) non-linear differential equations and it is difficult to find its exact equation. The model is divided into two populations, the host (human) population, and the vector (mosquito) population. The host (human) population is subdivided into five compartments, the Susceptible, the Exposed, the Infected, the Recovered, and the Protected (SPEIR). While the vector (mosquitoes) population is subdivided into three compartments, the Susceptible, the Exposed, and the Infected (SEI).

The SPEIR Model for the Host (human) population is given as;

$$\frac{dS_H}{dt} = \pi_H - \frac{b\beta_H S_H I_M}{1 + v_H I_M} - (\mu_H + e)S_H + \omega R_H \quad (1)$$

$$\frac{dE_H}{dt} = \frac{b\beta_H S_H I_M}{1 + v_H I_M} - (\varepsilon_H + \mu_H)E_H \quad (2)$$

$$\frac{dI_H}{dt} = \varepsilon_H E_H - (r + \mu_H + \varphi_H)I_H \quad (3)$$

$$\frac{dR_H}{dt} = rI_H - (\mu_H + \omega)R_H \quad (4)$$

$$\frac{dP_H}{dt} = eS_H - \mu_H P_H \quad (5)$$

The SEI Model for the Vector (mosquitoes) population is given as;

$$\frac{dS_M}{dt} = \pi_V - \frac{b\beta_M S_M I_H}{1 + v_M I_H} - \mu_M S_M \quad (6)$$

$$\frac{dE_M}{dt} = \frac{b\beta_M S_M I_H}{1 + v_M I_H} - (\varepsilon_V + \mu_M)E_M \quad (7)$$

$$\frac{dI_M}{dt} = \varepsilon_M E_M - (\mu_M + \varphi_M)I_M \quad (8)$$

The variables, parameters, and initial conditions are described below.

Table 1: Description of variables and parameters.

SYMBOL	DESCRIPTION OF VARIABLES AND PARAMETERS	SOURCES
S_H	Individuals who are susceptible to the disease = 100	Olaniyi and Obabiyi. (2013)
E_H	Individuals who are exposed to the disease = 20	Olaniyi and Obabiyi. (2013)
I_H	Individuals per unit of time who are infected with the disease = 10	Olaniyi and Obabiyi. (2013)
R_H	Individuals per unit of time who recovered from the disease = 0	Olaniyi and Obabiyi. (2013)
P_H	Individuals per unit of time who are protected from the disease = 0	Nagwari, et al., (2020).
S_M	Mosquitoes that are susceptible to the disease = 1000	Olaniyi and Obabiyi. (2013)
E_M	Mosquitoes that are exposed to the disease = 20	Olaniyi and Obabiyi. (2013)
I_M	Mosquitoes per unit of time that are infected with the disease = 30	Olaniyi and Obabiyi. (2013)
π_H	Recruitment Rate of Humans = 0.00125	Olaniyi and Obabiyi. (2013)
π_M	Recruitment Rate of Mosquitoes = 0.007	Olaniyi and Obabiyi. (2013)
μ_H	Death Rate of Humans = 0.0000548	Olaniyi and Obabiyi. (2013)
μ_M	Death Rate of Mosquitoes = 0.06667	Olaniyi and Obabiyi. (2013)
ε_H	Rate of Development fromE_H to I_H for Humans = 0.05882	Olaniyi and Obabiyi. (2013)
ε_M	Rate of Development fromE_H to I_H for Mosquitoes = 0.05556	Olaniyi and Obabiyi. (2013)
e	Per capita rate of behavioural change. = 0.25	Nagwari, et al., (2020).)
φ_H	Disease-induced death rate of humans = 0.001	Olaniyi and Obabiyi. (2013)
φ_M	Disease-induced death rate of mosquitoes = 0.01	Olaniyi and Obabiyi. (2013)
β_H	Probability that a bite by infectious mosquito results in the transmission of the disease to humans = 0.1	Olaniyi and Obabiyi. (2013)
β_M	Probability that a bite results in the transmission of the parasite to a susceptible mosquito = 0.09	Olaniyi and Obabiyi. (2013)
ω	Per capita rate of loss of immunity in humans = 1/730	Olaniyi and Obabiyi. (2013)
v_H	Proportion of antibodies produced by humans in response to the incidence of infection caused by humans = 0	Olaniyi and Obabiyi. (2013)
v_M	Proportion of antibodies produced by a mosquito in response to the incidence of infection caused by humans = 0	Olaniyi and Obabiyi. (2013)
r	Per capita recovery rate for humans from the infectious state of the recovered state = 0.05	Olaniyi and Obabiyi. (2013)
b	Biting rate of the mosquito = 0.12	Olaniyi and Obabiyi. (2013)

Derivation of DTM and MS-DTM

The differential transformation $F(k)$ of a function $f(t)$ is defined as follows:

$$F(k) = \frac{1}{k!}\left[\frac{d^k f(t)}{dt^k}\right]_{t=t_0} \quad (9)$$

where $f(t)$ is the original function and $F(k)$ is the transformedfunction.

The differential inverse transformation of $F(k)$is defined as follows:

$$f(t) = \sum_{k=0}^{\infty}(t-t_0)^k F(k) \quad (10)$$

From (5) and (6) , respectively, the arbitrary function $f(t)$expanded in the Taylor series is defined as;

$$f(t) = \frac{(t-t_0)^k}{k!}\sum_{k=0}^{N}\left[\frac{d^k f(t)}{dt^k}\right]_{t=t_0} \quad (11)$$

where N is a convergence of natural frequency.

If $g(t)$ and $h(t)$are two uncorrelated functions with t, where $G(t)$) and $H(t)$ are the transformed functions corresponding to $g(t)$ and $h(t)$) then, the fundamental mathematical operationsperformed by differential transform are listed blow

Table 2: The mathematical operations of the DTM

S/N	Original function	Transformed Function
1	$F(k) = G(t) \pm H(t)$	$f(t) = g(t) \pm h(t)$
2	$F(k) = \alpha G(k)$, where α is a constant	$f(t) = aG(t)$
3	$F(k) = (k+1)F(k+1)$	$f(t) = \frac{dg(t)}{dt}$
4	$F(k) = (k+1)(k+2) + \cdots (k+m)F(k+m)$	$f(t) = \frac{d^k g(t)}{dt^k}$
5	$F(k) = \delta(k)$, where δ is the Kronecker delta	$f(t) = 1$
6	$F(k) = \delta(k-1)$	$f(t) = t$
7	$F(k) = \delta(k-m) = \begin{cases}1, k^{\,m}\\ 0, k_{\neq m}\end{cases}$	$f(t) = t^m$
8	$F(k) = \sum_{m=0}^{k} G(m)H(k-m)$	$f(t) = g(t)h(t)$
9	$F(t) = e^{(\lambda t)}$	$f(t) = \frac{\lambda^k}{k!}$
10	$F(t) = (1+t)^m$	$f(t) = \frac{(m(m-1)\ldots(m-k+1))}{k!}$

Definition of Multi-Step Differential Transformation Method (MS-DTM).

The Multi-Step Differential Transformation method (MS-DTM) presented in the studies of (Jang, et. al., 2000; Bervillier, 2012) has been used. Let $[0,T]$ be the interval for nonlinear initial value problem $f(t,x,x',\ldots,x^n) = 0$ and this can be expressed by finite series as;

$$x(t) = \sum_{n=0}^{k} a_n t^n, t \in [0,T] \quad (12)$$

Subject to the initial condition $x^{(k)}(0) = c_k \; for \; k = 0,1,\ldots,n-1$. We assumed that the interval $[0,T]$ is divided into M sub-interval $[t_{m-1}, t_m]$ with $m = 1,2,\ldots M$ of equal step size $h = \frac{T}{M}$, by using the nodes $t_m = mh$ and the series solutions are obtained by applying DTM to $f(t,x,x',\ldots,x^n) = 0$ we have,

$$x_1(t) = \sum_{n=0}^{k} a_{1n} t^n, t \in [0,t_1] \quad (13)$$

Using the initial condition ${x_1}^{(k)}(0) = c_k \; for \; k = 0,1,\ldots,n-1$.

For $m \geq 2$ and at each subinterval $[t_{m-1}, t_m]$ with the initial conditions ${x_m}^{(k)}(t_{m-1}) = {x_{m-1}}^{(k)}(t_{m-1})$. The process is repeated and solutions $x_1(t), m = 1,2,\ldots,M$ with $N = K.M$ for the solution $X(t)$ and replacing t_0 with t_{m-1} in equation (11) we have,

$$x_m(t) = \sum_{n=0}^{k} a_{mn}(t-t_{m-1})^n, t \in [t_{m-1}, t_{m+1}] \quad (14)$$

APPLICATION OF THE MS-DTM TO THE SEIRP-SEI MALARIA MODEL

Using the transformed function of the original function in Table 2 to obtain the recurrence relation of SPEIR-SEI Malaria model in equations (1-8) we have;

$$S_H(k+1) = \frac{1}{k+1}\left(\pi_H - b\beta_H \sum_{l=0}^{k}\frac{S_H(l)I_M(k-l)}{1+v_H I_M(k)} - (\mu_H + e)S_H(k) + \omega R_H(k)\right) \quad (15)$$

$$P_H(k+1) = \frac{1}{k+1}(eS_H(k) - \mu_H P_H(k)) \quad (16)$$

$$E_H(k+1) = \frac{1}{k+1}\left(b\beta_H \sum_{l=0}^{k} \frac{S_H(l)I_M(k-l)}{1+v_H I_M(k)} - (\mu_H + \varepsilon_H)E(k)\right) \quad (17)$$

$$I_H(k+1) = \frac{1}{k+1}(\varepsilon_H E_H(k) - (r + \mu_H + \varphi_H)I_H(k)) \quad (18)$$

$$R_H(k+1) = \frac{1}{k+1}(rI_H(k) - (\mu_H + \omega)R_H(k) \quad (19)$$

$$S_M(k+1) = \frac{1}{k+1}\left(\pi_M - b\beta_M \sum_{l=0}^{k} \frac{S_H(l)I_H(k-l)}{1+v_M I_H(k)} - \mu_M S_H(k)\right) \quad (20)$$

$$E_M(k+1) = \frac{1}{k+1}\left(b\beta_H \sum_{l=0}^{k} \frac{S_H(l)I_H(k-l)}{1+v_M I_H(k)} - (\mu_H + \varepsilon_M)E_M(k)\right) \quad (21)$$

$$I_M(k+1) = \frac{1}{k+1}\left(\varepsilon_M E_M(k) - (\mu_M + \varphi_M)I_M(k)\right) \quad (22)$$

where$S_H(k)$,$P_H(k)$, $E_H(k)$, $I_H(k)$, $R_H(k)$, $S_M(k)$, $E_M(k)$and $I_M(k)$ are the differential transformation of $s_H(t)$, $e_H(t)$, $i_H(t)$, $r_H(t)$, $p_H(t)$, $s_M(t)$, $e_M(t)$ and $i_M(t)$ respectively. Therefore the DTM series solution of the SPEIR-SEI Malaria model is given as

$$s_H(t) = \sum_{n=0}^{k} S_H(k)t^k \quad (23)$$

$$p_H(t) = \sum_{n=0}^{k} P_H(k)t^k \quad (24)$$

$$e_H(t) = \sum_{n=0}^{k} e_H(k)t^k \quad (25)$$

$$i_H(t) = \sum_{n=0}^{k} I_H(k)t^k \quad (26)$$

$$r_H(t) = \sum_{n=0}^{k} R_H(k)t^k \quad (27)$$

$$s_M(t) = \sum_{n=0}^{k} S_M(k)t^k \quad (28)$$

$$e_M(t) = \sum_{n=0}^{k} E_M(k)t^k \quad (29)$$

$$i_M(t) = \sum_{n=0}^{k} I_M(k)t^k \quad (30)$$

The MS-DTM solution of the SPEIR-SEI Malaria model is given as:

$$X(t) = \begin{cases} x_1(t), t \in [0, t_1] \\ x_2(t), t \in [0, t_2] \\ \vdots \\ x_M(t), t \in [t_{M-1}, t_M] \end{cases} \quad (31)$$

Where $X(t)$ represents S_{Hj}, E_{Hj}, I_{Hj}, R_{Hj},P_{Hj}, S_{Mj}, E_{Mj} and I_{Mj} M, for $j = 1, 2, 3, 4, \dots, M$ to satisfy the recurrence relations given in equation (10):

$$S_{Hj}(k+1) = \frac{1}{k+1}\left(\pi_H - b\beta_H \sum_{l=0}^{k} \frac{S_{Hj}(l)I_{Mj}(k-l)}{1+v_H I_{Mj}(k)} - (\mu_H + e)S_{Hj}(k) + \omega R_{Hj}(k)\right) \quad (32)$$

$$P_{Hj}(k+1) = \frac{1}{k+1}\left(eS_{Hj}(k) - \mu_H P_{Hj}(k)\right) \quad (33)$$

$$E_{Hj}(k+1) = \frac{1}{k+1}\left(b\beta_H \sum_{l=0}^{k} \frac{S_{Hj}(l)I_{Mj}(k-l)}{1+v_H I_{Mj}(k)} - (\mu_H + \varepsilon_H)E_{Hj}(k)\right) \quad (34)$$

$$I_{Hj}(k+1) = \frac{1}{k+1}(\varepsilon_H E_{Hj}(k) - (r + \mu_H + \varphi_H)I_{Hj}(k)) \quad (35)$$

$$R_{Hj}(k+1) = \frac{1}{k+1}(rI_{Hj}(k) - (\mu_H + \omega)R_{Hj}(k) \quad (36)$$

$$S_{Mj}(k+1) = \frac{1}{k+1}\left(\pi_M - b\beta_M \sum_{l=0}^{k} \frac{S_{Hj}(l)I_{Hj}(k-l)}{1+v_M I_{Hj}(k)} - \mu_M S_{Hj}(k)\right) \quad (37)$$

$$E_{Mj}(k+1) = \frac{1}{k+1}\left(b\beta_H \sum_{l=0}^{k} \frac{S_{Hj}(l)I_{Hj}(k-l)}{1+v_M I_{Hj}(k)} - (\mu_H + \varepsilon_M)E_{Mj}\right) \quad (38)$$

$$I_{Mj}(k+1) = \frac{1}{k+1}\left(\varepsilon_M E_{Mj}(k) - (\mu_M + \varphi_M)I_{Mj}(k)\right) \quad (39)$$

Such that $S_{Hj}(0) = S_{H(j-1)}(0)$, $P_{Hj}(0) = P_{H(j-1)}(0)$, $E_{Hj}(0) = E_{H(j-1)}(0$, $I_{Hj}(0) = I_{H(j-1)}(0)$, $R_{Hi}(0) = R_{H(i-1)}(0)$, $S_{Mj}(0) = S_{M(j-1)}(0)$, $E_{Mj}(0) = E_{M(j-1)}(0)$ and $I_{Mj}(0) = I_{M(j-1)}(0)$,

SIMULATION RESULTS AND DISCUSSION

The SPEIR-SEI Malaria model was solved with the aid of Maple21 programming software. The initial conditions with the values of the parameters for the model in table1 were used for the numerical simulation.

Table 3: Comparison of the solutions obtained by MS-DTM, and RK4 for Susceptible Humans.

Time(t)	(S_H) MS-DTM	(S_H) $RK4$	|MS-DTM $-$ $RK4$|
0.00	100.0000000000000	100.0000000000000	0
0.01	99.39263091661203	99.3918741508497	0.000756766
0.02	98.79058370834239	98.7875802834613	0.003003425
0.03	98.19379131363868	98.1870864611084	0.006704853
0.04	97.60218775482758	97.5903612722981	0.011826483
0.05	97.01570811736572	96.9973736291060	0.018334488
0.06	96.43428852958498	96.4080927671777	0.026195762
0.07	95.85786614293220	95.8224882457274	0.035377897
0.08	95.28637911270354	95.2405299475385	0.045849165
0.09	94.71976657927317	94.6621880789638	0.0575785
0.1	94.15796864981649	94.0874331699250	0.07053548

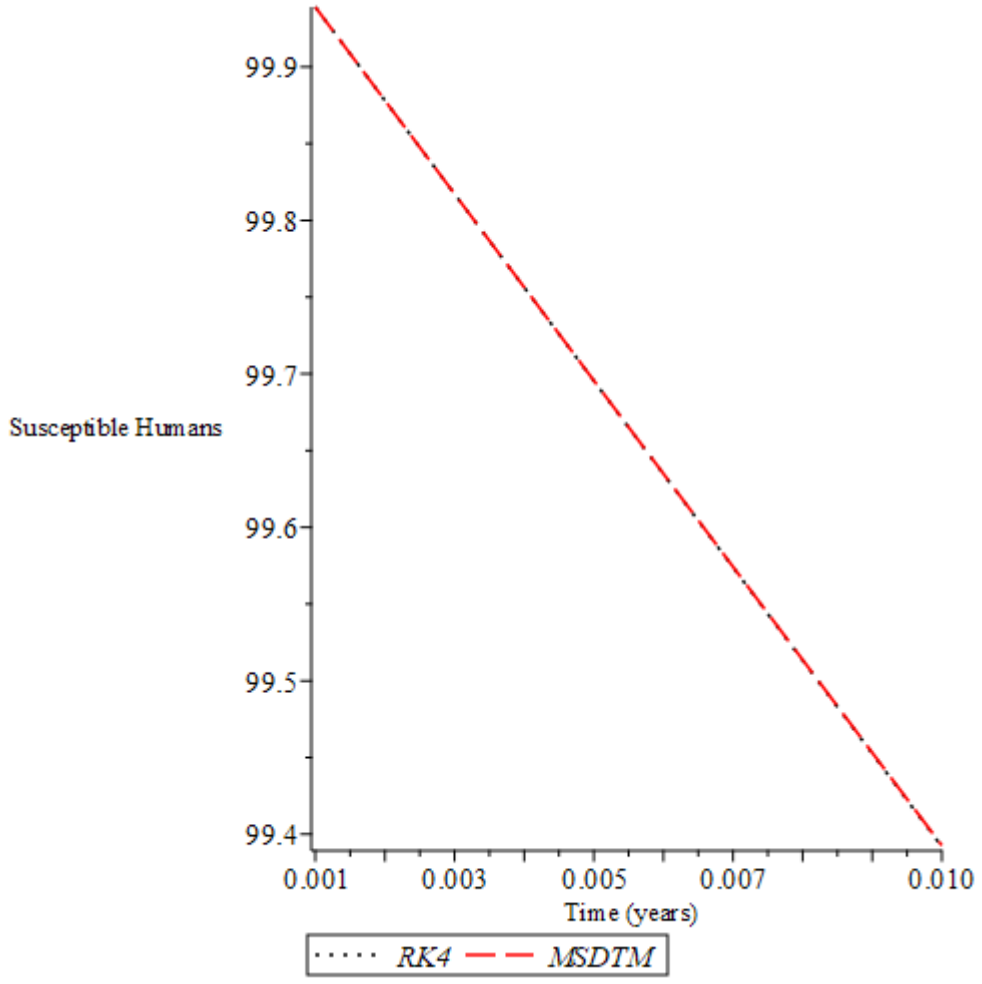

Figure 1: Plot showing the solutions of the Susceptible Humans by MS-DTM and RK4.

Table 4: Comparison of the solutions obtained by MS-DTM and RK4 for Protected Humans

Time(t)	(P_H) MS-DTM	(P_H) $RK4$	|MS-DTM $-$ $RK4$|
0.00	5.00000000000000	5.00000000000000	0
0.01	5.249236864503709	5.24923623266672	4.9956E-06
0.02	5.496961836561834	5.49695684095906	1.67665E-05
0.03	5.743188137631677	5.74317137115709	3.95612E-05
0.04	5.987928822866620	5.98788926162631	7.69046E-05
0.05	6.231196783795756	6.23111987916588	0.000132232

0.06	6.473004750948551	6.47287251900868	0.000208892
0.07	6.713365296424539	6.71315640482118	0.000310148
0.08	6.952290836408062	6.95198068870354	0.000439182
0.09	7.189793633628029	7.18935445118960	0.000599099
0.1	7.425885799762727	7.42528670124683	4.9956E-06

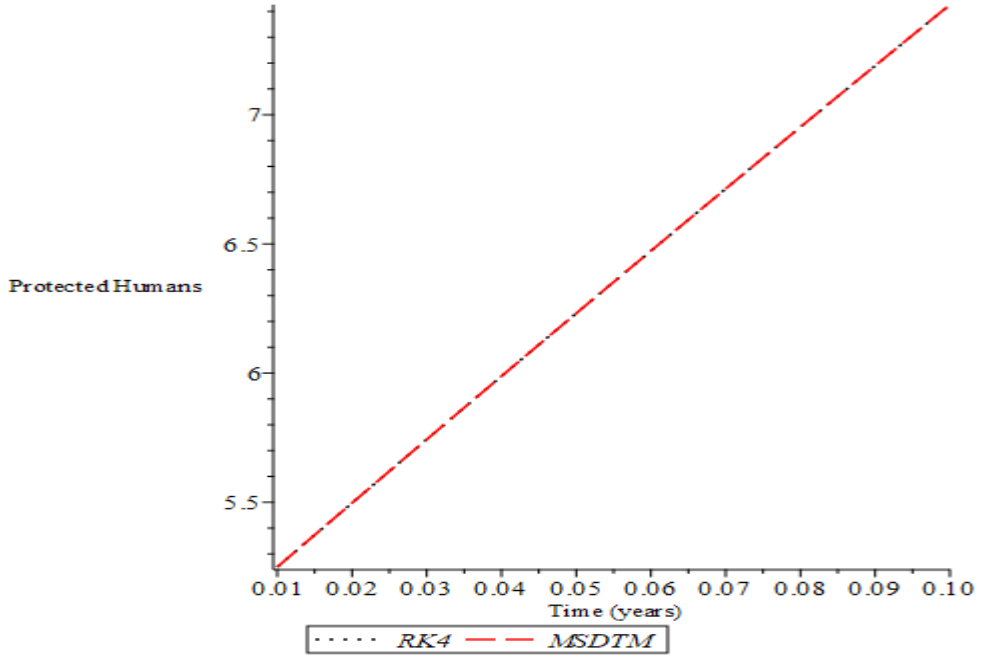

Figure 2: Plot showing the solutions of the Protected Humans by MS-DTM and RK4.

Table 4: Comparison of the solutions obtained by MS-DTM and RK4 for Exposed Humans.

Time(t)	**(E_H) MS-DTM**	**(E_H) $RK4$**	**MS-DTM $-$ $RK4$**
0.00	20.0000000000000	20.000000000000	0
0.01	20.35762667665543	20.3576363714703	9.69481E-06
0.02	20.71290034914333	20.7129354878407	3.51387E-05
0.03	21.06584907372839	21.0659198764134	7.08027E-05
0.04	21.41650047618613	21.4166116454263	0.000111169
0.05	21.76488175941470	21.765032649935	0.000150891
0.06	22.11101971087939	22.1112044918146	0.000184781
0.07	22.45494070988947	22.4551485197567	0.00020781
0.08	22.79667073470770	22.7968858292721	0.000215095
0.09	23.13623536949244	23.1364372626897	0.000201893
0.1	23.47365981107207	23.4738234091563	0.000163598

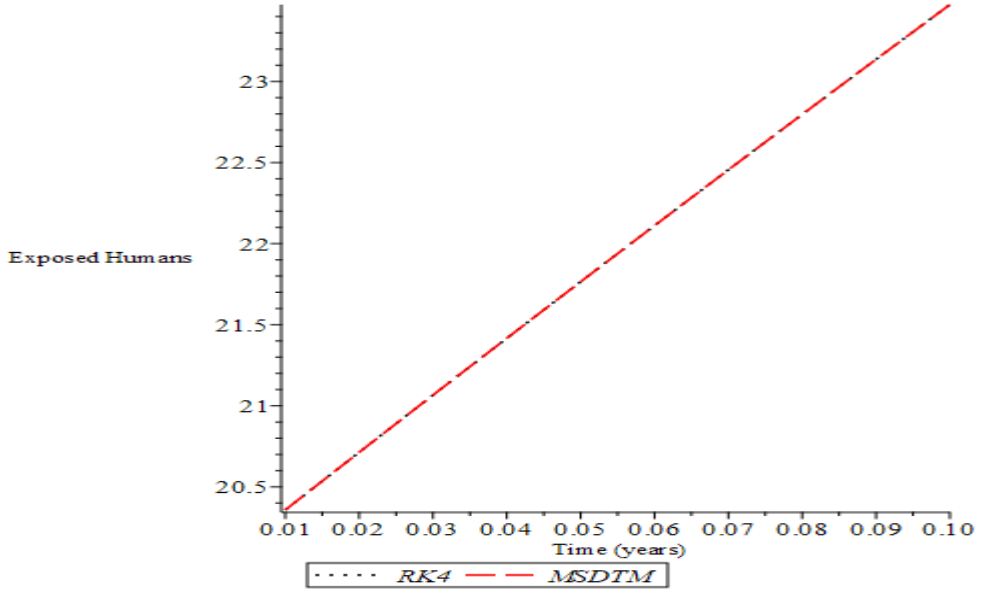

Figure 3: Plot showing the solutions of the Exposed Humans by MS-DTM and RK4.

Table 6: Comparison of the solutions obtained by MS- DTM and RK4 for Infected Humans.

Time(t)	**(I_H) MS-DTM**	**(I_H) $RK4$**	**MS-DTM $-$ $RK4$**
0.00	10.0000000000000	10.0000000000000	0
0.01	9.996082450432257	9.99608245062615	.939E-10
0.02	9.992187861354684	9.99218786231419	9.5951E-10
0.03	9.988316083506590	9.98831608649652	2.98993E-09
0.04	9.984466969340633	9.98446697646367	7.12304E-09
0.05	9.980640372996897	9.98064038675359	1.37567E-08
0.06	9.976836150277441	9.97683617315170	2.28743E-08
0.07	9.973054158621348	9.97305419269086	3.40695E-08
0.08	9.969294257080245	9.96929430365137	4.65711E-08
0.09	9.965556306294318	9.96555636556099	5.92667E-08
0.1	9.961840168468816	9.96184023919490	5.92667E-08

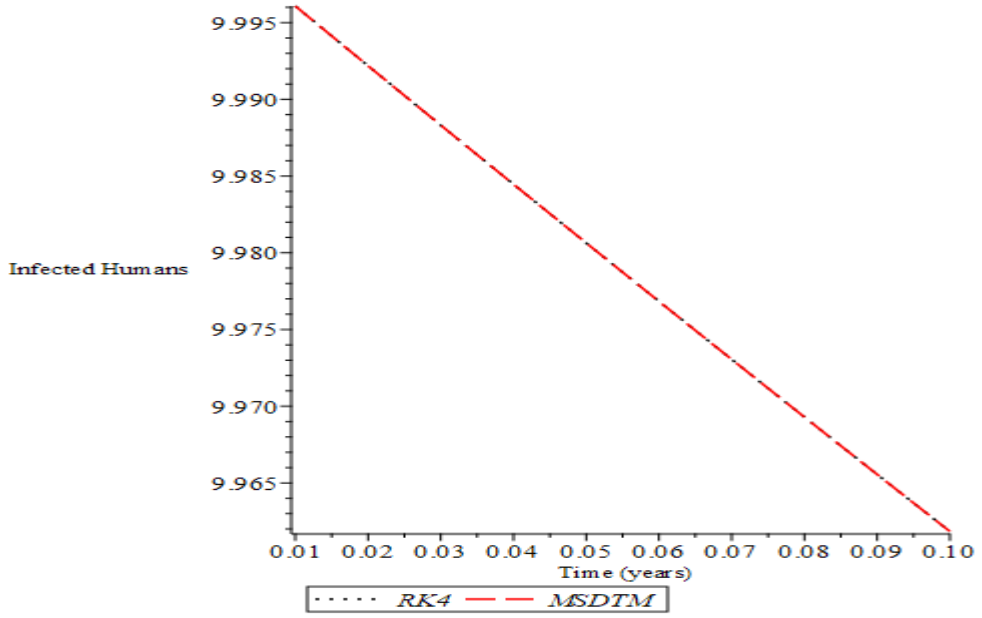

Figure 4: Plot showing the solutions of the Infected Humans by MS-DTM and RK4.

Table 7: Comparison of the solutions obtained by MS-DTM and RK4 for Recovered Humans.

Time(t)	R_H MS-DTM	R_H $RK4$	
0.00	0.5000000000000000	0.50000000000000000	0
0.01	0.004998984041039473	0.00499898404112516	8.56901E-14
0.02	0.009995943849427750	0.00999594388676876	3.7341E-11
0.03	0.01499089089677941	0.0149908910193964	1.22617E-10
0.04	0.01998383658034481	0.0199838368114170	2.31072E-10
0.05	0.02497479222386050	0.0249747925681116	3.44251E-10
0.06	0.02996376907838603	0.0299637695276343	4.49248E-10
0.07	0.03495077832312725	0.0349507788610115	5.37884E-10
0.08	0.03993583106624593	0.0399358316721421	6.05896E-10
0.09	0.04491893834565580	0.044918938997797	6.5E-10
0.1	0.04990011112980511	0.0499001118076224	6.52141E-10

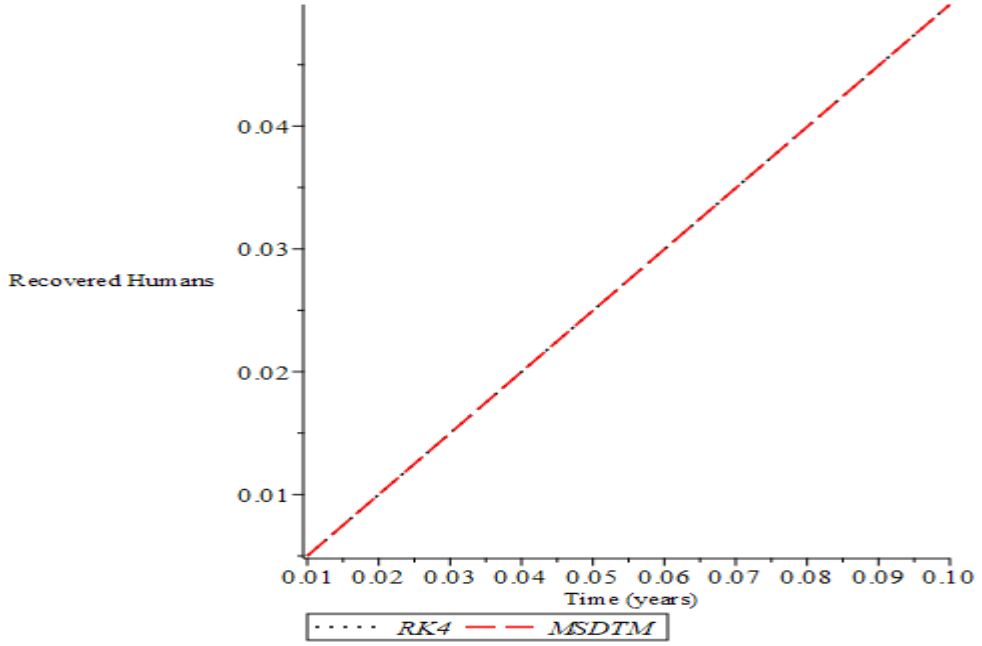

Figure 5: Plot showings the solution of the Recovered Humans by MS-DTM and RK4.

Table 8: Comparison of the solutions obtained by MS-DTM and RK4 for Susceptible Mosquitoes.

Time(t)	(S_M) MS-DTM	(S_M) $RK4$	|MS-DTM $- RK4$|
0.00	1000.00000000000	1000.00000000000	0
0.01	998.2556871402225	998.255105916992	0.000581223
0.02	996.5159964413853	996.513676975744	0.002319466
0.03	994.7809098016349	994.775703199738	0.005206602
0.04	993.0504092216594	993.041174681369	0.00923454
0.05	991.3244768038659	991.310081559535	0.014395244
0.06	989.6030947515721	989.582414019648	0.020680732
0.07	987.8862453682062	987.858162293624	0.028083075
0.08	986.1739110565213	986.137316659888	0.036594397
0.09	984.4660743178170	984.419867443372	0.046206874
0.1	982.7627177511759	982.705805015517	0.056912736

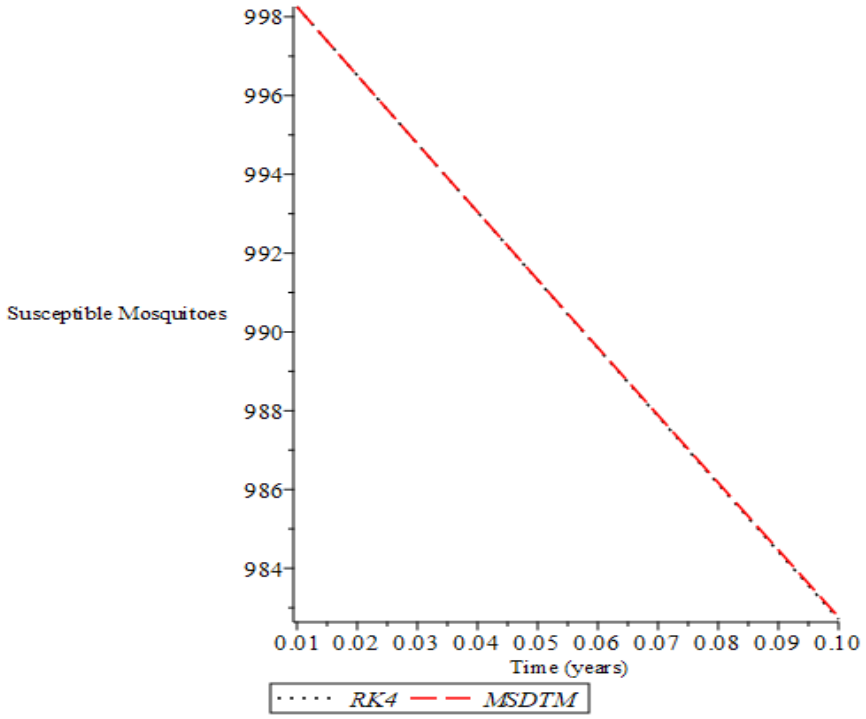

Figure 6: Plot showing the solution of the Susceptible Mosquitoes by MS-DTM and RK4.

Table 9: Comparison of the solutions obtained by MS-DTM and RK4 for Exposed Mosquitoes.

Time(t)	**(E_M) MS-DTM**	**(E_M) $RK4$**	**MS-DTM− $RK4$**
0.00	20.0000000000000	20.00000000000000	0
0.01	21.05311292558335	21.0537555673693	0.000642642
0.02	22.10136155944363	22.1039223487184	0.002560789
0.03	23.14477254866620	23.1505123931806	0.005739845
0.04	24.18337235686542	24.1935376715429	0.010165315
0.05	25.21718726579668	25.2330101003724	0.015822835
0.06	26.24624337694907	26.2689415420157	0.022698165
0.07	27.27056661311912	27.3013438045990	0.030777191
0.08	28.29018271996538	28.3302286420282	0.04004593
0.09	29.30511726754381	29.3556077539890	0.040045922
0.1	30.31539565182410	30.3774927859465	0.050490486

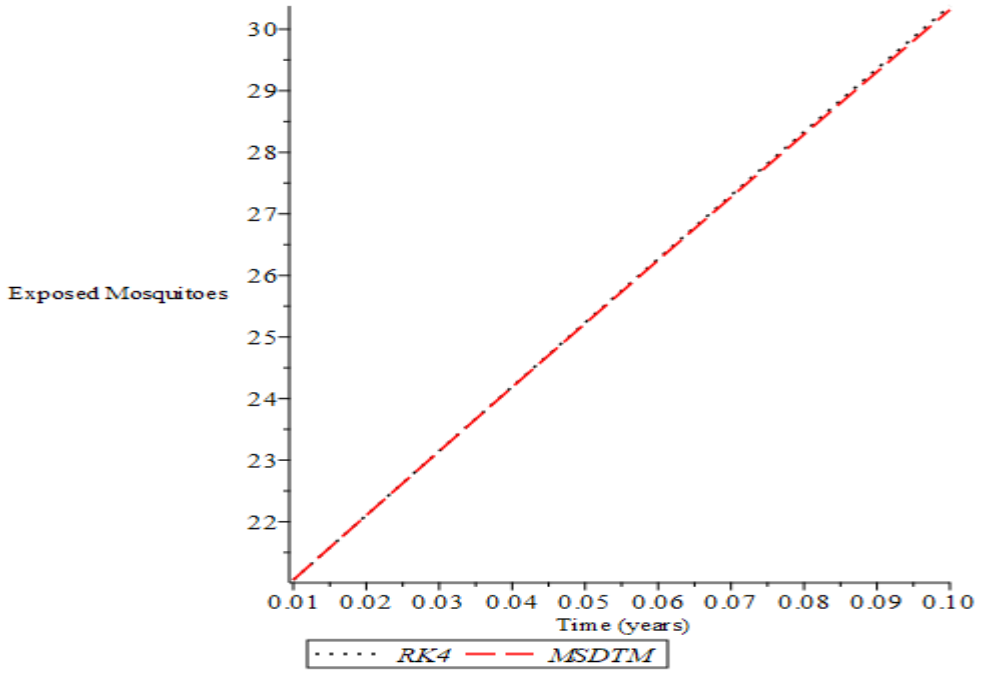

Figure 7: Plot showing the solutions of the Exposed Mosquitoes by MS-DTM and RK4.

Table 10: Comparison of the solutions obtained by MS-DTM and RK4 for Infected Mosquitoes.

Time(t)	**(I_M) MS-DTM**	**(I_M) *RK4***	**|MS-DTM− *RK4*|**
0.00	30.00000000000000	30.0000000000000	5.919E-10
0.01	29.98840826225117	29.9884083813568	1.19106E-07
0.02	29.97740894158618	29.9774098900576	9.48472E-07
0.03	29.96699888981741	29.9670020813996	3.19158E-06
0.04	29.95717497591850	29.9571825206669	7.54475E-06
0.05	29.94793408590970	29.9479487813357	1.46954E-05
0.06	29.93927312274444	29.9392984450747	2.53223E-05
0.07	29.93118900619669	29.9312291017449	4.00955E-05
0.08	29.92367867274943	29.9237383493992	5.96766E-05
0.09	29.91673907548421	29.9168237942834	8.47188E-05
0.1	29.91036718397161	29.9104830508350	0.000115867

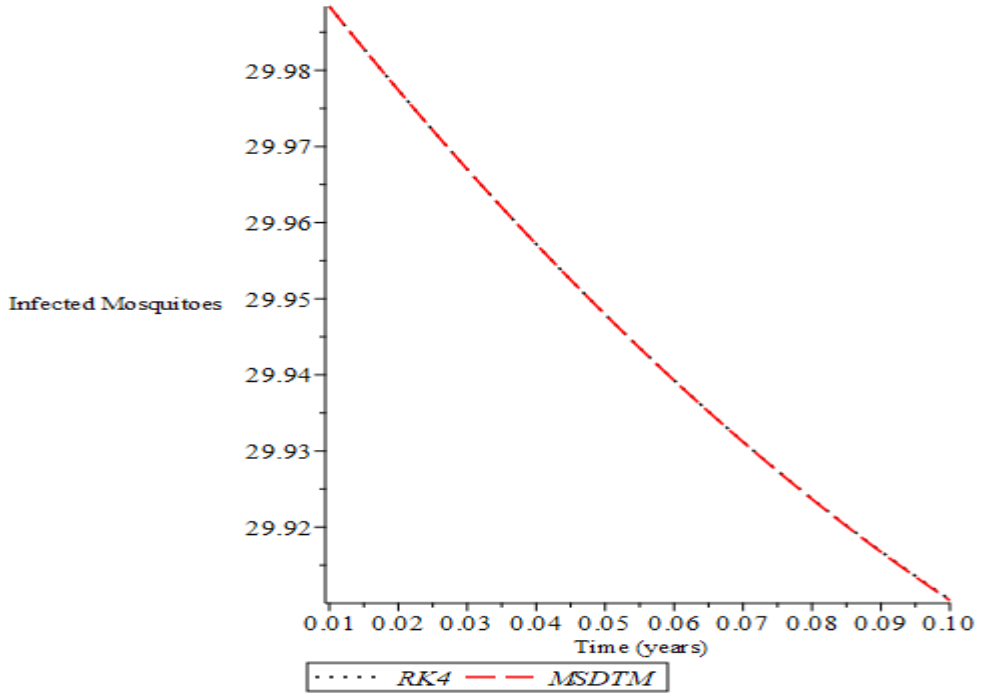

Figure 8: Plot showing the solutions of the Infected Mosquitoes by MS-DTM and RK4.

The graphs from figure 1-8 show that the solutions obtained by using the Multi-Step Differential Transform Method show a good correlation with the solution obtained using the fourth-order Runge-Kutta (RK4) method, which implies that MS-DTM has shown to be a reliable, efficient, and accurate with a high level of convergence.

CONCLUSION

The Multi-Step Differential Transform Method (MS-DTM) has been used to solve the SPEIR-SEI Malaria disease model with given initial conditions. The numerical results obtained show that MS-DTM is a reliable and excellent mathematical tool for conducting and conveying analysis on Malaria disease models.

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