MINISTERUL EDUCAȚIEI NAȚIONALE
ROMÂNIA
UNIVERSITATEA DE MEDICINĂ, FARMACIE, ȘTIINȚE ȘI TEHNOLOGIE „GEORGE EMIL PALADE" DIN TÂRGU MUREȘ

sciendo

Acta Marisiensis. Seria Technologica
Vol. 17 (XXXIV) no. 1, 2020
ISSN 2668-4217, ISSN-L 2668-4217

10.2478/amset-2020-0007

ANALYSIS OF ODE MODELS FOR MALARIA PROPAGATION

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Abstract

Epidemiological models play an important role in the study of diseases. These models belong to population dynamics models and can be characterized with differential equations. In this paper we focus our attention on two epidemic models for malaria spreading, namely Ross-, and extended Ross model. As both the continous and the corresponding numerical models should preserve the basic qualitative properties of the phenomenon, we paid special attention to its examination, and proved their invariance with reference to the data set. Moreover, existence and uniqueness of equilibrium points for both models of malaria are considered. We demonstrate the theoritical results with numerical simulations.

Key words: Epidemic, Extended Ross model, Positivity invariant, Equilibrium points, Ross model, Malaria propagation

1 Introduction and motivation

People of all eras had to cope with different diseases and despite of modern science today's population is no exception. Some of these diseases can decrease the size of the population dramatically. Therefore, it is extremely important to understand the mechanism of epidemics and try to prevent their outbreak and propagation.

Malaria is widespread in the tropical and subtropical regions, includes Asia, Sub-Saharan Africa and Latin America. It still occurs more than 200 million cases worldwide of which one-fifth ends in death. Since there is no effective vaccine, it is crucial to study the host-parasite biology and describe an effective mathematical model to its propagation.

Every mathematical model needs to reflect the main characteristic of the phenomenon. Since the unknown functions in the differential equations which describe the epidemic propagation give the number or the density of the different individuals, a reliable model could have only a non-negative solution. Therefore, one of the main requirements is the non-negativity property, which means that if the initial data are non-negative, then the solution of the models is also non-negative. In this paper we paid our attention to the analysis of this question for two ODE models for malaria propagation. Furthermore, the existence and uniqueness of the stationary points of both models are examined, which can give answer of how many infected people will be during the epidemic.

The basis of epidemic models is the so-called *SIR model*, which was created in 1927 by Kermack and McKendrick [12]. In this model there are three compartments, which are defined as below:

- ***(S)*** susceptibles - who have yet to contract the disease and become infectious,
- ***(I)*** infectives - who can pass on the disease to others,
- ***(R)*** removed - who have been infected but cannot transmit the disease for some reason.

The model has the form of a system of ordinary differential equations:

$$\begin{cases} \dfrac{dS(t)}{dt} = -aS(t)I(t) \\ \dfrac{dI(t)}{dt} = aS(t)I(t) - bI(t) \\ \dfrac{dR(t)}{dt} = bI(t), \end{cases} \tag{1}$$

where $S(t), I(t)$ and $R(t)$ are the number of susceptible, infective and recovered individuals as a function of time t. Contact rate a and recovery rate b are positive known parameters. It is easy to see that there is no vital dynamics in this model, and the movement between the three groups is one-way, which means that the recovered individuals do not become susceptible again. It is usually depicted as below

$$\text{(S)} \longrightarrow \text{(I)} \longrightarrow \text{(R)}$$

Some infections do not give immunity upon recovery from infection, and individuals become susceptible again. These are the so-called SIS models.

$$\text{(S)} \longrightarrow \text{(I)} \longrightarrow \text{(S)}$$

In other infections there is a significant incubation period during which the individual has been infected but is not yet infectious themselves. During this period the individuals are in the exposed (E) state, and this leads to the $SEIR$ models.

$$\text{(S)} \longrightarrow \text{(E)} \longrightarrow \text{(I)} \longrightarrow \text{(R)}$$

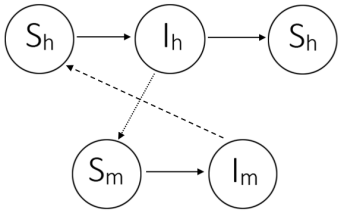
This paper is organised as follows. In Section 2 we introduce two mathematical models for malaria transmission including Ross and extended Ross model. Moreover, density preservation is proven for Ross model. In Section 3 we investigate the qualitative properties of the extended Ross model in detail. Section 4 addresses equilibrium points of both models and finally, in Section 5 we demonstrate the theoritical results on numerical examples.

2 Dynamics of malaria transmission

Models mentioned in Section 1 describe the direct type of epidemic propagation, which means that for the spread of the disease direct physical connection is required.
The most typical example for indirect type of epidemic propagation is malaria. In this case physical connection is not required directly between the infected individuals, rather the disease spreads through a vector. Hence this model usually called as host-vector-host model.

Ross model

Ronald Ross highlighted the role of mosquitoes in the spread of malaria and introduced a differential equation system to describe the dynamics of malaria transmission at a population level.
In the construction of the model the size of human and mosquito population considered as constant [11]. Both population is divided into two subgroups, including susceptibles and infected. In the human population the infected class returns to the susceptible again, unlike in the mosquito population where the mosquitoes dies due to their short lifetime. Therefore the Ross model can be considered as a modification of the SIR model, for humans it is an SIS model and SI model for mosquitoes. The movement between the compartments:



Ross model is formulated as follows:

$$\begin{cases} \dfrac{dS_h}{dt} = rI_h(t) - abmI_m(t)(1 - I_h(t)) \\ \dfrac{dI_h}{dt} = abmI_m(t)(1 - I_h(t)) - rI_h(t) \\ \dfrac{dS_m}{dt} = \mu I_m(t) - acI_h(t)(1 - I_m(t)) \\ \dfrac{dI_m}{dt} = acI_h(t)(1 - I_m(t)) - \mu I_m(t) \end{cases} \tag{2}$$

with given positive initial values which naturally satisfy the following conditions:

$$\begin{cases} S_h(0) + I_h(0) = 1 \\ S_m(0) + I_m(0) = 1 \end{cases} \tag{3}$$

Here $S_h(t)$ and $S_m(t)$ denotes the density of susceptible humans and mosquitoes at time t. The densitiy of infected humans and mosquitoes at

time t is characterized as $I_h(t)$ and $I_m(t)$. In (2) - (3), $S_h(t) + I_h(t) = 1$ for all t, and for mosquitoes $S_m(t) + I_m(t) = 1$ for all t, too.
Parameter a yields the number of bites per unit time, b is the proportion of bites that produce infection in humans, c represents the proportion of those bites by which a susceptible mosquito becomes infected. Parameter m is the ratio of number of female mosquitoes to that of humans. The parameter r is the average recovery rate of humans, and μ is the death rate of the vectors.

System (2) can be reduced as below:

$$\begin{cases} \dfrac{dI_h}{dt} = abmI_m(t)(1 - I_h(t)) - rI_h(t) \\ \dfrac{dI_m}{dt} = acI_h(t)(1 - I_m(t)) - \mu I_m(t) \end{cases} \tag{4}$$

With initial conditions (3) system (4) is a two-dimensional Cauchy problem. As the solution of system (4) is density, it should belong to interval $[0, 1]$. We will prove that if $I_h(0)$ and $I_m(0)$ are in interval $[0, 1]$, the solution of system (4) is in $[0, 1]$, too. This property is referred as density preservation (DP) property [13].

Theorem 1. *Ross model* (4) *possesses DP property.*

Proof. Assume that $I_h(0), I_m(0) \in [0, 1]$ and

$$\Omega := \{(I_h(t), I_m(t)) : 0 \leq I_h(t), I_m(t) \leq 1\}. \tag{5}$$

If $\bar{t}$ denotes the time-instant when the trajectories reach the boundary, the sign of the derivatives will be worth discussing. If we suppose $I_m(\bar{t}) \geq 0$ and $I_h(\bar{t}) = 0$ from the first equation of system (4) we get $\dot{I}_h(t) \leq 0$.
By similar reasoning for the second equation of system (4), the statement proves that set Ω is positively invariant with respect to Ross model (4). □

Despite that the Ross model possesses DP property, it has some shortcomings, too.

- As the total population is constant, the birth and mortality are assumed to be equal, i.e. there is no vital-dynamics.
- In reality there is a latency period which means that the transition from the susceptible state to the infected state is not direct. There is a state between the two compartments, the so-called exposed state.
- Since the Ross-model is based on SIS model for humans, there is no recovery state ($R(t)$).

Extended Ross model

To eliminate the above listed shortcomings we introduce another model for the malaria propagation, and we call it extended malaria model (c.f. [3]).
To follow the standard notation a new group has to be introduced: the class of exposed *(E)*, those individuals whom are infected but not able to pass on the infection to others.
In general we divide the human population into four groups: susceptible humans, exposed humans, infectious humans and recovered humans. Unlike human population, the mosquito population is divided into three subclasses. There is no recovered class due to their short life-cycle.
By some biological interpretations coming from [3] the progress of the disease can be described with the below seven-dimensional system of ordinary differential equations:

$$\begin{cases} \dfrac{dS_h(t)}{dt} = \Lambda_h - \dfrac{b\beta_h S_h(t) I_m(t)}{1 + \nu_h I_m(t)} - \mu_h S_h(t) + \omega R_h(t) \\ \dfrac{dE_h(t)}{dt} = \dfrac{b\beta_h S_h(t) I_m(t)}{1 + \nu_h I_m(t)} - (\alpha_h + \mu_h) E_h(t) \\ \dfrac{dI_h(t)}{dt} = \alpha_h E_h(t) - (r + \mu_h + \delta_h) I_h(t) \\ \dfrac{dR_h(t)}{dt} = rI_h(t) - (\mu_h + \omega) R_h(t) \\ \dfrac{dS_m(t)}{dt} = \Lambda_m - \dfrac{b\beta_m S_m(t) I_h(t)}{1 + \nu_m I_h(t)} - \mu_m S_m(t) \\ \dfrac{dE_m(t)}{dt} = \dfrac{b\beta_m S_m(t) I_h(t)}{1 + \nu_m I_h(t)} - (\alpha_m + \mu_m) E_m(t) \\ \dfrac{dI_m(t)}{dt} = \alpha_m E_m(t) - (\mu_m + \delta_m) I_h(t), \end{cases} \tag{6}$$

with the following initial conditions

$$\begin{cases} S_h(0) = S_{0h}, I_h(0) = I_{0h}, E_h(0) = E_{0h}, R_h(0) = R_{0h}, \\ S_m(0) = S_{0m}, E_m(0) = E_{0m}, I_m(0) = I_{0m}. \end{cases} \tag{7}$$

Here function $S_h(t)$ denotes the number of susceptible humans at time t, the number of humans exposed to malaria infection at time t is signified by $E_h(t)$ and the number of infectious and recovered humans at time t are characterized by $I_h(t)$ and $R_h(t)$. The variables for number of mosquitoes in the three compartments can be considered similarly.

Unlike Ross's model, this model takes into account the population dynamics by considering the birth rate and the death rate. In the extended model we assume that all children are born healthy, so the birth number (Λ_h, Λ_m) is only enters into the class of susceptibles (S_h, S_m).
Since malaria has a 2-4 weeks latent period, when the parasite is injected into the blood system with some probability (β_h), the susceptible human moves to the exposed class $E_h(t)$. Exposed humans are not able to transmitting the disease to the

susceptible mosquitoes as the parasites are in asexual stages [7].
When the incubation period is over the exposed human is progressed to the infectious state with some α_h rate. Then the individual in this class will either die or recover and moves to the recovered (R_h) class. The recovered human has some immunity to the disease, however after a few year the individual loses the immunity and become susceptible again.
As the model distinguish natural and disease induced death rate, every class is decreased by natural death rate μ_h, and only the infectious class is decreased by disease induced death rate δ_h.

In a similar way, when a susceptible mosquito $S_m(t)$ bites an infected human, the parasite enters the mosquito with some probability β_m and moves to the exposed class $E_m(t)$. After a given time it becomes infectious I_m. Mosquitoes leave the population by natural death rate μ_m or disease induced death rate δ_m.

Ratio $\dfrac{1}{1+\nu_h I_m(t)}$ denotes a saturating feature that inhibits the force of infection from infectious mosquitoes to susceptible humans. In other words $\nu_h \in [0,1]$ is the proportion of antibodies produced by human in response the incidence of antigens produced by infectious mosquito. This interpretation can be used for mosquitoes similarly, whereas $\nu_m \in [0,1]$ is the rate at which antibodies are produced against the antigens contacted from infectious humans.

In this model the movement between the compartments for human population is $SEIRS$, and for mosquitoes the movement is SEI.

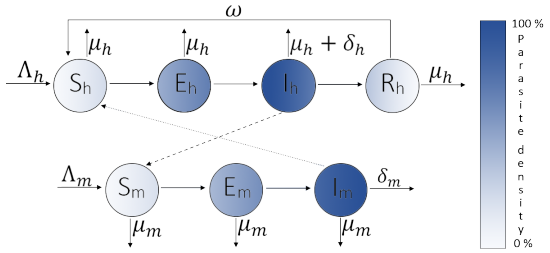


Figure 1: Mechanism in the extennded model. Colour bar indicates the density of malaria parasites in hosts / vectors in the different compartments $(0-100\%)$ [11].

3 Qualitative analysis of the extended model

We consider invariancy property of the extended malaria model.

Theorem 2. *Assume that $\Lambda_h, \Lambda_m > 0$ and all initial values in (7) are positive. Then the solution of the model (6)-(7) is positive for all t.*

Proof. We will prove the above theorem indirectly. Suppose that there exists $t < +\infty$ where our theorem is not true, which means that there exists at least one component which is equal to zero in that point. Let $t^\star$ be the infimum of such values. Then every component is positive on $[0, t^\star)$, and there exists at least one component which is equal to zero in $t^\star$. (This is due to the continuity of the functions.) In the sequel we show that no one of components can have this property.

1. Suppose that S_h has this feature, i.e., $S_h(t^\star) = 0$.

   Then the other components are non-negative on $[0, t^\star]$, that is the functions $E_h(t)$, $I_h(t)$, $R_h(t)$, $S_m(t)$, $E_m(t)$, $I_m(t)$ are non-negative on this interval. Let us consider the first equation in (6) at the point $t = t^\star$. We get

   $$S_h'(t^\star) = \Lambda_h - \frac{b\beta_h S_h(t^\star) I_m(t^\star)}{1+\nu_h I_m(t^\star)} - \mu_h S_h(t^\star) + \\ +\omega R_h(t^\star) = \Lambda_h + \omega R_h(t^\star) > 0.$$

   This means that $S_h(t)$ is strictly monotonically increasing at the point $t = t^\star$. Therefore $S_h(t) < S_h(t^\star)$ for all $t \in (t^\star - \varepsilon, t^\star)$ with some $\varepsilon > 0$. As $S_h(t^\star) = 0$ we get that $S_h(t) < 0$ on $(t^\star - \varepsilon, t^\star)$, which is a contradiction.

2. Assume that E_h has the above feature, i.e., $E_h(t^\star) = 0$. Multiplying both sides of the second equation in (6) with $e^{(\alpha_h+\mu_h)t}$, we obtain

   $$e^{(\alpha_h+\mu_h)t} E_h'(t) + e^{(\alpha_h+\mu_h)t}(\alpha_h+\mu_h) E_h(t) = \\ = e^{(\alpha_h+\mu_h)t} \frac{b\beta_h S_h(t) I_m(t)}{1+\nu_h I_m(t)}.$$

   Here on the left side stands the derivative of the function $e^{(\alpha_h+\mu_h)t} E_h(t)$. Hence, integrating this equality on the interval $[0,t]$ we get

   $$e^{(\alpha_h+\mu_h)t} E_h(t) - E_h(0) = \\ = \int_0^t e^{(\alpha_h+\mu_h)s} \frac{b\beta_h S_h(s) I_m(s)}{1+\nu_h I_m(s)} ds.$$

   Putting $t = t^\star$ this results in the relation

   $$E_h(t^\star) = e^{-(\alpha_h+\mu_h)t^\star} E_h(0) + \\ + \int_0^{t^\star} e^{-(\alpha_h+\mu_h)(t^\star - s)} \frac{b\beta_h S_h(s) I_m(s)}{1+\nu_h I_m(s)} ds.$$

   Hence $E_h(t^\star) > 0$, which yields a contradiction.

3. Assume now that I_h has the above feature, i.e., $I_h(t^\star) = 0$. Then the third equation in (6) at the point $t = t^\star$ results in the following:

   $$I_h'(t^\star) = \alpha E_h(t^\star) - (r + \mu_h + \delta_h) I_h(t^\star) = \\ = \alpha E_h(t^\star) > 0,$$

   which means that $I_h(t)$ is strictly monotonically increasing in $t^\star$. Hence, as in the first case, for S_h, we get again a contradiction.

4. Similarly we assume the above feature for the function $R_h(t)$ as well. Then

$$R_h'(t^\star) = rI_h(t^\star) - (\mu_h + \omega)R_h(t^\star) = rI_h(t^\star) > 0,$$

i.e., $R_h(t)$ is positive for all $t \in [0, t^\star]$, which contradicts the property $R_h(t^\star) = 0$.

For mosquitoes the proof is carried out analogously.

5 Suppose that $S_m(t)$ has the above feature, i.e., $S_m(t^\star) = 0$, and all the other components are non-negative at at the point $t = t^\star$. Then the the fifth equation in (6) at the point $t = t^\star$ results in the relation

$$S_m'(t^\star) = \Lambda_m - \frac{b\beta_m S_m(t^\star) I_h(t^\star)}{1 + \nu_m I_h(t^\star)} - \mu_m S_m(t^\star) = \\ = \Lambda_m > 0.$$

Hence, as in the case for $S_h(t)$, we got a contradiction.

6 Likewise for $E_m(t)$, by multiplication both sides of the corresponding equation by $e^{(\alpha_m + \mu_m)t}$, and then integrating on $[0, t]$, and substituting $t = t^\star$, we obtain

$$e^{(\alpha_m+\mu_m)t^\star} E_m(t^\star) - E_m(0) = \\ = \int_0^{t^\star} e^{(\alpha_m+\mu_m)t^\star} \frac{b\beta_m S_m(s) I_h(s)}{1 + \nu_m I_h(s)} ds.$$

Hence

$$E_m(t^\star) = e^{-(\alpha_m+\mu_m)t^\star} E_m(0) + \\ + \int_0^{t^\star} e^{-(\alpha_m+\mu_m)(t^\star - s)} \frac{b\beta_m S_m(s) I_h(s)}{1 + \nu_m I_h(s)} ds.$$

This means that $E_m'(t^\star) > 0$, which is the required contradiction.

7 Finally, for $I_m(t)$ we have

$$I_m'(t^\star) = \alpha E_m(t^\star) - (\mu_m + \delta_m) I_m(t^\star) = \\ = \alpha E_m(t^\star) > 0,$$

therefore $I_m(t^\star) > 0$, which is a contradiction.

These steps prove that there is no such $t^\star$ where any of the components turns into zero. Since at the initial point the components are positive, due to the continuity of the functions every component is positive for all t.

□

In theorem 2 we have proved the positivity of the solution, which means the model is bounded from below. In the following we consider its boundness from above.
Let V_h denote the total number of humans, i.e.

$$V_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t). \quad (8)$$

Similarly, for the mosquitoes we define

$$V_m(t) = S_m(t) + E_m(t) + I_m(t). \quad (9)$$

First we formulate the upper bound to V_h.

Theorem 3. *Suppose that at the initial time $t = 0$ the total population number is not equal with number $\frac{\Lambda_h}{\mu_h}$. Then the solution of the extended Ross model (6) – (7) is bounded from above by $\max\left(V_h(0), \frac{\Lambda_h}{\mu_h}\right)$ at any time t.*

Proof. Summing up the equations in (6) and using the definition of $V_h(t)$, we get

$$V_h'(t) = \Lambda_h - \mu_h V_h(t) - \delta_h I_h(t).$$

Hence, rearranging and multiplying both sides by $e^{\mu_h t}$, we obtain

$$V_h'(t) \cdot e^{\mu_h t} + \mu_h e^{\mu_h t} V_h(t) = (\Lambda_h - \delta_h I_h(t)) e^{\mu_h t}.$$

We notice that on the left side stands the derivative of $V_h(t) \cdot e^{\mu_h t}$. Hence, integrating both sides from 0 to t, we get

$$V_h(t) e^{\mu_h t} - V_h(0) = \int_0^t (\Lambda_h - I_h(s)) e^{\mu_h s} ds.$$

Hence

$$V_h(t) = e^{-\mu_h t} V_h(0) + e^{-\mu_h t} \int_0^t (\Lambda_h - I_h(s)) e^{\mu_h s} ds. \quad (10)$$

Since

$$e^{-\mu_h t} \int_0^t \Lambda_h e^{\mu_h s} ds = e^{-\mu_h t} \Lambda_h \frac{1}{\mu_h} (e^{\mu_h t} - 1) = \\ = \frac{\Lambda_h}{\mu_h} (1 - e^{-\mu_h t}),$$

and according to the Theorem 2, the function $I_h(t)$ is positive. From (10) we get the estimate

$$V_h(t) \le e^{-\mu_h t} V_h(0) + \frac{\Lambda_h}{\mu_h} \left[1 - e^{-\mu_h t}\right] = \\ = e^{-\mu_h t} \left[V_h(0) - \frac{\Lambda_h}{\mu_h}\right] + \frac{\Lambda_h}{\mu_h}. \quad (11)$$

Introduce the below notation for the right side

$$g(t) = e^{-\mu_h t} \left[V_h(0) - \frac{\Lambda_h}{\mu_h}\right] + \frac{\Lambda_h}{\mu_h}.$$

1. The first case is when

$$V_h(0) < \frac{\Lambda_h}{\mu_h}. \quad (12)$$

An easy computation shows that $g'(t) > 0$, which means that $g(t)$ is a monotonically increasing function. Therefore

$$g(t) \le \lim_{t\to\infty} g(t) = \frac{\Lambda_h}{\mu_h}. \tag{13}$$

Hence, (11) and (13) together imply the required estimate

$$V_h(t) < \frac{\Lambda_h}{\mu_h}$$

for any $t > 0$ under assumption (12).

2. If

$$V_h(0) > \frac{\Lambda_h}{\mu_h}, \tag{14}$$

then $g'(t) = -\mu_h e^{-\mu_h t}\left[V_h(0) - \frac{\Lambda_h}{\mu_h}\right] < 0$. It means that $g(t)$ is a monotonically decreasing function. Therefore

$$\sup g(t) = g(0) = \\ = e^{-\mu_h \cdot 0}\left(V_h(0) - \frac{\Lambda_h}{\mu_h}\right) + \frac{\Lambda_h}{\mu_h} = V_h(0). \tag{15}$$

Hence, (11) and (15) together imply the required estimate

$$V_h(t) \le V_h(0)$$

for any $t > 0$ under assumption (14).

The first and the second case together implies Theorem 3.

□

The statement for V_m is as follows.

Theorem 4. *Suppose that at the initial time $t = 0$ the total population number for the mosquitoes is not equal with number $\frac{\Lambda_m}{\mu_m}$. The solution of the extended Ross model (6)−(7) is bounded from above by $\max\left(V_m(0), \frac{\Lambda_m}{\mu_m}\right)$ at any time t.*

Proof. Since the proof is carried out analogously to the proof of Theorem 3, for brevity we omit it. □

Theorems 2, 3 and 4 imply that each component in the extended Ross model is on the interval $\left(0, \max\left\{V_h(0), \frac{\Lambda_h}{\mu_h}\right\}\right)$ and $\left(0, \max\left\{V_m(0), \frac{\Lambda_m}{\mu_m}\right\}\right)$, respectively.

4 Equilibrium points

The most important question during an epidemic is that how many person will be infected and when the spread of the disease will stop. This can be answered by finding the stationary points of the continous dynamical system which describe the epidemic model.

The stationary point of the Ross model (4) has to satisfies the following:

$$\begin{cases} abmI_m^*(1 - I_h^*) - rI_h^* = 0 \\ acI_h^*(1 - I_m^*) - \mu I_m^* = 0. \end{cases} \tag{16}$$

After solving the above algebraic system we get two equilibrium points:

$$(I_h^*, I_m^*)_1 = (0, 0) \text{ and} \\ (I_h^*, I_m^*)_2 = \left(\frac{a^2bcm - \mu r}{a^2bcm + acr}, \frac{a^2bcm - \mu r}{a^2bcm + abm\mu}\right). \tag{17}$$

Point $(I_h^*, I_m^*)_1$ is disease-free stationary point and point $(I_h^*, I_m^*)_2$ is endemic stationary point for system (4).

To get the equilibrium point of the extended model (6) let's denote $\gamma_1 := b\beta_h$ and $\gamma_2 := b\beta_m$ in system (6) as simplification. If there exists a stationary point $X \ge 0$ where $X = (S_h, E_h, I_h, R_h, S_m, E_m, I_m) \in \mathbb{R}^7$, it satisfies the following seven dimensional algebraic system:

$$\begin{cases} \Lambda_h - \frac{\gamma_1 S_h^* I_m^*}{1 + \nu_h I_m^*} - \mu_h S_h^* + \omega R_h^* = 0 \\ \frac{\gamma_1 S_h^* I_m^*}{1 + \nu_h I_m^*} - (\alpha_h + \mu_h)E_h^* = 0 \\ \alpha_h E_h^* - (r + \mu_h + \delta_h)I_h^* = 0 \\ rI_h^* - (\mu_h + \omega)R_h^* = 0 \\ \Lambda_m - \frac{\gamma_2 S_m^* I_h^*}{1 + \nu_m I_h^*} - \mu_m S_m^* = 0 \\ \frac{\gamma_2 S_m^* I_h^*}{1 + \nu_m I_h^*} - (\alpha_m + \mu_m)E_m^* = 0 \\ \alpha_m E_m^* - (\mu_m + \delta_m)I_h^* = 0. \end{cases} \tag{18}$$

From system (18) we get the following relations for the stationary points:

$$E_h^* = \frac{(r + \mu_h + \delta_h)I_h^*}{\alpha_h} \tag{19}$$

$$R_h^* = \frac{rI_h^*}{\mu_h + w} \tag{20}$$

$$S_m^* = \frac{\Lambda_m(1 + \nu_m I_h^*)}{\gamma_2 I_h^* + \mu_m(1 + \nu_m I_h^*)} \tag{21}$$

$$E_m^* = \frac{\gamma_2 S_m^* I_h^*}{(1 + \nu_m I_h^*)(\alpha_m + \mu_m)} \tag{22}$$

$$I_m^* = \frac{\alpha_m E_m^*}{\mu_m + \delta_m} \tag{23}$$

$$S_h^* = \frac{(\Lambda_h + wR_h^*)(1 + \nu_h I_m^*)}{\gamma_1 I_m^* + (1 + \nu_h I_m^*)\mu_h} \tag{24}$$

$$E_h^* = \frac{\gamma_1 S_h^* I_m^*}{(1 + \nu_h I_m^*)(\alpha_h + \mu_h)} \tag{25}$$

and I_h^* is a solution of a quadratic equation given by

$$(I_h^*)^2 - \frac{\mu_h\mu_m\Lambda_h(\mu_h+w)(R_0^2-1)}{\phi} I_h^* = 0. \quad (26)$$

here we have used the notation

$$\phi = w\mu_m\mu_h r R_0^2(\frac{(\alpha_h+\mu_h)(r+\mu_h+\delta_h)}{\alpha_h r} - 1)$$
$$+\mu_h\gamma_1\Lambda_h\mu_m C + (\mu_h+w)\Lambda_h\mu_h(\gamma_2+\mu_m\nu_m+\nu_h\mu_m C) \quad (27)$$

in which

$$C = \frac{\gamma_2\alpha_m\Lambda_m}{\mu_m(\delta_m+\mu_m)(\alpha_m+\mu_m)} \quad (28)$$

and

$$R_0 = $$
$$= \sqrt{\frac{\gamma_1\gamma_2\alpha_h\alpha_m\Lambda_h\Lambda_m}{\mu_h\mu_m(\alpha_h+\mu_h)(r+\mu_h+\delta_h)(\delta_m+\mu_m)(\alpha_m+\mu_m)}} \quad (29)$$

R_0 is called the basic reproduction ratio defined as the expected number of new cases of infection caused by a typical infected individual in a population of susceptibles only which is a criterion to determine a phenomenon is either disease-free, $R_0 < 1$, or endemic, $R_0 > 1$. To decide about this question we use linearization at disease-free stationary point ignoring the fact that the density of susceptibles decreases due to the infection process. The basic reproduction ratio is charcterized as a spectral radius of the next generation matrix of the model [9,10].

In absance of the epidemic in which the basic reproduction ratio $R_0 \leq 1$, $I_h^* = 0$ is a unique nonnegative solution for quadratic eqaution (25) and the other solution is negative. Therefore,

$$X^* = (S_h^*, E_h^*, I_h^*, R_h^*, S_m^*, E_m^*, I_m^*) =$$
$$= (\frac{\Lambda_h}{\mu_h}, 0, 0, 0, \frac{\Lambda_m}{\mu_m}, 0, 0) \quad (30)$$

is a unique posistive disease-free stationary point for system (6). Moreover, once the epidemic occurs, $R_0 > 1$, there exist two nonnegative solutions for (25) given by $I_h^* = 0$ and

$$I_h^{**} = \frac{\mu_h\mu_m\Lambda_h(\mu_h+w)(R_0^2-1)}{\phi} \quad (31)$$

hence,

$$X^{**} = (S_h^{**}, E_h^{**}, I_h^{**}, R_h^{**}, S_m^{**}, E_m^{**}, I_m^{**}) \quad (32)$$

in which all the components are occupied and positive is called endemic stationary point for system (6).

Theorem 5. *For system* (6)*, if* $R_0 < 1$*, there is a unique nonnegative disease-free stationary point and if* $R_0 > 1$*, there exist two nonnegative statioanry points.*

5 Numerical simulations

In Sections 3 and 4 we have shown that the solutions of Ross model (4) are in $[0,1]$, and the solutions of the extended Ross model (6) is on the interval $\left(0, \max\left\{V_h(0), \frac{\Lambda_h}{\mu_h}\right\}\right)$ and $\left(0, \max\left\{V_m(0), \frac{\Lambda_m}{\mu_m}\right\}\right)$, respectively. In this section we check it numerically.

For the numerical solution we used one of the simplest explicit method, the Explicit Euler method. Parameters are set according to Table 1 and 2, respectively.

In both simulations the solutions remain in the given domains as $t \to \infty$.

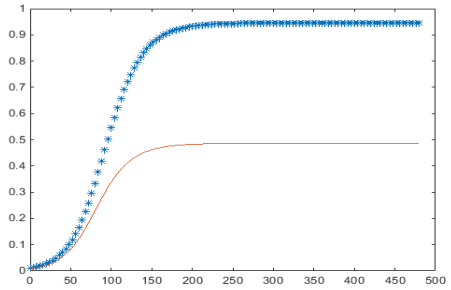


Figure 2: * denotes the density of infected humans and - visualizes the density of infected mosquitoes in Ross model (4).

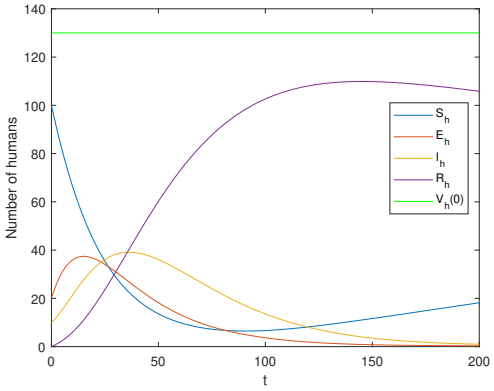


Figure 3: Number of humans in the four compartments in the extended Ross model (6).

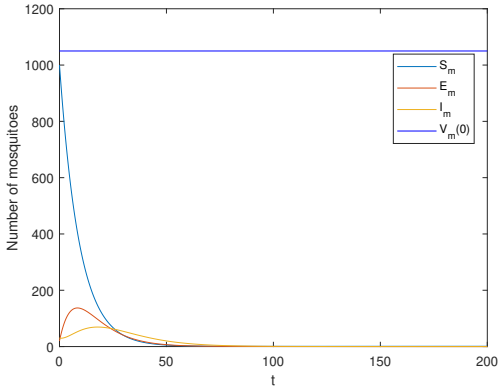


Figure 4: Number of mosquitoes in each compartments in the extended Ross model (6).

6 Summary

Since the solutions of Ross model are densities, it is proved that they are positively invariant in interval [0,1]. This results are visulalized numerically in Fig.2 in which the density of infected human and mosquito increases to reach the stationary points. Moreover, extended Ross model is considered qualitatively invariant in $\left(0, \max\left\{V_h(0), \frac{\Lambda_h}{\mu_h}\right\}\right)$ and $\left(0, \max\left\{V_m(0), \frac{\Lambda_m}{\mu_m}\right\}\right)$ for human and mosquito population respectively denoting in Fig. 3 and 4 by numeric simulation.

This paper proves that both models preserve the basic qualitative properties of the phenomenon. Since the Extended Ross model eliminates the shortcomings of the Ross model by considering the latency period, the vital dynamics and the recovery state, it is worth to use for simulate the propagation of malaria. That simulation can help to predict the peak of the epidemic and, as the stationary points of the continous models are given in this paper, an easy computation can give where the number of the infected and recovered individual tend during the epidemic.

Table 1: Values of the parameters in Fig.2.

Parameter	Value
a	0.4
m	0.6
b	0.3
c	0.5
r	0.002
μ	0.2

Table 2: Values of the parameters in Fig.3. and Fig.4.

$S_h(0) = 100$	$E_h(0) = 20$
$I_h(0) = 10$	$R_h(0) = 0$
$S_m(0) = 30$	$E_m(0) = 20$
$I_m(0) = 30$	
$\Lambda_h = 0.0004$	$\Lambda_m = 0.07$
$\beta_h = 0.2$	$\beta_m = 0.09$
$\mu_h = 0.00006$	$\mu_m = 0.067$
$\delta_h = 0.001$	$\delta_m = 0.01$
$\alpha_h = 0.06$	$\alpha_m = 0.055$
$r = 0.04$	$\omega = 0.0014$
$b = 0.15$	$\nu_h = 0.7$
$\nu_m = 0.3$	

Acknowledgement.
Many special thank to our supervisor, István Faragó, for his careful reading of our manuscript and his insightful comments and suggestions.

The project has been supported by the European Union, and co-financed by the European Social Fund (EFOP-3.6.3-VEKOP-16-2017-00002).

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