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Series solutions using variational iteration, differential transform and adomian decomposition methods.

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ABSTRACT

In this research work, a proposed Lassa fever model is solved by the Differential transform method (DTM), Variational Iteration Method (VIM) and Adomian decomposition methods (ADM). Prior to approximate solutions to the Epidemiology model, region of positive-invariant was examined. Results show that, the Variational Iterative Method converges faster than the two other methods.

1. Introduction

Lassa fever is a viral hemorrhagic fever that is often spread by multimammate rats (Mastomys natatesis). Its causative agent belongs to the family Arenaviride. The pathogen was identified in 1969 when three American nurses became infected in Lassa, Borno State of Nigeria (Macher and Wolfe, 2006). The virus is present in rodent excreta (e.g. urine, saliva and respiratory secretions). The rodent excretes the virus in urine for an extended time period and can therefore

contaminate peridomestic environments where food and non-food items are poorly stored. Transmission of Lassa virus occurs most commonly through ingestion or inhalation of contaminated items. Sexual transmission is possible (World Health Organizationon Lassa fever, 2016). Airborne transmission can also occur when cleaning dust contaminated by rodent.excreta. In addition, Lassa virus is transmitted from human to human by coming in contact with blood. Lassa Ribavirin is effective early in the course of the illness, notably when started within the first six days of illness (Cormick & Jonhson, 1984). There is currently no vaccine to the full blown disease, Therefore, primary prevention involves avoiding contact with items contaminated with rodent urine or faeces and implementing appropriate infection control measures in healthcare settings to minimise the risk of nosocomial transmission (Cormick & Jonhson, 1984). Rare cases have been reported among returning travellers with a history of exposure in rural areas or hospitals in countries where Lassa fever is known to be endemic. Laboratory infections by Lassa virus have been reported. Unlike other arena viruses, Lassa virus can be fairly easily transmitted from human to human. (Cormick & Jonhson, 1984) stated that humans can contact the disease from other humans via aerosol transmission (coughing), or from direct contact with infected human blood, urine, or semen. Lassa virus has been isolated from semen 6 weeks after acute illness; thus the virus can be transmitted to sexual partners by convalescent men (Tara, 2004). The symptoms of Lassa fever develop about 21 days after the infection with acute illness involving multi organs. Specific symptoms include fever, facial swelling, muscle fatigue, vomiting, cough, meningitis, and hypertension. In some patients neurological problems, including hearing loss which may be transient or permanent, tremors, and encephalitis, have been described (Omalibu *et al.*, 2003)

Recent reports show that between the first week and twenty third week of this year 2017, 301 suspected Lassa fever cases with 65 laboratory confirmed cases and 49 deaths Case of Fatality Rate (CFR, 16.28%) from 60 LGAs (22 States) were reported compared with 717 suspected cases with 71 laboratory confirmed cases and 87 deaths (CFR, 12.15%) from 125 LGAs (27 States) during the same period in 2016. Between weeks 1 and 52 2016, 921 suspected Lassa fever cases with 109 laboratory confirmed cases and 119 deaths (CFR, 12.92%) from 144 LGAs (28 States and FCT) were reported compared with 430 suspected cases with 25 laboratory confirmed cases and 40 deaths (CFR, 9.30%) from 37 LGAs (14 States and FCT) during the same period in

2015.Nigeria Center for Disease Control (Nigeria Center for Disease Control N.C.D.C., 2017). To stem the spread of the disease, medical experts say government should not only mount surveillance during an outbreak, the surveillance should be a way of life that must be sustained. Besides this, establishing aggressive campaigns to educate and enlighten the public on the disease will go a long way in creating the collective force to combat it. Mathematical models are useful weapons in fighting Epidemics. With the development of cheaper and more powerful computers, mathematical modeling of systems and the analysis of the resulting numerical solutions is becoming more popular. These solutions may be in the form of graphs showing the systems behavior over time as well as its sensitivity to variations in key model parameters. This research investigates the application of differential transform method (DTM), variational iteration method (VIM) and Adomian decomposition method (ADM) in finding the approximation solution to the Epidemiology model of Lassa fever developed.

2. Literature Review

Okuonghae and Okuonghae, (2006) developed a SIS model alongside with the population of rat species, for the transmission of Lassa fever disease. They obtained the equilibrium states of model that is the disease free equilibrium and the endemic equilibrium. Further, they calculated the basic reproductive number for their model and gave conditions for disease outbreak. In another development, Ogabi *et al.*, (2012), developed a SIR model for controlling Lassa fever transmission in northern part of Edo state, Nigeria. They advocated for health policies that will keep the basic reproductive number R_0 below 1, thereby keeping the transmission of the disease under control. The Lassa fever model developed by Bawa *et al.*, (2013) is a major paradigm shift from the first two papers motioned above in that these researchers divided the human population into susceptible human S_H and the Infect human I_H, the reservoir population they divided into Infant rat I_R and the Adult reservoir A_R and interestingly represented the Virus in the environment by V, they explained that the virus compartment is generated from the urine and faeces of infected Human and adult reservoirs. The major parameters of their model are b_H per capital birth rate of Human, b_R per capital birth rate of the reservoir, μ_H capital natural death rate of Human, μ_R per capital death rate of the reservoir, μ_H Lassa fever induced death rate, δ_R mortality death of the reservoir due to hunting, β_1 contact rate for

human, β_2 effective contact rate between reservoir and human, γ recovery rate of Infected human and σ progression rate from Infant to adult reservoir. They recommended that efforts should be made to keep the basic reproductive number below unity to ensure that the virus is contained. Abdullahi *et al.,* (2015) developed sensitivity analysis of a Lassa fever in which various parameters were analysed. Onuorah *et al.,* (2016) developed a Lassa fever model using the sex structure approach. Their model represented the transmission dynamics of the Lassa fever disease using a set of ordinary differential equations. The total human population at time t denoted by $N_H(t)$ was subdivided into four (4) mutually exclusive sub-populations of Susceptible Male $S_1(t)$, Infected Male $I_1(t)$, Susceptible Female $S_2(t)$, Infected Female $I_2(t)$, such that $N_H(t) = S_1(t) + I_1(t) + S_2(t) + I_2(t)$. Similarly, the total Natural Reservoir/host population at time t, denoted by $N_R(t)$ was sub-divided into dormant Reservoir/host $R_1(t)$, active Reservoir host $R_2(t)$, such that $N_R(t) = R_1(t) + R_2(t)$. Their model had the following assumptions. Susceptible individuals, male/female can be infected via interaction with the active Reservoir (Mastomys Natelensis), and via sexual interaction with opposite sex. Two major controls were considered, the use of condom to reduce contact via sexual interaction and the use of pesticide/Rat poison to kill the natural Reservoir (Mastomys Natelensis). And finally, horizontal transmission for human and vertical transmission for the Reservoir C.

Differential transform method has been successfully used to solve linear and nonlinear initial value problems in electric circuit analysis. In recent years, Differential transform method (DTM) has been used to solve one-dimensional planar Bratu problem, differential equation, delay differential equations, differential algebraic equation, integro-differential systems Stephenson *et al.,* (1984).

The Adomian decomposition method (ADM) is a semi-analytical method for solving ordinary and partial nonlinear differential equations. The method was developed from the 1970s to the 1990s by George Adomian, chair of the Center for Applied Mathematics at the University of Georgia. The crucial aspect of the method is employment of the "Adomian polynomials" which allow for solution convergence of the nonlinear portion of the equation, without simply linearizing the system.These polynomials mathematically generalize to a Maclaurin series about an arbitrary external parameter; which gives the solution method more flexibility than direct Taylor series expansion (Wazwaz, 2006).

In 1999, the variational iteration method (VIM) was proposed by He in (Wazwaz, 2006). The variational iteration method is useful to eliminate the small parameters that arise in the perturbation technique and gives exact solution of the problem. the variational iteration method uses a Lagrange multiplier which can be obtained optimally by the variational iteration method.

This model extends mathematical models for the transmission dynamics of Lassa fever proposed by (Bawa *et al.*, 2013). We propose an $S_r I_r S_H E_H I_H R_H P$ model where S_r is the susceptible rat population, I_r is infected rat population, S_H is the susceptible human population, E_H is the exposed or asymptomatic human population, R_H is the recovered human and P is the contaminated environment of Lassa virus. The contacting rate at which susceptible rats become infected is β_1, the rate which susceptible human becomes exposed is β_2, the exposed becomes infected by β_3 and the environment becomes contaminated by α_1 and α_2.

3. Results & Discussion

Model One Formulation and Analysis

The effects of immigrants to lassa fever susceptible population in Nigeria.

To formulating this model, the following assumptions are considered:

1. The rate of immigrants in to the infected compartment is considered less than the removal rate from the infected compartment.
2. Vertical transmission in this model is ignored.
3. The model considers a homogenous population i.e., every person has an chance of become infected with a infectious person.
4. Induced deaths as a result of infection occur at the infective compartment.

Base on the above assumptions, we have the following model consisting of Seven (7) ordinary differential equations:

$$\left.\begin{aligned}
\frac{dS_r}{dt} &= US_r - \beta_1 S_r I_r - \mu_r S_r \\
\frac{dI_r}{dt} &= \beta_1 S_r I_r - \mu_r I_r \\
\frac{dS_H}{dt} &= \pi S_H - \beta_2 S_H P - \beta_3 S_H I_H - \mu S_H \\
\frac{dE_H}{dt} &= \beta_2 S_H P + \beta_3 S_H I_H - \sigma E_H - \mu_H E_H - \varepsilon E_H \\
\frac{dI_H}{dt} &= \theta I_H + \sigma E_H - (\delta + \mu_H) I_H - \sigma I_H \\
\frac{dP}{dt} &= \alpha_1 I_r + \alpha_2 I_H - \phi P \\
\frac{dR_H}{dt} &= \sigma I_H + \varepsilon E_H - \mu_H R_H
\end{aligned}\right\} \quad (1)$$

3.1 Variables and Parameters

Table 1. Variable description

State Variables	Description
S_r	Susceptible Rat compartment
I_r	Infected Rat compartment
S_H	Human compartment
E_H	Exposed/ asymptomatic compartment
I_H	Infected humans
R_H	Recovered humans
P	Vector population Environment

Table 2. Parameter description

Parameter	Description
U	The rate of rat recruitment.
γ	The rate of progression of pathogens from the urine and faeces of infected Rats.
α_2	The rate of progression of pathogens from infective class to the Environment.
π	The rate of recruitment of susceptible human.
θ	Infective immigrants.
σ	The rate of progression from exposed class infective class.

τ	The rate of recovery from the infected class.
ϕ	Loss of Lassa virus in the Environment.
α_1	Interactions between infected Rats and the Lassa environment.
μ	Natural death of the Rats and Human population.
δ	Induced death due to infection.
G, Y	The force of infection: $G = (\beta_1 S_H E_H + \beta_2 E_1 I_H)$, $Y = \beta_3 S_r I_r$

Table 3. Baseline Parameter values for the model One equations

Parameter	Values	References
θ	0.02	Abdullahi *et al.* (2015)
τ	0.04	Abdullahi *et al.* (2015)
π_H	2000	Assumed
α_1	0.003	Assumed
α_2	0.003	Assumed
ϕ	0.009	Assumed
β_1	0.02	Abdullahi *et al.* (2015)
β_2	0.08	Abdullahi *et al.* (2015)
β_3	0.02	Abdullahi *et al.* (2015)
μ_r	0.0312	Abdullahi *et al.* (2015)
μ_H	0.05	Assumed
δ	0.01626	Nigeria Center for Disease Control N.C.D.C. (2017)
U_r	1500	Assumed

3.2 Invariant regions

The total population reservoir (Rat) is

$$N_r = S_r + I_r \tag{2}$$

The total population of Human is

$$N_H = S_H + E_H + I_H + R_H \tag{3}$$

The rate of change in population of Reservoir and that of Human by adding gives

$$\left.\begin{aligned}\frac{dN_r}{dt} &= U_r - \mu_r N_r \\ \frac{dN_H}{dt} &= \pi_H - \mu_r N_H + (\theta_H - \delta_H) I_H\end{aligned}\right\} \qquad (4)$$

Solving equations (4) by using integrating factor for $N_r(t)$ and $N_H(t)$ respectively we obtained

$$\left.\begin{aligned}N_r(t) &= \frac{U_r}{\mu_r}(1-\exp(-\mu_r t)) + N_r(0)\exp(-\mu_r t) \\ N_H(t) &= \frac{\pi_H}{\mu_H}(1-\exp(-\mu_H t)) + N_H(0)\exp-(\mu_H t)\end{aligned}\right\} \qquad (5)$$

Lemma 1:

The closed set $D = [(S_r, I_r, S_H, E_H, I_H, R_H) \in R_+^6 : \ S_r + I_r \le \frac{U_r}{\mu_r} \ ; \ S_H + E_H + I_H + R_H \le \frac{\pi}{\mu_H}]$ is positively-invariant and attracting with respect with the basic model equation (1)

Proof : From the above model equation, $\frac{dN_H}{dt} \le \pi_H - \mu_r N_H$, $\frac{dN_r}{dt} \le U_r - \mu_r N_r$

It follows that $\frac{dN_H}{dt} < 0$ and $\frac{dN_r}{dt} < 0$ if $N_H(t) > \frac{\pi_H}{\mu_H}$ and $N_r(t) > \frac{U_r}{\mu_r}$ respectively.

thus, a standard comparison theorem as in Onuorah, *et al.* [11] can be used to show that

$N_H(t) \le \frac{\pi}{\mu_H}(1-\exp(-\mu_H t)) + N_H(0)\exp(-\mu_H t)$ and $N_r(t) \le \frac{U_r}{\mu_r}(1-\exp(-\mu_r t)) + N_r(0)\exp(-\mu_r t).$

In particular, $N_H(t) \le \frac{\pi}{\mu_H}$ and $N_r \le \frac{U_r}{\mu_r}$ If $N_H(0) \le \frac{\pi}{\mu_H}$ and $N_r(0) \le \frac{U_r}{\mu_r}$ respectively. thus D is positively-invariant. Further,

$N_H(0) > \frac{\pi}{\mu_H}$ and $N_r(0) > \frac{U_r}{\mu_r}$ then either the solution enters D in finite time or $N_H(t)$ approaches $\frac{\pi}{\mu_H}$ and $N_r(t)$ approaches $\frac{\pi_r}{\mu_r}$, and the infected variables $I_H + I_r$ approaches 0. Hence D is attracting,

that is all solutions in R_+^6 eventually enters D. Thus in D, the basic mode equation (1) is well posed epidemiological and mathematically. Hence it is sufficient to study the dynamics of the basic model equation (1).

3.3 Variational Iteration Method (VIM)

The basic concept of this technique can be illustrated using the general form differential equation.

$$LU + NU = g(x) \qquad (6)$$

Where, L is a linear operator and g(x) is a forcing term. To use this method we construct a correction functional as follows.

$$U_{n+1}(x) = U_n(x) + \int_0^x \lambda(LU_n(t) + N\bar{U}_n(t) - g(x))dt \qquad (7)$$

Where, λ is a Lagrangian multiplier which can be identified optimally via the variational iteration method. The Lagrange

$$\lambda(t) = \frac{(-1)^m}{(m-1)!}(t-x)^{m-1} \qquad (8)$$

The subscript n and the superscript m denote the nth approximation and order of differential equation respectively . $\bar{U}_n$ is considered as a restricted variation that is $\delta\bar{U}_n = 0$. The above equation is referred to as correction functional. The successive approximation U_{n+1}; $n \geq 0$ of the solution of the correction functional will be readily obtained upon using the determined Lagrange multiplier and the first approximate (Venu and Lakshmi, 2012). Consider the model equation (1), we construct the correction functional as follows.

$$S_r(n+1) = S_r(n) - \int_0^t (\frac{d}{dt}S_r(n) - U_r + \beta_1 S_r(n)I_r(n) + \mu_r S_r(n))dt \qquad (9)$$

$$I_r(n+1) = I_r(n) - \int_0^t (\frac{d}{dt}I_r(n) - \beta_1 S_r(n)I_r(n) + \mu_r I_r(n))dt \qquad (10)$$

$$S_H(n+1) = S_H(n) - \int_0^t (\frac{d}{dt}S_H(n) - \pi_r + \beta_2 S_H(n)P(n) + \beta_3 S_H(n)I_H(n) + \mu_H S_H(n))dt \qquad (11)$$

$$E_H(n+1) = E_H(n) - \int_0^t (\frac{d}{dt}E_H(n) - \beta_2 S_H(n)P(n) + \beta_3 Sh(n)I_H(n) + \mu HE_H(n) + \sigma E_H(n) + \varepsilon E_H n)dt \qquad (12)$$

$$I_H(n+1) = I_H(n) - \int_0^t (\frac{d}{dt} I_H(n) - \theta I_H(n) - \sigma I_H(n) + \delta I_H(n) + \mu h I_H(n) + \sigma I_H(n))dt \quad (13)$$

$$P(n+1) = P(n) - \int_0^t (\frac{d}{dt} P(n) - \alpha_1 I_r(n) + \alpha_2 I_H(n) + \phi P(n))dt \quad (14)$$

$$R_H(n+1) = R_H(n) - \int_0^t (\frac{d}{dt} R_H(n) - \varepsilon E_H(n) - \sigma I_H(n) + \mu R_H(n))dt \quad (15)$$

With the initial conditions

$$S_H(0) = 990, S_R(0) = 500, I_H(0) = 100, I_r(0) = 10, E_H(0) = 300, R_H(20), P(0) = 200.$$

The solutions of the Model above using Maple 18 software respectively to the fourth-order approximate are,

$$\left.\begin{aligned}
S_r(t) &= \sum_{i=0}^{3} S_r(i) = 500 + 399.7t - 466.245t^2 - 1729.918412t^3 - 4970.563219t^4 \\
I_r(t) &= \sum_{i=0}^{3} I_r(i) = 10 + 85t + 458.9745t^2 + 1729.991117t^3 + 1275.721972t^4 \\
S_H(t) &= \sum_{i=0}^{3} S_H(i) = 990 + 15869.5t - 142849.1t^2 - 859681.179t^3 - 5501.8817t^4 \\
E_H(t) &= \sum_{i=0}^{3} E_H(i) = 300 + 17781t - 143608.0944t^2 + 863523.3788t^3 - 5422.123306t^4 \\
I_H(t) &= \sum_{i=0}^{3} I_H(i) = 100 + 60.374t - 634.2208295t^2 - 3267.61617t^3 - 69.788442t^4 \\
P(t) &= \sum_{i=0}^{3} P(i) = 200 - 5.6t + 0.311101t^2 + 1.090164219t^3 + 1.698725t^4 \\
R_H(t) &= \sum_{i=0}^{3} R_H(i) = 20 + 6t + 89.96248t^2 - 471.737450t^3 - 9.961748882t^4
\end{aligned}\right\} \quad (16)$$

3.4 Differential Transform Method

Differential function $Y(t)$ as in [1] is defined as follows.

$$Y(t) = \frac{1}{K!}[\frac{d^k y(t)}{dt^k}]_{t=0} \quad (17)$$

And the inverse differential transform of $Y(t)$ is

$$y(t) = \sum_{k=0}^{\infty} Y(K) t^K \quad (18)$$

Table 4. Differential Transform of various Functions (Akinboro *et al.*, 2014)

S/N	Functions	Differential Transform
1	$z(t) = I(t) \pm S(t)$	$z(k) = I(k) \pm S(k)$
2	$z(t) = \sin(\vartheta t + \alpha)$	$z(k) = \frac{\vartheta^k}{k!}\sin(\frac{\pi k}{2} + \alpha)$
3	$z(t) = e^{\beta t}$	$z(k) = \frac{\beta^k}{k!}$
4	$z(t) = \frac{dh(t)}{dt}$	$z(k) = (k+1)H(k+1)$
5	$z(t) = s\frac{d^2h(t)}{dt^2}$	$z(k) = (k+1)(k+2)H(k+2)$
6	$z(t) = \frac{d^n h(t)}{dt}$	$z(k) = (k+1)H(k+2)...$ $(k+n)H(k+n)$
7	$z(t) = I(t)S(t)$	$z(k) = \sum_{m=0}^{k} I(m)S(k-m)$
8	$z(t) = 1$	$z(k) = \delta(k)$
9	$z(t) = t$	$z(k) = \delta(k-1)$
10	$z(t) = t^n$	$z(t) = \delta(k-n) = \begin{cases} 1, k = m \\ 0, k \neq m \end{cases}$
11	$z(t) = au(t)$	$z(t) = aU(k)$

Implementing Model (1) using properties of differential transform above we obtained.

$$S_r(K+1) = \frac{1}{K+1}(U_r - \mu_r S_r(K) - (\beta_1 \sum_{m=0}^{k} S_r(M) I_r(K-M)) - \mu_r S_r(K) \quad (19)$$

$$I_r(K+1) = \frac{1}{K+1}((\beta_1 \sum_{m=0}^{k} Sr(M) Ir(K-M)) - \mu_r I_r(K) \quad (20)$$

$$S_H(K+1) = \frac{1}{K+1}(\pi_h - \mu_H S_H(K) - (\beta_2 \sum_{m=0}^{k} S_H(M) P(K-M)) - (\beta_3 \sum_{m=0}^{k} S_H(M) I_H(K-M)) \quad (21)$$

$$E_H(K+1) = \frac{1}{K+1}(\beta_2 \sum_{m=0}^{k} S_H(M) P(K-M)) + (\beta_3 \sum_{m=0}^{k} S_H(M) I_H(K-M)) - \sigma E_H(K) - \varepsilon E_H(K)) \quad (22)$$

$$I_H(K+1) = \frac{1}{K+1}(\theta I_H(K) + \sigma E_H(K) - \mu I_H(K) - \delta I_H(K) - \sigma I_H(K) \quad (23)$$

$$P(K+1) = \frac{1}{K+1}(\alpha_1 I_r(K) + \alpha_2 I_H(K) - \phi P(K) \quad (24)$$

$$R_H(K+1)=\frac{1}{K+1}(\sigma I_H(K)+\varepsilon E_H(K)-\mu R_H(K) \tag{25}$$

With the initial conditions

$$S_H(0)=990, S_R(0)=500, I_H(0)=100, I_r(0)=10, E_H(0)=300, R_H(20), P(0)=200.$$

The solutions of the Model above using Maple 18 software respectively to the fourth-order approximate are,

$$\left.\begin{aligned}
S_r(t)&=\sum_{i=0}^{3}S_r(i)=500+375t-296.845t^2-1850.047923t^3-5672544710t^4\\
I_r(t)&=\sum_{i=0}^{3}I_r(i)=10+99.9940t+537.4400018t^2+2021.554518t^3+5820.367075t^4\\
S_H(t)&=\sum_{i=0}^{3}S_H(i)=990-15869.50t+143849.0669t^2-865031.772t^3+3943423.385t^4\\
E_H(t)&=\sum_{i=0}^{3}E_H(i)=300+17781t-143608.0944t^2+869523.7721t^3-5422.123306t^4\\
I_H(t)&=\sum_{i=0}^{3}I_H(i)=100+60.374t+634.2208295t^2-3267.61617t^3-14895.02173t^4\\
P(t)&=\sum_{i=0}^{3}P(i)=200-5.67t+0.3256020t^2+1.16840411t^3+0.9433092728t^4\\
R_H(t)&=\sum_{i=0}^{3}R_H(i)=20+6t+89.96248t^2-471.73367450t^3+2147.030479t^4
\end{aligned}\right\} \tag{26}$$

3.5 Adomian Decomposition Method

Using the ADM, the differential operator L is given by $L(.)=\frac{d^n}{dt^n}(.)$ The inverse operator L^{-1}, this is n-fold integral operator defined by $L(.)=\int_0^1(.)_{n-times}\,dt$ Operating L^{-1} on the general form differential equation $Ly+Ry+Ny=f$ where Ny is the nonlinear term by Adomian polynomials (Bawa *et al.*, 2013). $Ny=\sum_{n=0}^{\infty}A_n$ and A_n are Adomian polynomials that can be generated for all forms non linearity as :

$$A_n=\frac{1}{n!}\frac{d^n}{dx^n}[N(\sum_{i=1}^{n}\alpha^i y_i)]_{\infty=0}\text{, where } i=0,1,2,3,...$$

$$A_0=f(y_0), A_1=y_1(\frac{d}{dy})f(y_0) \text{ gives}$$

$$L^{-}1Ly+L^{-1}Ry+L^{-1}Ny=L^{-1}f$$

Hence, the solution

$$\sum_{n=0}^{\infty} y_n = y_0 + L^{-1} f - L^{-1} R \sum_{n=0}^{\infty} y_n - L^{-1} \sum_{n=0}^{\infty} A_n$$

Implementing Model (1) we have,

$$S_r(K+1) = \int_0^t (U_r - \mu_r S_r(K) - (\beta_1 \sum_{m=0}^{k} S_r(M) I_r(K-M)) - \mu_r S_r(K))dt \quad (27)$$

$$I_r(K+1) = \int_0^t ((\beta_1 \sum_{m=0}^{k} Sr(M) Ir(K-M)) - \mu_r I_r(K))dt \quad (28)$$

$$S_H(K+1) = \int_0^t (\pi_h - \mu_H S_H(K) - (\beta_2 \sum_{m=0}^{k} S_H(M) P(K-M)) - (\beta_3 \sum_{m=0}^{k} S_H(M) I_H(K-M)))dt \quad (29)$$

$$E_H(K+1) = \int_0^t (\beta_2 \sum_{m=0}^{k} S_H(M) P(K-M)) + (\beta_3 \sum_{m=0}^{k} S_H(M) I_H(K-M)) - \sigma E_H(K) - \varepsilon E_H(K))dt \quad (30)$$

$$I_H(K+1) = \int_0^t (\theta I_H(K) + \sigma E_H(K) - \mu I_H(K) - \delta I_H(K) - \sigma I_H(K))dt \quad (31)$$

$$P(K+1) = \int_0^t (\alpha_1 I_r(K) + \alpha_2 I_H(K) - \phi P(K))dt \quad (32)$$

$$R_H(K+1) = \int_0^t (R_H(K+1) = \frac{1}{K+1} (\sigma I_H(K) + \varepsilon E_H(K) - \mu R_H(K))dt \quad (33)$$

With the initial conditions above

$$S_H(0) = 990, S_R(0) = 500, I_H(0) = 100, I_r(0) = 10, E_H(0) = 300, R_H(20), P(0) = 200.$$

The solutions of the Model above using Maple 18 software respectively to the fourth-order approximate are,

$$\left.\begin{aligned}
S_r(t) &= \sum_{i=0}^{4} S_r(i) = 500 + 1385t - 101.775t^2 - 584.8355834t^3 - 55.72610416t^4 \\
I_r(t) &= \sum_{i=0}^{4} I_r(i) = 10 + 99.7t + 87.0045t^2 + 584.9082884t^3 + 55.7261416t^4 \\
S_H(t) &= \sum_{i=0}^{4} S_H(i) = 990 + 11869t - 125172.23375t^2 - 86208287.3004t^3 + 51343.70657t^4 \\
E_H(t) &= \sum_{i=0}^{4} E_H(i) = 300 + 17781t - 125981.2650t^2 + 862087.3004t^3 - 51423.46456t^4 \\
I_H(t) &= \sum_{i=0}^{4} I_H(i) = 100 + 60{,}374t + 634.22.82995t^2 - 3276.32348t^3 - 69.78824218t^4 \\
P(t) &= \sum_{i=0}^{4} P(i) = 200 - 5.67t + 0.325161t^2 + 0.667937193t^3 + 0.19192255t^4 \\
R_H(t) &= \sum_{i=0}^{4} R_H(i) = 20 + 6t + 89.96248t^2 - 472.9806470t^3 - 9.969748882t^4
\end{aligned}\right\}$$

4. Conclusion

We extended and analyzed Mathematical model for the transmission dynamics of Lassa fever virus disease. The region of solutions to the model were found to exist and numerical methods solution were found to followed similar trend and thus recommended for solving any related problem. Finally Series solutions obtained by Differential transform method (DTM), Variational iteration method (VIM) and Adomian decomposition methods (ADM) using Maple 18 soft ware revealed that in terms of the time for simulation, VIM converges faster than the two other methods.

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