Towards a Safer Future

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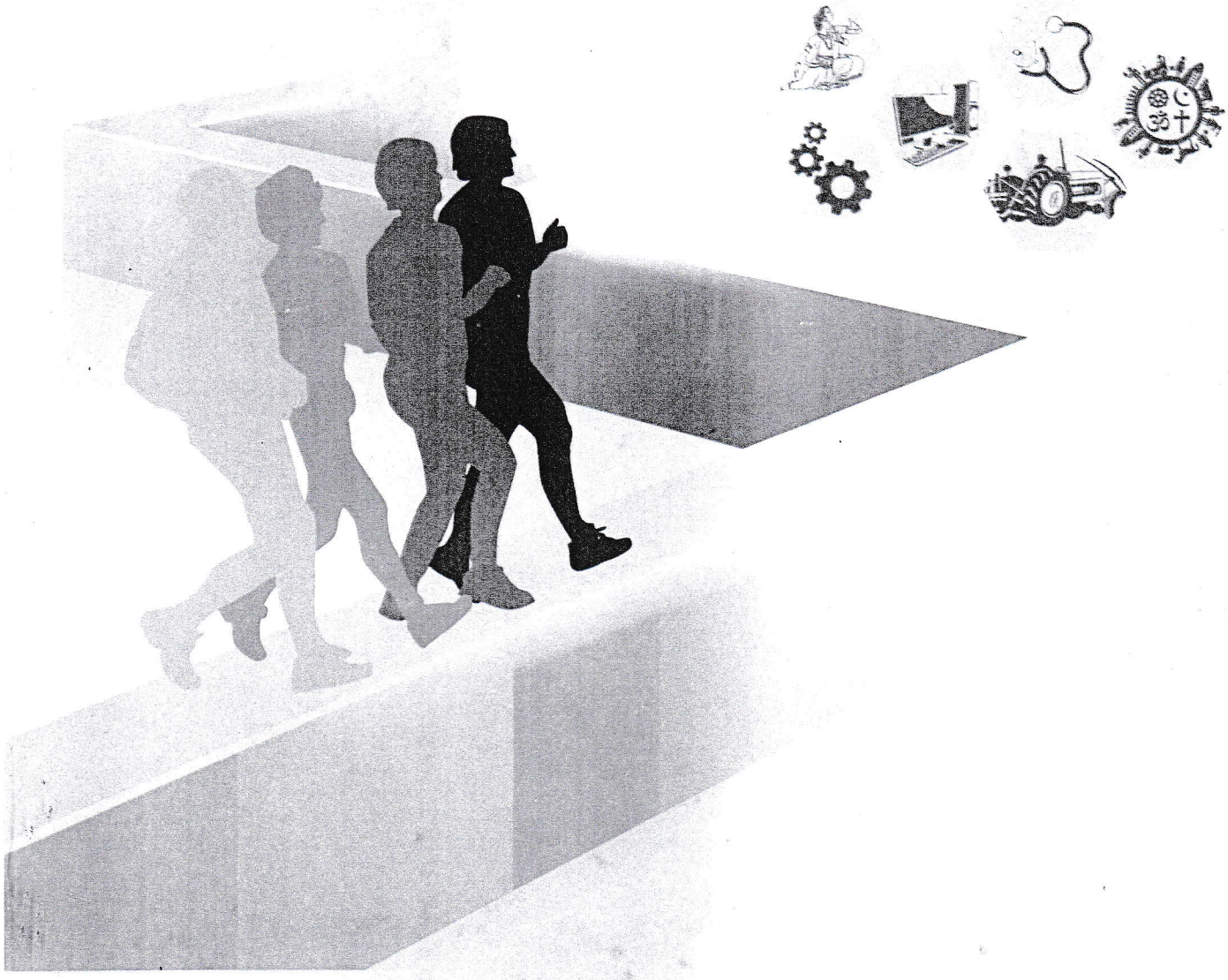

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A Kinetic-theory-based Model for Dengue Transmission

Erandi, K.K.W.H*, Perera, S.S.N , Mahasinghe, A.C.

Research & Development Centre for Mathematical Modelling, Faculty of Science, University of Colombo
**hasitha.erandi@yahoo.com*

Abstract - Dengue is the most critical mosquito-borne viral disease that has rapidly spread in tropical and subtropical regions. Understanding the dynamical behavior of Dengue transmission could provide efficient tools to control the spread and minimize the risk. In this study, we develop a simple mathematical model for Dengue transmission based on mathematical kinetic theory. Further, we derive another simplified model from the traditional compartment model for disease transmission. Finally, we compare these two models using numerical simulation results. Our results indicate that the dynamical behavior of Dengue transmission derived through the kinetic-theory-based model is similar to what was obtained from the simplified SIR model.

Keywords - Dengue transmission, Kinetic theory model, SIR model.

I. INTRODUCTION

Dengue is a mosquito-borne viral disease that has become a leading factor for illness and death in tropical and subtropical regions during the past few decades. There are currently four billion people living in high-risk areas of Dengue fever transmission, with 390 million cases reported annually [1]. Identified in Sri Lanka for the first time in 1962, it has now gained the status of an endemic disease. Statistics of the Epidemiology Unit of the Ministry of Health Sri Lanka indicate that 185,969 Dengue cases were reported in 2017. Every year the government and the private sector spend a significant amount of funds on individual healthcare and anti-Dengue campaigns. This is the context in which examining the dynamics of Dengue transmission becomes vital.

In order to capture the transmission of the Dengue virus, one might naturally look into well-known mathematical models of disease transmission based on classical compartments. In compartment models, the population is divided into categories for which the interactions and dynamics are formulated mathematically. Being one such model, the SIR classification divides the population into three compartments: susceptible (S), infected (I) and recovered (R) [2]. Thus, the SIR model consists of a system of differential equations which describes the dynamical behavior of the disease in terms of interactions between these compartments. Some recent works have suggested using the method of mathematical kinetic theory, which is a generalization of the Boltzmann equation, to model the evolution and the spread of epidemics [3]. A kinetic-theory-based-model is a spatial model which is capable of providing refined descriptions of each population based on the microscopic state of individuals. This motivates us to use the kinetic theory to model the Dengue transmission, as it seems to capture the microscopic picture which is scarcely taken into account in the SIR model.

Once a kinetic-theory-based model is developed for Dengue transmission, it is worthwhile to compare it with the standard SIR model. The SIR model, however, in its present format is incomparable to a kinetic-theory-based model. Therefore, we convert the standard SIR model to a comparable simplified version by adding certain assumptions. In order to make the comparison as much as compatible with the real phenomenon, we select the infected human density, which is the most critical factor in transmission of any disease, as the key ingredient for our comparison.

II. MODEL DEVELOPMENT

Kinetic-theory-based Model for Dengue Transmission

Recently, a mathematical kinetic theory has been used to model the evolution of large systems of interacting individuals [3]. Dynamics of Dengue transmission exhibits a similar behavior to that of particles considered in kinetic theory. This motivates us to use the mathematical structures developed in [3] and [4] to model Dengue transmission. First we build up a space-independent kinetic-theory-based model. Let f_i^h denote the i^{th} *population density in state h and* h_{ij} the encounter rate which gives the number of encounters per unit time between j^{th} and j^{th} populations. Also let β_{ij}^{pq} denote the discrete transition density which is the probability that a member of the i^{th} population with state p falls into state h after interacting with a member of the j^{th} population with state q and μ_{ij}^{pq} the source/sink rate. Thus, our model is described by equation (1) below, in which the time derivative of evolution function for ith population density in states h is equated to the difference between gthe gainand the loss terms.

$$\frac{df_i^h}{dt} = \sum_{j=1}^{2}\sum_{p,q=1}^{3}\eta_{ij}\beta_{ij}^{pq}(h)f_i^p f_j^q - f_i^h\sum_{j=1}^{2}\sum_{p,q=1}^{3}\eta_{ij}f_j^q + f_i^h\mu_i^h \quad (1)$$

Now we use equation (1) to describe Dengue transmission. It represents the rate of change of infected human population density. Infected human population increases due to interactions between *susceptible human* (f_h^s) and *infected vectors* (f_h^{inf} μ_h^{inf}) .and decreases due to human death rate and recovery rate which is represented by the *sink rate*

$(f_h^{inf}\mu_h^{inf})$

$$\frac{df_h^{inf}}{dt} = \eta_{hv}\beta_{hv}^{(s)(inf)}(inf)f_h^s f_v^{inf} - f_h^{inf}\mu_h^{inf} \quad (2)$$

Since infected vector density is proportional to per capita vector density ($n = \frac{N_v}{N_h}$), we use kn with constant value k instead of infected vector population function (f_v^{inf}).

One dimensional SIR Model for Dengue Transmission

Recall the standard SIR model captures the dynamics of an epidemic, a modified version of SIR model for Dengue transmission has been developed in [2], which represented interactions between human and vectors in terms of a

normalized system of non-linear ordinary differential equations. For the convenience of comparison, we simplify these differential equations, making justifiable assumptions for a real-world situation.

First, we convert the model in [2] into a dimensionless form. Let Sh, Ih, Sv and Iv denote the susceptible human, infected human, susceptible vector and infected vector densities respectively. Since Dengue virus comprises four distinct serotypes, sequential infection might take place. Thus, we simplify the model in [2] by omitting recovered human group and permanent immunized human fraction. Then, the recovery rate ($y\gamma\ I_h$) moves to the susceptible group. Let μ_h and μ_v denote the birth and death rates for human and vectors. Let the adequate contact rate of vectors to human and human to vectors be denoted by C_{vh} and C_{hv}. Also let N_v denote the vector population and N_h the total human population. Accordingly, Equations (3) to (6) represent a simplified SIR-based model.

$$\frac{dS_h}{dt} = \mu_h - C_{vh} I_v \frac{N_v}{N_h} S_h + \gamma_h I_h - \mu_h S_h \quad (3)$$

$$\frac{dI_h}{dt} = C_{vh} I_v \frac{N_v}{N_h} S_h - (\mu_h + \gamma_h) I_h. \quad (4)$$

$$\frac{dS_v}{dt} = \mu_v - C_{hv} I_h \frac{N_v}{N_h} S_v - \mu_v S_v \quad (5)$$

$$\frac{dI_v}{dt} = C_{hv} I_h \frac{N_v}{N_h} S_v - \mu_v I_v. \quad (6)$$

This is reducible further, as the sum of susceptible human density and infected human density is one. Thus, we reduce equation (3) and (4) into one dimensional system and replace S_h by 1- I_h. A similar reduction is applicable to Equations (5) and (6). In a pragmatic perspective, finding vector density is an infeasible task. Since per capita vector density ($n = \frac{N_v}{N_h}$) is proportional to infected mosquito density, Instead of using I_v, we use kn with constant value k. Then the entire system is reducible to Equation (7), which states the rate change of the infected human density.

$$\frac{dI_h}{dt} = C_{vh} nk(1 - I_h) - (\mu_h + \gamma_h) I_h \quad (7)$$

III. RESULTS AND DISCUSSION

We used numerical results obtained by MATLAB solver ode45 to study the dynamical behaviour of the models. For simplified SIR model, following [2], we took the values C_{vh}=0.75 and(μ_h+γ_h)=(1/3). In kinetic-theory-based model we selected η_{hv}=1, $\beta_{hv}^{(s)(inf)}$ (inf)=0.75 and μ_h^{inf}=(1/3) for equation (7). Assume that the initial infected human density is10^{-6} for both models. For the comparison, we assumed kn = 0.1 for both models. Figure 1 shows simulation results obtained by MATLAB ode45 solver for infected human density in the simplified SIR model and kinetic-theory-based models. We can see that infected human density curve of the simplified SIR model and space-independent kinetic-theory-based model coincide with each other.

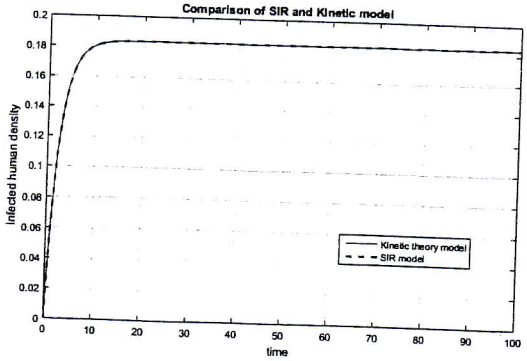

Fig. 1: Comparison of simplified SIR model and kinetic-theory-based model

IV. CONCLUSION

As mentioned in the introduction, our main purpose was to study the dynamical behaviour of Dengue transmission using a space-independent kinetic-theory-based model. As a tool of comparison, we used the SIR model. Since the standard SIR model is incomparable with the kinetic-theory-based model, we simplified the SIR to a comparable form by adding certain assumptions. For the simulations, we used infected human density as the key ingredient of comparison. Our simulation shows that the dynamical behaviour of Dengue transmission obtained by the kinetic-theory-based model coincides with the simplified SIR model. This result motivates us to do further research using functions such as uniform distribution and normal distribution instead of a fixed parameter for per capita mosquito density. Further, we hope to develop a functional for per capita mosquito density to capture the effects due to climate variation.

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