A First Stochastic Epidemic Model for Dengue Fever including vector dynamics

Alexandra Symeonides, Filipe Rocha & Nico Stollenwerk

Centro de Matemática e Aplicações Fundamentais. Avenida Prof. Gama Pinto 2, 1649-003 Lisboa, Portugal

authors' e-mails: alexandra.symeonides@gmail.com, frocha@ptmat.fc.ul.pt & nico@ptmat.fc.ul.pt

Abstract

A SISUV epidemic model describes the evolution of a vector-borne desease considering interactions between the vector and the host population. In the case of Dengue Fever the main vector that transmits the virus is the mosquito of the *Aedes'* genus and the main hosts are humans. We wrote the model's master equation and derived from that the Fokker-Planck and the Langevin-type equations. The first is a deterministic partial differential equation that describes the time evolution of the probability distribution, the second is a stochastic differential equation containing a deterministic part and an additional random white noise term. Stochastic computer simulations shows as in the deterministic case, that the dynamics of the vectors is completely slaved by the one of the humans because of their substantially different life spans.
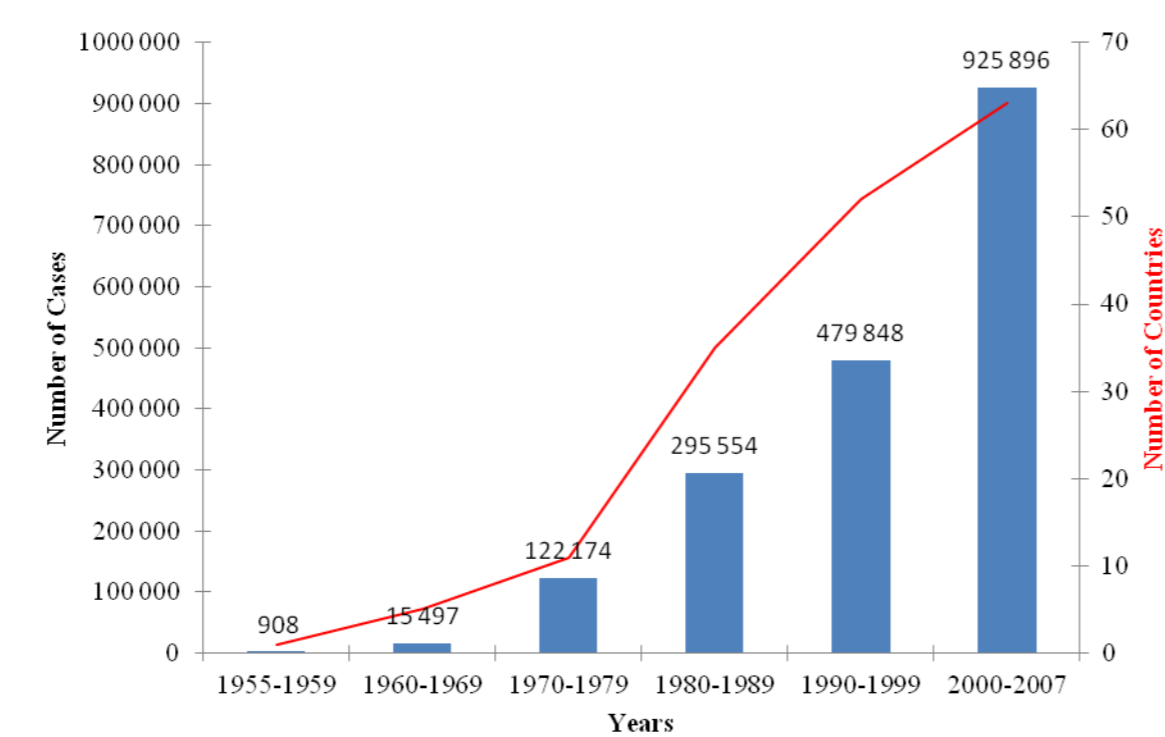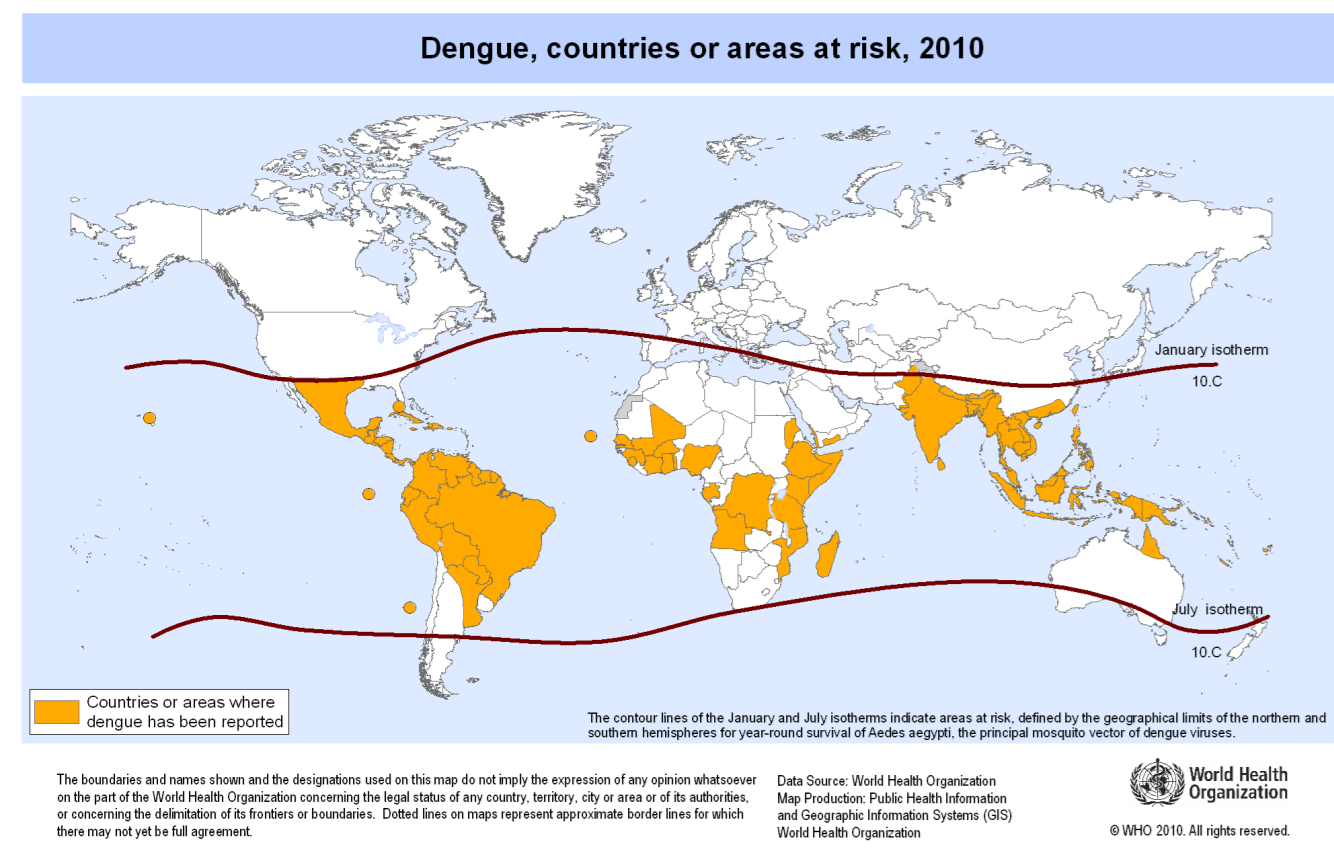
Figure 1. a) Zones where Dengue has been reported or where are infection risk [4]. b) Average annual number of DF/DHF cases reported to WHO & average annual number of countries reporting dengue.

1 Introduction

Dengue Fever (DF) is an infectious tropical desease. Incidence have increased dramatically from the 1960s due to a combination of population growth, increased international travel and global warming [4]. There exist four different serotypes of Dengue (DEN-1, DEN-2, DEN-3 and DEN-4). A first infection is characterized by flu-like symptoms and brings full life immunity relative to the contracted serotype and temporary cross immunity to the others, although a second infection can lead to a sever kind of infection called Dengue Hemorrhagic Fever (DHF), see Aguiar *et al.* (2008, 2011)[5,6]. Dengue Fever is endemic in more than 110 countries, and it is because of its wide and rapid diffusion more than its mortality rate that is object of research initiative. As still there does not exist any commercially available vaccine, vector control remains the main prevention measure. We propose a stochastic approach to a simple model including vector's dynamics.

1.1 The SIRUV model

The SIRUV is a basic model describing a vector-borne desease including the vector's dynamics. The scheme below shows the considered interactions where, S and U are respectively the susceptible humans and the susceptible mosquitos, I and V are respectively the infected humans and the infected mosquitos, and R is the class of the recovered people that are now immune to the contracted serotype. As mosquitos do not have an immune system there is no possibility of recovery.
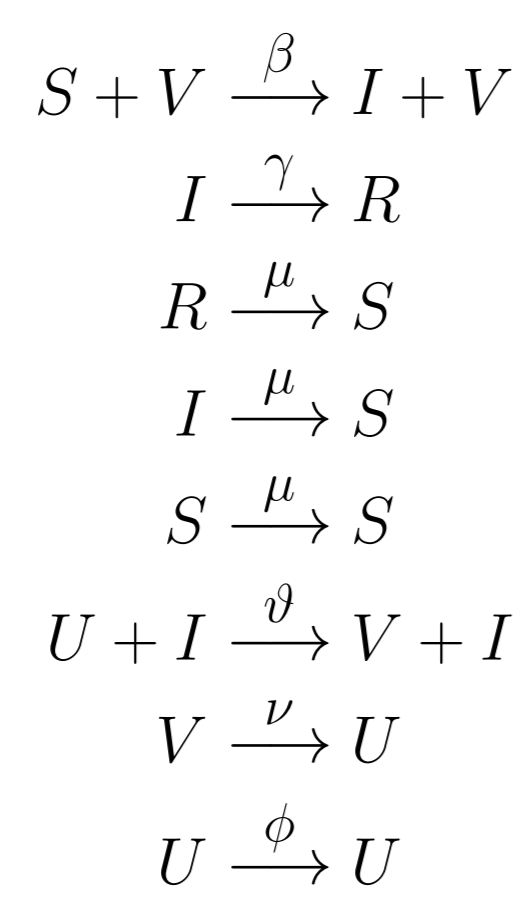
$$S + V \xrightarrow{\beta} I + V$$
$$I \xrightarrow{\gamma} R$$
$$R \xrightarrow{\mu} S$$
$$I \xrightarrow{\mu} S$$
$$S \xrightarrow{\mu} S$$
$$U + I \xrightarrow{\vartheta} V + I$$
$$V \xrightarrow{\nu} U$$
$$U \xrightarrow{\phi} U$$

Table 1. Realistic parameter's set for the SIRUV model (F. Rocha et al., 2012).

Parameter	Description	Simulation Values
μ	Human's birth and death rate	$1/65 y^{-1}$
β	Human's infection rate	2γ
γ	Human's recovery rate	$1/7 d^{-1}$
ν	Mosquito's death rate	$1/10 d^{-1}$
ϑ	Mosquito's infection rate	2ν
ϕ	Mosquito's birth rate	νM
N	Human's population size	1000
M	Mosquito's population size	$10N$

1.2 The simplified SISUV epidemic model

The SISUV is a simplified version of the SIRUV model where the class of the recovered people does not appear and an infected human just returns to be a susceptible with a new recovery rate α. This simplification causes a loss of reality in the modelling, but simplifies the calculations. To simulate as much as possible the original SIRUV system, the new recovery rate was set to $\alpha = 1/10 y^{-1}$, see F. Rocha *et al.* (2012), and the other parameters are kept as in Table 1. Supposing that $N = I(t) + S(t)$ and $M = V(t) + U(t)$ are constant for every time, the deterministic SISUV model is

$$\frac{dI}{dt} = \frac{\beta}{M}(N - I)V - \alpha I$$

$$\frac{dV}{dt} = \frac{\vartheta}{N}(M - V)I - \nu V$$

2 The master equation

The master equation is a *gain-loss* equation for the probability of each state, the positive terms are the gain due to a transitions from other states and the negative terms are the loss due to transitions into other states. The following is the master equation for the SISUV model just presented

$$\frac{dp(I, V, t)}{dt} = \frac{\beta}{M}(N - (I - 1))Vp(I - 1, V, t) + \alpha(I + 1)p(I + 1, V, t)$$

$$+ \frac{\vartheta}{N}(M - (V - 1))Ip(I, V - 1, t) + \nu(V + 1)p(I, V + 1, t)$$

$$- \left(\frac{\beta}{M}(N - I)V + \alpha I + \frac{\vartheta}{N}(M - V)I + \nu V\right)p(I, V, t)$$

Considering densities of populations $x := \frac{I}{N}$, $v := \frac{V}{M}$ and changing variables we obtain

$$\frac{dp(x, v, t)}{dt} = \beta N\left(1 - \left(x - \frac{1}{N}\right)\right)vp\left(x - \frac{1}{N}, v, t\right) + \alpha N\left(\left(x + \frac{1}{N}\right)\right)p\left(x + \frac{1}{N}, v, t\right)$$

$$+ \vartheta M\left(1 - \left(v - \frac{1}{M}\right)\right)xp\left(x, v - \frac{1}{M}, t\right) + \nu M\left(v + \frac{1}{M}\right)p\left(x, v + \frac{1}{M}, t\right)$$

$$- (\beta N(1 - x)v + \alpha x N + \vartheta M(1 - v)x + \nu v M)p(x, v, t)$$

2.1 The Fokker-Planck equation and the Stochastic ODE

We derive the Fokker-Planck equation from the latest expression of the master equation by Taylor's expansion up to second order around the state (x, v) with small deviation $\Delta x = 1/N$ and $\Delta v = 1/M$, also called Kramers-Moyal's expansion.

$$\partial_t p(x, v, t) = -\partial_x\left[(\beta(1 - x)v - \alpha x)p(x, v, t)\right] - \partial_v\left[(\vartheta(1 - v)x - \nu v)p(x, v, t)\right]$$

$$+ \frac{1}{2N}\partial_{xx}\left[(\beta(1 - x)v + \alpha x)p(x, v, t)\right] + \frac{1}{2M}\partial_{vv}\left[(\vartheta(1 - v)x + \nu v)p(x, v, t)\right]$$

The Fokker-Planck equation is a generalized diffusion equation where the *drift terms* gives the deterministic ODE system and a combination of this with the *diffusion terms* leads to the stochastic ODE system

$$\frac{dx}{dt} = \beta(1 - x)v - \alpha x + \frac{1}{N}\sqrt{\beta(1 - x)v + \alpha x}\,\varepsilon_x$$

$$\frac{dv}{dt} = \vartheta(1 - v)x - \nu v + \frac{1}{M}\sqrt{\vartheta(1 - v)x + \nu v}\,\varepsilon_v$$

that is a Langevin type equation

$$\frac{d\underline{z}}{dt} = \underline{f}(\underline{z}) + G(\underline{z})\Sigma\underline{\varepsilon}(t)$$

where $\underline{f}$ is a vector composed by the drift terms of the Fokker-Planck equation, G is a matrix depending on the states of the system $\underline{z}$ and Σ is a variance matrix for the Gaussian noise $\underline{\varepsilon}$ with zero mean and unit variance.

3 Stochastic simulation

The graphics below show that even for the stochastic simulation mosquito's dynamics is completely slaved by the human ones because of their different life spans, and from the state space plot is possible to visualize the stable manifold where the solutions of the model lies. The Gillispie algorithm was used to solve the master equation, while the following discretisation scheme (Itô formulation)

$$x_{t+\Delta t} = x_t + f(x_t)\Delta t + g(x_t)\sqrt{\Delta t}\,\sigma_t\,\varepsilon_t$$

was used for the stochastic ODE, where ε_t is a Gaussian white noise generated with the Box-Muller algorithm. In Table 1. there are the parameters used for the simulations. In every image there are represented the solutions in terms of densities of the master equation, of the stochastic ODE and of the deterministic ODE respectively with red, blue and black curves.
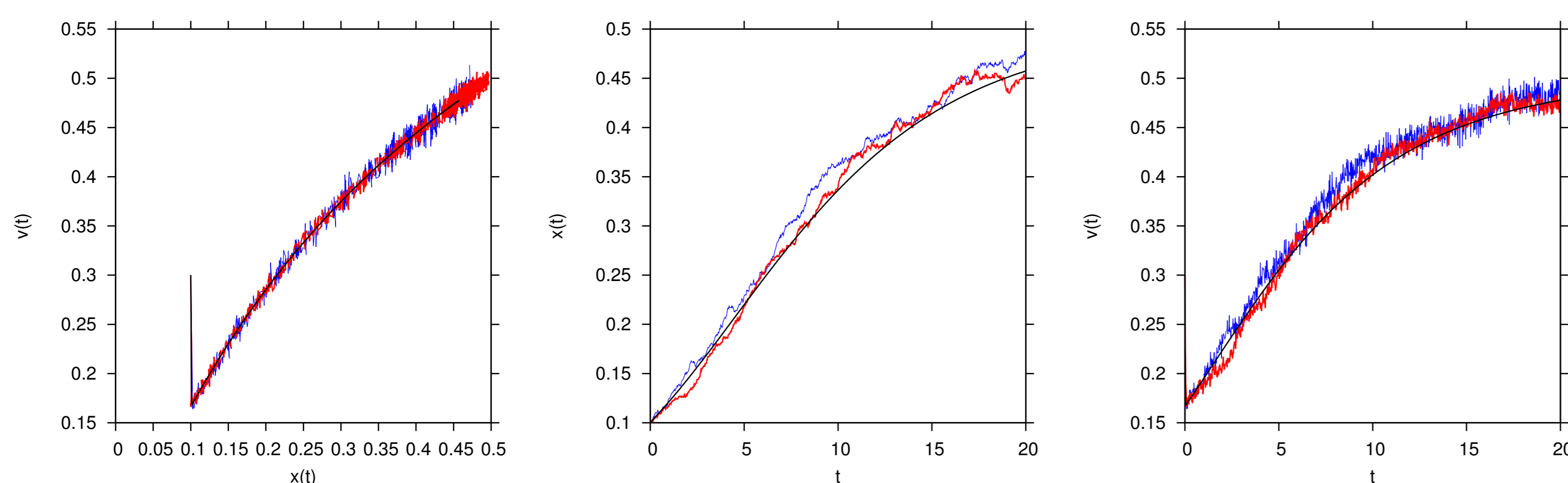

Figure 2. Respectively from left to right the state space plot and the time series for the humans and for the mosquitos all in terms of densities, with initial condition $x_0 = 0, 1$ for the humans and $v_0 = 0, 3$ for the mosquitos and parameters set as given in Table 1.

4 Conclusion

We proposed a first stochastic epidemic model for vector-borne desease taking into account mosquito's dynamics. We wrote the master equation and by Kramers-Moyal's expansion we derived the Fokker-Planck equation and the stochastic ODE. Computer simulations show that both approaches goes well presenting the expected behaviour. In fact as in the deterministic case vector's dynamics is slaved by the humans one, see F. Rocha *et al.* (2012). Future research is to extend this kind of approach for example to the SIRUV epidemic model and more complex vector-borne desease model.

Literature

[1] F. Rocha, M. Aguiar, M. Souza & N. Stollenwerk. (2012) *Time-scale separation and center manifold analysis describing vector-borne desease dynamics.* Accepted for publication in the International Journal of Computer Mathematics.

[2] N. Stollenwerk, V. Jansen. (2011) *Population Biology and Criticality*, London, Imperial College Press.

[3] N.G. Van Kampen. (1981) *Stochastic Processes in Physics and Chemistry*, Amsterdam, North-Holland Personal Library.

[4] Who-World Healt Organisation. (2012) Dendue/Dengue haemorragic fever. Accessible elettronically at http://www.who.int/crs/disease/dengue/en/index.html.

[5] M. Aguiar, S. Ballesteros, B. W. Kooi, N. Stollenwerk. (2011) *The role of seasonality and import in a minimalistic multi-strain dengue model capturing differences between primary and secondary infections: Complex dynamics and its implications for data analysis.* J. Theor. Biol. 289, 181-196.

[6] M. Aguiar, B. Kooi, N. Stollenwerk. (2008) *Epidemiology of Dengue Fever: A model with Temporary Cross-Immunity and Possible Secondary Infection Shows Bifurcations and Chaotic Behaviour in Wide Parameter Regions.* Math. Model. Nat. Phenom. 4, 48-70.