



Available online at <http://scik.org>

J. Math. Comput. Sci. 11 (2021), No. 2, 1242-1255

<https://doi.org/10.28919/jmcs/5288>

ISSN: 1927-5307

SOLUTION OF TYPHOID FEVER MODEL BY ADOMIAN DECOMPOSITION

METHOD

AJIMOT FOLASADE ADEBISI^{1,*}, OHIGWEREN AIRENONI UWAHEREN², OLUSOLA EZEKIEL

ABOLARIN³, MUSILIU TAYO RAJI⁴, JOSEPH A. ADEDEJI¹, OLUMUYIWA JAMES PETER²

¹Department of Mathematics, Osun State University, Oshogbo, Osun State, Nigeria

²Department of Mathematics, University of Ilorin, Ilorin, Kwara State, Nigeria

³Department of Mathematics, Federal University Oye Ekiti, Ekiti State, Nigeria

⁴Department of Mathematics, Federal University of Agriculture Abeokuta, Ogun State

Copyright © 2021 the author(s). This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract. In this paper, we presents a deterministic mathematical model on the dynamics of typhoid fever disease. The Adomian Decomposition Method (ADM) is used to solve the model equations. In solving the model, the validity of the ADM is established by the classical fourth-order Runge-Kutta method implemented in Maple 18. In other to confirm the accuracy of the method, a comparison was carried out between the ADM solution and Runge-Kutta(RK4). The findings obtained confirm the precision and accuracy of the ADM to cope with the study of morden epidemics.

Keywords: typhoid fever; Adomian Decomposition Method; Runge-Kutta Method.

2010 AMS Subject Classification: 93A30.

1. INTRODUCTION

Typhoid fever is a systemic infection, triggered by the ingestion of infected food or water, caused by the bacterium *Salmonella Typhi*. Prolonged fever, fatigue, nausea, loss of appetite, and diarrhea or even diarrhoea describe acute illness. Symptoms are often non-specific and other febrile

*Corresponding author

E-mail address: foladebisi@uniosun.edu.ng

Received December 1, 2020

disorders are clinically non-distinguishable [1]. There are also non-specific and clinically non-distinguishable signs of typhoid fever from other febrile diseases. Medical severity, however, varies and serious cases can lead to significant complications or even death. Recent findings indicate that an estimated 11–20 million people get sick from typhoid fever and between 128 000 and 161 000 people die from it every year. The disease is endemic in South America [2], Indian subcontinent [3], Southeast Asia [4] and mostly in Africa [5]. During year 2000, it was estimated that the disease caused illness is 21.6 million and 216,500 deaths worldwide. For many researchers, modeling the transmission dynamics of typhoid fever is an essential and important study. The study of infectious diseases in the past has concentrated primarily on their effects on the human population. Although, infectious diseases are present to some degree in human societies at all times, the results of epidemics are the most evident and spectacular [6].

George Adomian [7], an American mathematician, was the first to establish Method of Adomian decomposition. It is a form of semi-analysis that can be used in the solution of partial and ordinary differential equations in both nonlinear and linear order. It can also be used in solving higher order nonlinear differential equations. Also, it can be used in solving nonlinear differential equations of higher order. [8-9] considered Adomian Decomposition approach to solve deterministic models but not on the typhoid fever model. In fluid mechanics, [10-12] and in numerical analysis, [13,14]. Several mathematical models have been developed on this disease [15-32], but none has considered the solution of typhoid fever model by Adomian Decomposition Method.

The aim of this paper is to present the application of Adomian Decomposition Method to the proposed model and to verify the validity of the Adomian Decomposition Method in solving the model using Maple 18's classical fourth-order Runge-Kutta method as a basis for comparison.

2. MODEL FORMULATION

A deterministic, compartmental mathematical model is formulated in this chapter to explain the transmission dynamics of typhoid fever to extend and complement those existing in the literature.

The model is composed of four compartments: The Susceptible Class is for people vulnerable to typhoid fever. The infectious group consists of people who are aware of their infection and are in a position to transfer the disease to vulnerable people who are infected by the disease. The Carrier class involves individuals who are infected and are capable of infecting others but show no signs of infection. The recovered class comprises individuals who have been infected and then recovered from the disease, who will not be re-infected or transferred to those in this group.

The number of individuals in the Susceptible, Infected, Carrier, and Recovered classes are functions of time denoted by $S(t)$, $I(t)$, $I_c(t)$, $R(t)$ respectively.

Susceptible population are increased by immigration or birth at the rate θ . We assume that proportion ρ of susceptible class progress to carrier infected class, while the complement $1 - \rho$ migrate to infected class. We assumed that the rate of transmission β for carriers is higher than the rate of transmission γ of symptomatically infected individuals due to the fact that they are more likely to be unaware of their condition, and therefore continue with their regular activities. Carriers may become symptomatic at a rate α . Infectious individuals can receive treatment and recover at the rate δ . Susceptible individuals receive vaccination to protect themselves against infection at the rate ψ . $1 - \phi$ is an educational parameter that caters for limiting both carriers and symptomatic individuals from spreading typhoid. This parameter lies in the interval $0 < \phi < 1$. When $\phi = 0$ It means that there are no education programs in place so that vulnerable people are unaware of typhoid fever. $\phi = 1$, then it means that all susceptible individuals are fully aware of typhoid fever, that is to say they know what causes the diseases, how it is spread and how to avoid contracting the disease.

Table 1 gives a detailed summary of the parameters, while Figure 1 shows the model's compartmental flow diagram. The above description can be represented by a system of differential equations given as

SOLUTION OF TYPHOID FEVER MODEL BY ADOMIAN DECOMPOSITION METHOD

$$(1) \quad \left. \begin{aligned} \frac{dS}{dt} &= \theta - \mu_1 S - \lambda S(1 - \phi) - \psi S \\ \frac{dI_c}{dt} &= \rho \lambda S(1 - \phi) - \mu_2 I_c - \alpha(1 - \phi) I_c \\ \frac{dI}{dt} &= (1 - \rho) \lambda S(1 - \phi) + \alpha(1 - \phi) I_c - (\mu_3 + \delta) I \\ \frac{dR}{dt} &= \psi S + \delta I - \mu_4 R \end{aligned} \right\}$$

$$\lambda = \beta I_c + \gamma I$$

Substituting the value of force of infection in (1)

$$(2) \quad \left. \begin{aligned} \frac{dS}{dt} &= \theta - \mu_1 S - S(\beta I_c + \gamma I)(1 - \phi) - \psi S \\ \frac{dI_c}{dt} &= \rho S(\beta I_c + \gamma I)(1 - \phi) - \mu_2 I_c - \alpha(1 - \phi) I_c \\ \frac{dI}{dt} &= (1 - \rho)(1 - \phi) S(\beta I_c + \gamma I) + \alpha(1 - \phi) I_c - (\mu_3 + \delta) I \\ \frac{dR}{dt} &= \psi S + \delta I - \mu_4 R \end{aligned} \right\}$$

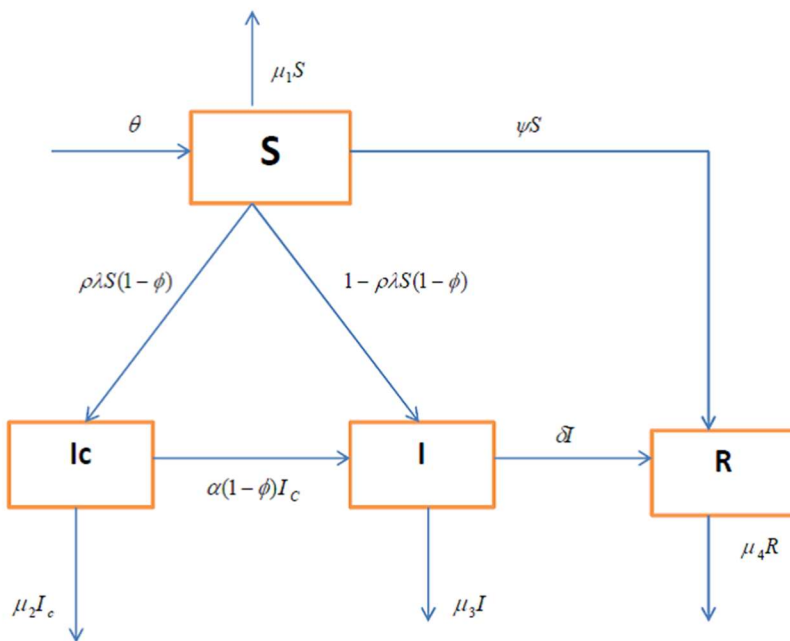


FIGURE 1: Pictorial Illustration of the Model

Table 1: Parameter values of the model

Variables	Description
$S(t)$	Susceptible population at time t
$Ic(t)$	Carrier infectious population at time t
$I(t)$	Infectious population at time t
$R(t)$	Recovered population at time t
Parameters	Interpretation
θ	Recruitment rate into susceptible class
μ_1	Natural mortality rate
μ_2	Natural rate for carrier class and disease induced death rate
μ_3	Natural death rate for infected class and disease induced death rate
μ_4	Natural mortality rate
α	Rate at which carriers develop symptom
ϕ	Education parameter
ψ	Vaccination rate
ρ	Probability that newly infected individuals are asymptomatic or carrier
β	Transmission rate for carrier group
γ	Transmission rate for infected group
λ	Force of infection
δ	Recovery rate for infected group

3. ADOMIAN DECOMPOSITION METHOD

3.1 Definition of Adomian Decomposition Method

Consider the equation

$$(3) \quad L(y) + R(y) + N(y) = f(t)$$

where $L(y)$ is the differential operator, $R(y)$ is the remainder of the differential operator,

$N(y)$ is the nonlinear terms, $f(t)$ is an inhomogeneous term and L can be defined as the

highest order of differential equation. Making $L^{-1}L(y)$ the subject of formula after (3) has been multiplying through by the inverse operator L (that is L^{-1}) to multiply (3), we obtain

$$(4) \quad L^{-1}L(y) = L^{-1}f(t) - L^{-1}R(y) - L^{-1}N(y)$$

For both $L^{-1}f(t)$ and $L^{-1}R(y)$ are linear which means they are integrable, $L^{-1}N(y)$ is nonlinear. Meanwhile, L^{-1} is an n-fold integration of an nth order L and the nonlinear term ($N(y)$) can be defined as

$$(5) \quad N(y) = \sum_{n=0}^{\infty} B_n(y_0, y_1, \dots, y_n)$$

where B_n is the Adomian polynomials and it can be derived from its iteration and its nonlinearity function. This B_n depends on the series of y_0 to y_n components. To derive B_n , we use the formula

$$(6) \quad B_n = \frac{1}{n!} \left\{ \frac{d^n}{d\chi^n} \left[N \left(\sum_{m=0}^{\infty} \chi^m y_m \right) \right] \right\}_{\chi=0} \quad n = 0, 1, 2, \dots$$

The composition solution series can be written as

$$(7) \quad y(t) = \sum_{k=0}^{\infty} y_k = y_0 + y_1 + y_2 + \dots$$

3.2 Solution of the Model Using Adomian Decomposition Method

From the model (2), since this model is the system of first order differential equations then we

define differential operation (L) and its inverse operator (L^{-1}) to be $L = \frac{d(\circ)}{dt}$ and $L^{-1} = \int_0^t (\circ) dt$

respectively with initial value problem. Applying (4) into (2), we have

$$(8) \quad \begin{aligned} L^{-1}L(S(t)) &= L^{-1}[\theta] - L^{-1}[\mu_1 S] - L^{-1}[S(\beta I_c + \gamma I)(1 - \phi)] - L^{-1}[\psi S] \\ L^{-1}L(I_c(t)) &= L^{-1}[\rho S(\beta I_c + \gamma I)(1 - \phi)] - L^{-1}[\mu_2 I_c] - L^{-1}[\alpha(1 - \phi)I_c] \\ L^{-1}L(I(t)) &= L^{-1}[(1 - \rho)(1 - \phi)S(\beta I_c + \gamma I)] + L^{-1}[\alpha(1 - \phi)I_c] - L^{-1}[(\mu_3 + \delta)I] \\ L^{-1}L(R(t)) &= L^{-1}[\psi S] + L^{-1}[\delta I] - L^{-1}[\mu_4 R] \end{aligned}$$

Simplifying the left hand side of (8) with the interval from 0 to t according to L^{-1} definition. We

have

$$\begin{aligned}
 (9) \quad & S(t) - S(0) = L^{-1}[\theta] - L^{-1}[\mu_1 S] - L^{-1}[S(\beta I_c + \gamma I)(1 - \varphi)] - L^{-1}[\psi S] \\
 & I_c(t) - I_c(0) = L^{-1}[\rho S(\beta I_c + \gamma I)(1 - \varphi)] - L^{-1}[\mu_2 I_c] - L^{-1}[\alpha(1 - \varphi)I_c] \\
 & I(t) - I(0) = L^{-1}[(1 - \rho)(1 - \varphi)S(\beta I_c + \gamma I)] + L^{-1}[\alpha(1 - \varphi)I_c] - L^{-1}[(\mu_3 + \delta)I] \\
 & R(t) - R(0) = L^{-1}[\psi S] + L^{-1}[\delta I] - L^{-1}[\mu_4 R]
 \end{aligned}$$

Solving (9) to obtain

$$\begin{aligned}
 (10) \quad & S(t) = S(0) + \theta t - (\mu_1 + \psi) \int_0^t \left(\sum_{n=0}^{\infty} S_n \right) dy - (1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} B_n \right) dy \\
 & I_c(t) = I_c(0) + \rho(1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} B_n \right) dy - (\mu_2 + \alpha(1 - \varphi)) \int_0^t \left(\sum_{n=0}^{\infty} I_{cn} \right) dy \\
 & I(t) = I(0) + (1 - \rho)(1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} B_n \right) dy + \alpha(1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} I_{cn} \right) dy - (\mu_3 + \delta) \int_0^t \left(\sum_{n=0}^{\infty} I_n \right) dy \\
 & R(t) = R(0) + \psi \int_0^t \left(\sum_{n=0}^{\infty} S_n \right) dy + \delta \int_0^t \left(\sum_{n=0}^{\infty} I_n \right) dy - \mu_4 \int_0^t \left(\sum_{n=0}^{\infty} R_n \right) dy
 \end{aligned}$$

$$(11) \quad \text{Where } B_n = \frac{d^n}{d\chi^n} \left[\sum_{m=0}^{\infty} S_m (\beta I_{cm} + \gamma I_m) \chi^m \right]_{\chi=0} \quad \text{for } n = 0, 1, 2, \dots$$

From (10), the initial stage gives

$$(12) \quad S_0(t) = S(0) + \theta t; I_{c0}(t) = I_c(0); I_0(t) = I(0); R_0(t) = R(0)$$

And the iteration can be written as

$$\begin{aligned}
 (13) \quad & S_{n+1}(t) = -(\mu_1 + \psi) \int_0^t \left(\sum_{n=0}^{\infty} S_n \right) dy - (1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} B_n \right) dy \\
 & I_{c(n+1)}(t) = \rho(1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} B_n \right) dy - (\mu_2 + \alpha(1 - \varphi)) \int_0^t \left(\sum_{n=0}^{\infty} I_{cn} \right) dy \\
 & I_{n+1}(t) = (1 - \rho)(1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} B_n \right) dy + \alpha(1 - \varphi) \int_0^t \left(\sum_{n=0}^{\infty} I_{cn} \right) dy - (\mu_3 + \delta) \int_0^t \left(\sum_{n=0}^{\infty} I_n \right) dy \\
 & R_{n+1}(t) = \psi \int_0^t \left(\sum_{n=0}^{\infty} S_n \right) dy + \delta \int_0^t \left(\sum_{n=0}^{\infty} I_n \right) dy - \mu_4 \int_0^t \left(\sum_{n=0}^{\infty} R_n \right) dy \\
 & \text{for } n = 0, 1, 2, \dots
 \end{aligned}$$

4. NUMERICAL SIMULATION AND GRAPHICAL ILLUSTRATION OF MODEL

In this section, we present the numerical simulation which demonstrates the analytical results for the model. This is accomplished by using the set of parameter values based on the literature and assumptions given in table 1, as well as assumptions. By substituting the following initial conditions for the different compartments. $S(0) = 60$, $I_c(0) = 40$, $I(0) = 20$, $R(0) = 10$ in equation (12) as well as solving equation (13), we obtain the following expansion up to 12th term. Further, the ADM is demonstrated against Maple 18's fourth order Runge-Kutta procedure for the solution of typhoid fever model. Fig (2) to (5) show the combined plots of the solutions of $S(t)$, $I_c(t)$, $I(t)$ and $R(t)$ by ADM and RK4

$$S(t) = 60 + 9.99931480 \times 10^5 t - 5.709649911 \times 10^5 t^2 + 98122.20012 \times t^3 - 9.186204736 \times 10^8 t^4 \\ + 6.704742248 \times 10^8 t^5 - 1.607645503 \times 10^{12} t^6 + 2.413714881 \times 10^{12} t^7 - 2.111060097 \times \\ 10^{15} t^8 + 5.668721345 \times 10^{15} t^9 - 2.220693766 \times 10^{18} t^{10} + 1.020803353 \times 10^{19} t^{11} - \\ 1.938795776 \times 10^{21} t^{12}$$

$$I_c(t) = 40 + 4.6000t + 1.749891240 \times 10^5 t^2 - 3.091519267 \times 10^4 t^3 + 4.593079843 \times 10^8 t^4 - \\ 3.322973422 \times 10^8 t^5 + 8.038207626 \times 10^{11} t^6 - 1.203182706 \times 10^{12} t^7 + 1.055525033 \times 10^{15} t^8 \\ - 2.830607448 \times 10^{15} t^9 + 1.110337658 \times 10^{18} t^{10} - 5.100793834 \times 10^{18} t^{11} + 9.693978882 \times \\ 10^{20} t^{12}$$

$$I(t) = 20 + 10.4000t + 1.749856100 \times 10^5 t^2 - 5.016288354 \times 10^4 t^3 + 4.593151062 \times 10^8 t^4 - \\ 3.626130224 \times 10^8 t^5 + 8.038438389 \times 10^{11} t^6 - 1.241080244 \times 10^{12} t^7 + 1.055579165 \times 10^{15} t^8 \\ - 2.869315751 \times 10^{15} t^9 + 1.110434763 \times 10^{18} t^{10} - 5.134030334 \times 10^{18} t^{11} + 9.693978882 \times \\ 10^{20} t^{12}$$

$$R(t) = 10 + 31.580t + 1.499913798 \times 10^5 t^2 - 2.044968858 \times 10^4 t^3 - 1.320411706 \times 10^3 t^4 + \\ 1.378007501 \times 10^7 t^5 - 1.212904500 \times 10^7 t^6 + 1.722727867 \times 10^{10} t^7 - 2.614274876 \times 10^{10} t^8 \\ + 1.759667562 \times 10^{13} t^9 - 4.53941743 \times 10^{13} t^{10} + 1.510749956 \times 10^{16} t^{11}$$

4.1. Comparison Graphs Between R-K 4 and ADM Methods

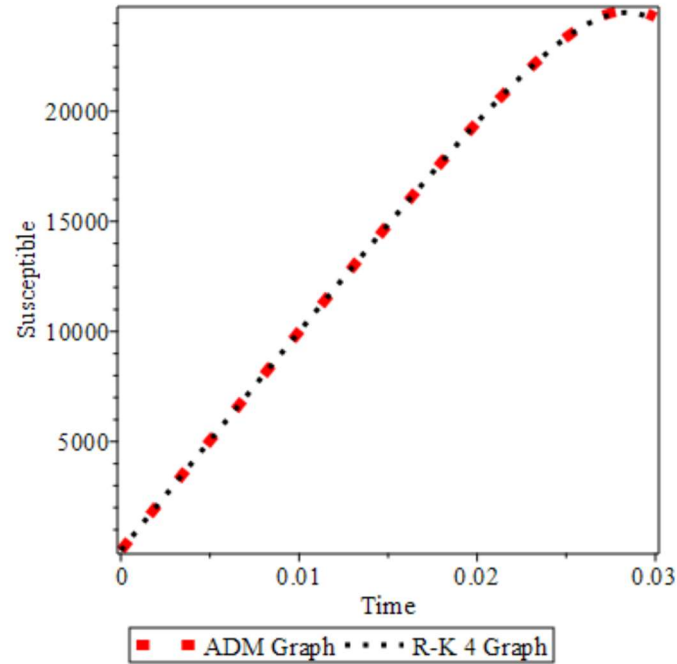


FIGURE 2. The graph of Susceptible against Time for both ADM and R-K 4

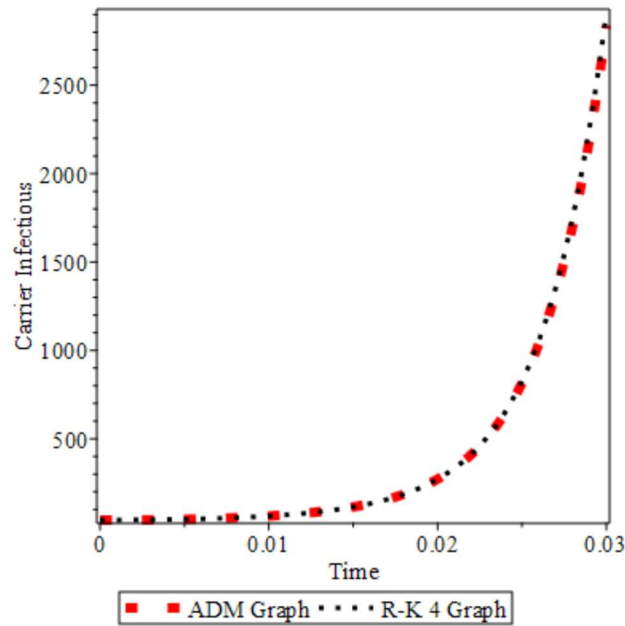


FIGURE 3. The graph of Carrier Infection against Time for both ADM and R-K 4

SOLUTION OF TYPHOID FEVER MODEL BY ADOMIAN DECOMPOSITION METHOD

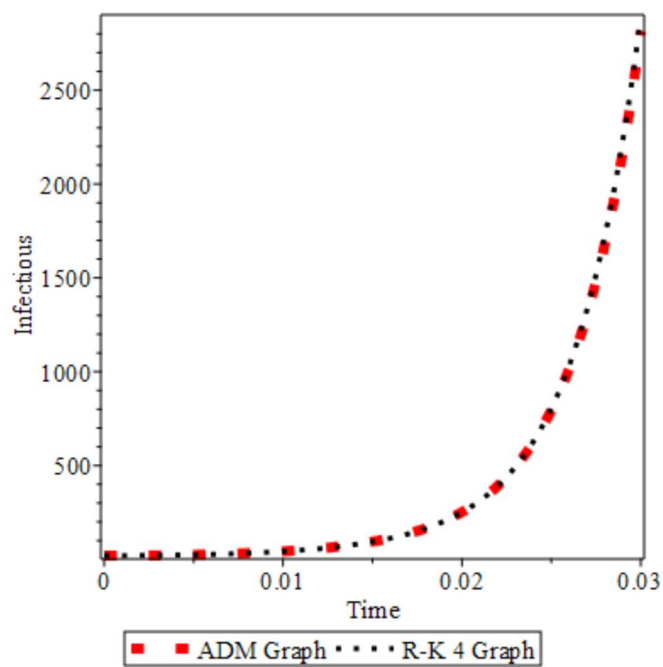


FIGURE 4. The graph of Infectious against Time for both ADM and R-K 4

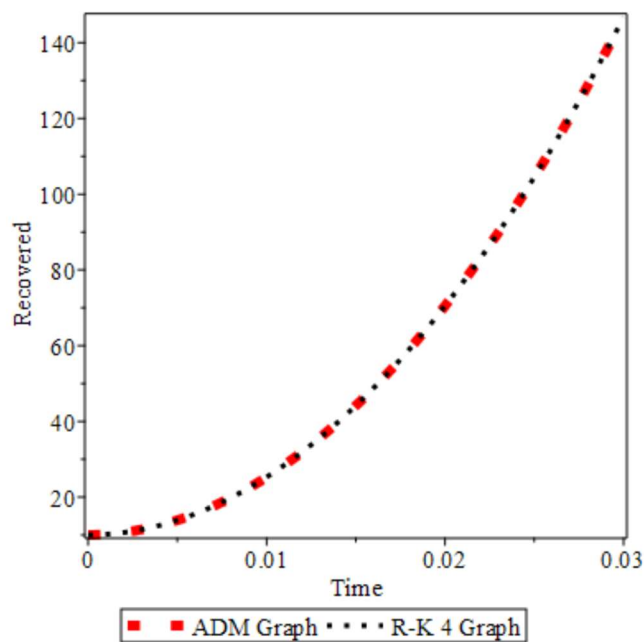


FIGURE 5. The graph of Recovered against Time for both ADM and R-K 4

Table 2: Parameters values for model

Parameter	Initial Value	Source
μ_2	0.2	Assumed
ψ	0.3	Assumed
μ_1	0.142	Mushayabasa, (2011)
μ_3	0.2	Assumed
μ_4	0.142	Mushayabasa, (2011)
α	0.3	Assumed
ρ	0.5	Assumed
β	0.02	Assumed
γ	0.01	Mushayabasa, (2011)
δ	0.75	Assumed
ϕ	0.3	Estimated
θ	10^6	Lauria <i>et al.</i> ,(2009)

Table 3. Comparison table between R-K 4 and ADM methods

TIME	$S(t)$		$I_c(t)$		$I(t)$		$R(t)$	
	R-K 4	ADM	R-K 4	ADM	R-K 4	ADM	R-K 4	ADM
0	60.0000	60.0000	40.0000	40.0000	20.0000	20.0000	10.0000	10.0000
0.001	1059.3597	1059.3597	40.1800	40.1800	20.1690	20.1858	10.1815	10.1816
0.002	2057.5654	2057.5651	40.7161	40.7163	20.6938	20.7277	10.6629	10.6630
0.003	3054.5841	3054.5830	41.6250	41.6256	21.5909	21.6424	11.4441	11.4441
0.004	4050.3582	4050.3556	42.9355	42.9368	22.8887	22.9587	12.5248	12.5249
0.005	5044.8031	5044.7977	44.6901	44.6928	24.6295	24.7192	13.9050	13.9052
0.006	6037.8016	6037.7921	46.9474	46.9522	26.8716	26.9825	15.5846	15.5849
0.007	7029.1983	7029.1827	49.7853	49.7931	29.6923	29.8264	17.5635	17.5639
0.008	8018.7906	8018.7662	53.3052	53.3174	33.1927	33.3527	19.8417	19.8421
0.009	9006.3163	9006.2797	57.6384	57.6566	37.5034	37.6926	22.4190	22.4195
0.01	9991.4384	9991.3852	62.9533	62.9799	42.7924	43.0150	25.2953	25.2960

5. DISCUSSION OF RESULTS FOR ADOMIAN DECOMPOSITION METHOD

The solutions obtained by using Adomian Decomposition Method with given initial conditions compared favourably with the solution obtained by using classical fourth-order Runge-Kutta method. The solutions of the two methods follows the same pattern and behaviour. This shows that Adomian Decomposition Method is suitable and efficient to conduct the analysis of typhoid models.

6. CONCLUSION

We presents a deterministic mathematical model on typhoid fever transmission, Adomian Decomposition Method is used to attempt the series solution of the model. Numerical simulations were carried out to compare the results obtained with the result of classical fourth-order Runge-Kutta method. The results of the simulations were displayed graphically. The results obtained from ADM when compared with RK4 confirm the accuracy of ADM in solving the typhoid fever model.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

REFERENCES

- [1] P. Roumagnac, F.-X. Weill, C. Dolecek, et al. Evolutionary History of Salmonella Typhi, *Science*. 314 (2006), 1301–1304.
- [2] S. Kariuki, G. Revathi, J. Muyodi, et al. Characterization of Multidrug-Resistant Typhoid Outbreaks in Kenya, *J. Clinic. Microbiol.* 42 (2004), 1477–1482.
- [3] A.E. Fica, S. Prat-Miranda, A. Fernandez-Ricci, K. D'Ottone, F.C. Cabello, Epidemic typhoid in Chile: analysis by molecular and conventional methods of Salmonella typhi strain diversity in epidemic (1977 and 1981) and nonepidemic (1990) years. *J. Clinic. Microbiol.* 34 (1996), 1701–1707.
- [4] P.M.A. Shanahan, M.V. Jesudason, C.J. Thomson, S.G.B. Amyes, Molecular Analysis of and Identification of Antibiotic Resistance Genes in Clinical Isolates of Salmonella typhi from India, *J. Clinic. Microbiol.* 36 (1998), 1595–1600.

- [5] S.H. Mirza, N.J. Beechmg, C.A. Hart, Multi-drug resistant typhoid: a global problem. *J. Med. Microbiol.* 44(5) (1996), 317-319.
- [6] S. Kariuki, Genotypic Analysis of Multidrug-Resistant *Salmonella enterica* Serovar Typhi, Kenya, *Emerg. Infect. Dis.* 6 (2000), 649–651.
- [7] G. Adomian, *Solving Frontier Problems of Physics: The Decomposition Method*. Kluwer Academic, Boston, 1994.
- [8] O.D. Makinde, Adomian decomposition approach to a SIR epidemic model with constant vaccination strategy, *Appl. Math. Comput.* 184 (2007), 842–848.
- [9] I. Elmojtaba, Using Adomian decomposition method for solving a vector-host model, *Int. J. Appl. Math. Res.* 5 (2016), 107-109.
- [10] M.J. M. Jiya, Adomian Decomposition Method for the Solution of Boundary Layer Convective Heat Transfer with Low Pressure Gradient over a Flat, *IOSR J. Math.* 4 (2012), 34–42.
- [11] A. Adeniyani, I.A. Abioye, Mixed convection radiating flow and heat transfer in a vertical channel partially filled with a Darcy-Forchheimer porous substrate. *Gen. Math. Notes*, 32(2) (2016), 80-104.
- [12] H. Heidarzadeh, J.M. Mashinchi, R. Asghari Application of Adomian Decomposition Method to Nonlinear Heat Transfer Equation, *J. Math. Computer Sci.* 4 (2012), 436-447.
- [13] M. Cakir, D. Arslan, The Adomian Decomposition Method and the Differential Transform Method for Numerical Solution of Multi-Pantograph Delay Differential Equations, *Appl. Math.* 6 (2015), 1332–1343.
- [14] G. Nhawu, P. Mafuta, J. Mushanyu, The Adomian decomposition method for numerical solution of first-order differential equations, *J. Math. Comput. Sci.* 6 (2016), 307-314
- [15] I.A. Adetunde, Mathematical models for the dynamics of typhoid fever in kassena-nankana district of upper east region of Ghana, *J. Mod. Math. Stat.* 2 (2008), 45-49.
- [16] V.E. Pitzer, C.C. Bowles, S. Baker, G. Kang, V. Balaji, J.J. Farrar, B.T. Grenfell, Predicting the Impact of Vaccination on the Transmission Dynamics of Typhoid in South Asia: A Mathematical Modeling Study, *PLoS Negl. Trop. Dis.* 8 (2014), e2642.
- [17] E. Joshua, Mathematical model of the spread of Typhoid fever. *World J. Appl. Sci. Technol.* 3(2) (2011),10-12.
- [18] D. Kalajdziewska, Modeling the Effects of Carriers on the Transmission Dynamics of Infectious Diseases, *Math. Biosci. Eng.* 8(3) (2011), 711–722.
- [19] O. J Peter, R. Viriyapong, F. A. Oguntolu, et al. Stability and optimal control analysis of an SCIR epidemic model, *J. Math. Comput. Sci.* 10 (2020), 2722-2753
- [20] M.A. Khan, M. Parvez, S. Islam, I. Khan, S. Shafie, T. Gul, Mathematical analysis of typhoid model with saturated incidence rate, *Adv. Stud. Biol.* 7 (2015), 65–78.
- [21] S. Mushayabasa, C.P. Bhunu, E.T. Ngarakana-Gwasira, Mathematical analysis of a typhoid model with carriers, direct and indirect disease transmission. *Int. J. Math. Sci. Eng. Appl.* 7(1) (2013), 79-90.

- [22] K. Moatlhodl, R.K. Gosaamang, Mathematical Analysis of Typhoid Infection with Treatment, *J. Math. Sci., Adv. Appl.* 40(1) (2017), 75-91.
- [23] J. Nthiiri, G. Lawi, C. Akinyi, D. Oganga, W. Muriuki, M. Musyoka, P. Otieno, L. Koech, Mathematical Modelling of Typhoid Fever Disease Incorporating Protection against Infection, *Br. J. Math. Computer Sci.* 14 (2016), BJMCS.23325, 1–10.
- [24] K. Moatlhodl, K.R. Gosaamang, Mathematical Analysis of Typhoid Infection with Treatment. *J. Math. Sci., Adv. Appl.* 40 (2017), 75-91.
- [25] [1]C.H. Watson, W.J. Edmunds, A review of typhoid fever transmission dynamic models and economic evaluations of vaccination, *Vaccine.* 33 (2015) C42–C54.
- [26] D.T. Lauria, B. Maskery, C. Poulos, D. Whittington, An optimization model for reducing typhoid cases in developing countries without increasing public spending, *Vaccine.* 27 (2009), 1609–1621.
- [27] A. Idowu Abioye, O. James Peter, A. Abayomi Ayoade, O. Airenoni Uwaheren, M. Olanrewaju Ibrahim, Application of Adomian Decomposition Method on a Mathematical Model of Malaria, *Adv. Math., Sci. J.* 9 (2020), 417–435.
- [28] O.J. Peter, M.O. Ibrahim, Application of Differential Transform Method in Solving a Typhoid Fever Model. *Int. J. Math. Anal. Optim., Theory Appl.* 1(1) (2017), 250-260.
- [29] M.O. Ibrahim, O.J. Peter, O.D. Ogwumu, O.B. Akinduko, On the Homotopy Analysis Method for Solving PSTIR Typhoid Model. *Trans. Nigerian Assoc. Math. Phys.* 4 (2017), 51-56.
- [30] O.J. Peter, M.O. Ibrahim, O.B. Akinduko, M. Rabi, Mathematical Model for the Control of Typhoid Fever. *IOSR J. Math.* 13(4) (2017), 60-66.
- [31] A.F. Adebisi, O.J. Peter, T.A. Ayoola, F.A. Oguntolu, C.Y. Ishola, Approximate Solution of Typhoid Fever Model by Variational Iteration Method ATBU, *J. Sci. Technol. Educ.* 6 (3) (2018), 254- 265.
- [32] O.J. Peter, O.A. Afolabi, F.A. Oguntolu, C.Y. Ishola, A.A. Victor, Solution of a Deterministic Mathematical Model of Typhoid Fever by Variational Iteration Method. *Sci. World J.* 13(1) (2018), 64-68.