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MODELING SPATIAL SPREAD OF AN EPIDEMIOLOGIC MODEL IN A SPATIALLY CONTINUOUS DOMAIN

Shousheng Zhu*, Nathalie Verdière[†], David Manceau[†], Lilianne Denis-Vidal* and Djalil Kateb*

Abstract. In this paper, we study a Chikungunya epidemic transmission model which describes an epidemic disease transmitted by Aedes mosquitoes. This model includes the spatial mobility of humans which is probably a factor that has influenced the re-emergence of several diseases. Assuming that the spatial mobility of humans is random described as Brownian random motion, an original model including a reaction-diffusion system is proposed. Since the displacement of mosquitoes is limited to a few meters, compared with humans, one can ignore mosquitoes mobility. Therefore, the complete model is composed of a reaction-diffusion system coupled with ordinary differential equations (ODEs). In this paper, we prove the existence and uniqueness, the positivity and boundedness of the global solution for the model and give some numerical simulations.

Keywords. Nonlinear model; Epidemiologic model; Chikungunya virus; Ordinary differential equations; Reactiondiffusion system.

1 Introduction

For many decades, our societies are confronted to recurrent epidemiological diseases due to, among others, the mobility of humans, the adaptation of their vectors, the virus itself or the environment changes. Global health authorities are now strongly engaged in the control of these diseases and describing their spread has become a major issue for predicting their evolution and controlling their outbreak. In order to better apprehend vector-borne infections, mathematical models are developed and studied since the 20th century. For example, models for the transmission of the dengue and chikungunya diseases transmitted by the the mosquito *Aedes albopictus* [15] had been proposed by [3] for the Dengue and [2] or [9] for the chikungunya. However, these first models do not consider space.

The description of the spread of such diseases can be done by epidemiological models, usually derived from the classical SIR models. These compartmental models consist of structuring the population in susceptible, infected and recovered individuals. Assuming that the spatial mobility is random and is described as Brownian random motion, the authors in [12] have proposed to add diffusion terms in system of ordinary differential equations to consider the spread of diseases. This modeling way is often used in order to take into account the spread of populations [1, 8].

In this paper, we focus on the chikungunya disease whose particularity is to reemerge regularly since the beginning of the 21th century. Until 2000, this virus was confined to African countries. However, because of the global warming and the development of transports, an unprecedented epidemic was observed in the Réunion island (a French island in the Indian Ocean) in 2005-2006 where one third of the total population was infected, the maximum number has been reached in February 2006 with 40 000 infected. The chikungunya epidemic affected for the first time Europe in 2007 from Italy. It was observed that the vector of this epidemic had developed capabilities to adapt to non tropical region. In 2014, this epidemic spreads to the whole of the Caribbean, the countries of America. Hundreds of cases of the islands of Oceania also exported to Europe and elsewhere in the world.

In [9], a SI-SIR model taken into account the mosquito biological life cycle and describing the virus transmission to human population was proposed. A parameter study of this model was done by [16]. But this model does not take into account spatial mobility of humans and mosquitoes which is a factor that has probably influenced the reemergence of several epidemics. In [11], a spatio-temporal model was proposed on the form of a metapopulation

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model. This model considers a graph where each node represents a real habitat of the environment. On each of them, the SI-SIR model is considered and to model the human mobility, each node is coupled with some neighboring nodes. This spatio-temporal model can be seen as a discrete model in space variable. In this paper, we propose a continuous model in space and time variables based too on the SI-SIR model proposed by [9]. We suppose that the displacements of mosquitoes are limited to a few meters compared to humans and thus, can be neglected. For modeling the human mobility the idea of [12] is taken again.

The paper is organized as follows. The model is presented in section 2. In the third section, the main result about the existence, the uniqueness, the positivity and boundedness of a global solution is given. Its proof is done at section 4. Some numerical simulations are proposed at section 5 and section 6 concludes the paper.

2 Presentation of the model

Different models for the spread of infectious diseases in populations have been analyzed mathematically and applied to specific diseases [4, 6, 14]. In [9], Moulay et al. proposed an epidemiological model of Chikungunya disease. This model couples a mosquito dynamics model and a transmission virus model between humans and mosquitoes populations. The vector dynamics model is based on the biological mosquito life cycle which considers three stages: E the number of eggs, L the number of larvae/pupae and A the number of adult females. This model is given by

$$\begin{cases} E'(t) = bA(t)(1 - \frac{E(t)}{K_E}) - (s+d)E(t), \\ L'(t) = sE(t)(1 - \frac{L(t)}{K_L}) - (s_L + d_L)L(t), \\ A'(t) = s_L L(t) - d_m A(t), \end{cases}$$
(1)

where

- b > 0 is the intrinsic rate, s > 0 (resp. $s_L > 0$) is transfer rate from E to L (resp. from L to A),
- $K_E > 0$ (resp. $K_L = K_E/2$) is the carrying capacity of E (resp. carrying capacity of L),
- d > 0, $d_L > 0$ and $d_m > 0$ are the mortality rate for E, L and A respectively.

For the transmission virus model, since the disease is transmitted by the adult female mosquitoes, only the stage A is considered. Thus, A is divided into two epidemiological states: S_m the density of susceptible and I_m the density of infective. Finally, the human population is divided into three stages given by their densities: S_H , susceptible humans, I_H , infected humans and R_H , recovered humans. With these notations, the transmission virus model is

$$\begin{cases}
I'_{m}(t) = -(s_{L}\frac{L(t)}{A(t)} + \beta_{m}I_{H}(t))I_{m}(t) + \beta_{m}I_{H}(t), \\
S'_{H}(t) = -(b_{H} + \beta_{H}I_{m}(t))S_{H}(t) + b_{H}, \\
I'_{H}(t) = \beta_{H}I_{m}(t)S_{H}(t) - (\gamma + b_{H})I_{H}(t),
\end{cases}$$
(2)

where

- $\beta_m > 0$ (resp. $\beta_H > 0$) is the infectious contact rate between susceptible mosquitoes and infected humans (resp. susceptible humans and vectors),
- $b_H > 0$ is the human birth rate,
- $\gamma > 0$ is the human recovery rate.

Note that we do not need to consider S_m and R_H since $S_m = 1 - I_m$ and $R_H = 1 - S_H - I_H$.

In this paper, under the same conditions as [11], we propose a continuous model in space and time variables. The human mobility is described by a Brownian motion leading to a model with diffusion (see e.g. [12]). Thus, this model is given by

$$\begin{cases} \partial_t E(t, \mathbf{x}) = bA(t, \mathbf{x})(1 - \frac{E(t, \mathbf{x})}{K_E(\mathbf{x})}) - (s+d)E(t, \mathbf{x}), \\ \partial_t L(t, \mathbf{x}) = sE(t, \mathbf{x})(1 - \frac{L(t, \mathbf{x})}{K_L(\mathbf{x})}) - (s_L + d_L)L(t, \mathbf{x}), \\ \partial_t A(t, \mathbf{x}) = s_L L(t, \mathbf{x}) - d_m A(t, \mathbf{x}), \end{cases}$$

$$\begin{cases} \partial_t I_m(t, \mathbf{x}) = -(s_L \frac{L(t, \mathbf{x})}{A(t, \mathbf{x})} + \beta_m I_H(t, \mathbf{x}))I_m(t, \mathbf{x}) + \beta_m I_H(t, \mathbf{x}), \\ \partial_t S_H(t, \mathbf{x}) = -(b_H + \beta_H I_m(t, \mathbf{x}))S_H(t, \mathbf{x}) + b_H + d_1\Delta S_H(t, \mathbf{x}), \\ \partial_t I_H(t, \mathbf{x}) = \beta_H I_m(t, \mathbf{x})S_H(t, \mathbf{x}) - (\gamma + b_H)I_H(t, \mathbf{x}) + d_2\Delta I_H(t, \mathbf{x}), \end{cases}$$
(3a)

where $d_1, d_2 > 0$ are diffusion coefficients, **x** is in a bounded domain $\Omega \subset \mathbb{R}^n$ with C^2 -boundary and t > 0. Note that the carrying capacities of mosquitoes stages K_E and K_L depend on the space variable **x** but still satisfy $K_L(\mathbf{x}) = K_E(\mathbf{x})/2$ for all $\mathbf{x} \in \Omega$. We also assume that $K_E(\mathbf{x})$ is continuous, strictly positive and uniformly bounded.

To avoid the difficulties due to the space dependance of K_E , we make the change of variables

$$Y_1 := E/K_E, \quad Y_2 := L/K_E \text{ and } Y_3 := A/K_E$$

Moreover, we note

$$\mathbf{u}_1 \ := \ I_m, \quad \mathbf{u}_2 \ := \ S_H$$
 and $\mathbf{u}_3 \ := \ I_H$

Then, model (3) can be written as

$$\begin{cases} \partial_{t}Y_{1} = bY_{3}(1 - Y_{1}) - (s + d)Y_{1}, \\ \partial_{t}Y_{2} = sY_{1}(1 - 2Y_{2}) - (s_{L} + d_{L})Y_{2}, \\ \partial_{t}Y_{3} = s_{L}Y_{2} - d_{m}Y_{3}, \end{cases}$$

$$\begin{cases} \partial_{t}\mathbf{u}_{1} = -(s_{L}\frac{Y_{2}}{Y_{3}} + \beta_{m}\mathbf{u}_{3})\mathbf{u}_{1} + \beta_{m}\mathbf{u}_{3}, \\ \partial_{t}\mathbf{u}_{2} = -(b_{H} + \beta_{H}\mathbf{u}_{1})\mathbf{u}_{2} + b_{H} + d_{1}\Delta\mathbf{u}_{2}, \\ \partial_{t}\mathbf{u}_{3} = \beta_{H}\mathbf{u}_{1}\mathbf{u}_{2} - (\gamma + b_{H})\mathbf{u}_{3} + d_{2}\Delta\mathbf{u}_{3}. \end{cases}$$
(4a)
$$(4b)$$

Thus, we obtain an ODE/reaction-diffusion system (4b) coupled with an ODE system (4a). Moreover, we need to add a boundary condition for \mathbf{u}_2 and \mathbf{u}_3 . We consider that there is no population flux across the boundary $\partial\Omega$ of Ω , thus homogeneous Neumann boundary conditions are considered:

$$\frac{\partial \mathbf{u}_2}{\partial \nu} = \frac{\partial \mathbf{u}_3}{\partial \nu} = 0, \quad \text{in } \mathbb{R}_+ \times \partial \Omega, \tag{5}$$

where ν is the unit outward normal at $\partial \Omega$. Finally, initial conditions are

$$\forall \mathbf{x} \in \overline{\Omega}, \begin{cases} Y_1(0, \mathbf{x}) = Y_{1,0}(\mathbf{x}), & Y_2(0, \mathbf{x}) = Y_{2,0}(\mathbf{x}), & Y_3(0, \mathbf{x}) = Y_{3,0}(\mathbf{x}), \\ \mathbf{u}_1(0, \mathbf{x}) = \mathbf{u}_{1,0}(\mathbf{x}), & \mathbf{u}_2(0, \mathbf{x}) = \mathbf{u}_{2,0}(\mathbf{x}), & \mathbf{u}_3(0, \mathbf{x}) = \mathbf{u}_{3,0}(\mathbf{x}), \end{cases}$$
(6)

where $Y_{1,0}, Y_{2,0}, Y_{3,0}, \mathbf{u}_{1,0}, \mathbf{u}_{2,0}, \mathbf{u}_{3,0}$ are continuous on $\overline{\Omega}$.

3 Existence and uniqueness of a global solution of (4)

Note that the ODE system (4a) is independent of the ODE/reaction-diffusion system (4b) and thus the two systems can be studied separately.

3.1 Properties of the ODE system

In all the sequel, X denotes the space of continuous functions on $\overline{\Omega}$, *i.e.* $X := C(\overline{\Omega})$, which is a Banach space endowed with the *sup* norm:

$$\forall f \in X, \quad \|f\|_{\infty} := \max_{\mathbf{x} \in \overline{\Omega}} |f(\mathbf{x})|.$$

For any function $f : \mathbb{R}_+ \times \overline{\Omega} \to \mathbb{R}$ continuous on $\overline{\Omega}$, we set $f(t) := f(t, \cdot) \in X$. With this notation, (4a) can be written under the form

$$Y'(t) = F(Y(t)),$$

where

$$\forall t > 0, \quad Y(t) := \begin{pmatrix} Y_1(t, \cdot) \\ Y_2(t, \cdot) \\ Y_3(t, \cdot) \end{pmatrix} \quad \text{and} \quad F(Y) \ := \ \begin{pmatrix} bY_3(1 - Y_1) - (s + d)Y_1 \\ sY_1(1 - 2Y_2) - (s_L + d_L)Y_2 \\ s_LY_2 - d_mY_3 \end{pmatrix}.$$

Since F is polynomial, F is locally Lipschitz continuous on X^3 and thus, for any $Y_0 \in X^3$, there exists T > 0 such that (4a) admits a unique solution $Y \in C^1([0,T); X^3)$. Moreover, F is of C^{∞} class on X^3 and thus $Y \in C^{\infty}([0,T); X^3)$. Following the work of [9], this solution is global and positive if the initial condition is positive. To state this result, we introduce the following notation

$$X_{+} := \left\{ f \in X \mid \forall \mathbf{x} \in \overline{\Omega}, \quad f(\mathbf{x}) \ge 0 \right\}.$$
(7)

Proposition 3.1 (Moulay et al. [9]). Let $Y_0 \in X^3_+$ and Y be the unique local solution of (4a) such that $Y(0) = Y_0$.

1. The solution Y is global and positive, i.e.

$$Y \in C^{\infty}\left([0,\infty); X^3_+\right)$$

2. The system has the following positive invariant set

$$\Sigma = \left\{ (Y_1, Y_2, Y_3) \in X^3 \mid 0 \le Y_1 \le 1, \quad 0 \le Y_2 \le \frac{1}{2}, \quad 0 \le Y_3 \le \frac{s_L}{2d_m} \right\},\tag{8}$$

i.e. if $Y_0 \in \Sigma$, then $Y \in C^{\infty}([0,\infty);\Sigma)$.

3. If

$$r = \frac{s_L}{d_m} \frac{b}{s+d} \frac{s}{s_L+d_L} > 1,$$
(9)

and $Y_0 \in int(\Sigma)$ (int(Σ) is the interior of Σ), then $Y \in C^{\infty}([0,\infty); int(\Sigma))$.

Remark 3.1. From [9], the case r > 1, with r given by (9), is the condition of survival of all populations of mosquitoes (eggs, larvae and adults). In all the sequel, we will assume that r > 1 and thus we have $Y_1, Y_2, Y_3 > 0$. In particular, we will suppose that there exists $\xi > 0$, such that for any $t \ge 0$, $Y_3(t) > \xi$.

3.2 Main result

In this section, we consider the ODE/reaction-diffusion system (4b) and state the main result of this paper: the existence and uniqueness of a global positive solution to (4b). First, we formulate problem (4b) as a system of semilinear evolution equations. We set

$$\forall t > 0, \quad \mathbf{u}(t) := (\mathbf{u}_1(t, \cdot), \mathbf{u}_2(t, \cdot), \mathbf{u}_3(t, \cdot))^{\mathrm{T}}.$$

Similarly to [14], we define the operator Λ on X^3 (recall that $X = C(\overline{\Omega})$) by

$$\Lambda := \operatorname{diag}(0, d_1 D_N, d_2 D_N), \tag{10}$$

whose domain is

$$D(\Lambda) := X \times D(D_N) \times D(D_N), \tag{11}$$

where D_N is the negative Neumann-Laplacian on X, *i.e.*

$$D_N \mathbf{u}_i := -\Delta \mathbf{u}_i, \quad \forall \ \mathbf{u}_i \in D(D_N) := \left\{ \mathbf{u}_i \in \bigcap_{p>1} W^{2,p}(\Omega) \mid \Delta \mathbf{u}_i \in X, \ \frac{\partial \mathbf{u}_i}{\partial \nu} = 0 \text{ on } \partial \Omega \right\}.$$

Then, $-\Lambda$ is the generator of the positive analytic C_0 -semigroup (see e.g. [7])

$$e^{-\Lambda t} = \operatorname{diag}(I, e^{-d_1 t D_N}, e^{-d_2 t D_N}) \in \mathcal{L}(X^3).$$

With these notations, system (4b)-(5)-(6) can be formulated as

$$\begin{cases} \mathbf{u}'(t) + \Lambda \mathbf{u}(t) &= G(\mathbf{u}(t)), \quad \forall t > 0, \\ \mathbf{u}(0) &= \mathbf{u}_0 \in X^3, \end{cases}$$
(12)

where

$$G(\mathbf{u}) := \begin{pmatrix} -(s_L \frac{Y_2}{Y_3} + \beta_m \mathbf{u}_3)\mathbf{u}_1 + \beta_m \mathbf{u}_3 \\ -(b_H + \beta_H \mathbf{u}_1)\mathbf{u}_2 + b_H \\ \beta_H \mathbf{u}_1 \mathbf{u}_2 - (\gamma + b_H)\mathbf{u}_3 \end{pmatrix} \text{ and } \mathbf{u} := (\mathbf{u}_1, \mathbf{u}_2, \mathbf{u}_3)^{\mathrm{T}}.$$

The main result of this paper and whose proof is given at section 4 is the following:

Theorem 3.1. Assume r > 1, where r is given by (9) and $Y_0 \in int(\Sigma)$ (see Proposition 3.1). Furthermore, we assume that Y_3 satisfies

$$Y_3(t) > \xi > 0$$
 for any $t \in [0, +\infty)$.

Let $\mathbf{u}_0 \in X^3$.

- 1. There exists $T := T(\mathbf{u}_0) > 0$ such that (4b) (5) (6) admits a unique solution $\mathbf{u} \in C([0, T]; X^3)$. Moreover, $\partial_t \mathbf{u}, \partial_{\mathbf{x}_i} \mathbf{u}_2, \partial_{\mathbf{x}_i} \mathbf{u}_3, \Delta \mathbf{u}_2$ and $\Delta \mathbf{u}_3$ are continuous on $(0, T] \times \overline{\Omega}$.
- 2. If $\mathbf{u}_0 \in X^3_+$, \mathbf{u} is a positive global solution, i.e. $\mathbf{u} \in C([0, +\infty); X^3_+)$. Moreover, \mathbf{u} is uniformly bounded with the given bounds:

$$\forall t \ge 0, \quad \|\mathbf{u}_1(t, \cdot)\|_{\infty} \le \max(\|\mathbf{u}_{1,0}\|_{\infty}; 1), \quad \|\mathbf{u}_2(t, \cdot)\|_{\infty} \le \max(\|\mathbf{u}_{2,0}\|_{\infty}; 1),$$

and

$$\|\mathbf{u}_{3}(t,\cdot)\|_{\infty} \leq \max\left(\|\mathbf{u}_{3,0}\|_{\infty};\frac{\beta_{H}}{\gamma+b_{H}}\right).$$

Remark 3.2. Since $\mathbf{u}_1, \mathbf{u}_2$ and \mathbf{u}_3 are densities, one important question is to know if they remain in the region of biological interest, that is [0, 1]. From Theorem 3.1, if $\mathbf{u}_{1,0}(\mathbf{x}), \mathbf{u}_{2,0}(\mathbf{x}), \mathbf{u}_{3,0}(\mathbf{x}) \in [0, 1]$ for any $\mathbf{x} \in \overline{\Omega}$, then $\mathbf{u}_1(t, \mathbf{x}), \mathbf{u}_2(t, \mathbf{x}) \in [0, 1]$ for all t > 0. Nevertheless this is not the case for $\mathbf{u}_3(t, \cdot)$, unless if $\frac{\beta_H}{\gamma + b_H} \leq 1$.

In the case without diffusion, it is proved in [9], that, for all t > 0, $\mathbf{u}_1(t)$ and $(\mathbf{u}_2 + \mathbf{u}_3)(t)$ are in [0, 1] if $\mathbf{u}_{1,0}, \mathbf{u}_{2,0} + \mathbf{u}_{3,0} \in [0, 1]$. In our case, arguing as in the proof below (subsection 4.3), we can obtain the same result as [9] if we assume $d_1 = d_2$. Nevertheless, since one can expect that infected people are less mobile than susceptible ones, it seems more realistic to assume that $d_2 < d_1$.

One way to obtain a similar result to [9] is to consider the total mass of $u_2 + u_3$. Indeed, we have the following:

Proposition 3.2. Let $\mathbf{u}_0 \in X^3_+$ and $\mathbf{u} \in C([0, +\infty); X^3_+)$ be the unique solution of (4b) - (5) - (6) given by Theorem 3.1. For any function $f \in L^1(\Omega)$, we set

$$\langle f \rangle := \frac{1}{|\Omega|} \int_{\Omega} f(\mathbf{x}) \, d\mathbf{x}.$$

If $\langle \mathbf{u}_{2,0} + \mathbf{u}_{3,0} \rangle \in [0, 1]$ *, then, for all* t > 0*,* $\langle \mathbf{u}_2 + \mathbf{u}_3 \rangle$ $(t) \in [0, 1]$ *.*

Proof. From Theorem 3.1, it suffices to prove that, for all t > 0, $\langle \mathbf{u}_2 + \mathbf{u}_3 \rangle$ $(t) \in [0, 1]$. Summing the second and third equation of (4b) and integrating on Ω , we get

$$\partial_t \langle \mathbf{u}_2 + \mathbf{u}_3 \rangle (t) = -\gamma \langle \mathbf{u}_3 \rangle (t) - b_H \langle \mathbf{u}_2 + \mathbf{u}_3 \rangle (t) + b_H \leq -b_H \langle \mathbf{u}_2 + \mathbf{u}_3 \rangle (t) + b_H,$$

since $\langle \mathbf{u}_3 \rangle$ (t) ≥ 0 . Applying Gronwall's lemma, we obtain

$$\langle \mathbf{u}_2 + \mathbf{u}_3 \rangle(t) \le \langle \mathbf{u}_{2,0} + \mathbf{u}_{3,0} \rangle e^{-b_H t} + 1 - e^{-b_H t},$$

which leads to the result.

4 **Proof of Theorem 3.1**

We divide the proof into three steps. First, we show the existence and uniqueness of a local solution with the appropriate regularity. Then, we show that for positive initial datum, the solution remains positive on its time interval of existence. Finally, we derive the bounds of statement 2 and deduce that the local solution is global.

4.1 Existence, uniqueness and regularity of the local solution

We follow the proof of Proposition 7.3.1 of [7], where the case of a reaction-diffusion system is considered but with positive diffusion coefficients, while in our case the first equation of (4b) has a zero diffusion coefficient.

The space X being endowed with the *sup* norm, we deduce that G is locally Lipschitz continuous on X^3 . Since $-\Lambda$ is the infinitesimal generator of an analytic C_0 -semigroup on X^3 , according to Theorem 7.1.2 of [7], there exists $T = T(\mathbf{u}_0) \in (0, +\infty)$ such that (12) admits a unique mild solution (see e.g. [7, 13] for the definition of mild solution)

$$\mathbf{u} \in C((0,T];X^3) \cap L^{\infty}(0,T;X^3).$$

Moreover, since Ω is bounded, $D(D_N)$ is dense in X (see Corollary 3.1.24 of [7]) and thus $\overline{D(\Lambda)} = X^3$. Then, from Proposition 7.1.10 of [7], we get that $\mathbf{u} \in C^1((0,T];X^3) \cap C((0,T];D(\Lambda))$ and $\Lambda \mathbf{u} \in C((0,T];X^3)$. Therefore, we deduce

 $\partial_t \mathbf{u} \in C((0,T]; X^3)$ and $\Delta \mathbf{u}_2, \Delta \mathbf{u}_3 \in C((0,T]; X).$

Finally, since $\mathbf{u} \in C((0,T]; D(\Lambda))$ we get $\mathbf{u}_2, \mathbf{u}_3 \in C((0,T]; D(D_N))$. Then, from Sobolev embedding theorem, we have $\mathbf{u}_2, \mathbf{u}_3 \in C((0,T]; C^1(\overline{\Omega}))$ and thus $\partial_{\mathbf{x}_i}\mathbf{u}_2$ and $\partial_{\mathbf{x}_i}\mathbf{u}_3$ are continuous on $(0,T] \times \overline{\Omega}$. Hence, statement 1 is proved.

4.2 **Positivity of the solution**

(1) Let $a \in (0,T)$. Since \mathbf{u}_1 is continuous on $[0,a] \times \overline{\Omega}$ and $\mathbf{u}_{1,0} \ge 0$,

$$M := \sup\{|\mathbf{u}_1(t, \mathbf{x})| \mid (t, \mathbf{x}) \in [0, a] \times \overline{\Omega}\} \in \mathbb{R}_+.$$

Let $\lambda > 0$ be such that $\lambda \ge \beta_H M - b_H$. Then, we have

$$b_H + \beta_H \mathbf{u}_1 + \lambda \ge 0$$
 on $[0, a] \times \overline{\Omega}$.

We set $\tilde{\mathbf{u}}_2(t, \mathbf{x}) := \mathbf{u}_2(t, \mathbf{x})e^{-\lambda t}$. Assume $\tilde{\mathbf{u}}_2$ has a negative minimum at $(t_0, \mathbf{x}_0) \in [0, a] \times \overline{\Omega}$. If $\mathbf{x}_0 \in \Omega$, from the maximum principle, and since $t_0 > 0$, we get

$$\partial_t \tilde{\mathbf{u}}_2(t_0, \mathbf{x}_0) - d_1 \Delta \tilde{\mathbf{u}}_2(t_0, \mathbf{x}_0) \le 0, \tag{13}$$

besides, since $b_H > 0$

$$\partial_t \tilde{\mathbf{u}}_2(t_0, \mathbf{x}_0) - d_1 \Delta \tilde{\mathbf{u}}_2(t_0, \mathbf{x}_0) = -(b_H + \beta_H \mathbf{u}_1(t_0, \mathbf{x}_0) + \lambda) \tilde{\mathbf{u}}_2(t_0, \mathbf{x}_0) + b_H e^{-\lambda t_0} > 0, \tag{14}$$

which leads to a contradiction. If $\mathbf{x}_0 \in \partial \Omega$, since $\tilde{\mathbf{u}}_2$ satisfies a homogeneous Neumann boundary condition, we obtain $\Delta \tilde{\mathbf{u}}_2(t_0, \mathbf{x}_0) \geq 0$ and, since the equations (13) and (14) are satisfied on $[0, a] \times \partial \Omega$, we get the same contradiction. Then, $\mathbf{u}_2 \geq 0$ on $[0, a] \times \overline{\Omega}$, since a is arbitrary, we deduce $\mathbf{u}_2 \geq 0$ on $[0, T) \times \overline{\Omega}$.

(2) First, assume \mathbf{u}_1 and \mathbf{u}_3 have a negative minimum on $[0, a] \times \overline{\Omega}$. We set

$$t_1 := \inf\{t \in [0, a] \mid \exists \mathbf{x}_1 \in \overline{\Omega}, \ \mathbf{u}_1(t, \mathbf{x}_1) < 0\} \text{ and } t_2 := \inf\{t \in [0, a] \mid \exists \mathbf{x}_2 \in \overline{\Omega}, \ \mathbf{u}_3(t, \mathbf{x}_2) < 0\}.$$

Since \mathbf{u}_1 and \mathbf{u}_3 are continuous on $[0, a] \times \overline{\Omega}$ and $\mathbf{u}_{1,0}, \mathbf{u}_{3,0} \ge 0$, we have

$$\mathbf{u}_1(t,\mathbf{x}) \geq 0, \quad \forall \ (t,\mathbf{x}) \in [0,t_1] \times \overline{\Omega} \quad \text{and} \quad \mathbf{u}_3(t,\mathbf{x}) \geq 0, \quad \forall \ (t,\mathbf{x}) \in [0,t_2] \times \overline{\Omega}$$

and there exist $\mathbf{x}_1, \mathbf{x}_2 \in \overline{\Omega}$ such that $\mathbf{u}_1(t_1, \mathbf{x}_1) = \mathbf{u}_3(t_2, \mathbf{x}_2) = 0$.

If $t_1 \leq t_2$. Then, we have $\partial_t \mathbf{u}_1(t_1, \mathbf{x}_1) = \beta_m \mathbf{u}_3(t_1, \mathbf{x}_1) \geq 0$ and thus, for $\varepsilon > 0$ small enough, we get

$$\mathbf{u}_1(t_1+\varepsilon,\mathbf{x}_1) = \mathbf{u}_1(t_1,\mathbf{x}_1) + \varepsilon \,\partial_t \mathbf{u}_1(t_1,\mathbf{x}_1) + o(\varepsilon) \ge 0,$$

which contradicts the definition of t_1 . So we have $t_1 > t_2$. Let $\mathbf{u}_3(t_*, \mathbf{x}_*)$ be the negative minimum of \mathbf{u}_3 on $[t_2, t_1] \times \overline{\Omega}$. Since $\mathbf{u}_1(t_*, \mathbf{x}_*) \ge 0$, from the maximum principle, we deduce

$$0 \ge \partial_t \mathbf{u}_3(t_*, \mathbf{x}_*) - d_2 \Delta \mathbf{u}_3(t_*, \mathbf{x}_*) = \beta_H \mathbf{u}_1(t_*, \mathbf{x}_*) \mathbf{u}_2(t_*, \mathbf{x}_*) - (\gamma + b_H) \mathbf{u}_3(t_*, \mathbf{x}_*) > 0,$$

which leads to a contradiction.

Second, if \mathbf{u}_1 has a negative minimum on $[0, a] \times \overline{\Omega}$ while $\mathbf{u}_3 \ge 0$, arguing as in the case $t_1 \le t_2$, we obtain a contradiction. Finally, if \mathbf{u}_3 has a negative minimum on $[0, a] \times \overline{\Omega}$ while $\mathbf{u}_1 \ge 0$, arguing as in the case $t_1 > t_2$, we obtain again a contradiction. Thus, we have $\mathbf{u}_1, \mathbf{u}_3 \ge 0$ on $[0, T] \times \overline{\Omega}$.

4.3 Boundedness and global existence of the solution

To show that **u** is a global solution, it suffices to show that

$$\lim_{t \to T} \|\mathbf{u}(t, \cdot)\|_{\infty} < \infty,$$

which holds obviously if u is uniformly bounded on [0, T). Thus we only have to obtain the bounds of statement 2 of Theorem 3.1. For this, we proceed as for the positivity by using the maximum principle. Let $a \in [0, T)$.

(1) Let $\mathbf{u}_1(t_0, \mathbf{x}_0)$ be the maximum of \mathbf{u}_1 on $[0, a] \times \overline{\Omega}$. If $t_0 = 0$, then we obtain $\|\mathbf{u}_1(t, \cdot)\|_{\infty} \le \|\mathbf{u}_{1,0}\|_{\infty}$. If $t_0 > 0$ and $\mathbf{u}_3(t_0, \mathbf{x}_0) \neq 0$, we obtain

$$0 \le s_L \frac{Y_2(t_0, \mathbf{x}_0)}{Y_3(t_0, \mathbf{x}_0)} \mathbf{u}_1(t_0, \mathbf{x}_0) \le \beta_m \mathbf{u}_3(t_0, \mathbf{x}_0)(1 - \mathbf{u}_1(t_0, \mathbf{x}_0)),$$

which leads to $\mathbf{u}_1(t_0, \mathbf{x}_0) \leq 1$. If $t_0 > 0$ and $\mathbf{u}_3(t_0, \mathbf{x}_0) = 0$, we obtain

$$\partial_t \mathbf{u}_1(t_0, \mathbf{x}_0) \ge 0$$

since (t_0, \mathbf{x}_0) is the maximum point. Besides,

0

$$\partial_t \mathbf{u}_1(t_0, \mathbf{x}_0) = -s_L \frac{Y_2(t_0, \mathbf{x}_0)}{Y_3(t_0, \mathbf{x}_0)} \mathbf{u}_1(t_0, \mathbf{x}_0) \le 0,$$

which leads to $\mathbf{u}_1(t_0, \mathbf{x}_0) = 0$ since $Y_2 > 0$ from Proposition 3.1 and the fact that r > 1. Thus, we obtain $\|\mathbf{u}_1(t, \cdot)\|_{\infty} \leq \max(\|\mathbf{u}_{1,0}\|_{\infty}; 1)$.

(2) Let $\mathbf{u}_2(t_1, \mathbf{x}_1)$ be the maximum of \mathbf{u}_2 on $[0, a] \times \overline{\Omega}$. If $t_1 > 0$ and $\mathbf{x}_1 \in \overline{\Omega}$, from the maximum principle, we get

$$\leq \partial_t \mathbf{u}_2(t_1, \mathbf{x}_1) - d_1 \Delta \mathbf{u}_2(t_1, \mathbf{x}_1) = -(b_H + \beta_H \mathbf{u}_1(t_1, \mathbf{x}_1)) \mathbf{u}_2(t_1, \mathbf{x}_1) + b_H.$$

Since $\mathbf{u}_1(t_1, \mathbf{x}_1) \ge 0$, we deduce $\mathbf{u}_2(t_1, \mathbf{x}_1) \le 1$. Thus, $\|\mathbf{u}_2(t, \cdot)\|_{\infty} \le \max(\|\mathbf{u}_{2,0}\|_{\infty}; 1)$.

(3) Let $\mathbf{u}_3(t_2, \mathbf{x}_2)$ be the maximum of \mathbf{u}_3 on $[0, a] \times \overline{\Omega}$. If $t_2 > 0$ and $\mathbf{x}_2 \in \overline{\Omega}$, from the maximum principle, we get

$$0 \le \partial_t \mathbf{u}_3(t_2, \mathbf{x}_2) - d_2 \Delta \mathbf{u}_3(t_2, \mathbf{x}_2) = \beta_H \mathbf{u}_1(t_2, \mathbf{x}_2) \mathbf{u}_2(t_2, \mathbf{x}_2) - (\gamma + b_H) \mathbf{u}_3(t_2, \mathbf{x}_2).$$

Since $\mathbf{u}_1(t_2, \mathbf{x}_2) \leq 1$ and $\mathbf{u}_2(t_2, \mathbf{x}_2) \leq 1$, we deduce $\mathbf{u}_3(t_2, \mathbf{x}_2) \leq \beta_H/(\gamma + b_H)$. Thus, we obtain

$$\|\mathbf{u}_{3}(t,\cdot)\|_{\infty} \leq \max\left(\|\mathbf{u}_{3,0}\|_{\infty};\frac{\beta_{H}}{\gamma+b_{H}}\right),$$

which leads to the desired bounds and then u is the global solution.

5 Numerical simulation

We will solve our model in two space dimensions where $\mathbf{x} = (x, y)$. While MATLAB's PDE Toolbox does not have an option for solving nonlinear parabolic PDE, we can make use of its tools to develop short M-files that will solve such equations [5].

The model parameters we will use for numerical simulations are noted in Table 1, the data come from table 1 of [10]. For the values d_1 and d_2 , we take $d_1 = 0.1$ and $d_2 = 0.01$, which signifies that the susceptible diffuse through the domain faster than the infected populations.

In general, initial and boundary conditions can be difficult to pin down for problems like this, but for this example we will assume that the domain is square of length 1 (denoted Ω), that neither human populations nor mosquitoes enters or exits the domain, and that initially the susceptible human density is mainly concentrated at the edges of the domain and the infected human density is mainly concentrated at the center. For the initial values of Y_i , we will take values obtained from an ODE model in [10] and $K_E(\mathbf{x})$ is also defined as a constant $K_E(\mathbf{x}) = 1000$. The initial conditions for model (4) are:

$$\begin{cases}
Y_1(t = 0, x, y) = 0.1, \\
Y_2(t = 0, x, y) = 0.04, \\
Y_3(t = 0, x, y) = 0.01, \\
\mathbf{u}_1(t = 0, x, y) = 0.2, \\
\mathbf{u}_2(t = 0, x, y) = 1 - N(x, y), \\
\mathbf{u}_3(t = 0, x, y) = N(x, y),
\end{cases}$$
(15)

Parameters	Description	Value
b	spawning rate	6
s	transfer rate from eggs to larvae	0.7
s_L	transfer rate from larvae to adult females	0.5
d	egg mortality rate	0.2
d_L	larvae mortality rate	0.2
d_m	adult female mortality rate	0.25
b_H	human birth rate	0.0000457
β_H	infection rate from human to vector	0.75
β_m	infection rate from vector to human	0.5
γ	human recovery rate	0.1428

Table 1: Values of the parameters

where N(x, y) is the probability density of the normal distribution,

$$N(x,y) = \frac{1}{\pi} e^{-((x-0.5)^2 + (y-0.5)^2)}.$$

The values of Y and u at times t = 0, t = 10 and t = 20 are given at Figures 1 and 2 respectively for surfaces and isovalues.

From Figures 1 and 2, we observe first that, in terms of time, Y_1 , Y_2 and Y_3 become larger and gradually tend to upper bounds, \mathbf{u}_1 has a very small change whereas \mathbf{u}_2 decreases rapidly and \mathbf{u}_3 first gradually increases, then gradually decreases which indicates that each member of the population typically progresses from susceptible to infectious to recovered. Then, in terms of space, Y_1 , Y_2 and Y_3 almost do not change, \mathbf{u}_1 has a very small change, \mathbf{u}_2 and \mathbf{u}_3 gradually spread and become smooth which indicates that susceptible and infected people tend to the same density at different points. These interpretations confirm that this first spatial PDE model models rather well the spread of chigungunya disease.

6 Conclusions

In this paper, an original epidemic transmission model composed of a reaction-diffusion system and ODEs is proposed. This model includes the spatial mobility of humans which is described as Brownian random motion and ignores mosquitoes mobility. Indeed, compared with humans, the displacement of mosquitoes is limited to a few meters. Then the existence and uniqueness, the positivity and the boundedness of the solution for the model are proved. We proved too that the global solution remains in the region of biological interest. Finally, we give some numerical simulations to show that this model can be well used to predict the processes of the evolution of the epidemic transmission. Our future work will consist in studying the identifiability of some parameters of this model and to propose a numerical procedure for estimating them.

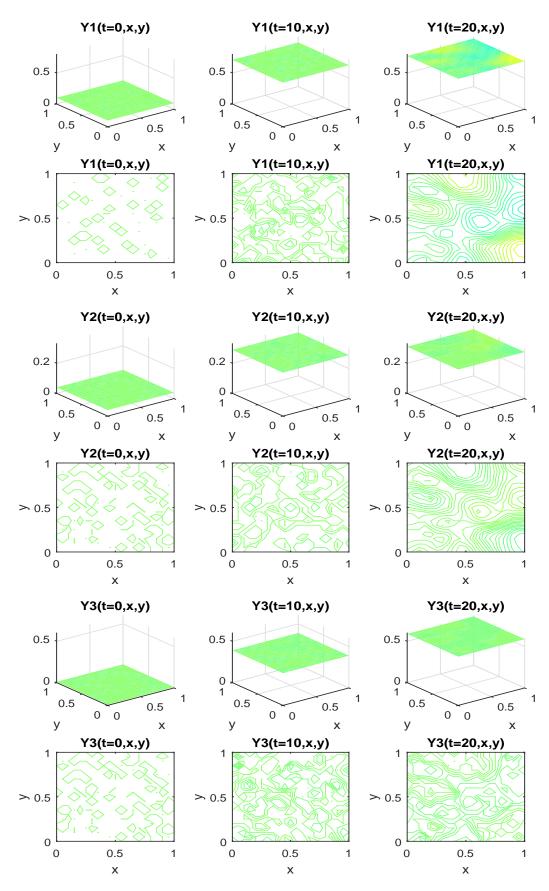


Figure 1: Values of (Y_1, Y_2, Y_3) in the domain Ω at t = 0 (left), t = 10 (mild) and t = 20 (right)

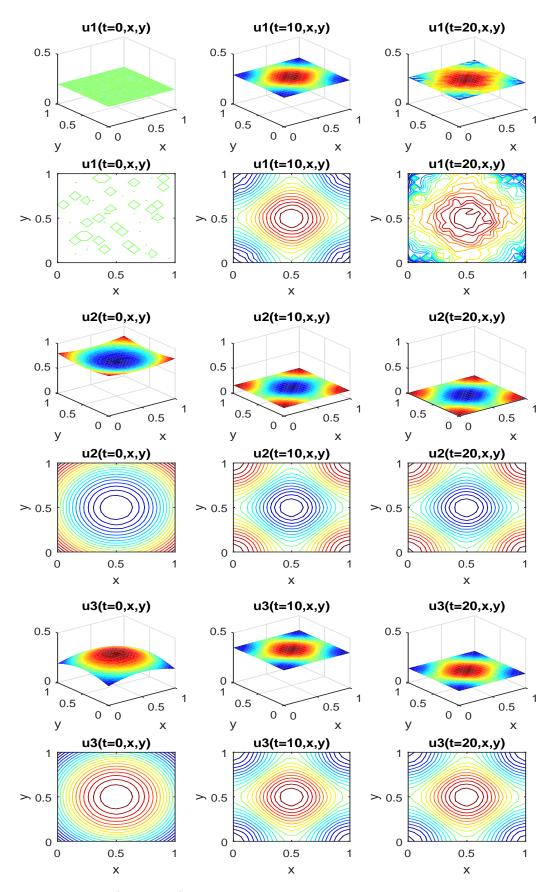


Figure 2: Values of $(\mathbf{u}_1, \mathbf{u}_2, \mathbf{u}_3)$ in the domain Ω at t = 0 (left), t = 10 (mild) and t = 20 (right)

References

- W. Abid, R. Yafia, M. Aziz-Alaoui, H. Bouhafa, A. Abichou, "Diffusion driven instability and hopf bifurcation in spatial predator-prey model on a circular domain", *Applied Mathematics and Computation*, vol. 260, pp. 292-313, 2015.
- [2] Y. Dumont, F. Chiroleu, C. Domerg, "On a temporal model for the Chikungunya disease: Modeling, theory and numerics", *Mathematical biosciences*, vol. 213 (1), pp. 80-91, 2008.
- [3] Z. Feng, J. X. Velasco-Hernández, "Competitive exclusion in a vector-host model for the dengue fever", *Journal of mathematical biology*, vol. 35 (5), pp. 523-544, 1997.
- [4] H. W. Hethcote, "The mathematics of infectious diseases", SIAM review, vol. 42 (4), pp. 599-653, 2000.
- [5] P. Howard, Partial Differential Equations in MATLAB 7.0, 2010.
- [6] S. Iwami, Y. Takeuchi, X. Liu, "Avian-human influenza epidemic model", *Mathematical biosciences*, vol. 207 (1), pp. 1-25, 2007.
- [7] A. Lunardi, *Analytic semigroups and optimal regularity in parabolic problems*, Springer Science & Business Media, 2012.
- [8] A. M. Lutambi, M. A. Penny, T. Smith, N. Chitnis, "Mathematical modelling of mosquito dispersal in a heterogeneous environment", *Mathematical biosciences*, vol. 241 (2), pp. 198-216, 2013.
- [9] D. Moulay, M. Aziz-Alaoui, M. Cadivel, "The chikungunya disease: modeling, vector and transmission global dynamics", *Mathematical biosciences*, vol. 229 (1), pp. 50-63, 2011.
- [10] D. Moulay, M. Aziz-Alaoui, H.-D. Kwon, "Optimal control of chikungunya disease: larvae reduction, treatment and prevention", *Mathematical Biosciences and Engineering*, vol. 9 (2), pp. 369-392, 2012.
- [11] D. Moulay, Y. Pigné, "A metapopulation model for chikungunya including populations mobility on a large-scale network", *Journal of theoretical biology*, vol. 318, pp. 129-139, 2013.
- [12] J. D. Murray, Mathematical Biology I: An Introduction, Springer, 2002.
- [13] A. Pazy, *Semigroups of linear operators and applications to partial differential equations*, Vol. 44, Springer Science & Business Media, 2012.
- [14] J. Prüss, R. Zacher, R. Schnaubelt, "Global asymptotic stability of equilibria in models for virus dynamics", *Mathematical Modelling of Natural Phenomena*, vol. 3 (07), pp. 126-142, 2008.
- [15] P. Reiter, D. Fontenille, C. Paupy, "Aedes albopictus as an epidemic vector of chikungunya virus: another emerging problem?", *The Lancet infectious diseases*, vol. 6 (8), pp. 463-464, 2006.
- [16] S. Zhu, L. Denis-Vidal, N. Verdière, "Identifiability study in a model describing the propagation of the chikungunya to the human population", *MOSIM 2014, 10ème Conférence Francophone de Modélisation, Optimisation et Simulation,* 2014.