# The influence of the vector *Aedes aegypti* in dynamics of the epidemiology of Dengue Fever

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*Figure 1:* The most important vector of dengue virus: *Aedes aegypti*

## 1. Introduction

Dengue Fever is a disease caused by an arboviral infection that infect between 50 and 100 millions of people every year [1]. Usually the Dengue Fever do not cause much deads, but in certain cases it develops to the Dengue Hemorragic Fever, which is much more severe and cause an higher number os deads, mainly when the pacients do not have adequade medical cares [3]. There are four antigenic distinct serotypes of dengue virus (DENV1-4). After being infected by one of these serotypes the human became resistant to this serotype, but remains susceptible to the others [1].

In order to infect other host, the virus needs a vector, in the case of the Dengue, it is passed by bites of a female mosquito of the species *Aedes aegypti*. Like other mosquitos species, females need mammal's blood to complete their eggs maturation [2]. The saliva of female mosquitos contains anti-coagulants which are released in order to facilitate feeding process.

When a mosquito bites an infected human, becames infected and the virus remains in its salivary glands and are released with the saliva when the mosquito bites another host [4].

In last years the populations of *A. aegypti* have experienced an expantion caused by the global changes, because of the increase of temperatures that make possible the ocurrence of the mosquito in areas where it could not survive before, and also the globalization of the human societies, that can transport the mosquitos to diferent areas [2]. The expansion of the mosquitos is not the expantion of the disease, in order to this it is necessary that a mosquito bite an infected person who travelled from a place where the disease exists.

## 2. The SIRUV model

The SIRUV epidemic model show the influence of the vector in the disease development, so there are some interection explaining the model:

$$S+V \xrightarrow{\beta} I+V$$

$$I \xrightarrow{\gamma} R$$

$$U+I \xrightarrow{\vartheta} V+I$$

$$S \xrightarrow{\mu} S$$

$$I \xrightarrow{\mu} S$$

$$R \xrightarrow{\mu} S$$

$$U \xrightarrow{\psi} U$$

$$V \xrightarrow{\nu} U$$

Where,
$S$ are the susceptible people;
$I$ are the infected people;
$R$ are the recovered people who became resistant;
$N$ is the total number of humans ($N = S+I+R$);
$U$ are the susceptibles mosquitos;
$V$ are the infected mosquitos;
$M$ is the total number of mosquitos ($M = U+V$);
$\beta$ is the infection rate;
$\gamma$ is the recovery rate;
$\alpha$ is the lost of imunity rate;
$\mu$ is the birth and death rate;
$\vartheta$ is the infection rate of mosquitos by biting infected humans;
$\nu$ is the death rate of mosquitos;
$\psi$ is the birth of mosquitos.

So, these interections can be used to construct the equation system which defines the model:

$$\begin{aligned}
\frac{d}{dt}S &= -\frac{\beta}{M}\cdot S\cdot V-\mu\cdot(N-S)\\
\frac{d}{dt}I &= \frac{\beta}{M}\cdot S\cdot V-\gamma\cdot I-\mu\cdot I\\
\frac{d}{dt}R &= \gamma\cdot I-\mu\cdot R\\
\frac{d}{dt}U &= \psi-\nu\cdot U-\frac{\vartheta}{N}\cdot U\cdot I\\
\frac{d}{dt}V &= \frac{\vartheta}{N}\cdot U\cdot I-\nu\cdot V
\end{aligned}$$

## Abstract

The epidemic modelling has been used to know the evolution of diseases over time, and allow to test different parameters in order to predict what will happen with the changes of the ecosystem. The Dengue Fever is caused by four serotypes of an arboviral virus. Like in other epidemics, the transmission of Dengue Fever between people needs a vector, for instance is a mosquito species, *Aedes aegypti*, which bite people and transmit the virus. In recent years it has been verified an expantion of the ecological niche of the mosquito *Aedes aegypti* thanks to the global changes and the facility of travelling between countries. So their expansion increase the risk of Dengue to infect a new area. The proposal of this work is to study an epidemic model (SIRUV) which include the influence of the vector in the evolution of the Dengue. The study of SIRUV model was based on finding the stationary states and to plot and compare the deterministic and the stochastic model.

## 2.1 The Stationary States

The stationary states of the SIRUV model are given by these equations in function of the stationary states of variable I:

$$\begin{aligned}
S^* &= N-\frac{(\mu+\gamma)}{\mu}I^*\\
R^* &= \frac{\gamma}{\mu}I^*\\
V^* &= \frac{\vartheta}{\nu\cdot N}\cdot\frac{\psi}{\nu+\frac{\vartheta}{N}\cdot I^*}\cdot I^*\\
U^* &= \frac{\psi}{\nu+\frac{\vartheta}{N}\cdot I^*}
\end{aligned}$$

The stationary states of the variable I are:

$$I_1^* = 0 \vee I_2^* = \frac{\beta N\vartheta\psi - MN\nu^2(\gamma+\mu)}{\vartheta(\gamma+\mu)\left(\nu M+\frac{\beta\psi}{\mu}\right)}$$

## 2.2. The Time Dependent Solution

The time dependent solution of the SIRUV model is given by:

$$I(t) = I(t_0)+\delta t\cdot\left(\frac{\beta}{M}\cdot S(t)\cdot V(t)-(\gamma+\mu)\cdot I(t_0)\right)$$

However, in order to plot the model it is necessary to define the parameters. With this propose the parameters used are as reals as possible. The population in study are closed, *i.e.* the number of humans remain constant (100 000 ) and the renovation of the populations happens each 65 years ($\mu$). The infection rate ($\beta$) is the time of incubation of virus (7 days) and the recover rate ($\gamma$) is the mean time to recover (14 days). The mosquitos population has 1 000 000 of individuals. The renovation of the population happens in 10 days (birth of musquitos ($\psi$) is the same of death mosquitos ($\nu M$)). The infection rate ($\vartheta$) is a value higher than the death rate (in this case it was used $5\cdot\nu$.

The simulation of the model using the this parameter set is plotted in following:

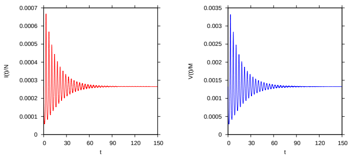

*Figure 3:* Plot of Determinisc SIRUV model using the parameters presented above. There are ploted the evolution of infected human and b) presents the evolution of infected mosquitos.

It is possible to see in figure 3 that the dynamic of infected mosquitos (b) is the same of the infected people (a). It shows the influence of the vector in the number of infected and its contribution in case of epidemiologies.

## 3. The Stochastic SIRUV Model

In natural systems there are some external and umpredictible forces influencing the evolution of the disease. The stochastic models allow to predict the effect of this external factors. So, using the same parameters as before, it was ploted the stochastic SIRUV model in figure 4.

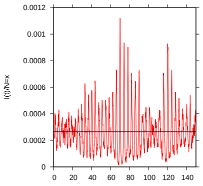

*Figure 4:* Plot of stochastic SIRUV model using the parameters presented above. The black line represents the stationary state.

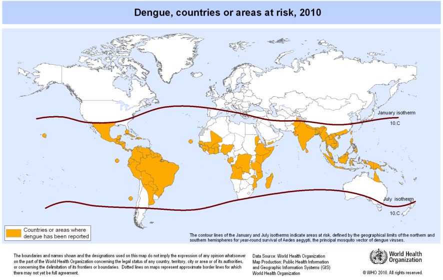

*Figure 2:* Map with zones where Dengue has been reported or where are risk of infection [3].

## 4. Deterministic vs. Stochastic

The Deterministic and Stochastic SIRUV model present lots of differences. In first, the behavior is completely different, while the deterministic starts with high oscilations, but the oscilations became smaller and smaller until the stationary state, and after that there are no more flactuations. In the stochastic happens almost the contrary, *i.e.* it starts in values relatively close to stationary state but with lots of noise and then the oscilations increase with the time. In this case the size of oscilations is almost cyclic, because there are times with high oscilations followed by smaller oscillations, but then they increase again. Contrary to deterministic, the stochastic model never stabilize in the stationary state.

Other interesting comparision is regarding frequency. In order to verify this, the figure 5 shows a 20 years part of the plots of the figures 3 (a) and 4.

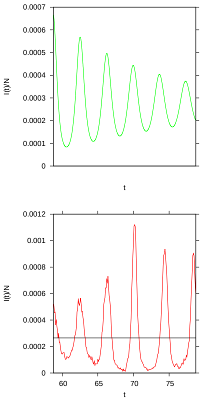

*Figure 3:* Fraction of 20 years of the deterministic (green) and stochastic (red) siruv model.

It is possible to see that the frequency of oscillations is 6 per twenty years for both cases, it means that both give the same information about the number of epidimies of Dengue. Although in the stochastic the curve remains more time in the the higher and lower values, and the transition is more quick than in deterministic.

## 5. Conclusion

The recent colonization of new areas by *A. aegypti*, combined with the increase of globalization and higher facility in travel between different world areas, is increasing the risk of new Dengue sites. In order to prevent this episode is important to increase the knowledge about the disease, and one of ways less explored is the effect of the vector. So, we are modelling the evolution of the Dengue with the influence of the mosquito because this can be an important tool for this propose.

## References

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