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Analytical Solution of Dynamical Transmission of Malaria disease Model Using Differential Transform Method

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Abstract: **The aim of this work is to compare analytical solution of Differential Transformation Method (DTM) with in-built solutions of Runge-Kutta Method (RK4) of MAPLE 18 software on dynamical transmission of malaria disease model. Mathematical model is developed in terms of nonlinear first order ordinary differential equations. Existence and uniqueness of model solution was determined and analytical solution of the model was obtained using Differential Transform Method. In order to show the efficiency of the method we compare the analytical solutions obtained by Differential Transform Method and fourth-order Runge-Kutta method. The validity of the DTM in solving the model is established by using the computer in-built RK4. We illustrated the profiles of the solutions of each of the compartments, from which we speculate that the DTM and RK4 solutions agreed well.**

Keywords: **Malaria disease, Existence and Uniqueness of solution, Differential Transformation Method and Runge Kutta Method.**

I. INTRODUCTION

The use of analytical method to obtain the solution mathematical models for solving biological problems varies from simple to complex analyses, depending on the nature of the research problems and applicability of the models. Adewale *et al*. (2017) used a system of differential equation approach to model the dynamical spread of malaria where humans and vectors interact and infect each other. The numerical result shows that the most effective strategies for controlling malaria is to reduce the vector biting rate and increased the human treatment. Peter *et al.* (2018) worked on series solution of typhoid fever model using differential transform method to study the transmission dynamics of typhoid fever diseases in a population. Differential Transformation Method was discussed, which later used to compute the series solution of the differential equation governing the model equations and graphical results confirm that (DTM) is in good agreement with RK-4 and this produced correctly same behavior of the model but not apply to Ebola virus and malaria disease model. Ghazala and Shaista (2019) worked on comparative study of mathematical model of Ebola virus disease via using differential transform method and variation of iteration method. The result revealed that both methods are in complete agreement, accurate and efficient for solving systems of ODEs. Omoloye *et al.*(2019) used differential transformation method to solve Lassa fever model. Firstly, existence and uniqueness of the solution was determined to establish that the model is mathematically well posed for the application of DTM. Numerically, simulations were conducted to compare the results obtained by DTM and that of fourth-order Runge-Kutta method and shown, DTM is very effective in predicting the solution of epidemics of Lassa fever model .This study investigates the analysis of Coronavirus disease model by Differential Transformation Method (DTM).

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Omoloye *et al.* (2021) worked on analysis of differential transformation method to obtain power series of Coronavirus disease model and accuracy of DTM is demonstrated against Runge-Kutta method of order four (RKM) numerical solution and it demonstrated high accuracy of the results. Plotted DTM solution is found to be in good agreement with the popular Runge-Kutta solution. Omoloye and Adewale (2021) developed an Ebola- Malaria co-infection model, in their work it shows that malaria is an important mimic or co-infection in potential Ebola virus disease patients. The model was analyzed for stability and it was established that the disease free equilibrium of each model and their co-infections were locally and globally asymptotically stable whenever the basic reproduction number is less than unity or endemic otherwise. Sensitivity analysis on the basic reproduction number reveal the most sensitive index value and the graph shows that by eliminating the co-infection contact rate of Ebola- malaria disease in the population in other to control Ebola-Malaria co-infections. To further extend the work of Omoloye and Adewale (2021) by performed the differential transform method on the malaria sub-model of Ebola- Malaria co-infection model in order to obtain the analytical solution of this model.

II. MALARIA DISEASE MODEL FORMULATION

The human population is divided into three classes; susceptible individuals $S_H(t)$, individuals exposed to malaria disease $E_M(t)$, individuals infected with malaria $I_M(t)$, individuals that recovered from malaria $R_M(t)$, therefore these give as;

$$N_H(t) = S_H(t) + E_M(t) + I_M(t) + R_M(t) \tag{1}$$

Similarly, the total vector (mosquito) population is sub-divided into susceptible mosquitoes $S_V(t)$, exposed mosquitoes $E_V(t)$ and the infected mosquitoes $I_V(t)$ so that the total population of mosquitoes is denoted by;

$$N_V(t) = S_V(t) + E_V(t) + I_V(t) \tag{2}$$

It is assumed that susceptible humans are recruited into the population at the constant rate π_H Susceptible individuals acquire infection with malaria following effective contact with infected mosquitoes (at a rate λ_M) and also Susceptible mosquitoes (S_V) are generated at a constant (recruitment rate π_V) and acquire malaria infection following effective contacts with humans infected with malaria at a rate λ_v.

Putting all these together to obtain the following as;

$$\left.\begin{aligned}
\frac{dS_H}{dt} &= \pi_H - \lambda_M S_H + \phi_1 R_M - \mu S_H \\
\frac{dE_M}{dt} &= \varepsilon_2 \lambda_M S_H - (\kappa_M + \mu) E_M - \tau_2 E_M \\
\frac{dI_M}{dt} &= (1-\varepsilon_2)\lambda_M S_H + \kappa_M E_M - (\tau_3 + r + \delta_{IM} + \mu) I_M \\
\frac{dR_M}{dt} &= \tau_2 E_M + \tau_3 I_M + r I_M - (\phi_1 + \mu) R_M \\
\frac{dS_V}{dt} &= \pi_V - \lambda_V S_V - \mu_V S_V \\
\frac{dE_V}{dt} &= \lambda_V S_V - (\sigma_V + \mu_V) E_V \\
\frac{dI_V}{dt} &= \sigma_V E_V - \mu_V I_V
\end{aligned}\right\} \tag{3}$$

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Where $\lambda_M = \frac{\beta_M b I_V}{N_H}$ and $\lambda_V = \frac{\beta_V b I_M}{N_V}$

Table 1.1: Definitions of parameters and variables used in the model formulation

PARAMETERS/ VARIABLES	DEFINITIONS
S_H	Susceptible individuals
E_M	Malaria exposed individuals
I_M	Malaria infected individuals
R_M	Malaria recovered individuals
S_V	Susceptible vectors (mosquitoes)
E_V	Exposed vectors (mosquitoes)
I_V	Infected vectors (mosquitoes)
π_H , π_V	Recruitment rate of human and vectors respectively
μ	Human death rate
μ_V	vectors (mosquitoes)death rate
τ_3, τ_2	Treatment rate for malaria exposed and malaria infected individuals
ε_2	Fraction of individuals with low immunity, Infected with malaria
δ_{IM}	Malaria induced death rate for classes E_M I_M
κ_M	Progression rate for malaria infection
β_M , β_V	Transmission probability from mosquito to human and human to mosquito respectively
σ_V	Progression rate of vectors (mosquitoes)
r	Recovery rate of malaria
b	Number of mosquito bites per unit time
λ_M , λ_V	Force of infection from mosquito to human and from human to mosquito respectively
ϕ_1	Rate of loose of immunity

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A. EXISTENCE AND UNIQUENESS OF THE SOLUTION

This is obtained by following (Derrick and Grossman, 1976) that is, linearized the equation (1) to obtained (2) below;

$$\left.\begin{aligned}
\frac{dS_H}{dt} &= f(S_H, E_M, I_M, R_M, S_V, E_V, I_V) = \pi_H - \lambda_M S_H + \phi_1 R_M - \mu S_H \\
\frac{dE_M}{dt} &= f(S_H, E_M, I_M, R_M, S_V, E_V, I_V) = \varepsilon_2 \lambda_M S_H - (\kappa_M + \mu) E_M - \tau_2 E_M \\
\frac{dI_M}{dt} &= f(S_H, E_M, I_M, R_M, S_V, E_V, I_V) = (1-\varepsilon_2)\lambda_M S_H + \kappa_M E_M - (\tau_3 + r + \delta_{IM} + \mu) I_M \\
\frac{dR_M}{dt} &= f(S_H, E_M, I_M, R_M, S_V, E_V, I_V) = \tau_2 E_M + \tau_3 I_M + r I_M - (\phi_1 + \mu) R_M \\
\frac{dS_V}{dt} &= f(S_H, E_M, I_M, R_M, S_V, E_V, I_V) = \pi_V - \lambda_V S_V - \mu_V S_V \\
\frac{dE_V}{dt} &= f(S_H, E_M, I_M, R_M, S_V, E_V, I_V) = \lambda_V S_V - (\sigma_V + \mu_V) E_V \\
\frac{dI_V}{dt} &= f(S_H, E_M, I_M, R_M, S_V, E_V, I_V) = \sigma_V E_V - \mu_V I_V
\end{aligned}\right\} \quad (4)$$

$$D = \left\{\begin{aligned}
&(S_H, E_M, I_M, R_M, S_V, E_V, I_V) : |S_H - S_{H0}| \le a, |E_M - E_{M0}| \le b, |I_M - I_{M0}| \le c, |R_M - R_{M0}| \le d, \\
&|S_V - S_{V0}| \le e, |E_V - E_{V0}| \le g, |I_V - I_{V0}| \le h
\end{aligned}\right\}$$

Taking the partial derivatives of each of the compartment of (4) at the origin, then obtain the following as;

$$\frac{\partial f_1}{\partial S_H} = |\mu| < \infty, \frac{\partial f_1}{\partial R_M} = |\phi_1| < \infty, \frac{\partial f_2}{\partial E_M} = |-(\kappa_M + \mu + \tau_2)| < \infty, \frac{\partial f_3}{\partial E_M} = |\kappa_M| < \infty,$$

$$\frac{\partial f_3}{\partial I_M} = |-(\tau_3 + r + \delta_{IM} + \mu)| < \infty, \frac{\partial f_4}{\partial E_M} = |\tau_2| < \infty, \frac{\partial f_4}{\partial I_M} = |\tau_3 + r| < \infty, \frac{\partial f_4}{\partial R_M} = |\mu - \phi_1| < \infty$$

$$\frac{\partial f_5}{\partial S_V} = |-\mu_V| < \infty, \frac{\partial f_6}{\partial E_V} = |-(\sigma_V + \mu_V)| < \infty, \frac{\partial f_7}{\partial E_V} = |\sigma_V| < \infty, \frac{\partial f_7}{\partial I_V} = |-\mu_V| < \infty.$$

Since the partial derivative of the model exist, continuous and bounded, hence the model has a unique solution *D*, which means that the model (3) is epidemiologically and mathematically well posed.

B. DIFFERENTIAL TRANSFORM METHOD (DTM)

The DTM is developed based on the Taylor series expansion, this method constructs an analytical or semi-analytical solution in term of polynomial. The following basic definitions and fundamental properties would be employed.

Descriptions of Differential Transform Method

Definition: The differential transformation method $Y(k)$ from the function $y(t)$ is defined as

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$$Y(k)=\frac{1}{k!}\left[\frac{d^k y(t)}{dt^k}\right]_{t=t_0} \tag{5}$$

$Y(k)$ is a transform function and $y(t)$ is the original function. The inverse of the DTM $Y(k)$ is defined as

$$y(t)=\sum_{k=0}^{\infty} Y(k)(t-t_0)^k \tag{6}$$

Substitute (5) in (6), obtained (7)

$$y(t)=\sum_{k=0}^{\infty}\frac{(t-t_0)^k}{k!}\frac{d^k y(t)}{dt^k}\bigg|_{t=t_0} \tag{7}$$

The equation (7) shows that DTM is derived from the Taylor series expansion and relative derivatives were calculated in a recurrent manner.

TABLE 1.2: Operations of differential transformation method

Original function	Transformed function
$y(t)=g(t)\pm h(t)$	$Y(k)=g(k)\pm h(k)$
$y(t)=\beta g(t)$	$Y(k)=\beta G(k)$
$y(t)=g(t)h(t)$	$Y(k)=\sum_{l=0}^{k} H(l)G(k-l)$
$y(t)=\frac{dg(t)}{dt}$	$Y(k)=(k+1)G(k+1)$
$y(t)=\frac{d^m g(t)}{dt^m}$	$Y(k)=(k+1)(k+2)\cdots(k+m)G(k+m)$
$y(t)=\int_{t_0}^{t} g(t)dt$	$Y(k)=\frac{G(k+1)}{k},k\geq 1$
$y(t)=t^m$	$Y(k)=\delta(k-m)$
$y(t)=\exp(\lambda t)$	$Y(k)=\frac{\lambda^k}{k!}$
$y(t)=\sin(wt+\beta)$	$Y(k)=\frac{w^k}{k!}\sin(\pi\frac{k}{2}+\beta)$
$y(t)=\cos(wt+\beta)$	$Y(k)=\frac{w^k}{k!}\cos(\pi\frac{k}{2}+\beta)$

C. APPLICATION OF DIFFERENTIAL TRANSFORMATION METHOD TO MALARIA MODEL

In this section, the steps involved in differential transform method was apply as follow. Using the transformed function of the original function in Table 1.2, obtained the recurrence relation of equation (3) that is malaria model only as.

$$S_H(k+1)=\frac{1}{k+1}\left[\pi_H-\beta_M b\left(\sum_{l=0}^{k} S_H(l)\frac{I_V(k-l)}{N_H}\right)+\phi_1 R_M(k)-\mu S_H(k)\right]$$

$$E_M(k+1)=\frac{1}{k+1}\left[\varepsilon_2\beta_M b\left(\sum_{l=0}^{k}S_H(l)\frac{I_V(k-l)}{N_H}\right)-k_1E_M(k)\right]$$

$$I_M(k+1)=\frac{1}{k+1}\left[(1-\varepsilon_2)\beta_M b\left(\sum_{l=0}^{k}S_H(l)\frac{I_V(k-l)}{N_H}\right)+\kappa_M E_M(k)-k_2I_M(k)\right]$$

$$R_M(k+1)=\frac{1}{k+1}\left[\tau_2E_M(k)+k_3I_M(k)-k_4R_M(k)\right] \quad (8)$$

$$S_V(k+1)=\frac{1}{k+1}\left[\pi_V-\beta_V b\left(\sum_{l=0}^{k}S_V(l)\frac{I_M(k-l)}{N_V}\right)-\mu_V S_V(k)\right]$$

$$E_V(k+1)=\frac{1}{k+1}\left[\beta_V b\left(\sum_{l=0}^{k}S_V(l)\frac{I_M(k-l)}{N_V}\right)-k_5E_V(k)\right]$$

$$I_V(k+1)=\frac{1}{k|+1}\left[\sigma_V E_V(k)-\mu_V I_V(k)\right]$$

Where $k_1=0.2728$, $k_2=0.2713$, $k_3=0.0213$, $k_4=0.48$, $k_5=0.15$, $k_6=0.22$, $k_7=1.06$

Subject to the following initial conditions $S_H(0)=1500$, $E_M(0)=1000$, $I_M(0)=900$, $R_M(0)=750$, $S_V(0)=100$, $E_V(0)=90$, $I_V(0)=60$. Using the initial conditions and the parameter values in the Table, the following series solutions were obtained;

When $k=6$ the solution to the system (3) in closed form is obtained as

$$S_H(t)=\sum_{k=0}^{N}S_H(k)t^k=1500+1709.739756t+681.4004976t^2+561.9236045t^3+420.9963904t^4$$
$$+343.2267488t^5+288.5407013t^6+\cdots$$

$$E_M(t)=\sum_{k=0}^{N}E_M(k)t^k=1000-272.6438554t+37.28541797t^2-3.361064516t^3+0.246002834t^4$$
$$-0.002841084004t^5+0.011796314t^6+\cdots$$

$$I_M(t)=\sum_{k=0}^{N}I_M(k)t^k=900-173.0659036t+13.86206369t^2-0.351555851t^3-0.02462913t^4$$
$$+0.011883503t^5+0.004095903942t^6+\cdots$$

$$R_M(t)=\sum_{k=0}^{N}R_M(k)t^k=750-339.03t+79.27866866t^2-12.56379508t^3+1.504270896t^4$$
$$-0.144426365t^5+0.011595443t^6+\cdots$$

$$S_V(t)=\sum_{k=0}^{N}S_V(k)t^k=100+382.04t+166.9388825t^2+115.2510667t^3+95.67593307t^4$$
$$+70.67715689t^5+64.91172457t^6+\ldots$$

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$$E_V(t)=\sum_{k=0}^{N}E_V(k)t^k = 90-0.54t+23.55061749t^2+14.2242105t^3+2.353837803t^4+8.295468648t^5$$
$$+0.958579068t^6+\cdots$$
$$I_V(t)=\sum_{k=0}^{N}I_V(k)t^k = 60+6t-0.177t^2+0.787970583t^3+0.343210894t^4+0.043644647t^5$$
$$+0.137894105t^6$$

D. NUMERICAL SIMULATION

The analytical results of this study are illustrated by carrying out numerical simulations of the models using parameter values from literature and estimated values as shown in Table (2). The simulations are carried out with the help of MAPLE 17 software

TABLE 2: Parameters values used for the numerical simulation

Parameters	Values	Sources
δ_{IM}	0.05	Mukandavire *et al.* (2009)
κ_M	0.071	Mueller *et al.*(2008)
β_M	0.03	Amoah-Mensah *et al*., (2018)
ε_2	0.6	Estimated
τ_3	0.0013	CDC (2014).
τ_2	0.0018	Estimated
π_V	400	Chitnis *et al.*(2006)
π_H	1800	Estimated
μ	0.2	Mueller *et al.*(2008)
μ_V	0.05	Okeke *et al.*(2014)
β_V	0.09	Blayneh and Kwon (2009)
σ_V	0.1	Chitnis *et al.*, (2006)
r	0.02	Abu-Raddad *et al*.,(2006)
b	0.4	Chitnis *et al.*(2008)

TABLE 3: The result obtained by DTM compared with result obtained by RK4 for Susceptible human malaria

t	DTM	$RK4$	$\lvert DTM-RK4\rvert$
0	1500	1500	0
0.01	1517.166104	1517.07556	0.090544404
0.02	1534.471918	1534.107531	0.364386615
0.03	1551.920974	1551.096048	0.824926089
0.04	1569.516908	1568.04124	1.475668467
0.05	1587.263472	1584.943236	2.32023594
0.06	1605.164538	1601.802167	3.362371127
0.07	1623.224104	1618.618161	4.605943069
0.08	1641.446293	1635.391347	6.054946235
0.09	1659.835366	1652.121852	7.713513518
0.1	1678.395726	1668.809806	9.585920237

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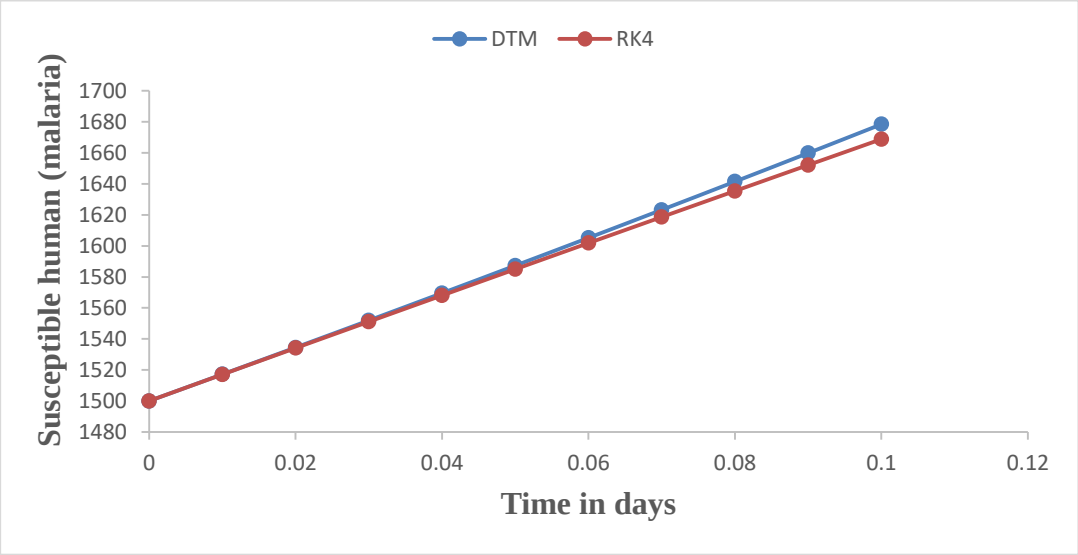

Figure 1: Graph of result obtained by DTM compared with result obtained by RK4 for Susceptible human malaria

TABLE 4: The result obtained by DTM compared with result obtained by RK4 for Exposed human

t	DTM	$RK4$	$\lvert DTM - RK4 \rvert$
0	1000	1000	0
0.01	997.2772865	997.2772866	9.76031E-08
0.02	994.5620102	994.5620099	2.80422E-07
0.03	991.8541507	991.8541496	1.10679E-06
0.04	989.153688	989.1536854	2.57301E-06
0.05	986.4606021	986.4605973	4.80951E-06
0.06	983.7748734	983.7748651	8.29484E-06
0.07	981.0964817	981.0964688	1.28557E-05
0.08	978.4254075	978.4253885	1.8967E-05
0.09	975.7616308	975.7616042	2.65517E-05
0.1	973.1051322	973.1050961	3.6081E-05

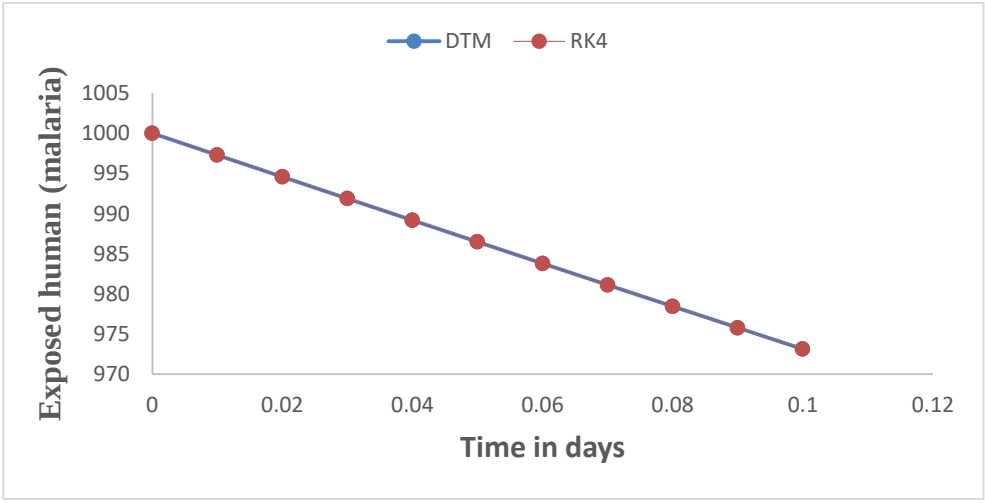

Figure 2: Graph of result obtained by DTM compared with result obtained by RK4 for Exposed human malaria

TABLE 5: The result obtained by DTM compared with result obtained byRK4 for Infected human (malaria)

t	DTM	$RK4$	$\lvert DTM - RK4 \rvert$
0	900	900	0
0.01	898.2707268	898.2707268	2.49702E-09
0.02	896.5442239	896.5442238	1.14341E-07
0.03	894.8204893	894.8204888	5.36143E-07
0.04	893.0995206	893.0995195	1.13314E-06
0.05	891.3813159	891.3813136	2.28138E-06
0.06	889.665873	889.6658689	4.06361E-06
0.07	887.9531897	887.9531831	6.56926E-06
0.08	886.2432639	886.2432539	9.99446E-06
0.09	884.5360936	884.536079	1.4642E-05
0.1	882.8316762	882.831656	2.02214E-05

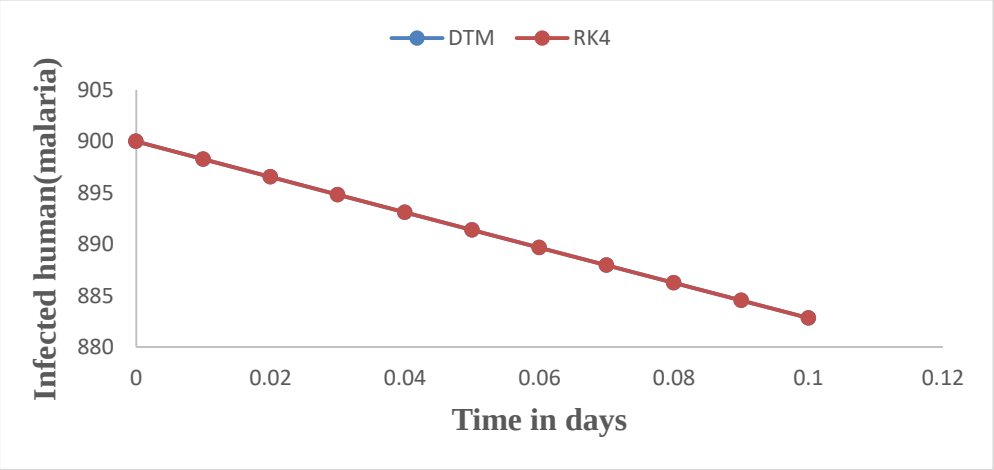

Figure 3: Graph of result obtained by DTM compared with result obtained by RK4 for Infected human malaria

TABLE 6: The result obtained by DTM compared with result obtained by RK4 for Recovered human (malaria)

t	DTM	$RK4$	$\lvert DTM - RK4 \rvert$
0	750	750	0
0.01	746.6176153	746.6176153	1.8097E-08
0.02	743.2510112	743.2510108	4.46862E-07
0.03	739.9001128	739.9001102	2.63892E-06
0.04	736.5648457	736.5648394	6.31488E-06
0.05	733.2451356	733.2451246	1.09701E-05
0.06	729.9409088	729.9408924	1.63658E-05
0.07	726.652092	726.6520697	2.23461E-05
0.08	723.3786119	723.3785835	2.8438E-05
0.09	720.120396	720.1203613	3.46513E-05
0.1	716.8773719	716.8773311	4.07786E-05

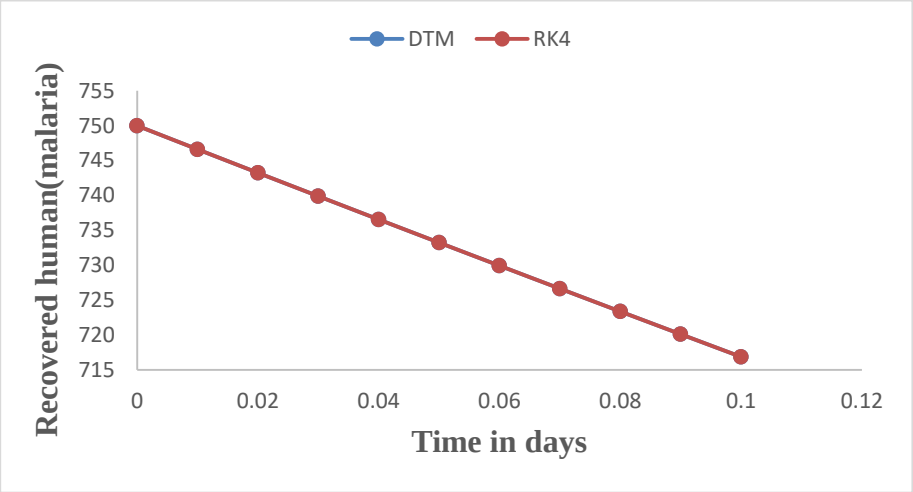

Figure 4: Graph of result obtained by DTM compared with result obtained by RK4 for Recovered human malaria

TABLE 7: The result obtained by DTM compared with result obtained by RK4 for Susceptible vector

t	DTM	$RK4$	$\lvert DTM - RK4 \rvert$
0	100	100	0
0.01	103.8372102	103.817099	0.020111232
0.02	107.7085131	107.6276162	0.080896858
0.03	111.614636	111.4315824	0.183053631
0.04	115.5563307	115.2290274	0.327303287
0.05	119.5343747	119.0199813	0.514393421
0.06	123.5495722	122.8044737	0.745098461
0.07	127.6027552	126.5825344	1.020220768
0.08	131.6947848	130.3541929	1.340591938
0.09	135.826552	134.1194784	1.707073599
0.1	139.9989792	137.8784203	2.120558914

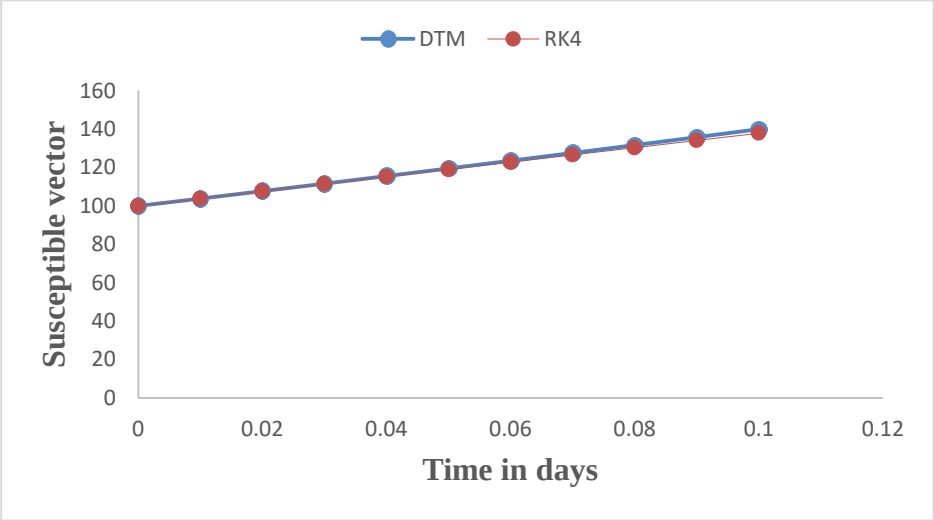

Figure 5: Graph of result obtained by DTM compared with result obtained by RK4 for Susceptible vector

TABLE 8: The result obtained by DTM compared with result obtained by RK4 for Exposed vector

t	DTM	$RK4$	$\lvert DTM - RK4 \rvert$
0	90	90	0
0.01	89.9969692	89.99694936	1.98434E-05
0.02	89.99897336	89.99857456	0.000398807
0.03	90.00537898	90.00484132	0.000537662
0.04	90.0169917	90.01571592	0.001275776
0.05	90.03365915	90.03116485	0.002494298
0.06	90.05546966	90.05115474	0.004314916
0.07	90.08251259	90.07565241	0.00686018
0.08	90.11487847	90.10462482	0.010253645
0.09	90.15265917	90.13803913	0.01462004
0.1	90.19594788	90.17586263	0.020085248

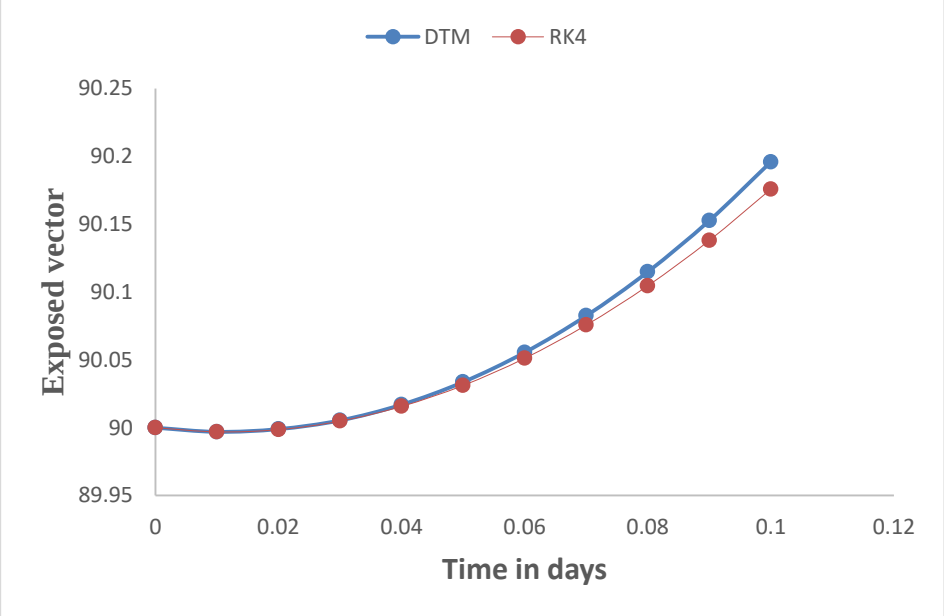

Figure 6: Graph of result obtained by DTM compared with result obtained by RK4 for Exposed vector

TABLE 9: The result obtained by DTM compared with result obtained by RK4 for Infected vector

t	DTM	$RK4$	$\lvert DTM - RK4 \rvert$
0	60	60	0
0.01	60.05998309	60.05998309	3.5545E-09
0.02	60.11993555	60.11993549	5.78151E-08
0.03	60.17986226	60.17986192	3.39678E-07
0.04	60.23976811	60.23976699	1.11852E-06
0.05	60.29965816	60.29965529	2.86995E-06
0.06	60.35953749	60.35953137	6.12247E-06
0.07	60.4194113	60.41939974	1.15575E-05
0.08	60.47928488	60.4792649	1.99794E-05
0.09	60.53916358	60.53913129	3.22855E-05
0.1	60.59905287	60.59900334	4.95258E-05

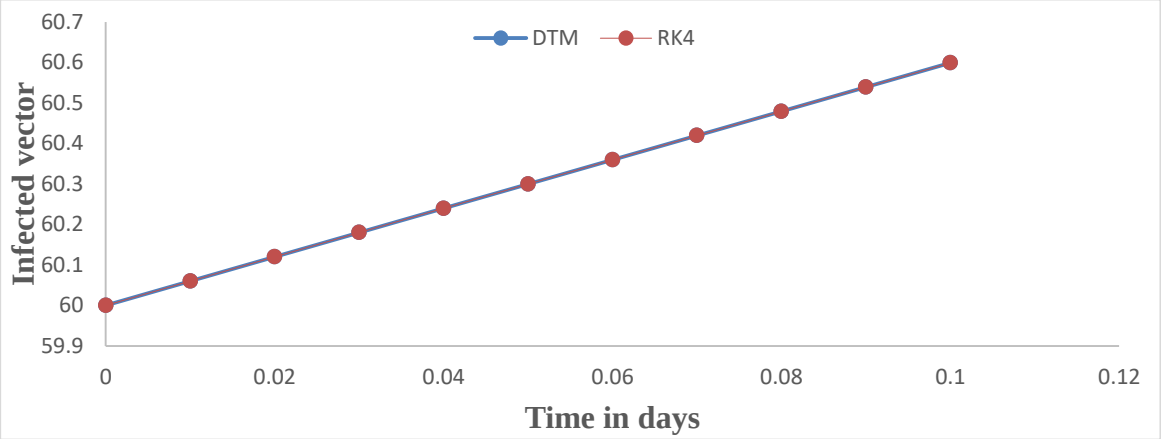

Figure 7: Graph of result obtained by DTM compared with result obtained by RK4 for Infected vector

III. DISCUSSION OF RESULTS

In Table 3-9 and Figure 1-7, shows the result obtained using the Differential Transform Method with given initial conditions favorably compared with the solution obtained using fourth-order Runge-Kuta Method, which implies that DTM was powerful tools to obtain analytical solution of malaria disease models in epidemic study.

IV. CONCLUSION

In this work, a differential transform method (DTM) has been successfully applied to solve malaria disease model with given initial conditions. This method provides an explicit solution which is very useful for understanding and analyzing an epidemic model. The comparison of the solutions obtained by DTM with RK4 shows the efficiency and accuracy of the method. From numerical results obtained so far, it was concluded that DTM is a mathematical tool which provide approximate analytical solutions for epidemiological models formulated by system of non-linear ordinary differential equations.

REFERENCES

[1] Abu-Raddad L. J., Patnaik P. and Kublin J. G. (2006). Dual infection with HIV and malaria fuels the spread of both diseases in sub-Saharan Africa. *Section 314(5805), Pp.1603-1606*

[2] Adewale S.O., Olopade I.A., Adeniran G.A., Mohammed I.T and Ajao S.O. (2015) Mathematical Analysis of effects of isolation on Ebola transmission Dynamics. *Research journalis. Journal of Mathematics vol. 2, No 2 Pp.1-20*

[3] Chitnis, N., Cushing, J. M. and Hyman, J. M. (2006). Bifurcation Analysis of a Mathematical Model for Malaria Tra nsmission, Submit ted: *SIAM Journal on Applied Mathematics.Vol. 67, N.1, Pp.24-45*

[4] CDC (2014). Method for Implementing and Managing Contact Tracing for Ebola VirusDisease in Less-affected Countries

[5] Omoloye, M. A., & Adewale, S.O. (2021). Mathematical Analysis of Sensitive Parameters on the Dynamical Transmission of Ebola-Malaria Co-infections. International Journal of Computer Science and Information Security (IJCSIS), Vol. 19, No. 7,Pp. 21-45, July 2021

[6] Omoloye, Musibau A., Adewale, Sunday O., Umar, Aliyu M., Oladapo Asimiyu O. Analysis of coronavirus disease model by differential transform method (DTM). *International Journal of Advance Research and Innovative Ideas in Education Vol. 7, Issue 3, Pp: 1410-1419*

[7] Okeke, I. N., Manning, R. S. and Pfeiffer, T. (2014). Diagnostic Schemes for Reducing Epidemic Size of African Vi ral Hemorrhagic Fever outbreaks. *Journal of Infection in Developing Countries, 8(9): Pp.1148-115*

[8] Mukandavire, Z., Gumel, A. B., Garira, W. and Tchuenche, J. M. (2009): Mathematical analysis of a model for HIV – Malaria co infection. *Mathematical Biosciences and Engineering vol 6, No. 2, Pp. 333-362*

[9] Mueller I., Zimmerman P. A. and Reeder J. C. (2008). Plasmodium malariae and Plasmodium ovale the" bashful" m alaria parasites ". *Trends in Parasitology 23 (6): 27883.doi:10.1016/j. pt.2007.04.009.PMC3728836.PMID 17459775*

[10] Peter O. J., Ibrahim M. O., Oguntolu F. A., Akinduko O. B. and Akinyemi S.T. (2018) Direct and Indirect Transmission Dynamics of Typhoid Fever Model by Differential Transform Method. *ATBU, Journal of Science, Technology & Education (JOSTE); vol. 6 (1), Pp.167-177*

[11] Ghazala Nazir, Shaista Gul (2019). Comparative Study Of Mathematical Model Of Ebola Virus Disease Via Using Differential Transform Method And Variation Of Iteration Method. *Matrix Science Mathematics*, 3(1) : 17-19