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# Identifiability study in a model describing the propagation of the chikungunya to the human population.

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**ABSTRACT:** *In different fields of research, modeling has become an interesting tool for studying and predicting the possible evolution of a system, in particular in epidemiology. Indeed, according to the globalization of our societies and the genetic mutation of transmission vectors, several epidemics have appeared in the last years in regions not yet concerned by such a catastrophe. One can name, for example, the chikungunya epidemic on the Réunion Island in 2005-2006. In this paper, a model describing the propagation of the chikungunya to the human population is taken again from (Moulay, Aziz-Alaoui & Cadivel 2011). In such models, some parameters are not directly accessible from experiments and have to be estimated numerically from an iterative algorithm. However, before searching for their values, it is essential to verify the identifiability of model parameters to assess whether the set of unknown parameters can be uniquely determined from the data. Indeed, this study insures that numerical procedures can be successful and if the identifiability is not ensured, some supplementary data have to be added or the set of admissible data has to be reduced. A first identifiability study had been done in (Moulay, Verdière & Denis-Vidal 2012) in considering that the number of eggs can be easily counted. However, after discussing with epidemiologist searchers, it appears that it is the number of larvae that can be estimated weeks by weeks. Thus, this paper proposes to do an identifiability study with this assumption and thanks to an integration of one of the model equations, some easier equations linking the inputs, outputs and parameters are obtained permitting a simpler identifiability study.*

**KEYWORDS:** *Identifiability; Nonlinear model; Epidemiologic model; Chikungunya virus*

## 1 Introduction

Studying and understanding transmission of epidemiologic diseases have become a major issue in our modern society. Indeed, due to modern conveyances as planes and actual climate change, their transmission vectors migrate to areas that previously were not affected. One can name, for example, mosquitoes of *Aedes* genus that transmit the chikungunya virus. Until 2000, this virus was confined to African countries. However, 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, the maximum number been reached in february 2006 with 40 000 infected. More worrying is the chikungunya epidemic in Italy in 2007 since it was the first time that such disease was observed in a non tropical region. This epidemic comes from the transmission vector, the *Aedes Albopictus* (Reiter, Fontenille & Paupy 2006) that has developed capabilities to adapt to non tropical region. Moreover, some mosquitoes of this species have been seen in the south of France. 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.

It is often a difficult task to collect sufficient data in order to do a complete study of the transmission, the emergence or re-emergence of such virus. For doing this, mathematical models have been proposed in the literature associating researchers from different fields such as epidemiology, biology, medicine or mathematics. For instance, Dengue, a vector borne disease mainly transmitted by *Aedes Aegypti* mosquitoes was the subject of several studies (Esteva & Vargas 1999, Esteva & Vargas 1998). For the chikungunya virus, (Dumont, Chiroleu & Domerg 2008), (Moulay, Aziz-Alaoui & Cadivel 2011) have recently proposed models of transmission. However, to do a complete study with such models, the main issue is to estimate numerically their parameters which are sometimes inaccessible to direct measurements. Thus, some algorithms

have to be implemented such as the minimal least squares algorithm. Their principles are to estimate the parameter vector such that the corresponding trajectories heat the output data set. However, an identifiability study has to be done before doing this numerical work. Indeed, identifiability consists in insuring that the set of unknown parameters can be uniquely determined from the data. If it is not the case, one can have a local minimum corresponding to an aberrant real solution or the iterative algorithm can fail.

In this paper, we propose to consider the models proposed by (Moulay, Aziz-Alaoui & Cadivel 2011) and used in (Moulay, Verdière & Denis-Vidal 2012). In the latter paper, the authors did an identifiability study but in supposing that the number of eggs can be observed. Concretely, this assumption appears unrealistic. Indeed, in order to study the evolution of the mosquitoes number, searchers install water tanks in concerned area and study their content each week. They can only count the larvae since the eggs are too small. This assumption changes the model and the identifiability results obtained by (Moulay, Verdière & Denis-Vidal 2012) are not yet valid. Thus, we suppose, in this paper, that only larvea can be observed and we propose to do an identifiability study on the new model.

For doing this, let us consider ordinary controlled or uncontrolled dynamical systems described in a general state-space form:

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

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  $f(\cdot, \theta)$ ,  $g(\cdot, \theta)$  and  $h(\cdot, \theta)$  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  $t \in [0, T]$ ). In the case of uncontrolled system  $u$  is equal to 0.

Since the initial conditions are not considered, the solution of  $\Gamma^\theta$  may be nonunique and some solutions might be of a degenerate character. Thus, the set of nondegenerate solutions will be denoted by  $\bar{x}(t, \theta)$ , the set of corresponding outputs by  $\bar{y}(t, \theta)$ . The definition introduced by (Ljung & T. Glad 1994) is adopted here. For uncontrolled systems, one gets:

**Definition 1.1.** *The model  $\Gamma^\theta$  is globally identifiable at  $\theta \in \mathcal{U}_p$  if  $\bar{y}(\theta) \neq \emptyset$  and for any  $\bar{\theta} \in \mathcal{U}_p$ ,  $\bar{\theta} \neq \theta$ ,  $\bar{y}(\theta) \cap \bar{y}(\bar{\theta}) = \emptyset$ .*

The identifiability definition of the controlled model

$\Gamma^\theta$  is the following:

**Definition 1.2.** *The model  $\Gamma^\theta$  is globally identifiable at  $\theta \in \mathcal{U}_p$  if there exists an input  $u$ , such that  $\bar{y}(\theta, u) \neq \emptyset$  and for any  $\bar{\theta} \in \mathcal{U}_p$ ,  $\bar{\theta} \neq \theta$ ,  $\bar{y}(\theta, u) \cap \bar{y}(\bar{\theta}, u) = \emptyset$ .*

Lots of methods to prove the identifiability of a model are available in the literature. For example, (Pohjanpalo 1978), (Ljung & T. Glad 1994), (Vajda, Godfrey & Rabitz 1989), (Verdière, Denis-Vidal, Joly-Blanchard & Domurado 2005) have proposed different approaches to study the global identifiability of nonlinear systems. But, three methods emerge. The first one is the Taylor Series approach proposed by (Pohjanpalo 1978) and consists in analyzing a power series expansion of the output(s), that is  $y$  in the case of model (1). This method can lead to complex systems essentially in the case of nonlinear systems and does not permit to obtain a good estimate of the unknown parameters. 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 partial differential equations. However, it does not induce a numerical method to estimate the parameters. A third one is a method based on differential algebra introduced by (Fliess & Glad 1993), (Ljung & T. Glad 1994) and (Ollivier 1997). It allows one to obtain relations linking the observations, the inputs and the unknown parameters of the system. From them, an identifiability study is done. It is this method which will be used in this paper. As it will be seen, thanks to an integration of one of the model equations, simple relations linking input, output and parameters of the model have been obtained. Furthermore, these relations can be used to obtain a first estimation of the unknown parameters without *a priori* any knowledge of them (Verdière, Denis-Vidal & Joly-Blanchard 2005). Indeed, the next step of this work will be to estimate the unknown parameters.

The paper is organized as follows. In the second section, models describing the transmission of the chikungunya virus to human population are presented. In the third section, the identifiability results are given. A conclusion and some perspectives are proposed in the fourth section.

## 2 Presentation of the models

Susceptible Infective Removed (SIR) models consist in subdividing the concerned population in the three classes: susceptible, infective and removed and to consider the different possible interactions among

these classes as contagion processes. One of the first model describing the *chikungunya* transmission virus using SI-SIR type models was proposed by (Bacaër 2007) who formulates several methods to compute the basic reproduction number for epidemiological models. Moreover, some biological parameter values was given. Another approach was proposed by (Dumont, Chiroleu & Domerg 2008). In their paper, a global aquatic stage for the mosquito dynamics supplements a classical transmission model. In (Dumont & Chiroleu 2010), authors formulated an ordinary differential equation system to study control of *chikungunya* virus using mechanical and chemical tools. In (Moulay, Aziz-Alaoui & Kwon 2012), control efforts was taken into account through the formulation of an optimal control problem, their objective was to control the mosquito proliferation and limit the number of human and mosquito infections.

It is the model proposed by (Moulay, Aziz-Alaoui & Cadivel 2011) which is considered in this paper. Its advantage is that it takes into account the mosquito biological life cycle and describes the virus transmission to human population. The mosquito biological life cycle is decomposed in four stages: eggs, larvae, pupae and adults. A stage structured model is used to describe the following stages: eggs number ( $E$ ), larvae and pupae number ( $L$ ), two stages biologically close and female adults number ( $A$ ). Only females are considered since male can not transmit the virus. This model is then included in a classical SI-SIR epidemiological model in order 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)  $R_H$ . The authors suppose first that there is no vertical transmission for both humans and mosquitoes. It means that the disease can not be passed on the future generation. Then, they suppose that the vector infection of susceptible mosquitoes ( $\bar{S}_m$ ) occurs when biting (necessary for females lay eggs) infectious humans ( $\bar{I}_H$ ). Conversely, the chikungunya infection among humans occurs when susceptible humans ( $\bar{S}_H$ ) are bitten by infection mosquitoes ( $\bar{I}_m$ ). In order to obtain a more simple model, density rather total number is considered that is  $S_m = \bar{S}_m/A$ ,  $I_m = \bar{I}_m/A$ ,  $S_H = \bar{S}_H/N_H$ ,  $I_H = \bar{I}_H/N_H$ ,  $R_H = \bar{R}_H/N_H$ . Then, with  $S_m = 1 - I_m$  and  $R_H = 1 - S_H - I_H$ , the model does not need to consider  $S_m$  and  $R_H$ .

The model derived in (Moulay, Aziz-Alaoui & Cadivel

2011) is the following:

$$\begin{cases} \begin{cases} E'(t) = bA(t) \left(1 - \frac{E(t)}{K_E}\right) - (s + d)E(t) \\ L'(t) = sE(t) \left(1 - \frac{L(t)}{K_L}\right) - (s_L + d_L)L(t) \\ A'(t) = s_L L(t) - d_m A(t) \end{cases} & (a) \\ \begin{cases} S'_H(t) = -(b_H + \beta_H I_m(t)) S_H(t) + b_H \\ I'_H(t) = \beta_H I_m(t) S_H(t) - (\gamma + b_H) I_H(t) \\ I'_m(t) = - \left( s_L \frac{L(t)}{A(t)} + \beta_m I_H(t) \right) I_m(t) + \beta_m I_H(t) \end{cases} & (b) \end{cases} \quad (2)$$

where

- $b$  is the intrinsic rate of eggs,  $s$  (resp.  $s_L$ ) is the transfer rate between  $E$  and  $L$  (resp. between  $L$  and  $A$ ),
- $K_E$  (resp.  $K_L$ ) is the carrying capacity of  $E$  (resp. carrying capacity of  $L$ ),
- $d$ ,  $d_L$  and  $d_m$  are the rates of natural deaths for eggs, larvae and adults,
- $b_H$  the human birth,
- $\gamma$  is the transfer rate between infected humans and recovered humans,
- $\beta_H$  (resp.  $\beta_m$ ) is the infectious contact rate between susceptible humans and vectors (resp. susceptible mosquitoes and humans).

The system is defined on  $\Delta \times \Omega$  where

$$\Delta = \left\{ (E, L, A) \in (\mathbb{R}^+)^3 \mid \begin{array}{l} 0 \leq E \leq K_E \\ 0 \leq L \leq K_L \\ 0 \leq A \leq \frac{s_L}{d_m} K_L \end{array} \right\} \quad (3)$$

and

$$\Omega = \left\{ (S_H, I_H, I_m) \in (\mathbb{R}^+)^3 \mid \begin{array}{l} 0 \leq S_H + I_H \leq 1 \\ 0 \leq I_m \leq 1 \end{array} \right\}. \quad (4)$$

The stability analysis of the model is detailed in (Moulay, Aziz-Alaoui & Cadivel 2011).

### 3 Identifiability Analysis

The first step in an identifiability study is to determine the outputs, that is the observable state variables. The second one consists in applying an identifiability method, here a method based on differential algebra. If the model is identifiable, we know that the set of unknown parameters can be uniquely determined from the data. If the model is not identifiable, it means that the numerical procedure to estimate the parameters of the model can fail : it can give either no

results or a local minimum corresponding to an aberrant real solution. In order to obtain an identifiable model, another state variable must be considered as observable by the experimenter (that implies to put other experimental procedures) or assumptions on the parameters must be done.

In the case of the *chikungunya* Réunion Island epidemic, authorities have registered the average number of larvae in each cottage in putting water tanks. Thus, ( $L$ ) can be considered as an observable variable. Furthermore, they estimate the number of new infections 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 which 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 field are:  $s, s_L, K_E, K_L$  for the system (2a) and  $\beta_H, \beta_m$  for the system (2b). Let us recall the main results of identifiability in differential algebra.

### 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  $\Gamma^\theta$  is rewritten as a differential polynomial system completed with  $\dot{\theta}_i = 0, i = 1, \dots, p$ , thus the following system composed of polynomial equations and inequalities is obtained:

$$\Gamma \begin{cases} p(\dot{x}, x, u, \theta) = 0, \\ q(x, y, \theta) = 0, \\ r(x, y, \theta) \neq 0, \\ \dot{\theta}_i = 0, i = 1, \dots, p. \end{cases} \quad (5)$$

Let us introduce some notations:

- $\mathcal{I}$  is the radical of the differential ideal generated by (5).  $\mathcal{I}$ , endowed with the following ranking which eliminates the state variables:

$$[\theta] \prec [y, u] \prec [x] \quad (6)$$

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

which has the following form:

$$\{\dot{\theta}_1, \dots, \dot{\theta}_p, P_1(y, u, \theta), \dots, P_m(y, u, \theta), Q_1(y, u, \theta, x), \dots, Q_n(y, u, \theta, x)\} \quad (7)$$

$\mathcal{C}(\theta)$  will denote the particular characteristic presentation  $\mathcal{C}$  evaluated in  $\theta$ .

- $\mathcal{I}_\theta$  is the radical of the differential ideal generated by (5) for the particular value of parameter  $\theta$  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 and the set  $\mathcal{C}_\theta^{i_0} = \mathcal{C}_\theta \cap \mathbb{Q}(\theta)\{U, Y\}$  is a characteristic presentation of this ideal.

The following proposition whose a proof can be found in (Noiret 2000) gives a necessary and sufficient condition in order to have the global identifiability.

**Proposition 3.1.** *If the system  $\Gamma$  does not admit non generic solution then the model is globally identifiable if and only if for all  $\bar{\theta} \in \mathcal{U}_p$ ,*

$$\mathcal{C}_\theta^{i_0} = \mathcal{C}_{\bar{\theta}}^{i_0} \Rightarrow \theta = \bar{\theta}.$$

This proposition is difficult to verify since the initial system should be evaluated in every parameter value as the associated characteristic presentation  $\mathcal{C}_\theta^{i_0}$ . The authors in (Noiret 2000) 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  $P_1(y, u, \theta), \dots, P_m(y, u, \theta)$ . The latter give the relations between input-output and parameters and can be expressed as

$$P_i(y, u, \theta) = \gamma_0^i(y, u) + \sum_{k=1}^{n_i} \gamma_k^i(\theta) m_{k,i}(y, u) \quad (8)$$

where  $(\gamma_k^i)_{1 \leq k \leq n_i}$  are rational in  $\theta$ ,  $\gamma_u^i \neq \gamma_v^i$  ( $u \neq v$ ),  $(m_{k,i})_{1 \leq k \leq n_i}$  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  $P_i$  and the polynomials  $P_i$  are called the input-output polynomials. The size of the system is the number of observations. The identifiability analysis is based on the following proposition (Denis-Vidal, Joly-Blanchard & Noiret 2001).

**Proposition 3.2.** *If for  $i = 1, \dots, m$ ,  $\Delta P_i(y, u, \theta) = \det(m_{k,i}(y, u), k = 1, \dots, n_i)$  is not in the ideal  $\mathcal{I}_\theta^{i_0}$ , then  $\Gamma^\theta$  is globally identifiable at  $\theta$  if and only if for every  $\bar{\theta} \in \mathcal{U}_p$  ( $\bar{\theta} \neq \theta$ ), the characteristic presentations  $\mathcal{C}_\theta^{i_0}$  and  $\mathcal{C}_{\bar{\theta}}^{i_0}$  are distinct.*

The function *belongs\_to* in Maple allows us to verify that the functional determinant does not vanish on the zeros of the radical differential ideal generated by  $\Gamma$ . Under this assumption, for proving that the model is globally identifiable, it is sufficient to verify for  $i = 1, \dots, m$  and  $k = 1, \dots, n_i$ :

$$\gamma_k^i(\theta) = \gamma_k^i(\bar{\theta}) \Rightarrow \theta = \bar{\theta}.$$

This work will be done in using the Rosenfeld-Groebner algorithm in the package Ddiffalg of Maple. To study the identifiability of the parameters  $s, s_L, K_E, K_L, \beta_L, \beta_m$  in (2a) and (2b), the two coupled systems can be considered as a unique system in which  $L, S_H$  and  $I_H$  are supposed to be observed. However, we will take again the procedure done in (Moulay, Verdière & Denis-Vidal 2012). Indeed, they study, first the mosquito model, then the human model. This procedure will permit to identify, first,  $s, s_L, K_E, K_L$ . Once these parameters known, model (2a) is well determined. Thus, the rational function  $L(t)/A(t)$ , which intervenes in (2b) can be considered as an input and an identifiability study can be done on  $s$  and  $s_L$ . Besides, this procedure can be easily put in form in order to do a parameter estimation. Recall that the use of differential algebra (Verdière et al. 2005) gives input-output polynomials that can be used to estimate the unknown parameters without *a priori* any knowledge of them.

### 3.2 Application to the Vector population

In order to obtain the input-output polynomials, we add  $y_1 = L$  to system (2a) and use the package ddiffalg of Maple with the elimination order  $[y_1] \prec [A, E, L]$ . Unfortunately, the exhaustive summary is constituted of 36 expressions, thus its study is difficult. Furthermore, derivatives of order 3 of  $y_1$ , that is  $L$ , appear in the input-output polynomial such that it will be difficult to use it for doing a parameter estimation. It would be better if this polynomial that will be used for parameter estimation is simple enough. For this reason, we will transform system (2a) by integrating its third equation. This integration leads us to let  $w(t) = e^{-d_m t}$ ,  $v(t) = e^{-d_m t} \int_0^t L(s) e^{d_m s} ds$  and  $A_0$ , the initial condition of  $A$ . Assume too that  $K_L = K_E/2$  ((Moulay, Aziz-Alaoui & Kwon 2012)). System (2a) can also be rewritten:

$$\left\{ \begin{array}{l} \left\{ \begin{array}{l} E'(t) = bA(t)\left(1 - \frac{E(t)}{K_E}\right) - (s + d)E(t) \\ L'(t) = sE(t)\left(1 - \frac{2L(t)}{K_E}\right) - (s_L + d_L)L(t) \\ A(t) = A_0w(t) + s_Lv(t) \\ v'(t) = L(t) - d_mv(t) \end{array} \right. \quad (a') \\ \left\{ \begin{array}{l} w'(t) = -d_mw(t) \\ S'_H(t) = -(b_H + \beta_H I_m(t))S_H(t) + b_H \\ I'_H(t) = \beta_H I_m(t)S_H(t) - (\gamma + b_H)I_H(t) \\ I'_m(t) = -(s_L \frac{L(t)}{A(t)} + \beta_m I_H(t))I_m(t) + \\ \beta_m I_H(t) \end{array} \right. \quad (b') \end{array} \right.$$

System (2) and System (9) are equivalent, and the stability analysis of the model (9) is the same as the model (2).

Since  $L$  is supposed to be observed,  $w$  and  $v$  can be calculated and equations  $y_1 = L$ ,  $y_2 = v$  and  $y_3 = w$  are added to system (9a'). With (9a'), the package ddiffalg of Maple with the elimination order  $[y_1, y_2, y_3] \prec [A, E, L, v, w]$  gives the characteristic presentation constituted of the following polynomials:

$$P_1 = -A_0y_3 - s_Ly_2 + A,$$

$$P_2 = -K_e s E + (K_e d_l + K_e s_l + 2sE)y_1 + K_e \dot{y}_1,$$

$$\begin{aligned} P_3 = & A_0 K_e^2 b s y_3 + K_e^2 b s s_l y_2 - \\ & K_e (b d_l s_l + 4b s s_l + b s_l^2) y_2 y_1 - \\ & K_e^2 (d d_l + d s_l + d_l s + s s_l) y_1 - \\ & K_e (A_0 b d_l + 4A_0 b s + A_0 b s_l) y_3 y_1 - \\ & K_e^2 (d + d_l + s + s_l) \dot{y}_1 - \\ & K_e b s_l y_2 \dot{y}_1 - A_0 K_e b y_3 \dot{y}_1 - K_e^2 \ddot{y}_1 + \\ & 2(b d_l s_l + 2b s s_l + b s_l^2) y_2 y_1^2 + \\ & 2(A_0 b d_l + 2A_0 b s + A_0 b s_l) y_3 y_1^2 + \\ & 2K_e (d d_l + d s_l + d_l s + s s_l) y_1^2 + \\ & 2b s_l y_2 \dot{y}_1 y_1 + 2K_e (d + s) \dot{y}_1 y_1 + \\ & 2A_0 b y_3 \dot{y}_1 y_1 - 2K_e (\dot{y}_1^2 - \ddot{y}_1 y_1), \end{aligned}$$

$$P_4 = d_m y_2 + \dot{y}_2 - y_1.$$

$$P_5 = d_m y_3 + \dot{y}_3.$$

The polynomials  $P_1, P_2$  permit to express  $E$  and  $A$  from  $y_1, y_2$  and the parameters of the model. The polynomials  $P_4, P_5$  are input-output polynomials which contain no parameters. The third one,  $P_3$ , is an input-output polynomial and links the outputs with the parameters. The polynomial  $\tilde{P}_3 = \frac{P_3}{K_e}$  is considered in order to obtain an expression of the form (8). With the function *belongs\_to*, we verify that the functional determinant  $\Delta \tilde{P}_3$  is not in the ideal  $\mathcal{I}_\theta^{i_0}$ . The exhaustive summary is constituted of 15 expressions. In using the Rosenfeld-Groebner algorithm, we obtain the identifiability of the parameters  $s, s_L, K_E, K_L$  and  $A_0$ . Finally, from the observation  $L$  and by using  $\tilde{P}_3$ , the unknown parameters  $s, s_L, K_E, K_L$  and  $A_0$  can be estimated.

Compared with the system (2a), system (9a') has the following advantages:

1. The list of the exhaustive summary obtained with system (9a') is shorter than the one obtained with system (2a). The first list contains 15 expressions contrary to the second one which contains 36 expressions.

2. The higher order derivative of  $y_1 = L$  in  $\tilde{P}_3$  is lower than in the corresponding polynomial obtained with system (2a). Indeed, the latter contains derivatives of order 3 while  $\tilde{P}_3$  contains only two expressions of derivatives of order 2. Numerically, estimating derivatives of order 3 can be a difficult task so  $\tilde{P}_3$  is more adapted for doing a parameter estimation.
3. The initial condition  $A_0$  for female adults can be estimated which is an interesting information.

### 3.3 Application to the population Model

The third equation of (9b') links the human population to the vector population with the term  $L(t)/A(t)$ . According to the previous section,  $A(t)$  and  $L(t)$  are known. Thus  $L(t)/A(t)$  can be considered as a known input  $u$ . As previously, in adding  $y_1 = I_H$ ,  $y_2 = S_H$  to (9b') and in considering the elimination order  $[y_1, y_2, u] \prec [I_H, S_H, I_m]$ , one gets for the following output polynomials:

$$P_6 = -b_H s_I u y_2 + b_H \dot{y}_2 + b_H s_I u y_2^2 + s_I u \dot{y}_2 y_2 - \dot{y}_2^2 + \ddot{y}_2 y_2 - b_H \beta_m y_1 y_2 + (b_H \beta_m + \beta_H \beta_m) y_1 y_2^2 + \beta_m y_1 \dot{y}_2 y_2,$$

$$P_7 = -b_H + (\beta_H I_m + b_H) y_2 + \dot{y}_2,$$

$$P_8 = -b_H + b_H y_2 + \dot{y}_2 + (\gamma + b_H) y_1 + \dot{y}_1.$$

Only the polynomial  $P_6$  contains the parameters  $\beta_H$  and  $\beta_m$  and is used to study the identifiability of the model with respect these two parameters. The polynomial  $P_6$  is of the form (8). The functional determinant  $\Delta P_6$  is proved not to be in the ideal  $\mathcal{I}_\theta^{i_0}$ . In studying the exhaustive summary of  $P_6$ , we conclude that the parameters  $\beta_H$  and  $\beta_m$  are identifiable. From this identifiability result, a numerical procedure may be implemented in order to estimate uniquely the unknown parameters of the model from the data. The value of the parameters may differ according to the study site since their estimation depends on the data, in particular on the number of observed larvae or on human population. Once their estimation done, the model is well defined and can be used to better apprehend the evolution of the epidemic on a specific site or to improve results in the control study of the chikungunya disease presented in (Moulay, Aziz-Alaoui & Kwon 2012) for example.

## 4 Conclusion

In this paper, we have done an identifiability study of models describing the transmission of the chikungunya virus to human population in supposing, among other, that the number of mosquitoes larvae

are observed. For doing this, a differential algebra method has been used and thanks to an integration of one of the equations, simpler input-output polynomials has been obtained, hence an easier identifiability study. Furthermore, since only derivatives of order two appear in this polynomial, a numerical procedure in order to estimate the unknown parameters may be implemented and this will be the following step of this work.

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