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Solution of SIR Model of ZIKA Virus – A Numerical Approach

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Abstract: ***Zika virus (ZIKV) is a flavivirus which is transmitted by mosquitoes and has a close relationship with the yellow fever virus as well as the dengue virus. It is currently responsible for causing a large outbreak in Americas. In this study, the susceptible-infected-recovered (SIR) model of Zika virus is presented and is solved by the incorporation of a technique known as the Runge-Kutta method. The case of Brazil has been taken to illustrate our epidemiological modeling by simulation through graphs. The results of the study help us to analyze the transmission dynamics, severity of infection and the fatality of the Zika virus.***

Keywords: Zika Virus, Epidemiology, SIR Modeling, Numerical Solution, Runge-Kutta

1. Introduction

The Zika virus (ZIKV) belongs to the category of Flavivirus, family Flaviviridae. The other flaviviruses which are of great importance to medical research are dengue virus and yellow fever virus. ZIKV first originated from a forest named Zika situated in Uganda in the year 1947 and cases closely associated with it were reported in both Africa and South East Asia for duration of around 50 years. The African lineage and the Asian lineage form the two lineages of the ZIKV. The virus spreading in the American region is known as the African lineage and the virus that disseminated in French Polynesia during the 2013–2014 outbreaks is known as the Asian lineage.

The Pan American Health Organization (PAHO), the Regional Office of the WHO for Americas, issued an alert about possible autochthonous transmission of the ZIKV in Brazil, South America in May 2015. Since then the virus has been spreading at a rapid rate in the Caribbean, Middle and South America affecting 29 countries and thousands of people. By August 2016, more than 50 countries have experienced active transmission of ZIKV. These facts are profoundly documented in the literature: refer M. Goeijenbier, L. Slobbe [10].

Mosquitoes, sexual contact, contaminated blood transfusion and pregnancy form the primary factors for the rapid transmission of the ZIKV. ZIKV is primarily spread by the female Aedes A.egypti mosquito, which is the same mosquito that transmits dengue, chikungunya and yellow fever; and is active mostly during daytime. The potential societal risk of ZIKV can be delimited by the distribution of the mosquito species that transmit it. Cases of ZIKV being transmitted sexually has been reported in seven countries – Argentina, Brazil, Chile, France, Italy, New Zealand, and the United States. A mathematical model of this problem available in the literature: refer T. Alex Perkins [9].

The infection due to the ZIKV, known as Zika fever or Zika virus disease is very similar to a very mild form of dengue fever which often causes no or only mild symptoms. Symptoms may include fever, red eyes, joint pain, headache, and a maculopapular rash. . There is also a potential risk that the virus is transferred from the mother to the fetus during pregnancy or delivery. This can result in a situation called as microcephaly, severe brain malformations, and other birth defects. Microcephaly is the situation in which a baby is born with an abnormal size of the head. Infection in adults has been linked to Guillain–Barré syndrome (GBS). No deaths have been reported during the initial stages of infection caused by the ZIKV.

In order to have a higher clarity, more comprehensive knowledge about the transmission characteristics of these diseases and to prepare counter measures strategically, mathematical modeling becomes an essential tool. The mathematical model allows us to simulate the real world which enhances the possibility of tests for sensitivity and comparison of conjunctures.

2. Sir Mathematical Modelling

Epidemiology studies the spread of diseases in population, primarily the human population. The work of an epidemiologist is to model the existing scenario, estimate parameters and investigate the sensitivity of the model to make changes in the parameters and numerical simulations. These chronological processes followed are expected to yield information about the spread of the disease in a population. One such epidemiological modeling is the SIR mathematical model. David Smith, Lang Moore [8] and Guillerno Abramson [10] have discussed several aspects of the SIR model in more detail.

The S-I-R was first introduced by W.O. Kermack and has proved its dominance in the field of epidemiological

modeling. The empirical use of this model is based on the fact that it can be kept realistic enough. The model makes use of first order; first degree differential equations and one can derive several important implications from it.

The entire population is divided into three categories: the susceptible (S), who have the capability to acquire the disease, the infected (I), who have the disease and are capable of transferring it, the removed (R), either recovered or sadly dead and N is the total population. Then:

$$S + I + R = N \quad (1)$$

Let us assume $S(t)$, $I(t)$, $R(t)$ as the number density (fraction of the population) of the members of each class. Then

$$S(t) + I(t) + R(t) = 1 \quad (2)$$

We now make assumptions which are necessary to proceed with the mathematical modeling:

1) The diseases unfurls itself in a closed environment; that is none of the members of any group leave the group nor is any other member allowed inside the group, so the whole population remains a constant N.
2) The number of susceptible individuals who are getting infected by an infected individual per unit of time, at any given time t, is considered to be proportional to the total number of susceptible individuals with the proportionality constant (transmission coefficient) 'r', such that the total number of new susceptible individuals at time t, is $rS(t)I(t)$.
3) The number of individuals withdrawn from the group which is infected per unit of time at any given time t is $aI(t)$, where 'a' is known as the recovery rate coefficient or removal rate coefficient.
4) Any other element such as age, gender, societal status does not affect the likelihood of an individual being infected and that the individuals constituting the environment mix homogeneously.
5) The incubation period of the infected individual is ignored and he/she is assumed to be capable of transmitting the disease as soon as he/she is infected.

The model's equations are delineated as shown below:

$$\frac{dS}{dt} = -rSI \quad (3)$$

$$\frac{dI}{dt} = rSI - aI \quad (4)$$

$$\frac{dR}{dt} = aI \quad (5)$$

Here 'r' is the transmission or infection rate and 'a' is the recovery or removal rate.

3. Numerical Simulation

The traditional methods of solving differential equations (variable separable, homogeneous etc.) are applicable only to limited types of differential equations. More often we happen to come across equations which do not belong to any of these familiar forms and one is obliged to resort to numerical methods of computation. Different numerical approaches have been exceptionally written in the document: refer F.S Akinboro[2], S.O. Maliki[4]. There are various numerical methods to solve differential equation, Picard's, Euler, Runge-Kutta, Milne, Adams-Bashforth methods to name a few. The epidemiological model is an initial value problem where one knows the initial values and is required to determine the values after a certain interval. Here we try to solve this model [(1) – (5)] using fourth order Runge-Kutta algorithm popularly called as the Runge-Kutta method itself.

The constant 'r' defined as the rate of spread of infection is determined to be 0.011. This 'r' reduces by a rate of 20% for nearly 5-10% increase in the infected group, taking into account that the entire population is constant. The constant 'r' reduces only till the population of the infected group is less than half of the total population. Once the population of infected exceeds half the population of infected it remains constant. The constant 'a' defined as the rate of removal is determined to be $1.22*10^{-7}$. Please note that the determination of these constants has been done based on the analysis of statistical data.

The SIR modeling is a special case of the Runge-Kutta method. It's a case of simultaneous first order differential equation of the form:

$$\frac{dy}{dx} = f(x, y, z) \quad (6)$$

$$\frac{dz}{dx} = g(x, y, z) \quad (7)$$

We assume the initial conditions i.e. $S(0) = S_0$, $I(0) = I_0$, $R(0) = R_0$. From the statistics we have S_0=0.6255, I_0 =0.3744, R_0=0. We follow the working procedure for the Runge-Kutta method and find the increment 'p' of 'y', 'q' of 'z' corresponding to and increment 'h' of 'x_0'. So for any point x, $y(x)$ is given by $y(x_0 + h)$ and $z(x)$ is given by $z(x_0 + h)$. Here p and q are weighted means of p_1, p_2, p_3, p_4 and q_1, q_2, q_3, q_4 respectively which are calculated in the Runge-Kutta algorithm.

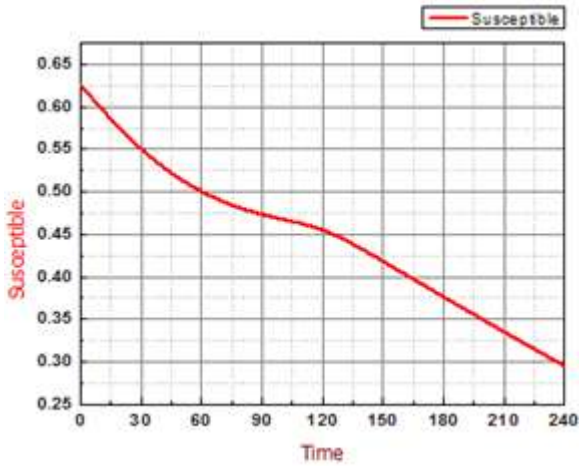

Figure 1: Graphical representation of the susceptible human population

From this graph we can infer that the population of the susceptible group of population reduces with the increase in time i.e after the population has been infected by the virus.

The recovered members (if any) are not added back into the susceptible group as they are considered to have developed immunity towards the disease. Thus only the susceptibles become infected and this explains the descent of the graph.

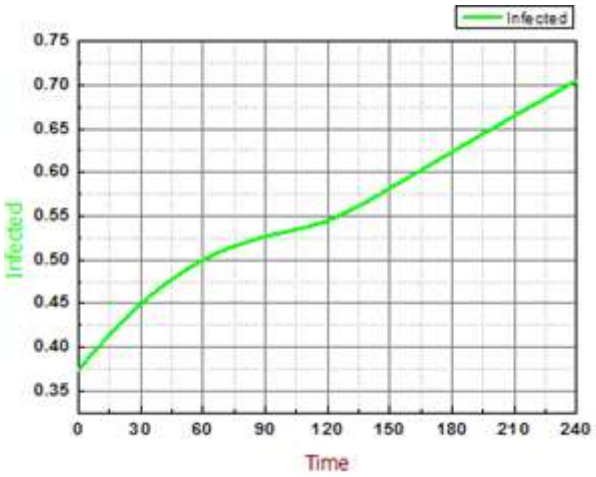

Figure 2: Graphical representaiton of the infected human population.

From the infected human population graph we get to know that the population of the infected group is constantly on the rise. We can conclude by this that the ZIKV is very infectious and is capable of infecting a large amount of area within a short span of time. When ZIKV causes situations like microcephaly in an individual, there is absolutely no scope for recovery and hence he/she remains infected till he/she is alive. Hence the ZIKV is capable of infecting the entire population if not acted upon wisely.

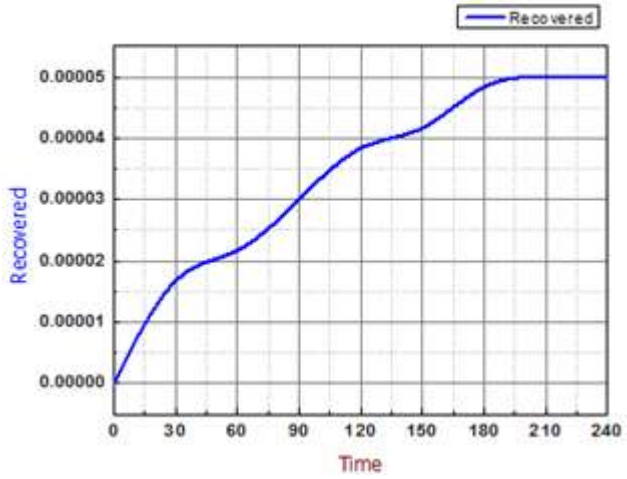

Figure 3: Graphical representation of the removed human population

The interesting factor of ZIKV is that it has a low mortality rate. Hence if we compare the scaling factor of the Y axis of the removed population graph with the suscpetible and infected population graphs' Y axis we can see that there is a huge difference. This only proves the fact that once an individual is infected with ZIKV he/she has to bear with it for his/her lifetime as one doesn't die within a short span of time as in cases of Ebola where the infected individual dies within 7 days.

4. Conclusion

This research work investigates the approximation of susceptible, infected and recovery model of ZIKV. It also goes to prove that the fourth order Runge-Kutta method can be employed to solve the equations and has a greater accuracy in finding out the efficient solution for the basic spread of ZIKV. We conclude by stating that one can rely on Runge-Kutta algorithm for solving dynamical problems of a broad array as it is consistent in the longer time frame. This might prove as a tool for the medical society in developing counter measures for the elimination of the disease completely.

5. Acknowledgment

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