Applied Mathematics & Information Sciences
An International Journal

http://dx.doi.org/10.18576/amis/120420

Probabilistic Model of Dengue

German Marcillo[1,*], *Anibal Muñoz*[2] *and Gerard Olivar Tost*[3]

[1] Faculty of Education, Mariana University, San Juan de Pasto, Nariño, Colombia
[2] University of Quindio, Armenia, Colombia
[3] National University of Colombia, Manizales, Colombia

Received: 25 Apr. 2018, Revised: 1 Jun. 2018, Accepted: 25 Jun. 2018
Published online: 1 Jul. 2018

Abstract: The article presents the stochastic modeling of a particular dynamic of dengue cases for a constant population with an initial number of susceptible and infected members, a time-dependent force of infection and a probability-generating function from which a linear partial differential equation (PDE) of first order is derived whose solution can assign probabilities to each of the states of the model and the transitions between them. The force of infection is estimated numerically based on a dynamic system of ordinary differential equations. The method of characteristics applied to find the analytical solution of the PDE and subsequently the marginal probabilities of the stochastic process are derived analytically. Furthermore, by applying the cumulative generating function, a system of ordinary differential equations is derived, and the numerical solution determines the values of statistical measures over time. Finally a comparison of the results of the simulations is undertaken to understand the probabilistic dynamics of the process of infection in a population.

Keywords: Aedes aegypti, Dengue, Stochastic Processes, Force of Infection, Prediction, Probability Generating Function

1 Introduction

Viral diseases transmitted by arthropods have today become a global public health problem due to factors such as climate change, population increase, accumulation of waste and pollutants, inadequate forms of recycling and insufficient controls on transmission. Dengue is an acute viral disease caused by the dengue virus and transmitted to man by the mosquito *Aedes aegypti*, as its main transmitter. The virus is caused by four serotypes (DENV1, DENV2, DENV3, DENV4), which circulate simultaneously in tropical and subtropical areas, although recent studies have confirmed the finding of a new serotype called DENV5 [1]. Serotypes do not trigger cross-immunity, which means that individuals recovering from one of them acquire permanent immunity against it, but only temporary and partial immunity against the others [2]. It is estimated that there are between 50 and 100 million cases of dengue worldwide [3].

Different theories and mathematical models applied to epidemiology have made it possible to understand the dynamics of these viruses and their effects on the population. Also, important tools such as numerical methods and computational simulations have been used to study and understand more complex dynamics, even being used to predict the future effects of an outbreak in a particular population and the probabilities over time of the states of a given disease. Many researchers have used stochastic models to study particular viral infections that have been a major global health problem; such as Bailey (1950) [4], who studied the simplest process disease propagation, in which there are only two transition states: susceptible and infected. Bailey analyzed the deterministic and stochastic cases of the dynamics, making a comparison and calculating the probability generating functions and moments, as well as analysing the behaviour in the limit. Gani and Purdue (1984) [5], who studied the simplest process disease propagation, in which there are only two transition states: studied the SI dynamics for a generalized infection, formulating a geometric matrix, and calculating the probability for survivors of a certain epidemic, agreeing with Whittle's stochastic threshold theorem. Also, Lounes and Arazoza (1998) [6] who investigated the deterministic and stochastic dynamics with immigration for two populations corresponding to known cases of HIV-AIDS, according to a health program implemented in Cuba.

* Corresponding author e-mail: gmarcillo@umariana.edu.co

More recent cases, such as that of Khan *et al* (2013)[7], who based their work on a deterministic model of the dynamics of Dengue viruses, formulated a stochastic model using Markov chains in continuous time and observed stability and equilibrium characteristics for the virus; and the case of Lee *et al* (2012)[8] who proposed an efficient and precise numeric scheme using characteristic curves to determine probability-generating functions that arise in the stochastic models of first-order general reaction networks.

In this investigation, a stochastic mathematical model is formulated and analyzed on the basis of a SIR [9] [10] system for an outbreak of dengue, with a force of infection that varies over time and is estimated from a dynamic model and parameters from the literature. Analytical formulas are derived for marginal probabilities and particular probabilities are estimated numerically as the statistical measures of the random variables of the stochastic dynamic of dengue.

2 Force of Infection

The force of infection (IF) is considered as a parameter that depends on time and represents the way in which the susceptible members of the population (S) become infected (I) [11]. There is no single defined model to estimate or calculate the force of infection, and so both simple and complex relationships have been used to represent it. Some of these models can be found in such articles as Griffiths (1973), [12]; Shkedy, Aerts, *et al* (2003) [13]; or that of Massad et al (2008) [14], which is precisely what is applied in the present investigation to estimate the force of infection. Thus the mathematical model is as follows:

$$\lambda(t) = a\beta \int_0^t \frac{x_2(s)}{N(s)} ds \int_0^t \frac{y_2(s)}{Y(s)} ds$$

where, x_2 is the average number of infectious people at time t, y_2 is the average number of mosquitos carrying the virus at time t, N is the total human population changing with time, Y is the average total population of mature mosquitos at time t, β is the proportion of mosquito bites that infect humans, and a is the rate at which mosquitos bite humans.

As is clear from the model, it is necessary to determine each of the variables and parameters that make it up, so we opt for the deterministic model of Lopez *et al* (2012, p.519)[15], whose system of ordinary differential equations does not consider controls or latency, that is, $u_1 = u_2 = u_3 = 0$ and $\tau = T_1 = T_2 = T_3 = 0$. The model and its parameters can be consulted on page 518 of the cited paper.

The solution of the system is found numerically by applying the Runge-kutta method using Matlab. The numerical values of the necessary variables for the IF model are integrated as vectors, and then, using the algorithm for the Simpson method adapted for this particular case, we estimate the force of infection over time (weeks) for a constant population (figure 1). The IF model consists of the product of two definite integrals and, as mentioned, to generate their respective curves over time we use numerical methods in Matlab, in this case of Simpson rule. The algorithm has been constructed based on the computational theory and implementation set out in Ojeda's book (2011, p.166-169)[16] and in Mora's book (2014, p.174)[17].

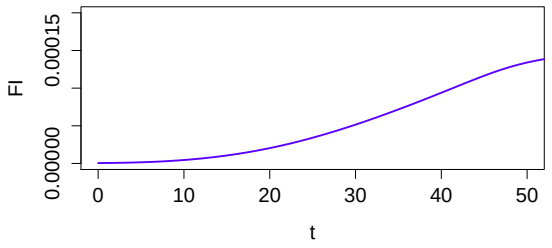

Fig. 1: Estimated force of infection: $\lambda(t)$, with $a = 0.97$, $\beta = 1$, $x_{2_0} = 39$, $y_{2_0} = 200$, $N_0 = 1000$, $Y_0 = 239$

$\lambda(t)$ is an increasing function over time, for this particular case we take a bite rate a of 97%, a proportion of bites that infect of 100%, a constant average total population of 1000 people, a constant average total number of de 239 mature mosquitos, an average number of infectious people of 30 and an average number of mosquitos carrying the virus of 200. The initial conditions and parameters used for the estimation of the force of infection are the average number of people infected per week according to the reports of the annual number cases of dengue fever in tropical areas.

Thus, in the following, the estimated force of infection is a time-dependent function in the stochastic model and the corresponding mathematical models derived from it. In addition it becomes a non-homogeneous Poisson process, a situation that is explained later. For simulation purposes, the force of infection is taken as a vector of data.

3 SIR Stochastic Model

The model features three states of the Dengue dynamic: susceptible S, infected I and recovered R ($R = S - I$). These states are represented by the random variables (r.v.) $X(t)$, $Y(t)$ and $Z(t)$ respectively, with $t \geq 0$.

The variables and parameters of the model are therefore: $X(t)$, the number of susceptible people at time t; $Y(t)$, the number of infected people at time t; $Z(t)$, the number of recovered people at time t; and $\lambda(t)$, the force

of infection at time t; θ, the rate at which infected people recover. Since the number of recovered people depends only on the number of susceptible and infected, the stochastic analysis is performed only on the bivariate process $(X(t),Y(t))$.

To derive the stochastic model, it is necessary to analyze particular probabilistic characteristics correspnding to the changes of state that each person undergoes and the transitions from one r.v. to another, following the path susceptible-infected-recovered. The dynamics over time of the infection process is random in character because the number of people who are infected (being bitten by a carrier mosquito) is random. Furthermore, depending on the time interval over which the phenomenon is observed, there may be subintervals in which the rate at which people are bitten is higher (periods of the day when there are more insects) and therefore the rate of infection is higher. This example indicates that the infectious process is not homogeneous because the chances of becoming infected depend on time. The distribution of the infected cases is also proportional to the interval, so if we take an infinitesimal time interval at most one infection occurs in the period, with the probability proportional to the length of the infinitesimal interval. In addition, the distribution of the number of infected cases in time intervals are independent, i.e. in each new interval the process starts again. These characteristics make the SIR stochastic dynamics of dengue a Poisson process [18] which is, in addition, non-homogeneous because the Poisson parameter λ is a function that depends on time and is represented by the force of infection over time $\lambda(t)$.

By probabilistic methods, in an interval $(t,t+\Delta t)$ of infinitesimal length, the process can either undergo a single change or stay the same. Thus for the bivariate stochastic process $\{X(t),\,Y(t)\}_{t\geq 0}$ the transition probabilities are:

$$\begin{aligned} P(X(t+\Delta t) &= x-1, Y(t+\Delta t) = y+1 / X(t)=x, Y(t)=y) \\ &= \lambda(t)x\Delta t + o(\Delta t) \end{aligned}$$

$$\begin{aligned} P(X(t+\Delta t) &= x, Y(t+\Delta t) = y-1 / X(t)=x, Y(t)=y) \\ &= \theta y\Delta t + o(\Delta t) \end{aligned}$$

$$\begin{aligned} P(X(t+\Delta t) &= x, Y(t+\Delta t) = y / X(t)=x, Y(t)=y) \\ &= 1-(\lambda(t)x+\theta y)\,\Delta t + o(\Delta t) \end{aligned}$$

with initial conditions $X(0)=x_0$, $Y(0)=y_0$ y $\lim\limits_{\Delta t\to 0}\frac{o(\Delta t)}{\Delta t}=0$

By the law of total probability and by independence, the joint probability of the bivariate process at the instant $t+\Delta t$ is given by:

$$p_{x,y}(t+\Delta t) = \sum_{x',y'} P\left\{X(t+\Delta t)=x', Y(t+\Delta t)=y'\right\} p_{x,y}(t) \tag{1}$$

Where, $P\{X(t)=x, Y(t)=y\} = p_{x,y}(t)$

if $\Delta t \to 0$, the difference quotient becomes the differential equation

$$\begin{aligned} \frac{dp_{x,y}(t)}{dt} &= \lambda(t)(x+1)p_{x+1,y-1}(t) \\ &+ \theta(y+1)p_{x,y+1}(t) - \lambda(t)xp_{x,y}(t) - \theta y p_{x,y}(t) \end{aligned} \tag{2}$$

which plays an important role in finding the probabilistic model of the system, being used to determine the probability generating function (PGF) of the bivariate case.

4 Probability Generating Function (PGF)

For the bivariate stochastic process $\{X(t),\,Y(t)\}_{t\geq 0}$ with probability distribution given by: $P\{X(t)=x, Y(t)=y\} = p_{x,y}(t)$, the PGF is defined as [19] [20]

$$\psi(u,v,t) = \sum_{x,y\geq 0} u^x v^y p_{x,y}(t) \tag{3}$$

This is absolutely convergent for $u,v\in[-1,1]$ and with initial and boundary conditions given by:

$$\begin{cases} \psi(u,v,t) = u^{x_0}v^{y_0}; \quad x(0)=x_0, y(0)=y_0 \\ \psi(0,0,t) = p\{X(t)=0, Y(t)=0\} = 0 \\ \psi(1,1,t) = \sum\limits_{x,y} p\{X(t)=x, Y(t)=y\} = 1 \end{cases} \tag{4}$$

On differentiating the PGF with respect to t we obtain

$$\frac{\partial\psi(u,v,t)}{\partial t} = \sum_{x,y\geq 0} u^x v^y \frac{dp_{x,y}(t)}{dt} \tag{5}$$

Replacing equation 2 in 5 results in the following partial differential equation (PDE)

$$\frac{\partial\psi}{\partial t} = \lambda(t)(v-u)\frac{\partial\psi}{\partial u} + \theta(1-v)\frac{\partial\psi}{\partial v} \tag{6}$$

The derived PDE is a first-order linear equation in the variables u,v y t, with the Cauchy initial condition

$$\psi(u,v,0) = u^{x_0}v^{y_0} \tag{7}$$

The process starts at $t=0$ and therefore the initial probability that the process is at x_0 y y_0 is certain and

equal to 1, while the joint probabilities that the random variables take other initial values are zero.

The PDE can be written in vector form as

$$\psi_t + [\lambda(t)(v-u), \theta(v-1)] \cdot [\psi_u, \psi_v] = 0$$

if $r = [\psi_u, \psi_v]$, the Cauchy problem becomes

$$\begin{cases} \psi_t + r\nabla\psi = 0 \ \ in\ (-1,1)^2 \times (0,\infty) \\ \psi = g(u,v,0) = u^{x_0} v^{y_0} \ on\ (-1,1)^2 \times \{t=0\} \end{cases} \tag{8}$$

The above problem can be solved in a closed or numerical way by the method of the characteristics [21] [8] which is expanded and developed in the following section.

5 Solution of the PDE - Method of Characteristics

In this section we present the method of the characteristics to solve a homogeneous first-order linear PDE at a given point (u_0, v_0).

To describe the application of the method of characteristics, the PDE ref sys53 is written as a typical transport equation [21]

$$\begin{cases} \psi_t + r\nabla\psi = 0 \ \ in\ (-1,1)^2 \times (0,\infty) \\ \psi = g(u,v,0) = u^{x_0} v^{y_0} \ on\ (-1,1)^2 \times \{t=0\} \end{cases} \tag{9}$$

Where the initial condition $g(u,v,0)$ is a function continuous on $(-1,1)^2$. It is assumed that the curve is described parametrically by the function $s(\xi) = (u(\xi), v(\xi))$, where the parameter ξ is in R. We now define the function z as

$$z(\xi) := \psi(u(\xi), v(\xi), t-\xi) \tag{10}$$

Differentiating $z(\xi)$ with respect to ξ

$$\begin{aligned} \frac{d}{d\xi} z(\xi) &= \frac{\partial\psi}{\partial u}\frac{du}{d\xi} + \frac{\partial\psi}{\partial v}\frac{dv}{d\xi} - \frac{\partial\psi}{\partial t} \\ &= r \cdot \nabla\psi(u(\xi), v(\xi), t-\xi) \\ &\quad - \psi_t(u(\xi), v(\xi), t-\xi) = 0 \end{aligned} \tag{11}$$

Thus, $z(\xi)$ is a constant function of ξ and, as a result, for each point (u,v,t). This implies that ψ is also a constant function on the curve $r(u(\xi), v(\xi)) \in R^2$ on $(u(\xi), v(\xi))$. Because the initial value of ψ is given for some point of every curve, we can find the value of $u(\xi)$ y $v(\xi)$ everywhere in $R^2 \times (0,\infty)$. It is important to observe that in the general form of the method of characteristics, the coefficients of the gradient terms of equation 6 are never both zero. That is, $(\lambda(t)(u-v))^2 + (\theta(v-1))^2 \neq 0$ because u y v are in the open interval $(-1,1)$.

Now, taking the fixed starting point (u_0, v_0), we want to obtain directly the value of $\psi(u_0, v_0, t)$ for $t \geq 0$. The value at $(u(t), v(t))$ is found by following the characteristic curve back to the initial condition $(u(0), v(0))$.

Since ψ is constant on the characteristic curve and taking equations 7, we have

$$z(0) = z(t) \tag{12}$$

For any value of t, we deduce from here that

$$\begin{aligned} \psi(u_0, v_0, t) &= \psi(u(0), v(0), t) \\ &= \psi(u(t), v(t), 0) = g(u(t), v(t), 0) \end{aligned} \tag{13}$$

for an initial position $u_0 = u(0)$ and $v_0 = v(0)$, $(u(t), v(t)) \in (-1,1)^2$ y $t \geq 0$

Finally, the solution of the PDE in terms of the initial conditions u_0 y v_0 is given by

$$\psi(u_0, v_0, t) = u_0^{x_0} v_0^{y_0} \tag{14}$$

The method of the presented characteristics to find a solution of the linear first-order PDE homogeneous in the variables u, v, t is applied to the PDE 6 with the initial condition 7, to then find the probabilistic model for the bivariate stochastic process of the SIR dynamics.

From equation 11 we establish two ordinary differential equations (ODEs) given by:

$$\frac{du}{d\xi} = \lambda(\xi)(u(\xi) - v(\xi)) \tag{15}$$

$$\frac{dv}{d\xi} = \theta(v(\xi) - 1) \tag{16}$$

From equation 12 we have that $\xi = t$, and so the ODEs depending on t with their respective initial conditions are:

$$\frac{dv}{dt} = \theta(v-1);\ v_0 = v(0) \tag{17}$$

$$\frac{du}{dt} = \lambda(t)(u-v);\ u_0 = u(0) \tag{18}$$

The equations are solved analytically by the method of separable variables and the integral factor method respectively. Thus the solutions for v_0 and u_0 in terms of v and u, respectively are:

$$v_0 = (v-1)e^{-\theta t} + 1 \tag{19}$$

$$u_0 = ue^{-\int_0^t \lambda(s)ds} - \int_0^t \lambda(s)\left[(1-v)e^{-\theta s} - 1\right] e^{-\int_0^t \lambda(s)ds} ds \tag{20}$$

Replacing (19) and (20) in (14), we obtain the closed soluction for the PDE ψ

$$\psi(u_0,v_0,t) = \left[ue^{-\int_0^t \lambda(s)ds} - \int_0^t \lambda(s)\left[(1-v)e^{-\theta s}-1\right]e^{-\int_0^t \lambda(s)ds}ds\right]^{x_0} \cdot \left[(v-1)e^{-\theta t}+1\right]^{y_0} \quad (21)$$

ψ as well as being the analytical solution of the PDE is the FGP of the SIR stochastic process, so from this we can find the marginal probability distributions of the r.v. X_t and Y_t a process of higher-order partial differentiation of ψ.

6 Probability Distributions

By definition, the probability distribution for the random variable X_t is given by [8] [22]

$$X \sim P(X(t)=x) = \begin{cases} \frac{1}{x!}\frac{\partial^x \psi}{\partial u^x}(0,1,t) \; if \quad x=0,1,... \\ 0 \; otherwise \end{cases} \quad (22)$$

Similarly, the probability distribution for the r.v. Y_t is given by

$$Y \sim P(Y(t)=y) = \begin{cases} \frac{1}{y!}\frac{\partial^y \psi}{\partial v^y}(1,0,t) \; si \quad y=0,1,... \\ 0 \; otherwise \end{cases} \quad (23)$$

This means that we must necessarily partially derive the function *psi*, k times with respect to the variable u or v, if we want to find the probabilities in time that X or Y respectively will be equal to k. It is then necessary to find a formula for the derivatives of higher order with respect to a single variable, by a recurrence relation.

As we follow a process of successive differentiation of the function ψ given by the equation 21, it is convenient to rewrite the equation as

$$\psi(u_0,v_0,t) = [uA_1 - A_2 + vA_2 + A_3]^{x_0}[vA_4 + A_5]^{y_0} \quad (24)$$

Where

$$A_1 = e^{-\int_0^t \lambda(s)ds}; \quad A_2 = \int_0^t \lambda(s)e^{-\theta s - \int_0^t \lambda(s)ds}ds$$

$$A_3 = \int_0^t \lambda(s)e^{-\int_0^t \lambda(s)ds}ds; \quad A_4 = e^{-\theta t}; \quad A_5 = 1-e^{-\theta t}$$

Then we define a formula for the k-th derivative of ψ with respect to u as

$$\frac{\partial^k \psi}{\partial u^k}(0,1,t) = \frac{x_0!}{(x_o-k)!}[A_3]^{x_0-k}A_1^k[A_4+A_5]^{y_0}$$

Replacing the values of A_1, A_3, A_4 y A_5, we have the k-th partial derivative of ψ with respect to u evaluated at the point $(0,1,t)$ is

$$\frac{\partial^k \psi}{\partial u^k}(0,1,t) = \frac{x_0!}{(x_o-k)!}\left[\int_0^t \lambda(s)e^{-\int_0^t \lambda(s)ds}ds\right]^{x_0-k} \cdot \left[e^{-\int_0^t \lambda(s)ds}\right]^{k} \quad (25)$$

Finally, the probability distribution for the r.v. X_t representing the number of people susceptible to Dengue at time t, is

$$X \sim P(X(t)=x) = \begin{cases} \frac{x_0!}{(x_o-x)!x!}\left[\int_0^t \lambda(s)e^{-\int_0^t \lambda(s)ds}ds\right]^{x_0-x} \\ \left[e^{-\int_0^t \lambda(s)ds}\right]^{x} \; if \quad x=0,1,... \\ 0 \; otherwise \end{cases} \quad (26)$$

Also, the recurrence formula for the k-th derivative of *psi* with respect to v is

$$\frac{\partial^k \psi}{\partial v^k} = \sum_{i=0}^{k} \frac{k!}{(k-i)!i!}\frac{x_0!}{(x_0-(k-i))!}\frac{y_0!}{(y_0-i)!} [uA_1 - A_2 + vA_2 + A_3]^{x_0-(k-i)}A_2^{k-i} \cdot [vA_4 + A_5]^{y_0-i}A_4^i.$$

Then evaluating the partial derivative of *psi* of order k with respect to v at point $(1,0,t)$, we obtain

$$\frac{\partial^k \psi}{\partial v^k}(1,0,t) = \sum_{i=0}^{k} \frac{k!}{(k-i)!i!}\frac{x_0!}{(x_0-(k-i))!}\frac{y_0!}{(y_0-i)!} \cdot [A_1 - A_2 + A_3]^{x_0-(k-i)}A_2^{k-i}[A_5]^{y_0-i}A_4^i$$

In conclusion, the probability distribution for the r.v. Y_t representing the number of people infected with Dengue at time t, is

$$P(Y(t)=y) = \frac{1}{y!}\sum_{i=0}^{y} \frac{y!}{(y-i)!i!}\frac{x_0!}{(x_0-(y-i))!}\frac{y_0!}{(y_0-i)!} [A_1 - A_2 + A_3]^{x_0-(y-i)} \cdot A_2^{y-i}[A_5]^{y_0-i}A_4^i \quad (27)$$

for $y = 0,1,2,...$

It is important in the infection process of the dengue virus to analyze the behavior of those that recover, which as already mentioned corresponds to the difference between susceptible and infected individuals over time. Furthermore, as the two sets are mutually exclusive, that is $S \cap I = \{\phi\}$, then the probability distribution of the recovered population R represented by the r.v. $Z(t)$, is

$$\begin{aligned} P(Z(t)=z) &= P(X(t)-Y(t)=x-y) \\ &= P(X(t)=x)-P(Y(t)=y) \end{aligned} \tag{28}$$

With the calculated distributions, it is now possible to make numerical simulations in Matlab of the probabilities over time of susceptible, infected and recovered individuals when there is an outbreak of dengue. The probability of infection $\lambda(t)$ estimated in section 1 is included in the probabilistic models.

Figure 2*a* shows the behaviour over time of the probabilities that the number of susceptible individuals remain at least 20, 40 and 60 people, given an initial susceptible population of 100 people with a single infected person and an infection force estimated by $\lambda(t)$, that is to say that $P(X(t) = 20)$; $P(X(t) = 40)$; $P(X(t) = 60)$ with $x_0 = 100$ y $y_0 = 1$.

It is observed that the probability of finding exactly 20 susceptible persons over time is greater than finding 40 or 60 people susceptible to the disease, because the infection begins to spread in the population, since the model does not consider migration or natural death of the susceptible population. In addition, after 15 weeks the odds begin to decrease more rapidly. A possible explanation is that the incubation period of dengue fever lasts from 1 to 2 weeks per person, which implies that in the first weeks the number of infected individuals is very low, a situation that is observed in figure 2*b* corresponding to the probability of finding exactly 20, 40 or 60 infected individuals over time, under the same initial conditions. The probability of finding exactly 20 infected is maximum and equal to 50% around the 5th week of the process, and then decreases until it disappears as individuals recover from the infection.

Meanwhile, the probability of finding 40 infected individuals reaches a maximum of 38% around 18 weeks of the infection process and for 60 infected people, the maximum probability is almost 37% after aproximately 35 weeks before the probability vanishes as the infected people move to a different state. In this way, the probabilistic model reveals the behavior of Dengue dynamic states over time and more precisely with what probability all or part of the population become infected and when this occurs.

Given the probabilistic behavior over time of the susceptible and infected states, it is possible to simulate the behavior of the probabilities of the recovered population, as dipicted in figure 2*c*. We observe that the minimum probability of finding 20, 40 and 60 recovered individuals is 50%, 60% and 61% occurring around 5, 18 and 33 weeks respectively after the infection process has started.

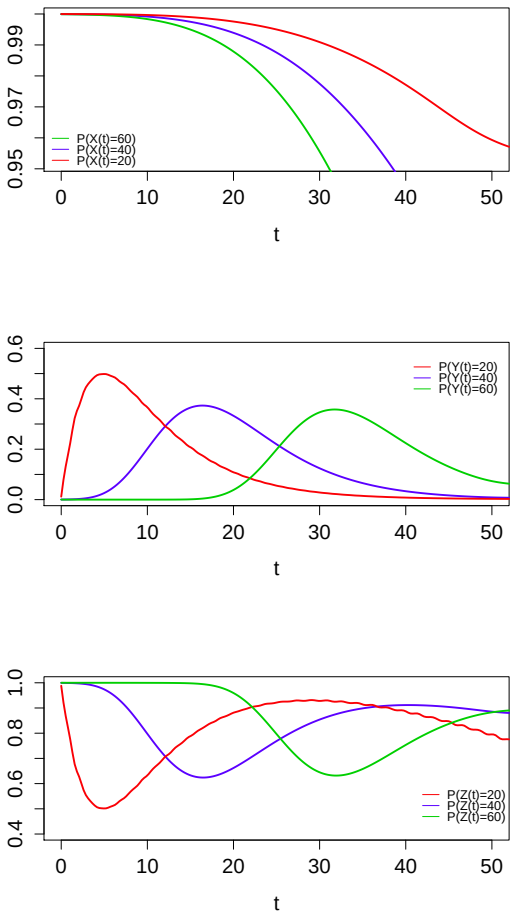

Fig. 2: probability over time of susceptible, infected and recovered individuals with $\lambda(t)$

7 Cumulant-Generating Function

The cumulant-generating function (CGF) for the bivariate process, taking the definitions and properties set forth in Bailey (1990) [23] y Severini (2005) [24] is the natural logarithm of the PGF for $u = e^a$ y $v = e^b$. That is to say that $k(a,b,t) = \ln \psi(u,v,t)$

from where,

$$\frac{\partial \psi}{\partial t} = \psi \frac{\partial k}{\partial t}, \quad \frac{\partial \psi}{\partial u} = \psi e^{-a} \frac{\partial k}{\partial a}, \quad \frac{\partial \psi}{\partial v} = \psi e^{-b} \frac{\partial k}{\partial b}$$

In consequence, a differential equation for the CGF is,

$$\frac{\partial k}{\partial t} = \lambda(t)\left(e^{b}-e^{a}\right)e^{-a}\frac{\partial k}{\partial a} + \theta(1-e^{b})e^{-b}\frac{\partial k}{\partial b} \quad (29)$$

This equation allows us to derive the system of ordinary differential equations whose solutions represent the statistical measures sought. We use Taylor series and the properties of moments of order k centred at the origin. By definition in descriptive statistics the first two moments centered correspond to the expectation and variance of a random variable.

The CGF is also approximately given by [25]

$$k(a,b,t) = \sum_{x,y\geq 0} k_{x,y}(t)\frac{a^{x}b^{y}}{x!y!} \quad (30)$$

The expansion of which is

$$k(a,b,t) = ak_{10}(t) + bk_{01}(t) + \frac{a^{2}}{2!}k_{20} + \frac{b^{2}}{2!}k_{02} + abk_{11} + \cdots \quad (31)$$

where,
$k_{10}(t) = E[X(t)] = \mu_X(t)$, $k_{01}(t) = E[Y(t)] = \mu_Y(t)$,
$k_{20} = Var[X(t)] = \sigma_X^2(t)$, $k_{02}(t) = Var[Y(t)] = \sigma_Y^2(t)$,
$k_{11}(t) = \mathrm{cov}[X(t),Y(t)]$
Now, differentiating equation 31 with respect to time, expanding the functions e^{a}, e^{-a}, e^{b}, e^{-b} in Taylor series, and substituting the expanded series in equation 29 we obtain a system of linear equations for the expected value, the variance and the covariance of $X(t)$ y $Y(t)$

$$\begin{aligned}
&\frac{d\mu_X(t)}{dt} = -\lambda(t)\mu_X(t)\\
&\frac{d\mu_Y(t)}{dt} = \lambda(t)\mu_X(t) - \theta\mu_Y(t)\\
&\frac{d\sigma_X^2(t)}{dt} = \lambda(t)\mu_X(t) - 2\lambda(t)\sigma_X^2(t)\\
&\frac{d\sigma_Y^2(t)}{dt} = 2\lambda(t)\,\mathrm{cov}_{XY}(t) + \lambda(t)\mu_X(t)\\
&\frac{d\mathrm{cov}_{XY}(t)}{dt} = -\lambda(t)\mu_X(t) + \lambda(t)\sigma_X^2(t) - \lambda(t)\,\mathrm{cov}_{XY}(t)\\
&-\theta\mathrm{cov}_{XY}(t)
\end{aligned} \quad (32)$$

with initial conditions $\mu_X(0) = x_0$, $\mu_Y(0) = y_0$, $\sigma_X^2(0) = 0$, $\sigma_Y^2(0) = 0$ y $\mathrm{cov}_{XY}(0) = 0$

The system can be solved numerically in Matlab, by applying Runge-Kutta because the force of infection $\lambda(t)$ is an estimated vector. This follows below the simulated scenarios of statistical measures such as the expected value, variance and covariance with an initial population of 100 people, that is $x_0 = 100$, and a single infected individual, $y_0 = 1$ who interacts with the susceptible population via the mosquito vector.

Figure 3 shows that the expected value of the susceptible population over time is 20 people and more or less a constant value, while the expected value of the infected population decreases to zero over time. This agrees with the previous simulation which shows that the probability of a particular number of infected individuals grows initially but then vanishes. That is to say that the probability that a number of infected individuals is maintained for all time is equal to zero.

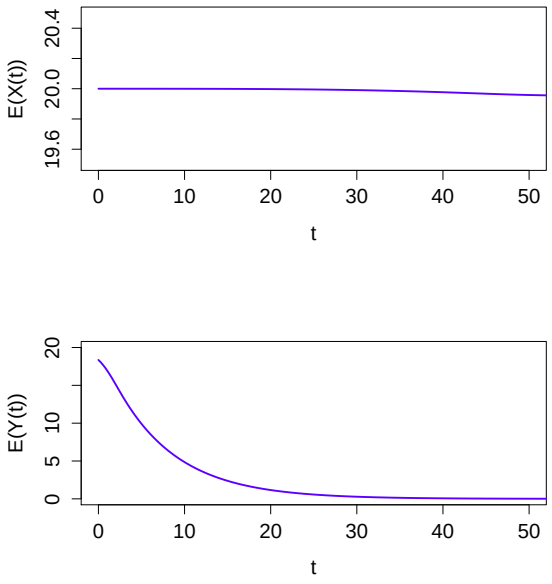

Fig. 3: Expected value of the susceptible and infected populations over time

The behaviour of the variances of the the susceptible and infected populations is similar, being lower for the infected individuals. In addition, the spread of the population figures for susceptible and infected individuals is very small, almost negligible, as can be seen in figure 4.

Finally, figure 5 indicates that the covariance of the susceptible and the infected populations is negative over time because they are inverse processes, that is, the greater the number of infected individuals, the fewer susceptible individuals there are.

8 Conclusion

Combining deterministic and stochastic models when studying phenomenon of an epidemiological type makes the results closer to reality and therefore they become tools that can be used to solve many problems caused by viruses in a community of susceptible individuals. In particular, this investigation demonstrates this combination in the deterministic model used to estimate the force of infection over time and the stochastic model formulated from the SIR dynamics of dengue with their respective probability distributions over time.

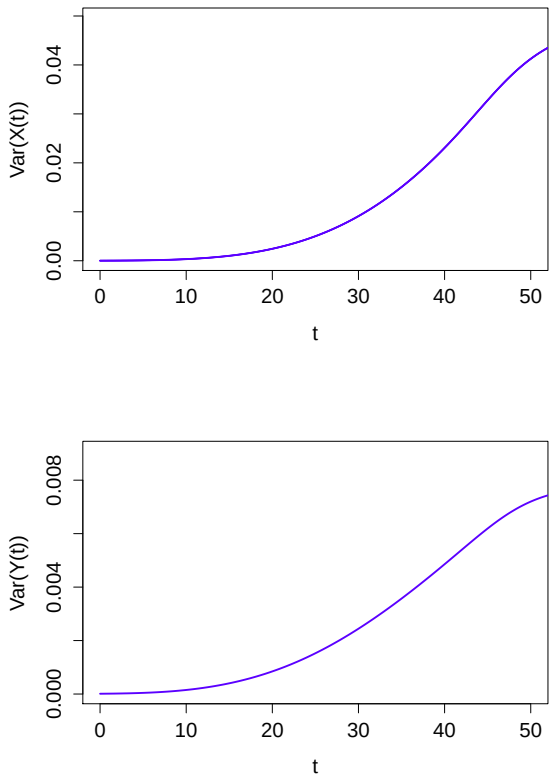

Fig. 4: Variance of the susceptible and infected populations over time

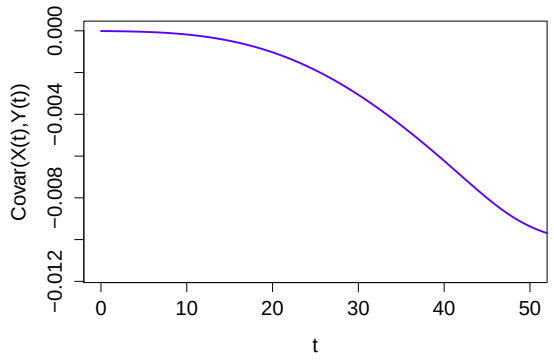

Fig. 5: Covariance over time of the r.v. $X(t)$ and $Y(t)$

The calculation of the probability distributions for the random variables that represent the susceptible, infected and recovered populations from the solution of a partial differential equation shows the great importance of this type of equation in the modeling, not only of epidemiological phenomena but also of other types of natural phenomena which they represent a world that can be explored and exploited using numerical methods. The calculation of both theoretical and numerical probabilities over time and the estimation of basic statistical measures such as expected value, variance and covariance give another facet to the analysis and understanding of the Dengue SIR dynamics.

References

[1] D. Normile, Surprising new dengue virus throws a spanner in disease control efforts, Science, Vol. 342, No. 6157, pp. 415-415 (2013).
[2] S. Thomas, D. Strickman, and D. Vaughn, Dengue epidemiology: virus epidemiology, ecology, and emergence, Advances in virus research, Vol. 61, pp. 235-290 (2003).
[3] M. Bogantes, and W. Montoya, Boletin: Dengue, Chikungunya o Zika?, Revista Clinica Escuela de Medicina UCR-HSJD, Vol. 6, No. 5, pp. 1-6 (2016).
[4] N. Bailey, A simple stochastic epidemic, Biometrika Trust, Vol. 37, pp. 193-202 (1950).
[5] J. Gani, and P. Purdue, Matrix-Geometric methods for the general stochastic epidemic, IMA Journal of Mathematics Applied in Medicine and Biology, Vol. 1, No. 4, pp. 333-342 (1984).
[6] R. Lounes, and H. Arazoza, A two-type model for the Cuban national programme on HIV/AIDS, IMA Journal of Mathematics Applied in Medicine and Biology, Vol. 16, No. 2, pp. 143-154 (1999).
[7] A. Khan, M. Hassan, and M. Imran, The effects of a backward bifurcation on a continuous time markov chain model for the transmissions dynamics of single strain dengue virus, Scientific Research, Applied Mathematics, Vol. 4, No. 04, pp. 663-674 (2013).
[8] C. Lee, J. Shin, and J. Kim, A numerical characteristic method for probability generating functions on stochastic first-order reaction networks, Journal of Mathematical Chemistry, Vol. 51, No. 1, pp. 316-337 (2013).
[9] R. Anderson, and R. May, Infectious diseases of humans, Dynamics and control. Oxford: Oxford University Press, (1991).
[10] L. Allen, Some discrete-time SI, SIR, and SIS epidemic models, Department of mathematics, Texas: Texas Tech University, Vol. 124, No. 1, pp. 83-105 (1994).
[11] H. Muench. Catalytic models in epidemiology, Harvard University Press, (1959).
[12] D. Griffiths, A catalytic model of infection for measles, Applied Statistics, Vol. 23, No. 3, pp. 330-339, (1974).
[13] Z. Shkedy, M, Aerts, G. Molenberghs, P. Beutels, and P. Damme, Modelling forces of infection by using monotone local polynomials, Journal of the Royal Statistical Society: Series C (Applied Statistics), Vol. 52, No. 4, pp. 469-485 (2003).
[14] E. Massad, M. Chen, C. Struchiner, N. Stollenwerk, and M. Aguiar, Scale-free network of a dengue epidemic, Applied Mathematics and Computation, Vol. 195, No. 2, pp. 376-381 (2008).

[15] L. Lopez, A. Muñoz, G. Olivar, and J. Betancourt, Modelo matematico para el control de la transmision del Dengue, Revista de Salud Publica, Journal of Public Health, Vol. 14, No. 3, pp. 512-523 (2012).
[16] L. Ojeda. Análisis numérico básico, Un enfoque algorítmico con el soporte de Matlab, Guayaquil: Escuela Superior Politecnica del Litoral, (2011), http://www.fcnm.espol.edu.ec/sites/fcnm.espol.edu.ec/files /ANALISIS_NUMERICO_BASICO_V4P4.pdf.
[17] F. Walter. Introducción a los Métodos Numéricos. Revista Digital, Escuela de matematica,(2014).
[18] J. Kingman, Poisson processes, John Wiley & Sons, Ltd, (1993).
[19] M. Esquivel, Probability generating functions for discrete real-valued random variables, Theory of Probability & Its Applications, Vol. 52, No. 1, pp. 40-57 (2008).
[20] I. Gerst, The bivariate generating function and two problems in discrete stochastic processes, SIAM Review, Vol. 4, No. 2, pp. 105-114 (1962).
[21] L. Evans, Partial differential equations and Monge-Kantorovich mass transfer, Current developments in mathematics, Vol. 1997, No. 1, pp. 65-126 (1997).
[22] V. Iório, EDP: un curso de graduacion, IMCA, (1999).
[23] N. Bailey, The elements of stochastic processes with applications to the natural sciences, Vol. 25, John Wiley & Sons (1990).
[24] T. Severini, Elements of distribution theory, Vol. 17, Cambridge University Press (2005).
[25] R. Bhattacharya, and E. Waymire, Stochastic processes with applications, Society for Industrial and Applied Mathematics, Vol. 61, Siam (2009).

Germán Arturo Marcillo Hernández received the title of Bachelor of Mathematics from the Nariño University of Colombia in 2009. He received the title of Magister in Sciences - Applied Mathematics from the National University of Colombia in 2017. Researcher at the Faculty of Education, Mariana University , San Juan de Pasto - Colombia. His subjects of interest are in Mathematical Epidemiology, Applied Mathematics and Probability.

Anibal Muñoz Loaiza Specialization in Biomathematics, University of Quindo, Colombia; Dr. in Mathematical Sciences, FCFM-BUAP, Mexico; Researcher at the Faculty of Education, Universidad del Quindo, Colombia and director of the Mathematical Modeling in Epidemiology Group (GMME). 45 articles in different journal, numerous presentations as speaker and lecturer in events in different countries. At present, he is developing a postdoctoral project on Mathematical Modeling with new technologies and inclusion of limiting factors to control vectors of arbovirosis, in the Federal Center of Technological Education of Minas Gerais, Department of Physics and Mathematics (DFM), Brazil. With Dr. Rodrigo Toms Nogueira Cardoso and his doctoral students.

Gerard Olivar received the title of Mathematician from the University of Barcelona (Barcelona, Spain) in 1987 and the Doctor of Sciences - Mathematics by the Universitat Politcnica de Catalunya (Barcelona, Spain) in 1997 (Cum Laude). From 1987 to 2005 he was assigned to the Department of Applied Mathematics IV at the Universitat Politcnica de Catalunya, where he was Professor. Since 2005 he has been linked to the National University of Colombia, where he currently works as a Full Professor. His subjects of interest are in Mathematical Engineering and Applied Mathematics. Specifically, in applications to science and engineering modeling and simulation, nonlinear dynamics and complex systems. Since 2011, he has held the Presidency of the Colombian Section of the Society for Industrial and Applied Mathematics (SIAM).