Modelling the Spread of Dengue in Singapore

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This project is a joint effort between NIE and the Ministry of the Environment under the ENV-NTU Joint Research Project Scheme. The aim of the study is to develop a mathematical model which can represent and describe the dynamics of the spread of Dengue in Singapore.

The specific objectives of this project are to:

- construct, from basic principles, a mathematical model which can be used to study or explain the dynamics of dengue spread in Singapore.
- use the resulting model to investigate the rate of the spread of the disease and to monitor and predict trends of the disease development in a chosen sensitive area.
- model and simulate the interaction between the host and vector populations, and to compare it with collected data.
- use the model to examine the effectiveness of the control measures.

Background

Dengue is a viral disease which is transmitted when infected female species of the Aedes mosquitoes, notably the *Aedes aegypti* and *Aedes albopictus,* bite human beings. After an incubation period of 5 to 8 days, dengue fever manifests itself with symptoms such as severe headaches, bone or joint and muscular pains, fever and rash. A complete recovery takes place after 4 to 7 days and is rarely fatal.

Despite the Aedes control programs, public health education and law enforcement, there has been a resurgence of dengue in Singapore in the past decade. The majority of the cases reported were Dengue Fever (DF), with Dengue Haemorrhagic Fever (DHF) constituting around 5.6%. As the trend points towards an increase in dengue infection in Singapore for the next few years, it is therefore in our interest to carry out a study to investigate the dynamics of the disease. This will help us interpret observed epidemiological trends, to guide the collection of data towards further understanding and to design programmes for the control of infection and disease.

Mathematical Models

A number of models have been studied and tested. In particular, three models were developed and investigated in detail. All three models are deterministic models based on a set of non-linear differential equations, subject to given initial conditions. Results from the modelling study are briefly described here.

1) *Model I : A Basic Model (qualitative study)*

Firstly, a qualitative model was developed to assess the suitability of using deterministic models in such epidemic studies. This model yielded fairly positive results, indicating that assuming that sufficient and accurate data can be obtained, deterministic models can provide valuable information on possible outbreaks of the disease. The drawback is that it is based on theoretical variables with no real data involved. In fact, in this model, certain parameters (such as transmission rate, and birth and death rates of the vector) had to be estimated.

2) Model II : SEIR Model (with real data)

A second model, called the SEIR (Susceptible-Exposed-Infected-Recovered)model, was then constructed. Based on the model developed by Newton and Reiter, this model used data on Singapore's vector and host populations obtained over a two-year period (from **1995** to 1996). **The** model was solved using Maple V. Results from this model indicated that while the model was able to predict possible outbreaks, comparison with actual Dengue cases was not as good.

The strength of this model lies in the fact that real data had been used to determine various parameters arising from the mathematical equations. However, the variables representing infected and uninfected vector were grouped as one variable representing total vector population. This is not satisfactory. In practice it is daunting task to determine the proportion of infected and uninfected vector based on the collected data.

3) Model III : The Final Model

The next model developed attempts to address the weaknesses of the previous models. In this model, larvae densities were used to represent a varying vector population. In particular, the model assumed that the proportion of infected vectors is a function of rainfall level since the arrival of rainfall increases potential breeding sites.

Results from this model show that the proportion of infected vectors is approximately 0.9 at the peak of the Dengue outbreak in October **1996.** Moreover, increase in rainfall levels and larvae densities precede an increase in Dengue incidence by 8 and 2 weeks respectively. This model compares much better with the actual number of Dengue cases during the simulation period than previous models (see figure below). We believe that Model III can be considered as a possible form of a mathematical model for predicting future Dengue outbreaks in Singapore.

Comparison between Actual Data and Model Prediction
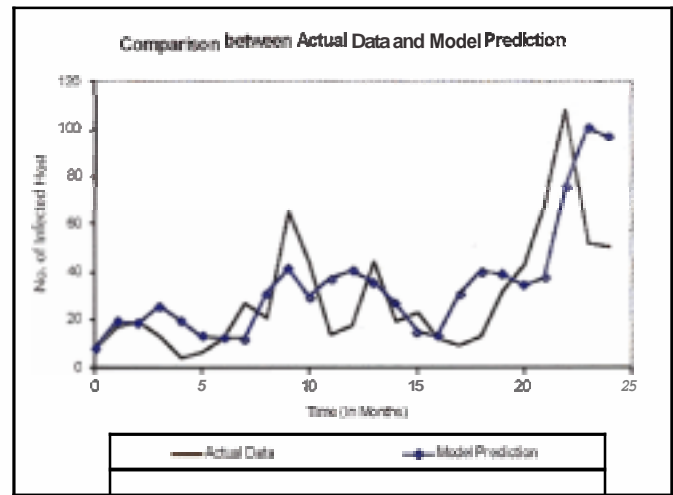
[1] Note: Pang, E.Y., previously affiliated to ENV, is currently a staff member of NEA (National Environment Agency).