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ABSTRACT : *In the last years, several epidemics have been reported in particular the chikungunya epidemic on the Réunion Island. For predicting its possible evolution, new models describing the transmission of the chikungunya to the human population have been proposed and studied in the literature. In such models, some parameters are not directely accessible from experiments and for estimating them, iterative algorithms can be used. However, before searching for their values, it is essential to verify the identifiability of models parameters to assess wether the set of unknown parameters can be uniquely determined from the data. Thus, identifiability is particularly important in modeling. Indeed, if the model is not identifiable, numerical procedures can fail and in that case, some supplementary data have to be added or the set of admissible data has to be reduced. Thus, this paper proposes to study the identifiability of the proposed models by (Moulay, Aziz-Alaoui & Cadivel 2011).*

KEY WORDS : *Identifiability, Nonlinear models, Epidemiologic model, Chikungunya virus.*

1 Introduction

The *chikungunya* virus is a vector-borne disease transmitted by mosquitoes of *Aedes* genus. Several epidemics of this tropical disease have been reported this last 50 years. Recently an unprecedented epidemic has been observed in the Réunion island (a French island in the Indian Ocean) in 2005-2006 where one third of the total population has been infected. A pic of 40 000 infected per week has been reached in february 2006. An other *chikungunya* epidemic has been reported in Italy in 2007. It was the first time that such disease is observed in a non tropical region. The responsible vector of these two epidemics is identified: the *Aedes Albopictus* mosquito (Reiter, Fontenille & Paupy 2006). Contrary to *Aedes Aegipty*, the main vector of Dengue, which also transmits the chikungunya virus, *Aedes Albopictus* has developed capabilities to adapt to non tropical region. Chikungunya is now a major health problem. European health authorities are now strongly engaged in the control of this disease. Since there is no vaccine nor specific treatment, efforts are mostly directed towards prevention measures and the control of mosquito proliferation. Since these events, several works and models are proposed to try to understand their emergence or re-emergence. Various fields of research are concerned, such as epidemiology, biology, medicine or mathematics. For instance, Dengue, a vector borne disease mainly transmitted by *Aedes Aegipy* mosquitoes was the subject of several studies (Esteva & Vargas 1999, Esteva & Vargas 1998).
Models for the chikungunya virus have been recently proposed (Dumont, Chiroleu & Domerg 2008), (Moulay, Aziz-Alaoui & Cadivel 2011).... Since the models are recent, the not well-known parameters have not yet been studied. In this paper, we propose to take again the models proposed by (Moulay, Aziz-Alaoui & Cadivel 2011) and to do an identifiability study. In their paper, the models are uncontrolled and can be described in a general state-space form:

$$\Gamma^\theta = \begin{cases} \dot{x}(t,\theta) = f(x(t,\theta)), \\ y(t,\theta) = h(x(t,\theta),\theta). \end{cases} \quad (1)$$

Here $x(t,\theta) \in \mathbb{R}^n$ and $y(t,\theta) \in \mathbb{R}^m$ denote the state variables and the measured outputs, respectively and $\theta \in \mathcal{U}_p$ the unknown parameters vector ($\mathcal{U}_p$ is an open subset in $\mathbb{R}^p$). The functions $f(.,\theta)$ and $h(.,\theta)$ are real, rational and analytic for every $\theta \in \mathcal{U}_p$ on M (a connected open subset of $\mathbb{R}^n$ such that $x(t,\theta) \in M$ for every $\theta \in \mathcal{U}_p$ and every $t \in [0,T]$).
The identifiability definition of the uncontrolled model Γ^θ is the following:

Definition 1.1. *The model Γ^θ is globally identifiable at $\theta \in \mathcal{U}_p$ if there exists a finite time $t_1 > 0$ such that if $y(t,\theta) = y(t,\bar{\theta})$ ($\bar{\theta} \in \mathcal{U}_p$) for all $t \in [0,t_1]$ then $\bar{\theta} = \theta$.*
The model Γ^θ is locally identifiable at $\theta \in \mathcal{U}_p$ if there exists an open neighborhood W of θ such that Γ^θ is

globally identifiable at θ with $\mathcal{U}_\theta$ restricted to W.

The identifiability of models has been extensively studied (Ljung & Glad 1994), (Vajda, Godfrey & Rabitz 1989), (Verdière, Denis-Vidal, Joly-Blanchard & Domurado 2005) and different approaches have been proposed for studying the global identifiability of nonlinear systems. We can mention for example, the Taylor Series approach of (Pohjanpalo 1978). He proposed a method based on the analysis of a power series expansion of the output which gives rise to an algebraic system constituted of an infinite number of equations. A second method is based on the local state isomorphism theorem ((Walter & Lecourtier 1982), (Chappell & Godfrey 1992), (Denis-Vidal, Joly-Blanchard & Noiret 2001), (Chapman, Godfrey, Chappell & Evans 2003)). It leads to study the solution of a specific set of differential partial equations. A third one is a method based on differential algebra that was introduced by (M. Fliess 1993), (Ljung & Glad 1994) and (Ollivier 1997). It allows one to obtain relations linking the observations, the inputs and the unknown parameters of the system. These relations can be used to obtain a first estimation of the unknown parameters without *a priori* any knowledge of them (Verdière et al. 2005). It is the latter method which will be used in this paper for studying the models identifiability.

The paper is organized as follows. In the second section, models describing the transmission of the chikungunya virus to human population are presented. Some results obtained in (Moulay, Aziz-Alaoui & Cadivel 2011) will be recalled since they will give us first, the framework of our study then, the steps to study the identifiability of the not well-known parameters. In the third section, the identifiability results are given.

2 Presentation of the models

In (Bacaër 2007) the author formulate several methods to compute the basic reproduction number for epidemiological models. One of the first models describing the *chikungunya* transmission virus using SI-SIR type models is proposed. Moreover, some biological parameter values are given. An other approach is describe in (Dumont et al. 2008), where a global aquatic stage for the mosquito dynamics supplements a classical transmission model. In (Dumont & Chiroleu 2010), authors formulate an ordinary differential equation system to study control of *chikunugunya* virus using mechanical and chemical tools. In (Moulay, Aziz-Alaoui & Kwon 2011), control efforts are taken into account through the formulation of an optimal control problem, where the objective is to control the mosquito proliferation and limit the number of human and mosquito infection. This papers deal with the Réunion Island epidemic.

Our model given in (Moulay, Aziz-Alaoui & Cadivel 2011, Moulay, Aziz-Alaoui & Kwon 2011) takes into account the mosquito biological life cycle and describe the transmission virus to human population. For the reader convenience, we briefly recall the modeling steps. The mosquito biological life cycle consists in four stages: eggs, larvae, pupae and adults. We use a stage structured model to describe the following stages: eggs (E), larvae and pupae (L, two stages biologically close) and female adults (A, only females can transmit the virus) stages. The density variation of each stage is describe by the following scheme:

$$density\ variation = entering - (leaving + death)$$

The egg density variation is then described by the number of eggs laid by females b, by eggs becoming larvae with a transfer rate s and by eggs death with a natural mortality rate d. We assume that the number of eggs is proportional to the number of females $b(t)A(t)$, and regulated by a carrying capacity K_E since mosquitoes are able to detect the best breeding site ensuring the egg development, then $b(t) = bA(t)(1 - E(t)/K_E)$. Other stages, are described in the same way. The input in the larvae stage, given with a transfer s is also assumed to be regulated by a carrying capacity K_L which characterizes the availability of nutrients and space. The number of new larvae entering the L stage is then given by $s(t) = sE(t)(1-L(t)/K_L)$. These larvae become adult females with a transfer rate s_L. Natural deaths occur with a rate d_L, d_m for larvae and adults respectively.

This model is then included in a classical SI-SIR epidemiological model to describe the virus transmission to human population. To this aim, the adult stage A is divided into two epidemiological states: susceptible S_m and infective I_m, since mosquitoes carry the infection along their life. The human population N_H is subdivided into three stages: susceptible S_H, infected I_H and recovered (or immune) R_H. We assume that there is no vertical transmission for both humans and mosquitos. This means that human birth, with a rate b_H from susceptible, infected and removed are susceptible and eggs laid by susceptible or infected mosquitoes are susceptible. The vector infection of susceptible mosquitoes ($\bar{S}_m$) occurs during the blood meal (necessary to the female egg laying) from infectious humans ($\bar{I}_H$). The force of infection (or per-capita incidence rate among mosquitoes) given by $\beta_m \bar{I}_H/N_H$ depends on the fraction of infectious individuals $\bar{I}_H/N$ and the number of bites that would result in an infection β_m. Conversely, the *chikungunya* infection among humans occurs when suscep-

tible humans ($\bar{S}_H$) are bitten by infectious mosquitoes ($\bar{I}_m$) during blood meal. The force of infection given by ($\beta_H \bar{I}_m/A(t)$) depends on the fraction of infectious mosquitoes ($\bar{I}_m/A(t)$) and the number of bites that would result an infection β_H. Infected humans are infectious during $1/\gamma$ days, called the viremic period, and then become immune.

All previous assumptions are summed up in Fig. 1.

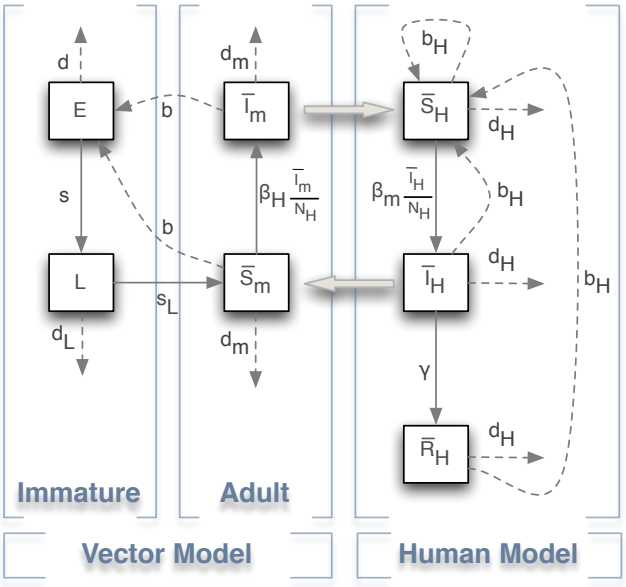

FIG. 1: Compartmental model for the dynamics of *Aedes albopictus* mosquitos and the virus transmission to human population.

Based on our model description (see Fig.1) and assumptions, we establish the following equations:

$$\begin{cases} \frac{dE}{dt}(t) &= bA(t)\left(1-\frac{E(t)}{K_E}\right) - (s+d)E(t) \\ \frac{dL}{dt}(t) &= sE(t)\left(1-\frac{L(t)}{K_L}\right) - (s_L+d_L)L(t) \\ \frac{dA}{dt}(t) &= s_L L(t) - d_m A(t) \\ \frac{d\bar{S}_m}{dt}(t) &= s_L L(t) - d_m \bar{S}_m(t) - \beta_m \frac{\bar{I}_H(t)}{N_H(t)}\bar{S}_m(t) \\ \frac{d\bar{I}_m}{dt}(t) &= \beta_m \frac{\bar{I}_H(t)}{N_H(t)}\bar{S}_m(t) - d_m \bar{I}_m(t) \\ \frac{d\bar{S}_H}{dt}(t) &= -\beta_H \frac{\bar{I}_m(t)}{A(t)}\bar{S}_H(t) - d_H \bar{S}_H(t) \\ & \quad +b_H(\bar{S}_H(t)+\bar{I}_H(t)+\bar{R}_H(t)) \\ \frac{d\bar{I}_H}{dt}(t) &= \beta_H \frac{\bar{I}_m(t)}{A(t)}\bar{S}_H(t) - \gamma \bar{I}_H(t) - d_H \bar{I}_H(t) \\ \frac{d\bar{R}_H}{dt}(t) &= \gamma \bar{I}_H(t) - d_H \bar{R}_H(t) \end{cases} \tag{2}$$

Using the following variable changes $S_m = \bar{S}_m/A$, $I_m = \bar{I}_m/A$ $S_H = \bar{S}_H/N_H$, $I_H = \bar{I}_H/N_H$ and $R_H = \bar{R}_H/N_H$ and the fact that then $S_m = 1 - I_m$ et $R_H = 1 - S_H - I_H$, system (2) reads as:

$$\begin{cases} \begin{cases} E'(t) = bA(t)\left(1-\frac{E(t)}{K_E}\right) - (s+d)E(t) \\ L'(t) = sE(t)\left(1-\frac{L(t)}{K_L}\right) - (s_L+d_L)L(t) \\ A'(t) = s_L L(t) - d_m A(t) \end{cases} & (a) \\ \begin{cases} S_H'(t) = -\left(b_H + \beta_H I_m(t)\right) S_H(t) + b_H \\ I_H'(t) = \beta_H I_m(t) S_H(t) - (\gamma + b_H) I_H(t) \\ I_m'(t) = -\left(s_L \frac{L(t)}{A(t)} + \beta_m I_H(t)\right) I_m(t) + \beta_m I_H(t) \end{cases} & (b) \end{cases} \tag{3}$$

and it is defined on $\Delta \times \Omega$ where

$$\Delta = \left\{ (E,L,A) \mid \begin{array}{l} 0 \le E \le K_E \\ 0 \le L \le K_L \\ 0 \le A \le \frac{s_L}{d_m} K_L \end{array} \right\} \tag{4}$$

and

$$\Omega = \left\{ (S_H, I_H, I_m) \in (\mathbb{R}^+)^3 \mid \begin{array}{l} 0 \le S_H + I_H \le 1 \\ 0 \le I_m \le 1 \end{array} \right\}. \tag{5}$$

The stability analysis of the model is detailed in (Moulay, Aziz-Alaoui & Cadivel 2011). We briefly recall some results about this model. The study was conducted in two steps and they will be taken again for the identifiability study. First, we analyze the mosquito dynamics in the absence of virus, which correspond to the subsystem (3a). The mosquito dynamic is governed by the following threshold:

$$r = \left(\frac{b}{s+d}\right)\left(\frac{s}{s_L+d_L}\right)\left(\frac{s_L}{d_m}\right) \tag{6}$$

obtained from computation of the equilibrium.

Theorem 2.1.

- *System (3a) always has the mosquito-free equilibrium* $(0,0,0)$*, which is globally asymptotically stable (GAS) if* $r \le 1$ *and unstable otherwise*
- *If* $r > 1$ *system (3a) has an endemic equilibrium* (E^*, L^*, A^*) *wich is GAS, where*

$$\begin{pmatrix} E^* \\ L^* \\ A^* \end{pmatrix} = \left(1 - \frac{1}{r}\right) \begin{pmatrix} \frac{K_E}{\gamma_E} \\ \frac{K_L}{\gamma_L} \\ \frac{s_L}{d_m}\frac{K_L}{\gamma_L} \end{pmatrix}$$

$$\gamma_E = 1 + \tfrac{(s+d)d_m K_E}{b s_L K_L} \quad \text{and} \quad \gamma_L = 1 + \tfrac{(s_L+d_L)K_L}{s K_E}$$

In both cases, the global stability is obtained by using Lyapunov function theory.

Now we assume $r > 1$, the biological interesting case, in order to ensure the persistence of mosquito population and we consider the subsystem (3b).

The stability of equilibrium of the transmission dynamics model is described thanks to the basic reproduction number (van den Driessche & Watmough 2002, Diekmann & Heesterbeek 2000), computed in the case $r > 1$ which is the biologically interesting case:

$$R_0 = \frac{\beta_m \beta_H}{d_m(\gamma + b_H)} \tag{7}$$

We show the following result

Theorem 2.2. *Assume $r > 1$ and let us denote (E^*, L^*, A^*) the endemic equilibrium of (3a).*

- *System (3b) always has the disease-free equilibrium $(1, 0, 0)$, which is GAS if $R_0 \leq 1$ and unstable otherwise.*
- *If $R_0 > 1$ system (3a) has an endemic equilibrium (S_H^*, I_H^*, S_m^*) which is GAS and where*

$$\begin{pmatrix} S_H^* \\ I_H^* \\ I_m^* \end{pmatrix} = \begin{pmatrix} \frac{b_H}{\beta_H + b_H} + \frac{\beta_H}{(\beta_H + b_H)R_0} \\ \frac{d_m b_H}{\beta_m(\beta_H + b_H)}(R_0 - 1) \\ \frac{b_H}{\beta_H + b_H R_0}(R_0 - 1) \end{pmatrix}$$

The first part of the theorem is obtained using Lypunov function theory. The case of the endemic equilibrium needs more study. The idea here is that the mosquito dynamic system drove the transmission dynamics. It may be assimilated to master-slave system. The coupling term is $s_L \frac{L(t)}{A(t)}$.

In order to study the equilibrium stability we consider the limit system associated to (3b) and use the result of (Vidyasagar 1980) :

Theorem 2.3. *Consider the following $\mathcal{C}^1$ system*

$$\begin{cases} \frac{dx}{dt} = f(x) \\ \frac{dy}{dt} = g(x, y), \end{cases} \tag{8}$$

with $(x, y) \in \mathbb{R}^n \times \mathbb{R}^m$. Let (x^*, y^*) be an equilibrium point. If x^* is GAS in $\mathbb{R}^n$ for the system $\frac{dx}{dt} = f(x)$ and if y^* is GAS $\mathbb{R}^n$ for the system $\frac{dy}{dt} = g(x^*, y)$, then (x^*, y^*) is (locally) asymptotically stable for system (8). Moreover, if all trajectories of (8) are forward bounded, then (x^*, y^*) is GAS for (8).

The GAS of the endemic equilibrium (S_H^*, I_H^*, S_m^*) of system (3b) where $s_L \frac{L(t)}{A(t)}$ is replaced by $s_L \frac{L^*}{A^*}$ is then shown using the theory of competitive systems (Hirsch & Smale 1974), (Hirsch 1990)(Smith 1995) and the Poincaré-Bendixson property (Thieme 1992).

3 Identifiability Analysis

Recall that the identifiability analysis of models parameters consists in assessing wether the set of unknown parameters can be uniquely determined from the data. Thus, it is essential to determine the state variables that can be considered as observable. In the case of the *chikungunya* Réunion Island epidemic, authorities have registered the average number of eggs in a number if sites. Thus, (E) can be considered as an observable variable. Furthermore, they estimate the number of new infection week by week. More generally, it seems to be realistic to assume that data about human population may be obtained. For instance, we know that the entire Réunion island before the epidemic was susceptible. Data indicating week per week new cases of the disease may be provided by the INVS (French Institute for Health Care). We know that the epidemic was declared over by April 2006. In the end the INVS counted 265,733 cases of chikungunya from March 2005 to April 2006. This represents more than 35% of the total population of the Island. That is why it seems reasonable to assume that susceptible (S_H) and infected human (I_H) are observable.
The parameters whose values are not directly accessible from the fiel are: s, s_l, K_e, K_l for the system (3a) and d_l, d_m for the system (3b). Let us recall main results in differential algebra for proving the parameters identifiability.

3.1 Differential Algebra

This method consists in eliminating unobservable state variables in order to get relations between outputs and parameters. Let us recall the methodology. The system Γ^θ is rewritten as a differential polynomial system completed with $\dot{\theta}_i = 0$, $i = 1, \ldots, p$, thus the following system composed of polynomial equations and inequalities is obtained:

$$\begin{cases} p(\dot{x}, x, \theta) = 0, \\ q(x, y, \theta) = 0, \\ r(x, y, \theta) \neq 0, \\ \dot{\theta}_i = 0,\ i = 1, \ldots, p. \end{cases} \tag{9}$$

Let us introduce some notations:

- $\mathcal{I}$ is the radical of the differential ideal generated by (9). $\mathcal{I}$, endowed with the following ranking which eliminates the states variables:

$$[\theta] \prec [y, u] \prec [x] \tag{10}$$

is assumed to admit a characteristic presentation $\mathcal{C}$ (i.e., a canonical representant of the ideal) which has the following form:

$$\Big\{\dot{\theta}_1, \dots \dot{\theta}_p, P_1(y,u,\theta), \dots, P_m(y,u,\theta), Q_1(y,u,\theta,x), \dots, Q_n(y,u,\theta,x), \} \tag{11}$$

- $\mathcal{I}_\theta$ is the radical of the differential ideal generated by (9) for the particular value of parameter θ and $\mathcal{C}_\theta$ is the characteristic presentation associated with the ranking $[y,u] \prec [x]$.
- Finally, $\mathcal{I}_\theta^{i_0}$ is the ideal obtained after eliminating state variables, the set $\mathcal{C}_\theta^{i_0} = \mathcal{C}_\theta \cap \mathbb{Q}(\theta)\{U,Y\}$ is a characteristic presentation of this ideal.
  The authors in (Denis-Vidal, Joly-Blanchard, Noiret & Petitot 2001) have given some technical conditions for having the equality $\mathcal{C}_\theta = \mathcal{C}(\theta)$. Under these assumptions, the characteristic presentation $\mathcal{C}_\theta$, that is, $\mathcal{C}_\theta^{i_0}$ of $\mathcal{I}_\theta^{i_0}$ is proved to contain the differential polynomials $P_1(y,u,\theta), \dots, P_m(y,u,\theta)$ which can be expressed as

$$P_i(y,u,\theta) = \gamma_0^i(y,u) + \sum_{k=1}^{n_i} \gamma_k^i(\theta) m_{k,i}(y,u) \tag{12}$$

  where $(\gamma_k^i)_{1\le k\le l}$ are rational in θ, $\gamma_u^i \neq \gamma_v^i$ $(u \neq v)$, $(m_{k,i})_{1\le k\le l}$ are differential polynomials with respect to y and u and $\gamma_0^i \neq 0$.

The list $\{\gamma_1^i(\theta), \dots, \gamma_{n_i}^i(\theta)\}$ is called the exhaustive summary of P_i. The size of the system is the number of observations. The identifiability analysis is based on the following proposition (Denis-Vidal, Joly-Blanchard, Noiret & Petitot 2001).

Proposition 3.1. *If for $i = 1, \dots, m$, $\triangle P_i(y,u,\theta) = \det(m_{k,i}(y,u), k = 1, \dots, n_i)$ is not in the ideal $\mathcal{I}_\theta^{i_0}$, then Γ^θ is globally identifiable at θ if and only if for every $\bar{\theta} \in \mathcal{U}_\theta$ $(\bar{\theta} \neq p)$, the characteristic presentations $\mathcal{C}_\theta^{i_0}$ and $\mathcal{C}_{\bar{\theta}}^{i_0}$ are distinct.*

For studying the identifiability of the parameters s, s_l, K_e, K_l, d_l, d_m in (3a) and (3b), the two coupled systems can be considered as a unique system in which E, S_H and I_H are supposed to be observed. However, we will take again the procedure done in (Moulay, Aziz-Alaoui & Kwon 2011) and presented in section 2, that is, decompose the identifiability analysis in two steps. Indeed, for studying the parameters of the second system it is essential to know those of the first one. Besides, our aim is to propose an identifiability study which can be used for a numerical procedure. Indeed, as it was done in (Verdière et al. 2005), the use of differential algebra gives output polynomials usable for estimating the unknown parameters.

3.2 Application to the Vector population

Since E is supposed to be observed, the equation $y = E$ is added to the sytem (3a). In using the elimination order $[y] \prec [E, L, A]$, the package diffalg of Maple gives the caracteristic presentation constituted of the three following polynomials (13):

$$\begin{aligned}
P_1 &= (-bK_e + by)A + \dot{y}K_e + K_e sy + K_e dy \\
P_2 &= (bK_e^2 s_l - 2K_e bys_l + by^2 s_l)L - K_e^2 d\dot{y} - K_e^2 s\dot{y} \\
&\quad -K_e^2 \ddot{y} + K_e \ddot{y}y - K_e^2 d_m \dot{y} - K_e^2 d_m sy - K_e^2 d_m dy \\
&\quad -K_e \dot{y}^2 + d_m K_e \dot{y}y + d_m K_e sy^2 + d_m K_e dy^2 \\
P_3 &= (K_e^3 s_l K_l d_m d + K_e^3 K_l d_l d_m s + K_e^3 K_l d_l d_m d \\
&\quad +K_e^3 s_l K_l d_m s - bK_e^3 s_l s K_l)y + (K_e^3 K_l d_l s + K_e^3 K_l d_m d \\
&\quad +K_e^3 K_l d_l d_m + K_e^3 s_l K_l d + K_e^3 s_l K_l s + K_e^3 s_l K_l d_m \\
&\quad +K_e^3 K_l d_l d + K_e^3 K_l d_m s)\dot{y} + (K_e^3 K_l d_l + K_e^3 K_l d \\
&\quad +K_e^3 K_l d_m + K_e^3 K_l s + K_e^3 s_l K_l)\ddot{y} \\
&\quad +K_l K_e^3 \dddot{y} + (3K_e^2 bs_l s K_l - 2K_e^2 s_l K_l d_m d + K_e^3 s d_m d \\
&\quad -2K_e^2 K_l d_l d_m s - 2K_e^2 K_l d_l d_m d + K_e^3 s^2 d_m - 2K_e^2 s_l K_l d_m s)y^2 \\
&\quad +(-2K_e^2 K_l d_l d_m + K_e^3 s d_m - K_e^2 K_l d_l s - K_e^2 K_l d_l d + K_e^3 s d \\
&\quad -K_l d_m K_e^2 d - K_e^2 s_l K_l s - K_e^2 s_l K_l d - 2K_e^2 s_l K_l d_m - K_l d_m K_e^2 s \\
&\quad +K_e^3 s^2)\dot{y}y + (K_e^2 K_l d_l + K_l d_m K_e^2 + 2K_e^2 K_l s + 2K_e^2 K_l d + \\
&\quad K_e^2 s_l K_l)\dot{y}^2 + (-2K_e^2 K_l d_l - 2K_l d_m K_e^2 - K_e^2 K_l s \\
&\quad -2K_e^2 s_l K_l - K_e^2 K_l d + K_e^3 s)\ddot{y}y + 3K_l K_e^2 \ddot{y}\dot{y} \\
&\quad -2K_l K_e^2 \dddot{y}y + (s_l K_l d_m K_e s - 2K_e^2 s^2 d_m - 3K_e bs_l s K_l \\
&\quad +K_l d_l d_m K_e s + s_l K_l d_m K_e d - 2K_e^2 s d_m d + K_l d_l d_m K_e d)y^3 \\
&\quad +(-K_e^2 s^2 - 2K_e^2 s d_m - K_e^2 s d + s_l K_l d_m K_e + K_l d_l d_m K_e)\dot{y} \\
&\quad y^2 + (-K_e K_l d_l + K_e^2 s - K_e s_l K_l - K_l d_m K_e)\dot{y}^2 y \\
&\quad +2K_l K_e \dot{y}^3 + (-2K_e^2 s + K_l d_m K_e + K_e K_l d_l + K_e s_l K_l)\ddot{y}y^2 \\
&\quad -3K_l K_e \ddot{y}\dot{y}y + K_l K_e \dddot{y}y^2 + (s^2 d_m K_e + s d_m K_e d \\
&\quad +bs_l s K_l)y^4 + s d_m K_e \dot{y}y^3 - sK_e \dot{y}^2 y^2 + sK_e \ddot{y}y^3.
\end{aligned} \tag{13}$$

The polynomials P_1 and P_2 used to express L and A as a function of y and the parameters of the model. The third one, P_3, links the output with the parameters: it is the output polynomial. With the function *belong_to*, we verifie that the functional determinant $\triangle(P_3)$ is not in the ideal $\mathcal{I}_\theta^{i_0}$. The exhaustive summary is constituted of 21 expressions. In using the Rosenfeld-Groebner algorithm, we obtain the identifiability of the parameters K_e, K_l, s, s_l. Thus, from the observation E, the unknown parameters can be estimated.

3.3 Application to the population Model

The third equation of (3b) links the human population to the vector population with the term $L(t)/A(t)$. According to the previous section, they can be explicitely determined from $E(t)$ thus the ratio $L(t)/A(t)$ can be considered as a known input u. As previously, in adding $y_1 = I_H$, $y_2 = S_H$ to (3b) and in considering the elimination order $[y_1, y_2, u] \prec [I_h, S_H, I_m]$, one gets for the two following output

polynomials:

$$P_4 = y_2\ddot{y}_2 - \dot{y}_2^2 + (\beta_H\beta_m + \beta_m b_H)y_1y_2^2 + s_l u y_2\dot{y}_2 \\ +s_l b_H u y_2^2 - s_l b_H u y_2 + b_H\dot{y}_2 + \beta_m y_2 y_1\dot{y}_2 - \beta_m b_H y_2 y_1$$

$$P_5 = \dot{y}_2 + \dot{y}_1 - b_H + b_H y_2 + (b_H + \gamma)y_1. \tag{14}$$

Only the polynomial P_4 contains the parameters β_H and β_m and is used for studying their identifiability. The functional determinant $\triangle P_4$ is proved not to be in the ideal $\mathcal{I}_\theta^{i_0}$. In studying the exhaustive summary of P_4, we conclude that the parameters β_H and β_m are identifable.

4 Conclusion

In this paper, the identifiability of models describing the transmission of the chikungunya virus to human population has been studied. According to the re-emergence of this virus, the chikungunya becomes a major health problem especially since the main vector has developed capabilities to adapt to non tropical region. The identifiability is an important step in the modeling. Indeed, the identifiability study enables one to know if a model is well-posed and if the unknown parameters can be assess from some observations done in the field.

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