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Research Article

Parameter Estimation of Chikungunya in the Case of Incomplete Information about Its Model

Feranmi E Olayiwola*, Michael Y Shatalov, Samuel A Surulere

Department of Mathematics and Statistics, Tshwane University of Technology, Pretoria, ZA, 0081 South Africa
E-mail: salawuferanmi@gmail.com

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Abstract: This paper presents solutions to the problem of parameter estimation of mathematical model of Chikungunya with incomplete information about the model parameters. The process involves finding a set of unknown parameters from the given model such that the behavior of the predicted system reflects the original behavior (measurement) using the same scientific assumptions. To achieve this, we solve the differential equations which describe the relation between unknown functions and their derivatives using the fundamental theorem of ordinary differential equation (ODE) (i.e., the theorem of existence) to obtain solutions for the initial value problems. The solutions to the ODE give unknown parameters which functionally depend on the original unknown parameters. And these parameters have two constraints between them. We further find solutions to the constraints minimization problem to obtain estimations of a-parameters. But, the method of constraint minimization problem stipulates the ill-conditioned problem and makes it impossible to accurately identify a-parameters. It is necessary therefore to formulate the goal function using the Least squares method to determine the unknown parameters. This method works reliably well and converges at a large interval of initial guess values of parameters.

Keywords: mathematical modeling, parameter estimation, differential equation, least squares, initial value problem, numerical differentiation, numerical integration

MSC: 92D25, 34A12, 65D25, 65D30, 65D10

1. Introduction

More than 17% of all infectious diseases are considered to be vector-borne diseases. These vector-borne diseases are human illnesses caused by parasites, viruses and bacteria that are transmitted by vectors [1]. Fleas, ticks and mosquitoes are vectors which spread the pathogens that cause illness. Malaria being a parasitic infection is transmitted by Anopheles mosquitoes with an estimated 350-500 million cases occurring yearly [2]. Each year, over 500 million people suffer clinical malaria episodes caused by P.falciparum infection alone, resulting in a conservative estimate of 1 million deaths annually [2, 3]. Chikungunya on the other hand is a viral disease spread to humans by Aedes albopictus or Aedes aegypti mosquitoes [4]. This mosquito-borne viral disease caused by Chikungunya virus (CHIKV) has its origin traced to Tanzania in 1952, where from a word in the Kimakonde language, the name Chikungunya was derived which means “that which bends” [5]. The noticeable symptoms of a Chikungunya virus infection includes headache, fever, severe joint pain, nausea,

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fatigue and muscle pain which last for 2-7 days [6–8]. Subsequently, the CHIKV has been identified in other Africa and Asia countries. For instance, in Kenya during a severe outbreak of Chikungunya disease in 2004, about 13,500 lives were lost [9]. Another example is Southern Asia and India near adjoining continents and Islands of the Indian Ocean with the established populations of Aedes albopictus or Aedes aegypti mosquitoes [10]. Vector-borne diseases have become a threat to many countries especially countries where there is poor water storage and sanitation; no public awareness that can reduce the spread of the disease and no access to management technologies [11].

The distribution of vector-borne diseases is influenced by climatic factors, majorly high and low temperature extremes and precipitation patterns putting large risk on travelers [12, 13]. Different aspects of the spread of Chikungunya disease and behavior have been studied in many literature [14–18]. For example, the study of vector-borne diseases has been carried out using ODE models and reasonable insights to better our understanding of transmission and effective measure control have been provided [19, 20]. To address the problem of incomplete information which may arise due to several reasons such as incorrect measurements, equipment errors, and loss of values, this study considers a mathematical model of Chikungunya given by a system of differential equations describing human and vector populations with incomplete information about the model parameters.

Efforts have been made by various scholars to develop and analyze the mathematical model that describes the population dynamics of Chikungunya. A deterministic mathematical model was proposed in [21] for Chikungunya infection, where the authors considered that virus transmission exists between humans and mosquitoes. In their work, two infected human sub-populations designated as symptomatic and asymptomatic are used to classify the humans responsible for transmitting the virus. The results of their model yielded a close approximation of the peak incidence of the outbreak and the final epidemic size.

In [22], Wang and Liu proposed and analyzed a within-host CHIKV model which comprises four compartments namely; uninfected-monocytes (s), infected monocytes (y), free CHIKV-particles (p) and antibodies (x). This model was extended by A.M Elaiw et al. in [23, 24] where they took into consideration the general CHIKV-monocyte incidence rate with the assumption that the uninfected monocyte becomes infected by contacting CHIKV (i.e., CHIKV-to-monocyte transmission) [22–24].

Between February 2005 and August 2006, the Indian Ocean Islands experienced a large Chikungunya fever outbreak [25, 26], which included La Reunion Island since April 2005. Authors in [27] worked on estimating the Chikungunya attack rate at the upsurge of La Reunion Island by serosurveys. They found out that at the time of emergency when large seroprevalence studies can not be done, a rapid serosurvey in a targeted population can be helpful to assess the extent of epidemic.

In [28], the authors introduced differential-delay equation (DDE) models which is different from frequently used ordinary differential equation (ODE) because its derivative at any time depends on the solution at prior times. This is done for disease to reflect intra-annual fluctuations that are common in diseases spread by vectors. Additionally, they introduced the original ODE version of the Ross-MacDonald model for vector-borne diseases and modified the model by suggesting different types of naturally occurring delays. In [19], the authors proposed and investigated a mathematical model where the populations of host and mosquito are homogeneous using a system of nonlinear differential equations. They further considered a chronic sub-population of the model which helped in giving recommendations to the health institution.

Chikungunya disease, along with other infectious diseases such as dengue, cholera, diphtheria, plague, yellow fever, tuberculosis, HIV/AIDS, typhoid, and influenza, has been a subject of analysis and simulation using mathematical models in various research studies. In [29–31], a mathematical model was developed for typhoid disease, incorporating different interventions aimed at controlling the spread of the disease and reducing infection risk, with treatment being the predominant intervention used.

Additionally, authors in [32–35] conducted a study on dengue fever epidemiology using a mathematical model, which compared deterministic and stochastic modeling frameworks. The focus of their research was on optimizing interventions to prevent disease outbreaks, aiming to identify solutions to optimization problems in dynamic systems, such as infections and deaths.

In this paper, our aim is to solve the problem of complete parameter estimation of the Chikungunya mathematical model [19] in the presence of incomplete information about healthy and ill human populations and the mosquito populations. The model describes interaction between the susceptible, exposed, infected, recovered, chronically infected (SEIRC) human population and susceptible, exposed, infected (SEI) mosquito vector. Hence, the model is characterized by eight functions depending on time and connected between each other by the system of eight nonlinear ordinary differential equations. In the frame of this model, the growth rate of the susceptible human population is increasing proportionally to the existing human population and decreases proportionally to the product of the susceptible human population and relative infected mosquito vector. The rate of growth of the exposed human population increases proportionally to the product of the susceptible human population and relative infected mosquito vector with the same coefficient of proportionality and decreases proportionally to the susceptible human population including their transfer to the group of infected human population. The rate of growth of the infected human population increases proportionally to the exposed human population with the same coefficient of proportionality and decreases proportionally to the infected human population including their transfer to the group of recovered human population. The rate of growth of the recovered human population increases proportionally to the infected human population with the same coefficient of proportionality and decreases proportionally to the recovered human population including their transfer to the group of chronically infected human population.

This model can describe either constant or exponentially increasing or exponentially decaying total human population on a limited time interval. Furthermore, the present model describes the dynamics of mosquito population interacting with the human population. In the frame of this model, the rate of growth of the susceptible mosquitoes increases proportionally to their total population and decreases proportionally to the susceptible mosquito vector and product of the susceptible mosquito population and relative infected human population. The rate of growth of the exposed mosquito population increases proportionally to the product of the susceptible mosquito population and relative infected human population with the same coefficient of proportionality and decreases proportionally to the susceptible mosquito population including their transfer to the group of infected mosquito vectors. The infected mosquito rate increases proportionally to the exposed population with the same factor and decreases proportionally to the infected one. This model can also describe either constant or exponentially increasing or exponentially decaying total mosquito population on a limited time interval.

The solution to the problem of parameter determination in the case of incomplete information about human and mosquito populations is based on the assumption that: it is enough to know the total populations of human and mosquito vectors, and susceptible human and infected mosquitoes at discrete time instants. Moreover, only initial and terminal values of other human (exposed, infected, recovered, chronically infected) and mosquitoes (susceptible, exposed) populations are necessary for determination of all parameters. Knowing parameters and initial conditions of humans and mosquitoes, one can solve the initial value problem and restore the unknown populations on the given time interval. Hence, the problem of complete identification of the system in the case of incomplete information is solved. The theoretical results in this paper are supported by numerical simulations carried out using the adaptive Runge-Kutta 4 method which is built in software Mathcad 15.

2. Mathematical model

Let us consider the mathematical model of Chikungunya which was introduced by Gonzalez-Parra et al. [19], with the first five equations of system (1) describing the dynamics of the human population with total population $N_h(t)$ and the last three equations of system (1) describes the dynamics of the mosquito vector with the total population $N_v(t)$.

$$\frac{dS_h(t)}{dt} = \mu_h \cdot N_h(t) - S_h(t) \cdot \left[d_h + \beta_1 \cdot \frac{I_v(t)}{N_v(t)} \right],$$

$$\frac{dE_h(t)}{dt} = \beta_1 \cdot \frac{I_v(t)}{N_v(t)} \cdot S_h(t) - (d_h + \alpha) \cdot E_h(t),$$

$$
\begin{aligned}
\frac{dI_h(t)}{dt} &= \alpha \cdot E_h(t) - (d_h + \gamma) \cdot I_h(t), \\
\frac{dR_h(t)}{dt} &= \gamma \cdot I_h(t) - (d_h + \rho) \cdot R_h(t), \\
\frac{dC_h(t)}{dt} &= \rho \cdot R_h(t) - d_h \cdot C_h(t), \\
\frac{dS_v(t)}{dt} &= \mu_v \cdot N_v(t) - S_v(t) \cdot \left[d_v + \beta_2 \cdot \frac{I_h(t)}{N_h(t)} \right], \\
\frac{dE_v(t)}{dt} &= \beta_2 \cdot \frac{I_h(t)}{N_h(t)} \cdot S_v(t) - (d_v + \phi) \cdot E_v(t), \\
\frac{dI_v(t)}{dt} &= \phi \cdot E_v(t) - d_v \cdot I_v(t).
\end{aligned}
\tag{1}
$$

where, functions and parameters in equations of system (1) are described in Table 1.

Table 1. Description of the model parameters

Parameters	Description
$S_h(t)$	Susceptible human population
$E_h(t)$	Exposed humans population
$I_h(t)$	Infected humans population
$R_h(t)$	Recovered humans population
$C_h(t)$	Chronically infected humans population
$S_v(t)$	Susceptible mosquitoes vector
$E_v(t)$	Exposed (latent) mosquitoes vector
$I_v(t)$	Infected mosquitoes vector
μ_h	The birth rate of humans
μ_v	The birth rate of mosquitoes
d_h	The death rate of humans
d_v	The death rate of mosquitoes
β_1	Transmission rate due to a bite of an infected mosquito from a susceptible human population to the latent sub population
β_2	Transmission rate due to a bite from an infected human to a susceptible mosquito
γ	The rate at which the infected humans recovers
ρ	The rate at which the recovered humans moves to the chronic class
α	The period between human exposure and the virus infection
ϕ	The rate at which the exposed (latent) mosquitoes becomes infected mosquitoes

In this study, it is assumed that the total human population $N_h(t)$ and susceptible population $S_h(t)$ are known in $N+1$ points t_i of time interval $t_i \in [0,\ T]$, where $i = 0,\ 1,\ \cdots,\ N$ and $t_0 = 0, t_N = T$.

This is a general model which is different from the model presented in [19] because we assume that μ_h and d_h can be different (although, it can also be the same but in a particular case). Analogously, we make similar assumption about the total vector population $N_v(t)$ and infected mosquitoes vector $I_v(t)$.

Other functions are assumed to be known only at the initial and terminal points of the time interval for the human population:

$$E_h(t=0)=E_{h,\,0},\quad E_h(t=T)=E_{h,\,N},\quad I_h(t=0)=I_{h,\,0},$$

$$I_h(t=T)=I_{h,\,N},\quad R_h(t=0)=R_{h,\,0},\quad R_h(t=T)=R_{h,\,N}. \tag{2}$$

And

$$\begin{aligned} C_{h,\,0}&=N_{h,\,0}-S_{h,\,0}-E_{h,\,0}-I_{h,\,0}-R_{h,\,0},\\ C_{h,\,N}&=N_{h,\,N}-S_{h,\,N}-E_{h,\,N}-I_{h,\,N}-R_{h,\,N}. \end{aligned} \tag{3}$$

For the mosquitoes vector population:

$$\begin{aligned} &E_v(t=0)=E_{v,\,0},\quad E_v(t=T)=E_{v,\,N},\\ &S_{v,\,0}=N_{v,\,0}-I_{v,\,0}-E_{v,\,0},\quad S_{v,\,N}=N_{v,\,N}-E_{v,\,N}-I_{v,\,N}. \end{aligned} \tag{4}$$

Inside the time interval $t\in[0,\ T]$ values of $E_h(t), I_h(t), R_h(t), C_h(t), S_v(t)$ and $E_v(t)$ are assumed to be unknown. All parameters μ_h, d_h, β_1, γ, α, ρ, μ_v, d_v and ϕ are also not known. This study demonstrates that all unknown functions and parameters can be determined in the case of the above-mentioned incomplete information about the populations.

2.1 *Method of solution*

By adding the first five terms of equation (1) and equalizing them to the sum of the five corresponding terms in the right hand side, we obtain:

$$\begin{aligned} \frac{dN_h(t)}{dt}&=\frac{d\left[S_h(t)+E_h(t)+I_h(t)+R_h(t)+C_h(t)\right]}{dt},\\ &=(\mu_h-d_h)\cdot N_h(t), \end{aligned} \tag{5}$$

where, $N_h(t)$ is the total human population. It follows from equation (5) that

$$N_h(t)=N_{h,\,0}\cdot e^{(\mu_h-d_h)\cdot t}, \tag{6}$$

where, $N_{h,\,0} = N_h(t=0)$ is the initial total human population. Hence, in the given model it is possible to analyze three different scenarios of the human population dynamics:

- if $\mu_h - d_h > 0$, then $N_h(t)$ is growing exponentially,
- if $\mu_h - d_h < 0$, then $N_h(t)$ is decaying exponentially,
- if $\mu_h - d_h = 0$, then $N_h = N_{h,\,0}$ equals a constant.

Analogously, adding both left and right hand sides of the last three equations of system (1) we obtain:

$$\begin{aligned} \frac{dN_v(t)}{dt} &= \frac{d\left[S_v(t)+E_v(t)+I_v(t)\right]}{dt}, \\ &= (\mu_v - d_v)\cdot N_v(t), \end{aligned} \tag{7}$$

where, $N_v(t)$ is the total mosquitoes vector population. Solution of equation (7) is

$$N_v(t) = N_{v,\,0}\cdot e^{(\mu_v - d_v)\cdot t}. \tag{8}$$

Hence, in addition to the conditions of existence of the human population mentioned above, we need to add one of the three possible conditions of application of mathematical model (1):

- exponential growth of the total mosquitoes vector population if $(\mu_v > d_v)$,
- exponential decay of the total mosquitoes vector population if $(\mu_v < d_v)$,
- constant mosquitoes vector population $N_v(t) = N_{v,\,0}$ if $(\mu_v = d_v)$.

Difference $\mu_h - d_h$ in equation (6) is found from statistics about the total human population by means of the Least squares method as follows:

$$\mu_h - d_h = \frac{1}{N+1}\cdot\sum_{i=0}^{N}\ln\left(\frac{N_{h,\,i}}{N_{h,\,0}}\right). \tag{9}$$

where, $N_{h,\,i} = N_h(t_i)$.

Analogously, difference $\mu_v - d_v$ in equation (8) is found from statistics about the total mosquitoes vector population as:

$$\mu_v - d_v = \frac{1}{N+1}\cdot\sum_{i=0}^{N}\ln\left(\frac{N_{v,\,i}}{N_{v,\,0}}\right), \tag{10}$$

where, $N_{v,\,i} = N_v(t_i)$.

Both human and mosquitoes populations are normalized as follows:

$$\begin{aligned} s_h(t) &= \frac{S_h(t)}{N_h(t)}, \quad e_h(t) = \frac{E_h(t)}{N_h(t)}, \quad i_h(t) = \frac{I_h(t)}{N_h(t)}, \\ r_h(t) &= \frac{R_h(t)}{N_h(t)}, \quad c_h(t) = \frac{C_h(t)}{N_h(t)}. \end{aligned} \tag{11}$$

and

$$s_v(t) = \frac{S_v(t)}{N_v(t)}, \quad e_v(t) = \frac{E_v(t)}{N_v(t)}, \quad i_v(t) = \frac{I_v(t)}{N_v(t)}. \tag{12}$$

Hence,

$$\begin{aligned} s_h(t) + e_h(t) + i_h(t) + r_h(t) + c_h(t) &= 1, \\ s_v(t) + e_v(t) + i_v(t) &= 1. \end{aligned} \tag{13}$$

Differentiating $S_h(t) = N_h(t) \cdot s_h(t)$ with respect to time (keeping in mind equation (5)), we obtain:

$$\begin{aligned} \frac{dS_h(t)}{dt} &= \frac{ds_h(t)}{dt} \cdot N_h(t) + s_h(t) \cdot \frac{dN_h(t)}{dt}, \\ &= \frac{ds_h(t)}{dt} \cdot N_h(t) + s_h(t) \cdot (\mu_h - d_h) \cdot N_h(t). \end{aligned} \tag{14}$$

Equalizing it to the right hand side of the first equation of system (1) and using equation (11), we obtain:

$$\frac{ds_h(t)}{dt} \cdot N_h(t) + (\mu_h - d_h) \cdot s_h(t) \cdot N_h(t) = \mu_h \cdot N_h(t) - s_h(t) \cdot N_h(t) \cdot [d_h + \beta_1 \cdot i_v(t)]. \tag{15}$$

From this equation, it immediately follows that

$$\frac{ds_h(t)}{dt} = \mu_h \cdot [1 - s_h(t)] - \beta_1 \cdot i_v(t) \cdot s_h(t). \tag{16}$$

Analogously, other four equations from the second to the fifth equation of system (1) can be transformed to obtain the following system:

$$\begin{aligned} \frac{ds_h(t)}{dt} &= \mu_h \cdot [1 - s_h(t)] - \beta_1 \cdot i_v(t) \cdot s_h(t), \\ \frac{de_h(t)}{dt} &= -(\mu_h + \alpha) \cdot e_h(t) + \beta_1 \cdot i_v(t) \cdot s_h(t), \\ \frac{di_h(t)}{dt} &= -(\mu_h + \gamma) \cdot i_h(t) + \alpha . e_h(t), \\ \frac{dr_h(t)}{dt} &= -(\mu_h + \rho) \cdot r_h(t) + \gamma \cdot i_h(t), \end{aligned} \tag{17}$$

$$\frac{dc_h(t)}{dt} = -\mu_h \cdot c_h(t) + \rho \cdot r_h(t).$$

By further differentiating $S_v(t) = N_v(t) \cdot s_v(t)$ and keeping in mind expression (7), we obtain

$$\begin{aligned} \frac{dS_v(t)}{dt} &= \frac{ds_v(t)}{dt} \cdot N_v(t) + s_v(t) \cdot \frac{dN_v(t)}{dt}, \\ &= \frac{ds_v(t)}{dt} \cdot N_v(t) + s_v(t) \cdot (\mu_v - d_v) \cdot N_v(t). \end{aligned} \tag{18}$$

Substituting equation (18) in the sixth equation of system (1) using (11), we obtain

$$\frac{ds_v(t)}{dt} \cdot N_v(t) + (\mu_v - d_v) \cdot s_v(t) \cdot N_v(t) = \mu_v \cdot N_v(t) - s_v(t) \cdot N_v(t) \cdot [d_v + \beta_2 \cdot i_h(t)]. \tag{19}$$

The above relationship yields the following equations:

$$\frac{ds_v(t)}{dt} = \mu_v[1 - s_v(t)] - \beta_2 \cdot i_h(t) \cdot s_v(t). \tag{20}$$

Analogously, transforming the sixth, seventh and eighth equations of system (1), we obtain system:

$$\begin{aligned} \frac{ds_v(t)}{dt} &= \mu_v[1 - s_v(t)] - \beta_2 \cdot i_h(t) \cdot s_v(t), \\ \frac{de_v(t)}{dt} &= -(\mu_v + \phi) \cdot e_v(t) + \beta_2 \cdot i_h(t) \cdot s_v(t), \\ \frac{di_v(t)}{dt} &= -\mu_v \cdot i_v(t) + \phi \cdot e_v(t). \end{aligned} \tag{21}$$

Steady-state solutions of system (17) and (21) with ($\dot{s}_h = \dot{e}_h = \dot{i}_h = \dot{r}_h = \dot{c}_h = \dot{s}_v = \dot{e}_v = \dot{i}_v = 0$) are of two sorts namely;

1. Healthy populations of the humans and mosquitoes vectors:

$$\begin{aligned} s_h^* = 1, \quad e_h^* = i_h^* = r_h^* = c_h^* = 0, \\ s_v^* = 1, \quad e_h^* = i_h^* = 0. \end{aligned} \tag{22}$$

2. Infected human and mosquitoes vector population:

$$s_h^* = \frac{A \cdot B \cdot C \cdot (\mu_v + \beta_2 \cdot i_h^*)}{\alpha \cdot \beta_1 \cdot \beta_2 \cdot \phi}, \quad e_h^* = \frac{\beta \cdot i_h^*}{\alpha}, \quad r_h^* = \frac{\gamma \cdot i_h^*}{\mu_h + \rho},$$

$$c_h^* = \frac{\rho \cdot \gamma \cdot i_h^*}{\mu_h \cdot (\mu_h + \rho)}, \quad s_v^* = \frac{\mu_v}{\mu_v + \beta_2 \cdot i_h^*}, \quad e_v^* = \frac{\mu_v \cdot \beta_2 \cdot i_h^*}{C \cdot (\mu_v + \beta_2 \cdot i_h^*)}, \quad i_v^* = \frac{\beta_2 \cdot \phi \cdot i_h^*}{C \cdot (\mu_v + \beta_2 \cdot i_h^*)}, \tag{23}$$

where, $i_h^* = \dfrac{\mu_h(1 - 1/R_0^2)}{\dfrac{A \cdot B}{\alpha} \cdot \left(1 + \dfrac{\mu_h \cdot C}{\beta_1 \cdot \phi}\right)}$, $A = \mu_h + \alpha$, $B = \mu_h + \gamma$, $C = \mu_h + \phi$ and $R_0 = \sqrt{\dfrac{\alpha \cdot \beta_1 \cdot \beta_2 \cdot \phi}{\mu_v \cdot A \cdot B \cdot C}}$ is the reproduction number.

In [19] it is proven that if $0 < R_0 < 1$, then the steady-state values (22) corresponding to healthy human and mosquito vector populations are stable. If $R_0 > 1$ then both human and mosquitoes vector populations are stable.

The steady-states of equations (17) and (21) are derived as follows; if $\dfrac{ds_h(t)}{dt} = \dfrac{de_h(t)}{dt} = \dfrac{di_h(t)}{dt} = \dfrac{dr_h(t)}{dt} = \dfrac{ds_h(t)}{dt} = 0$ and $\dfrac{ds_v(t)}{dt} = \dfrac{de_v(t)}{dt} = \dfrac{di_v(t)}{dt} = 0$, then we have the following systems of equations:

$$\begin{aligned}
&\mu_h [1 - s_h^*] - \beta_1 \cdot i_v^* \cdot s_h^* = 0,\\
&-(\mu_h + \alpha) \cdot e_h^* + \beta_1 \cdot i_v^* \cdot s_h^* = 0,\\
&-(\mu_h + \gamma) \cdot i_h^* + \alpha \cdot e_h^* = 0,\\
&-(\mu_h + \rho) \cdot r_h^* + \gamma \cdot i_h^* = 0,\\
&-\mu_h \cdot c_h^* + \rho \cdot r_h^* = 0,\\
&\mu_v [1 - s_v^*] - \beta_2 \cdot i_h^* \cdot s_v^* = 0,\\
&-(\mu_v + \phi) \cdot e_v^* + \beta_2 \cdot i_h^* \cdot s_v^* = 0,\\
&-\mu_v \cdot i_v^* + \phi \cdot e_v^* = 0.
\end{aligned} \tag{24}$$

Assume that the infected human population is non-zero ($i_h^* > 0$), we obtain from equations three and four of system (24)

$$\begin{aligned}
e_h^* &= \frac{\mu_h + \gamma}{\alpha} \cdot i_h^* = \frac{\beta}{\alpha} \cdot i_h^*,\\
r_h^* &= \frac{\gamma}{\mu_h + \rho} \cdot i_h^*.
\end{aligned} \tag{25}$$

In the original work of Gonzalez-Parra et al. [19], there were some misprints and they are corrected in this paper. The global asymptotic stabilities of the disease-free equilibrium $(1,\ 0,\ 0,\ 0,\ 0,\ 1,\ 0,\ 0)$ and endemic equilibrium $(s_h^*,\ e_h^*,\ i_h^*,\ r_h^*,\ c_h^*,\ s_v^*,\ e_v^*,\ i_v^*)$ are proven in [19]. Furthermore, the positiveness of systems (1), (17) and (21) are proven in the Appendix 4.

To determine parameter α, we need to use the second equation of system (17). Let us re-write the equation as follows:

$$\frac{de_h(t)}{dt} + (\bar{\mu}_h + \alpha) \cdot e_h(t) = \bar{\beta}_1 \cdot i_v(t) \cdot s_h(t). \tag{26}$$

The initial value problem for ODE (26) with initial conditions $t = 0$ such that $e_h(t=0) = \dfrac{E_{h,\,0}}{N_h(t=0)} = e_{h,\,0}$ has a unique solution at fixed value α. The first order differential equation given by equation (26) can be solved analytically or using integrating factor as follows:

$$e_h(t,\ \alpha) = e_{h,\,0} \cdot e^{-(\bar{\mu}_h+\alpha)t} + \bar{\beta}_1 \cdot \int_0^t e^{-(\bar{\mu}_h+\alpha)(t-\tau)} \cdot i_v(\tau) \cdot s_h(\tau) d\tau. \tag{27}$$

Parameter α is selected so that at $t = T$

$$e_h(t=T,\ \bar{\alpha}) = e_{h,\,T} = \frac{E_{h,\,T}}{N_h(t=T)}, \tag{28}$$

and solution $\bar{e}_h(t) = e_h(t,\ \bar{\alpha})$ satisfy the boundary condition at right end of the time interval $t = T$. Analogously, parameter γ can be determined from equation (17) by re-writing the equation as follows:

$$\frac{di_h(t)}{dt} + (\bar{\mu}_h + \gamma) \cdot i_h(t) = \bar{\alpha} \cdot \bar{e}_h(t). \tag{29}$$

Solving ODE (29) with initial condition $t = 0$ such that $i_h(t=0) = \dfrac{I_{h,\,0}}{N_h(t=0)} = i_{h,\,0}$ gives solution (30):

$$i_h(t,\ \gamma) = i_{h,\,0} \cdot e^{-(\bar{\mu}_h+\gamma)t} + \bar{\alpha} \cdot \int_0^t e^{-(\bar{\mu}_h+\gamma)(t-\tau)} \cdot \bar{e}_h(\tau) d\tau, \tag{30}$$

and define parameter γ so that at $t = T$

$$i_h(t=T,\ \bar{\gamma}) = i_{h,\,T} = \frac{I_{h,\,T}}{N_h(t=T)}. \tag{31}$$

Solution of $\bar{i}_h(t) = i_h(t,\ \bar{\gamma})$ satisfies both the initial and boundary conditions at $t = T$. Similarly, the fourth equation of system (17) can be written as:

$$\frac{dr_h(t)}{dt} + (\bar{\mu}_h + \rho) \cdot r_h(t) = \bar{\gamma} \cdot \bar{i}_h(t). \tag{32}$$

Solving ODE (32) with initial condition $t = 0$ such that $r_h(t = 0) = \dfrac{R_{h,\,0}}{N_h(t = 0)} = r_{h,\,0}$ gives solution (33):

$$r_h(t,\ \rho) = r_{h,\,0} \cdot e^{-(\bar{\mu}_h + \rho)t} + \bar{\gamma} \cdot \int_0^t e^{-(\bar{\mu}_h + \rho)(t-\tau)} \cdot \bar{i}_h(\tau) d\tau. \tag{33}$$

Solving equation $r_h(t = T,\ \rho) = r_{h,\,\mu} = \dfrac{R_{h,\,\mu}}{N_h(t = T)}$ with respect to ρ, we obtain estimation of parameter $\bar{\rho}$ and solution $\bar{r}_h(t) = r_h(t,\ \bar{\rho})$. Estimation of function $\bar{c}_h(t)$ is given as follows:

$$\bar{c}_h(t) = 1 - s_h(t) - \bar{e}_h(t) - \bar{i}_h(t) - \bar{r}_h(t). \tag{34}$$

Now, we need to consider how to determine parameters μ_v, ϕ and β_2 from three equations of system (21) with the assumption that $i_v(t) = \dfrac{I_v(t)}{N_v(t)}$ and its known at $t \in [0,\ T]$ whereas, functions $s_v(t)$ and $e_v(t)$ are unknown. Starting with the last equation of system (21) and solving it with respect to $e_v(t)$, we have

$$e_v(t) = \frac{\dfrac{di_v(t)}{dt} + \mu_v \cdot i_v(t)}{\phi}. \tag{35}$$

Substituting equation (35) into the second equation of system (21) we obtain:

$$\frac{d^2 i_v(t)}{dt^2} + (2\mu_v + \phi)\frac{di_v(t)}{dt} + \mu_v \cdot (\mu_v + \phi) \cdot i_v(t) - \beta_2 \cdot \phi \cdot \bar{i}_h(t) \cdot s_v(t) = 0, \tag{36}$$

where, $\bar{i}_h(t)$ is described by equation (30) at $\gamma = \bar{\gamma}$ and $s_v(t)$ is given as

$$\begin{aligned} s_v(t) &= 1 - e_v(t) - i_v(t), \\ &= 1 - \frac{\dfrac{di_v(t)}{dt} + (\mu_v + \phi) \cdot i_v(t)}{\phi}. \end{aligned} \tag{37}$$

By substituting equation (37) into equation (36), we obtain the following equation:

$$\frac{d^2 i_v(t)}{dt^2} + a_1 \cdot i_v(t) + a_2 \cdot \bar{i}_h(t) + a_3 \cdot i_v(t) \cdot \bar{i}_h(t) + a_4 \cdot \frac{di_v(t)}{dt} + a_5 \cdot \bar{i}_h(t) \cdot \frac{di_v(t)}{dt} = 0, \tag{38}$$

where, $a_1 = \mu_v \cdot (\mu_v + \phi)$, $a_2 = -\beta_2 \cdot \phi$, $a_3 = \beta_2 \cdot (\mu_v + \phi)$, $a_4 = 2\mu_v + \phi$ and $a_5 = \beta_2$ are new unknown parameters which functionally depend on the original unknown parameters μ_v, ϕ and β_2. Parameters $a_1,\ a_2,\ \ldots,\ a_5$ has two constraints between them as given below:

$$a_2 + 2a_3 - a_4 a_5 = 0,$$
$$(a_2 + a_3) \cdot a_3 - a_1 a_5^2 = 0. \tag{39}$$

After solution of the constraint minimization problem, we obtain estimation $\bar{a}_1,\ \bar{a}_2,\ \ldots,\ \bar{a}_5$ of a-parameters and further find the estimations of the original unknown parameters:

$$\bar{\mu}_v = \frac{\bar{a}_2 + \bar{a}_3}{\bar{a}_5}, \quad \bar{\phi} = \frac{\bar{a}_2}{\bar{a}_5}, \quad \bar{\beta}_2 = \bar{a}_5. \tag{40}$$

Using finite difference representation of derivative $\dfrac{di_v(t)}{dt}$, the normalized value of $\bar{e}_v(t)$ can be approximately calculated from the last equation of system (21) as follows:

$$\begin{aligned} \bar{e}_v(t_j) &= \frac{\dfrac{di_v(t)}{dt}\Big|_{t_j} + \bar{\mu}_v \cdot i_v(t_j)}{\bar{\phi}}, \\ &\cong \frac{\dfrac{i_{v,\ j+1} - i_{v,\ j-1}}{2 \cdot (t_{j+1} - t_j)} + \bar{\mu}_v \cdot i_{v,\ j}}{\bar{\phi}}, \end{aligned} \tag{41}$$

where, $j = 1,\ 2,\ \ldots,\ N-1$. Bearing in mind that $e_{v,\ 0} = e_v(t_0 = 0)$ and $e_{v,\ \mu} = e_v(t = T)$ are assumed to be known. Lastly, $\bar{s}_{v,\ j} = \bar{s}_v(t_j)$ is calculated as:

$$\begin{aligned} \bar{s}_v(t_j) &= 1 - \bar{e}_{v,\ j} - i_{v,\ j}, \\ &= \bar{s}_{v,\ j}, \end{aligned} \tag{42}$$

where, $j = 1,\ 2,\ \ldots,\ N-1$. Remember that $s_{v,\ 0} = s_v(t_0 = 0)$ and $s_{v,\ \mu} = s_v(t = T)$ are known.

By multiplying $\bar{e}_h(t)$, $\bar{i}_h(t)$, $\bar{r}_h(t)$ and $\bar{c}_h(t)$ by $N_h(t)$ we obtain estimations of $\bar{E}_h(t)$, $\bar{I}_h(t)$, $\bar{R}_h(t)$ and $\bar{C}_h(t)$. Analogously, by multiplying $\bar{s}_v(t)$ and $\bar{e}_v(t)$ by $N_v(t)$ we also obtain estimations of $\bar{S}_v(t)$ and $\bar{E}_v(t)$.

Unfortunately, the described method stipulates the ill-conditioned problem and it is impossible to accurately identify parameters $a_1,\ a_2,\ \ldots,\ a_5$. We therefore need to describe another reliable method of estimation of parameters μ_v, β_2 and ϕ.

The ill-conditioned nature of the previous method is explained by lack of information in function $i_v = i_v(t)$. In particular, the method described above does not take into consideration the initial and terminal values of functions $s_v = s_v(t)$ and $e_v = e_v(t)$ at $t_0 = 0$ and $t = T$.

For instance, if we assume that $i_v = i_v(t)$ together with the initial and terminal values $s_{v,\ 0} = s_v(t = 0)$, $e_{v,\ 0} = e_v(t = 0)$, $s_{v,\ T} = s_v(t = T)$ and $e_{v,\ T} = e_v(t = T)$ are known, then the goal function for determination of parameters μ_v, β_2 and ϕ can be formulated as follows:

$$
\begin{aligned}
G = G(\mu_v,\ \beta_2,\ \phi) = D(t,\ z) &\to [\mu_v - (1 - Z_0) - \beta_2 \cdot Z_0 \cdot \bar{i}_h(t) - \beta_2 \cdot Z_0 \cdot \bar{i}_h(t) - (\mu_v + \phi) \cdot Z_1], \\
&= Z \to ODESolve(Z,\ 0,\ T,\ \mu,\ D), \\
&= G_1 \to \frac{1}{2}\left[\left(Z_\mu^{\prec 1\succ} - s_{v,\,T}\right)^2 + \left(Z_\mu^{\prec 2\succ} - e_{v,\,T}\right)^2\right], \\
&= G_2 \to \frac{1}{2}\sum_{i=1}^{N}\left[Z_i^{\prec 1\succ} + Z_i^{\prec 2\succ} + i_{v,\,i} - 1\right]^2, \\
&= G \to G_1 + G_2,
\end{aligned}
\tag{43}
$$

where, $i_{v,\,i} = i_v(t = t_i)$ and $\bar{i}_h(t)$ are calculated by equation (30).

By minimizing function $G = G(\mu_v,\ \beta_2,\ \phi)$ given by equation (43), we obtain estimations of parameters $\bar{\mu}_v$, $\bar{\beta}_2$ and $\bar{\phi}$. This method works reliably well and converges for large intervals of initial guess values of parameters.

3. Numerical analysis of the result

In this section we demonstrate the principle of possibility of realization of the algorithm of parameter identification of Chikungunya model with incomplete information about the populations. We take parameters of the model, which are close to those discussed in [19], then select initial conditions and solve the corresponding initial value problem on finite time interval divided by thirty sub-intervals ("days"). As a result, we obtain thirty one points for each component of the human and mosquito vector populations. Further, we assume that known values are only initial and terminal values of all populations as well as susceptible human and infected venomous mosquitoes populations. Total human and mosquito populations are also supposed to be known. We do not give absolute values of these populations because only relative normalized values of all populations, described by system (1) are considered.

Thereafter, we "forget" about all parameters other than susceptible human and infected mosquito normalized populations. And working toward recovering all parameters as well as "unknown" populations (keeping in mind that only initial and terminal values of all populations are known). "Forgotten" values of parameters are used in calculating absolute and percentage errors of estimated parameters and "Forgotten" populations are used in calculating absolute errors of their identification. By means of the explained method, one can draw conclusions about practical application of the described algorithm.

Let us solve initial value problem for systems (17) and (21) with initial values; $s_{h,\,0} = 0.8$, $e_{h,\,0} = 0.1985$, $i_{h,\,0} = 0.007$, $r_{h,\,0} = 0.0003$, $c_{h,\,0} = 0.0005$, $s_{v,\,0} = 0.7$, $e_{v,\,0} = 0.299$ and $i_{v,\,0} = 0.001$ and parameters $\mu_h = 4.10\times^{-5}$, $\mu_v = 0.0713$, $\beta_2 = 14.9233$, $\beta_1 = \dfrac{1}{600} = 0.001667$, $\phi = 0.0333$, $\gamma = 0.066$, $\alpha = 0.13333$ and $\rho = 0.003333$. These parameters are close to the one described by [19] in their article. For solution of this problem, we use the Runge-Kutta 4 method which is a built-in algorithm in Mathcad 15 on time interval $t \in [0,\ T]$, where $T = 30$ days.

Figures 1 and 2 shows the solutions at $t_i = 0,\ 1,\ 2,\ \ldots,\ N = 30$ (days) for $s_{h,\,i} = s_h(t_i)$ and $i_{v,\,i} = i_v(t_i)$.

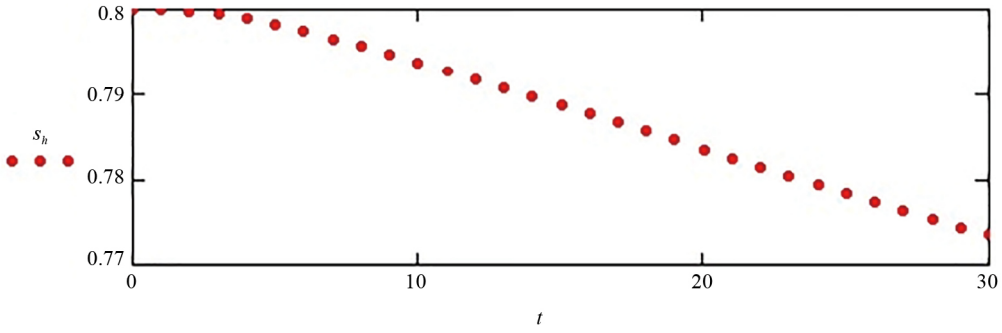

Figure 1. Given relative values of the susceptible human population $N+1=31$ data points, on given time interval $t \in [0,\ 30]$ days

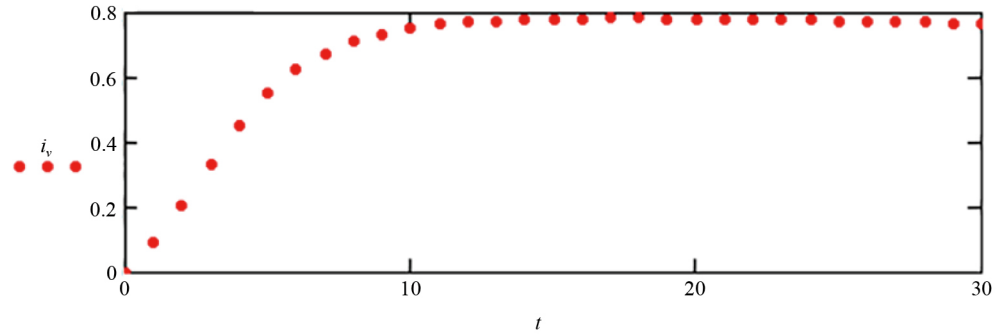

Figure 2. Given relative values of the infected vector population ($N+1=31$ data points) on given time interval $t \in [0,\ 30]$ days

The data shown are assumed to be known together with the total population $n_{h,\,i} = n_h(t_i) = 1$ and $n_{v,\,i} = n_v(t_i) = 1$, but other unknown populations as well as the unknown parameters must be found from these data. In line with this, we will rewrite equation (16) as over determined system of equations which will be used to estimate parameters μ_h and β_1 as follows:

$$\mu_h \cdot J_{1\cdot i} + \beta_1 \cdot J_{2\cdot i} - \Delta s_{h\cdot i} = 0, \quad (i = 1,\ 2,\ \ldots,\ N), \tag{44}$$

where,

$$J_{1,\,i} = \int_0^{t_i} [1 - s_h(\tau)]\, d\tau, \quad J_{2,\,i} = -\int_0^{t_i} [i_v(\tau) - s_h(\tau)]\, d\tau, \quad \Delta s_{h,\,i} = s_{h,\,i} - s_{h,\,0}. \tag{45}$$

We find μ_h and β_1 as follows:

$$[\mu_h\, \beta_1]^T = (\mu_1^T \cdot \mu_1)^{-1} \cdot (\mu_1^T \cdot \Delta s_h), \tag{46}$$

where, matrix N_1 and vector Δs_h are

$$\underbrace{N_1}_{N\times 2} = [J_{1,\,i}\; J_{2,\,i}], \quad (i = 1,\, 2,\, \ldots,\, N), \quad \underbrace{\Delta s_h}_{N\times 1} = \left[\Delta s_{h,\,i}\right]. \tag{47}$$

Hence, numerical estimation of the parameters $\bar{\mu}_h$ and $\bar{\beta}_1$ are given as $\bar{\mu}_h \cong 3.97 \times 10^{-5}$ and $\bar{\beta}_1 \cong 1.667 \times 10^{-3}$ and the percentage errors are $\bar{\mu}_h \cong 0.75\%$ and $\bar{\beta}_1 \cong 0.02\%$.

Parameter α is therefore calculated as a solution of equation (48)

$$e_{h,\,0} \cdot e^{-(\bar{\mu}_h+\alpha)T} + \bar{\beta}_1 \cdot \int_0^T e^{-(\bar{\mu}_h+\alpha)(T-\tau)} \cdot i_v(\tau) \cdot s_h(\tau) d\tau = e_{h,\,T}, \tag{48}$$

where, $e_{h,\,0} \cong 0.1985$ and $e_{h,\,T} \cong 9.701 \times 10^{-3}$.

The graph of $\log(|e_h(T,\,\alpha) - e_{h,\,T}|)$ against α for $\alpha = 0.001, 0.002, \ldots, 0.3$ is shown in Figure 3 with the estimated value of $\bar{\alpha} \cong 0.133$ and % Error $(\alpha) \cong 0.25\%$.

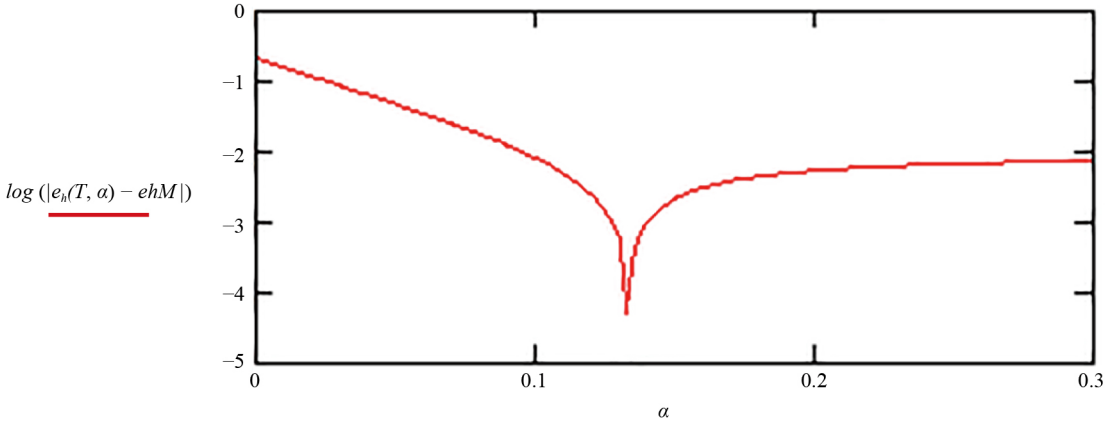

Figure 3. Graphical determination of guess value of parameter α (period between human exposure and the virus infection) with the known terminal value of the relative exposed human population $ehM = e_{h,\,T}$ at $t = T = 30$

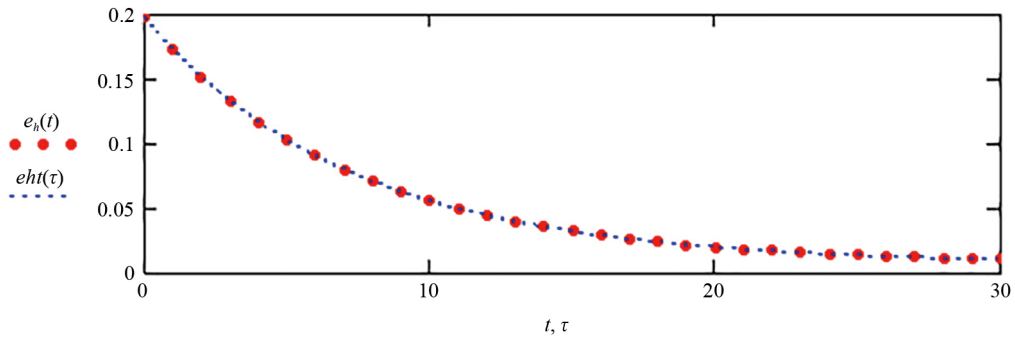

Figure 4. Calculated relative values of the estimated exposed human population $eht(\tau)$ and its comparison with preliminary calculated result $e_{h,\,i}$ in $N + 1 = 31$ data points on given time interval $t, \tau \in [0,\, 30]$ days

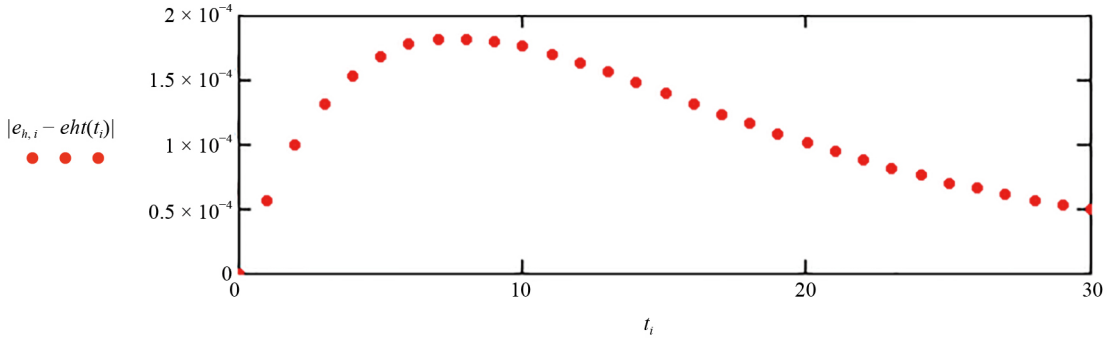

Figure 5. Absolute error between the estimated exposed human population $eht(t_i)$ and preliminary calculated result $e_{h,\,i}$ in $N+1=31$ data points on given time interval $t \in [0,\ 30]$ days

In equation (48), parameter α is not known but parameters s_h and i_v are known. And parameter e_h is known only at initial value $e_h(0)$ and terminal value $e_h(T)$ at a given time interval. And we start to solve initial value problem for different values of α using shooting method. When a particular terminal value is reached, a sharp negative spike is seen as shown in Figure 3.

In Figure 4, the estimation of $\bar{e_h}(t) = e_h(t,\ \bar{\gamma})$ against time is shown. And its absolute error is shown in Figure 5. The error is quite small, on the level of 10^{-4}.

Furthermore, parameter γ is estimated from equation (49)

$$i_{h,\,0} \cdot e^{-(\bar{\mu}_h+\gamma)T} + \bar{\alpha} \cdot \int_0^T e^{-(\bar{\mu}_h+\gamma)(T-\tau)} \cdot \bar{e}_h(\tau) d\tau = i_{h,\,T}, \tag{49}$$

where, $i_{h,\,0} \cong 7.01 \times 10^{-4}$ and $i_{h,\,T} \cong 0.0555$.

The graph of $\log(|i_h(T,\ \gamma) - i_{h,\,T}|)$ against γ for $\gamma = 0.001, 0.002, \ldots, 0.1$ is shown in Figure 6 as a sharp negative spike.

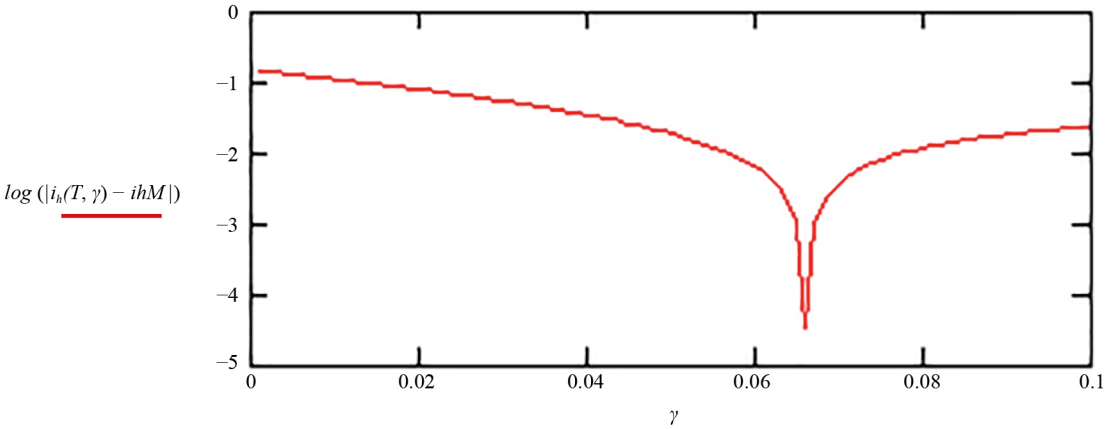

Figure 6. Graphical determination of parameter γ (the rate of recovery for human populations) with known terminal value of the relative infected human population $ihM = i_{h,\,T}$ at $t = T = 30$

In equation (49), the initial and terminal values of i_h are known. Parameter μ is known and γ is not known. But by means of solving initial value problem at different values of γ, it can be deduced from Figure 6 that as the logarithm turns zero, the terminal value of the solution corresponds to the known terminal value.

The estimation of $\bar{i_h}(t) = i_h(t,\ \bar{\gamma})$ against time is shown in Figure 7 and it's absolute error in Figure 8.

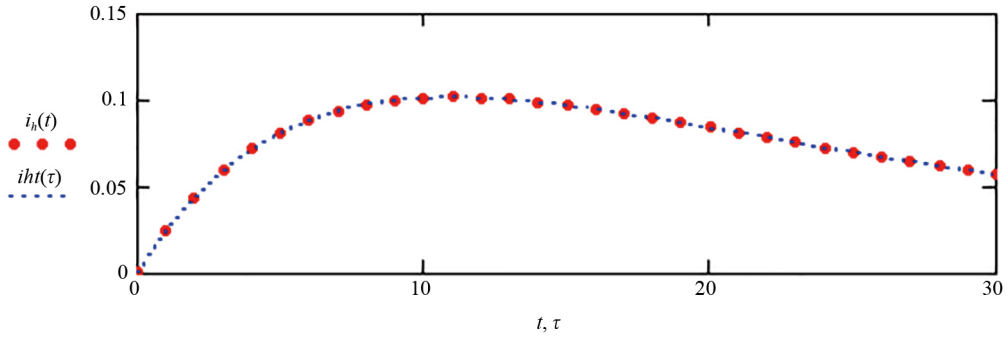

Figure 7. Calculated relative values of the estimated infected human population $iht(\tau)$ and it's comparison with preliminary calculated result $i_{h,\,i}$ in $N+1=31$ data points on given time interval $t, \tau \in [0,\ 30]$ days

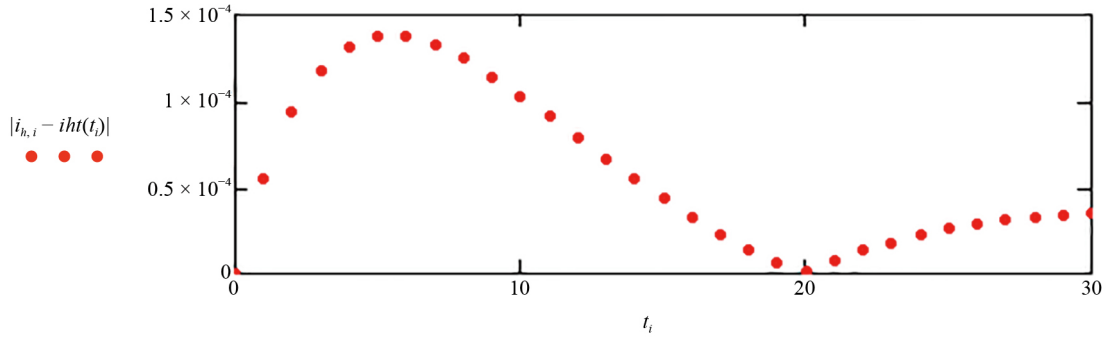

Figure 8. Absolute error between the estimated infected human population $iht(t_i)$ and preliminary calculated result $i_{h,\,i}$ in $N+1=31$ data points on given time interval $t \in [0,\ 30]$ days

Analogously, parameter ρ can be estimated from equation (50)

$$r_{h,\,0} \cdot e^{-(\bar{\mu}_h+\rho)T} + \bar{\rho} \cdot \int_0^T e^{-(\bar{\mu}_h+\rho)(T-\tau)} \cdot \bar{i}_h(\tau) d\tau = r_{h,\,T}. \tag{50}$$

The graph of $\log(|r_h(T,\ \rho) - r_{h,\,T}|)$ against ρ for $\rho = 0.001, 0.002, \ldots, 0.1$ is shown in Figure 9 from where we obtained $\bar{\rho} \cong 0.0033$ with % Error $(\rho) \cong 1\%$. That is, in Figure 9 the modulus of the difference between the predicted and the preliminary obtained value is not more than 1% and this gives an error not more than 8×10^{-3}.

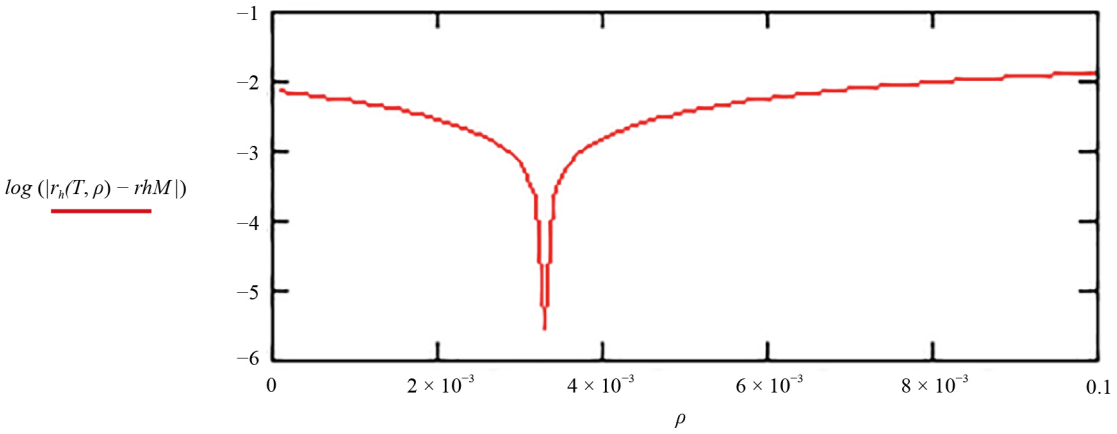

Figure 9. Graphical determination of parameter ρ (the rate at which the recovered humans moves to the chronic class) with known terminal value of the relative recovered human population $rhM = r_{h,\,T}$ at $t = T = 30$

The estimation of $\bar{r_h}(t) = r_h(t,\ \bar{\gamma})$ against time is shown in Figure 10 and its absolute error in Figure 11.

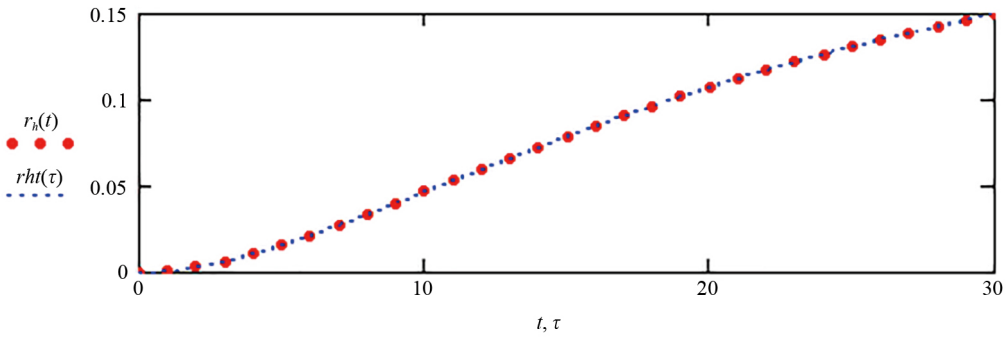

Figure 10. Calculated relative values of the estimated recovered human population $rht(\tau)$ and its comparison with preliminary calculated result $r_{h,\,i}$ in $N+1 = 31$ data points on given time interval $t, \tau \in [0,\ 30]$ days

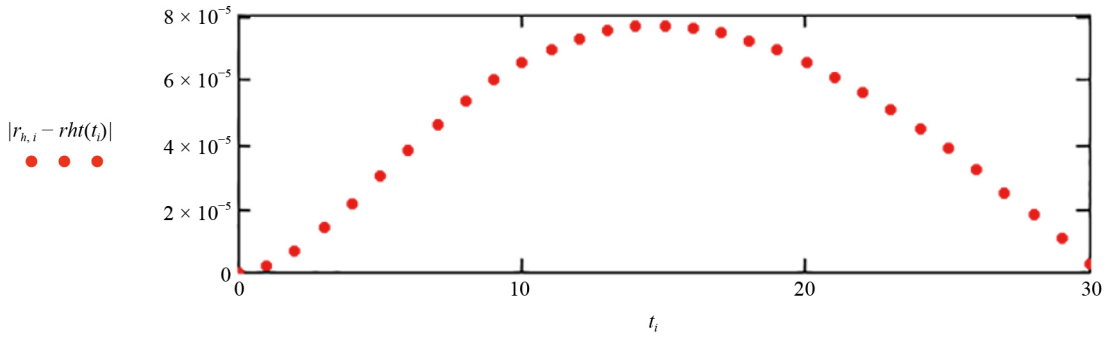

Figure 11. Absolute error between the estimated recovered human population $rht(t_i)$ and preliminary calculated result $r_{h,\,i}$ in $N+1 = 31$ data points on given time interval $t \in [0,\ 30]$ days

We therefore calculate the estimation of $\bar{c}_h(t)$ as

$$\bar{c}_h(t) = 1 - \bar{s}_h(t) - \bar{e}_h(t) - \bar{i}_h(t) - \bar{r}_h(t). \tag{51}$$

And its graphical representation is shown in Figure 12 with its absolute error demonstrated in Figure 13.

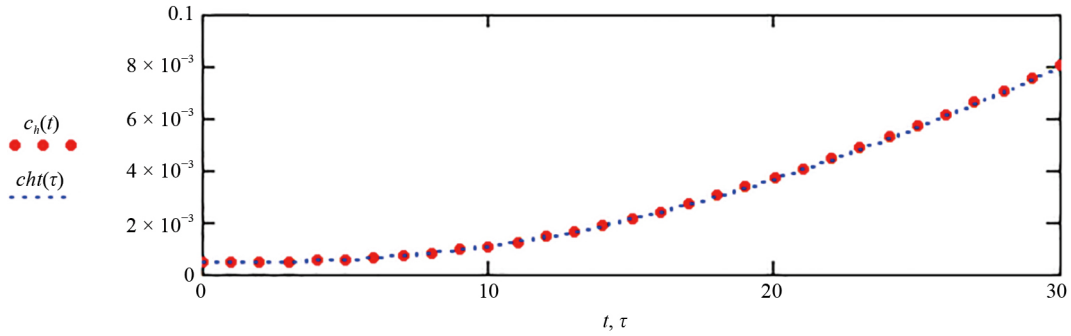

Figure 12. Calculated relative values of the estimated chronically infected human population $cht(\tau)$ and its comparison with preliminary calculated result $(c_{h,\,i})$ in $N+1=31$ data points on given time interval $t,\ \tau \in [0,\ 30]$ days

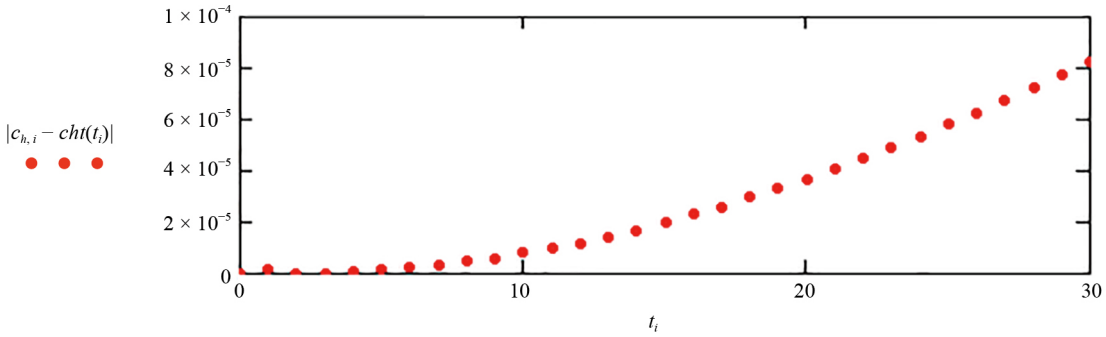

Figure 13. Absolute error between the estimated chronically infected human population $cht(t_i)$ and preliminary calculated result $c_{h,\,i}$ in $N+1=31$ data points on given time interval $t \in [0,\ 30]$ days

Lastly, to find estimate of parameters μ_v, β_2 and ϕ we use the goal function (43) and minimize it at guess values of parameters $\mu_v = 0.1$, $\beta_2 = 1.0$ and $\phi = 0.1$. The results of the minimization are $\bar{\mu}_v \cong 0.0714$, $\bar{\beta}_2 \cong 3.2372$ and $\bar{\phi} \cong 0.3338$ with their corresponding percentage errors at % error $(\bar{\mu}_v) \cong 0.11\%$, % error $(\bar{\beta}_2) \cong 0.12\%$ and % error $(\bar{\phi}) \cong 0.13\%$. It is observed that the convergence of the algorithm is faster in a broad range of guess values as seen in Table 2.

Table 2. Comparison between the guess values and estimated values of the parameters for vector population

Parameters	μ_v	ϕ	β_2
Original values	0.07133	0.3333	14.92333
Estimated values	0.0714	0.3336	14.9356
% Error	0.08%	0.08%	0.08%

Using the obtained parameters, we solve the system of ordinary differential equations:

$$\frac{d\bar{s}_v(t)}{dt} = \bar{\mu}_v \cdot [1 - \bar{s}_v(t)] - \bar{\beta}_2 \cdot \bar{s}_v(t) \cdot \bar{i}_h(t),$$

$$\frac{d\bar{e}_v(t)}{dt} = \bar{\beta}_2 \cdot \bar{s}_v(t) \cdot \bar{i}_h(t) - \left(\bar{\mu}_v + \bar{\phi}\right) \cdot \bar{e}_v(t), \tag{52}$$

with initial conditions $\bar{s}_{v,\,0} = \bar{s}_v(t=0) = s_{v,\,0} = 0.7$, $\bar{e}_{v,\,0} = \bar{e}_v(t=0) = 0.299$ we obtain estimations of functions $\bar{s}_v = \bar{s}_v(t)$ and $\bar{e}_v = \bar{e}_v(t)$ (see Figures 14 and 15). The estimation of functions $\bar{s}_v(t)$ and $\bar{e}_v(t)$ with their absolute error are shown respectively in Figures 16 and 17.

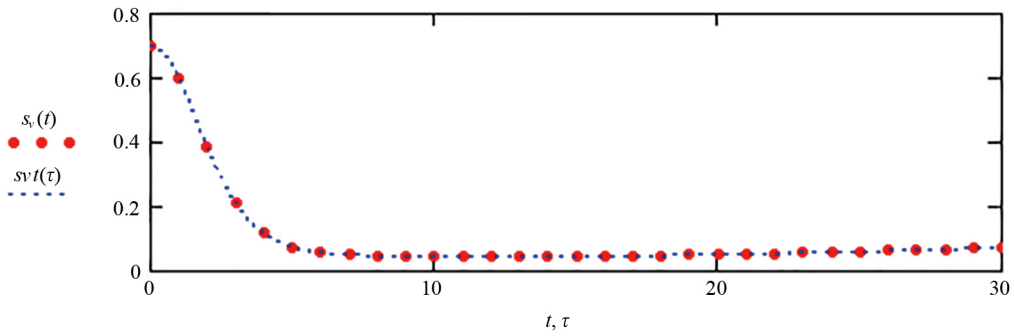

Figure 14. Calculated relative values of the estimated susceptible vector population $svt(\tau)$ and its comparison with preliminary calculated result $s_{v,\,i}$ in $N+1=31$ data points on given time interval $t, \tau \in [0,\ 30]$ days

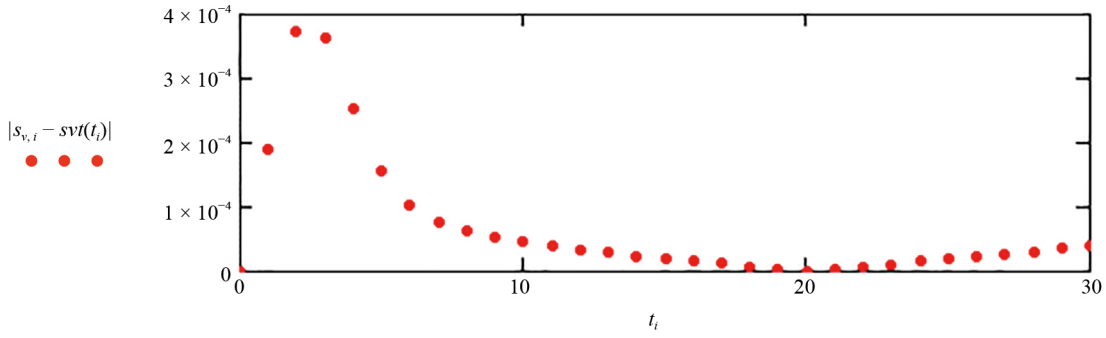

Figure 15. Absolute error between the estimated susceptible vector population $iht(t_i)$ and preliminary calculated result $s_{v,\,i}$ in $N+1=31$ data points on given time interval $t \in [0,\ 30]$ days

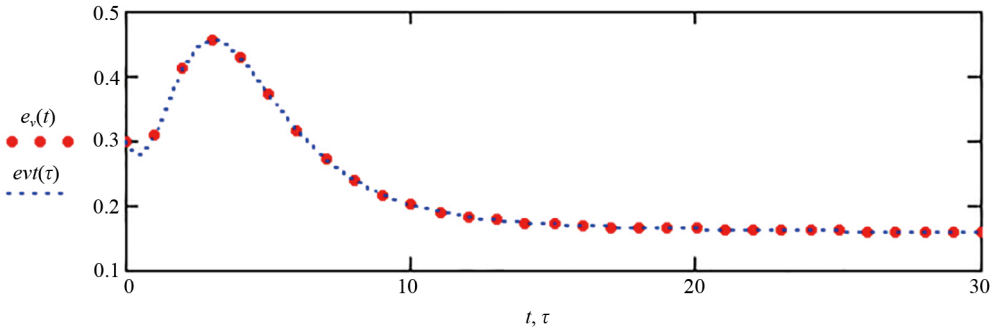

Figure 16. Calculated relative values of the estimated exposed vector population $evt(\tau)$ and its comparison with preliminary calculated result $e_{v,\,i}$ in $N+1=31$ data points on given time interval $t, \tau \in [0,\ 30]$ days

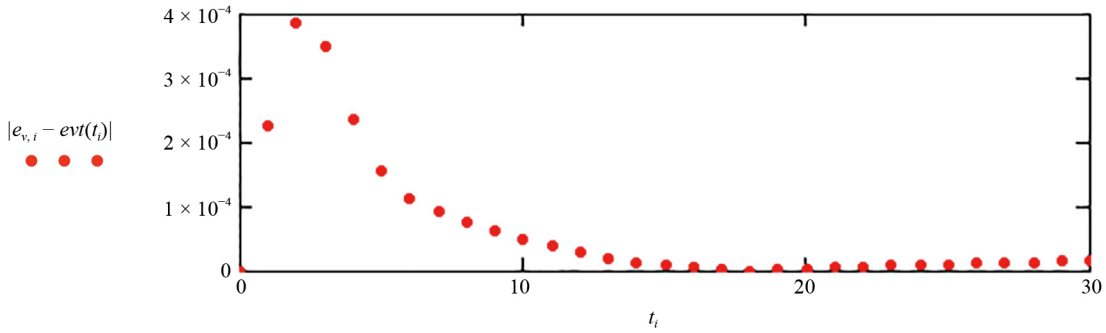

Figure 17. Absolute error between the estimated exposed vector population $evt(t_i)$ and preliminary calculated result $e_{v,\,i}$ in $N+1=31$ data points on given time interval $t \in [0,\ 30]$ days

The expected number of secondary cases produced by a single infection in a population that is completely disease free is called basic reproductive number, denoted by R_0 [36, 37]. It follows from the estimated parameters that the basic reproduction number:

$$R_0 = \sqrt{\frac{\alpha \cdot \beta_1 \cdot \beta_2 \cdot \phi}{(d_h+\alpha)(d_h+\gamma)\cdot \mu_v \cdot (\mu_v+\phi)}} \cong 2.085 > 1. \tag{53}$$

Hence, both human and mosquito vectors are stable.

4. Conclusions

The investigation carried out on the mathematical model for Chikungunya in this paper begins with the description of a basic model for vector transmitted disease, in which we stated that human populations satisfy a SEIRC model and mosquito populations satisfy SEI model. The model of the Chikungunya disease was generalized by assuming that the total human and mosquito populations can not only be constant but also exponentially increased and decreased populations. It was proven that both human and mosquito populations are positive provided that all coefficients of the model are positive.

The problem of complete identification of the system was formulated with the assumption that incomplete information on both human and mosquito populations are available. The complete identification in this case means that

all parameters of the model are found and calculated together with all unknown populations at the given time interval ($t \in [0,\ T]$), ($T = 30$). Furthermore, in the formulated identification problem it was assumed that only the total human and mosquito vector populations as well as the susceptible human and infected mosquito populations are known at discrete time instants of the given time interval ($t \in [0,\ T]$). In addition to this information, we also assumed that values of the exposed, infected, recovered human and susceptible, exposed mosquito populations are given at initial time instant ($t = 0$) and terminal time instants ($t = T$). In the above-mentioned situation, it was shown that it is possible to obtain the complete parameter identification of the Chikungunya model by demonstrating that all unknown human and mosquito vector populations can be recovered on the given time interval ($t \in [0,\ T]$). Errors of recovered estimated functions characterizing the unknown human and mosquito populations were also estimated. The estimated parameters gave the possibility to calculate the basic reproductive number R_0, which in the considered situation was larger than one ($R_0 > 1$). Hence, the conclusion about stability of the human and mosquito vector populations was formulated.

In the general mathematical model of Chikungunya studied in this paper, the parameters of the model were estimated in the case of incomplete information about them. The proposed technique of the system identification in section 2 makes it possible to solve the problem of prediction of the Chikungunya disease which will be considered in future publications.

As it follows from the conclusions, the present mathematical model of Chikungunya is limited by either constant human and mosquito populations, or their exponential growth/decay. This and some other obvious limitations need further development of the present model and will be directed to the improvement of the model in the following aspects: more general model of total human and mosquito populations will be introduced; different death rates of susceptible, exposed, infected, recovered and chronically infected human and susceptible, exposed mosquito populations will be introduced in the model. Moreover, the problems of prediction of future dynamics of the Chikungunya will be solved on the basis of the existing and more advanced mathematical models.

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Conflict of interest

The authors declare no competing financial interest.

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Appendix A

In [19], the authors used the facts of positivity of solutions of systems (17) and (21) as well as possibility of their continuation on infinite time interval $t \in [0, +\infty)$. These facts were neither validated nor proven by the authors. In this Appendix, we prove the following theorem.

A.1 *Notes on positivity of solutions of systems (17) and (21)*

Theorem Provided that all parameters $\mu_h, \beta_1, \alpha, \gamma, \rho, \mu_v, \beta_2, \phi$ of systems (17) and (21) are positive. If the initial conditions $s_h(0), e_h(0), i_h(0), r_h(0), c_h(0), s_v(0), e_v(0)$ and $i_v(0)$ are positive and satisfy conditions $s_h(0)+e_h(0)+i_h(0)+r_h(0)+c_h(0)=1$ and $s_v(0)+e_v(0)+i_v(0)=1$, then solutions $s_h(t), e_h(t), i_h(t), r_h(t), c_h(t), s_v(t), e_v(t), i_v(t)$ of systems (17) and (21) are positive for all t and can be continued on infinite time interval $t \in [0, +\infty)$.

Proof. Systems (17) and (54) satisfies the local theorem of continuation and hence all solutions $s_h(t), e_h(t), \cdots, i_v(t)$ exist on time interval $[0, t]$, where $t > 0$. It follows from the first equation of system (17) that:

$$s_h(t) = s_h(0) \cdot \exp\left\{-\int_0^t [\mu_h + \beta_1 \cdot i_v(\tau)]d\tau\right\} + \mu_h \cdot \int_0^t \exp\left\{-\int_\tau^t [\mu_h + \beta_1 \cdot i_v(\xi)]d\xi\right\} d\tau \tag{54}$$

Hence, due to $s_h(0) > 0$, $\mu_h > 0$ and $\exp\left\{-\int_0^t [\mu_h + \beta_1 \cdot i_v(\tau)]d\tau\right\} > 0$, $s_h(t) > 0$ is independent on sign of $i_v(t)$. Solution of the second equation of system (17) is:

$$e_h(t) = e_h(0) \cdot \exp\{-(\mu_h + \alpha)t\} + \beta_1 \cdot \int_0^t i_v(\tau) \cdot s_h(\tau) \cdot \exp\{-(\mu_h + \alpha) \cdot (t - \tau)\} d\tau \tag{55}$$

The first term is definitely positive due to $e_h(o) > \varepsilon$. In the second term $\beta_1 > 0$, $s_h(t) > 0$ and $i_v(\tau)$ is positive due to continuity of function $i_v(t)$ (because $i_v(\tau)$ is differentiable and $i_v(0) > 0$). Let us assume that $i_v(T_1) = 0$ and also $i_v(t) < 0$ for $t > T_1$, where $T_1 > 0$ is the first time instant at which it become equal to zero. (If T_1 does not belong to the considered interval of existence of the solutions of system (17) and (21), we continue the solution on the interval $t \in [0, T_1]$). Hence $e_h(t) > 0$ for $t \in [0, T_1]$.

From the third equation of (17) it follows that:

$$i_h(t) = i_h(0) \cdot \exp\{-(\mu_h + \gamma) \cdot t\} + \alpha \cdot \int_0^t e_h(\tau) \cdot \exp\{-(\mu_h + \gamma) \cdot (t - \tau)\} d\tau \tag{56}$$

is positive for $t \in [0, T_1]$.

Analogously, it is possible to prove that $r_h(t) > 0$ and $c_h(t) > 0$ for $t \in [0, T_1]$. From the first equation of (21) we obtain

$$s_v(t) = s_v(0) \cdot \exp\left\{-\int_0^t [\mu_v + \beta_2 \cdot i_h(\tau)]d\tau\right\} + \mu_v \cdot \int_0^t \exp\left\{-\int_\tau^t [\mu_h + \beta_2 \cdot i_h(\xi)]d\xi\right\} d\tau > 0 \tag{57}$$

for $t \in [0, T_1]$, because $s_v(0) > 0$, $\mu_v > 0$ and all exponents are positive.

From the second equation of (21) we have:

$$e_v(t) = e_v(0) \cdot \exp\{-(\mu_v + \phi)t\} + \beta_2 \cdot \int_0^t i_h(\tau) \cdot s_v(\tau) \cdot \exp\{-(\mu_v + \phi) \cdot (t - \tau)\} d\tau > 0 \tag{58}$$

for $t \in [0,\ T_1]$, because $e_v(0) > 0$, $\beta_2 > 0$ and $i_h(t) > 0$ for $t \in [0,\ T_1]$.

Finally, from the last equation of (21) we obtain:

$$i_v(t) = i_v(0) \cdot \exp\{-\mu_v \cdot t\} + \phi \cdot \int_0^t e_v(\tau) \cdot \exp\{-\mu_v \cdot (t - \tau)\} d\tau > 0 \tag{59}$$

for $t \in [0,\ T_1]$. But, $i_v(T_1) > 0$ which contradicts assumption that $i_v(T_1) = 0$. Therefore, we have proven that time instant T_1 at which $i_v(T_1) = 0$ does not exist and $i_v(t) > 0$ for $t \in [0,\ +\infty)$. Thus, all other equations of (17) and (21) are also positive for $t \in [0,\ +\infty)$. Due to relationship (13) all these functions are less than 1 and hence, exist on time interval $t \in [0,\ +\infty)$.