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Application of Computer Algebra into the Analysis of a Malaria Model using MAPLE™

Davinson Castaño Cano
EAFIT University
Colombia

1. Introduction

At the moment, we are at the edge of a possible biological trouble. Some people say that the 19th century was the century of chemistry, the 20th was the century of physics, and they say that the 21st will be the century of biology. If we think, the advances in the biological field in the recent years have been incredible, and like the physics and its atomic bomb, with biology could create global epidemics diseases. Also the climate change could produce a new virus better than the existing virus, creating an atmosphere of panic, such as the influenza A (H1N1) in recent years or Malaria who still killing people. To go a step further, we use computer science in the improvement of disease prevention (Baker, 2007; Magal & Rouen, 2008).
For beginning, we mention quickly some plagues in history such as the Black Death as an example of Bubonic plague, and we present from their basic concepts the most common classical epidemic models.
We present a transmission malaria model with inhomogeneities in a human population, which is proposed in terms of SIR coupled models for human and mosquitoes, which are described by differential equations. The human population is considered divided into several groups depending on genetics profiles, social condition, differentiation between rural or urban people, etc. Within malaria model we consider that mosquitoes bite humans in a differentiated way in accordance with the inhomogeneity. We use an algorithm for the analysis from local stability of the infection-free equilibrium and that algorithm is implemented on Maple™. This algorithm consists on determinate the characteristic polynomial from Jacobian matrix of the model and the analysis of their eigenvalues using Routh-Hurwitz theorem. As a result we obtain the basic reproductive number for malaria (R_o) and the threshold condition for a malaria epidemic triggering ($R_o>1$). From this result we can derivate effective control measures for avoiding malaria outbreaks and determinate the minimum level of income for a community becomes free of malaria infection. This work pretend to show the symbolic computing potential from CAS (Computer Algebra Systems), in our case Maple™, for analysing automatically complex epidemic models and the usefulness of them for designing and implementing public health politics.

2. Historical survey of epidemiological models

In this first part of the chapter, we are going to mention two aspects to capture your attention, the first one is a little tour for history where we refer to some of the most tragic

plagues, but we just pretend to show some examples of diseases for that reason it is not all the history of each plague, and the second one is a presentation of the most common models used in epidemics problems such as SIS, SIR and SEIR models, trying to explain their dynamics. This model models can be used in other sciences such as economics, biology, etc. (Perthame, 2007)

2.1 Epidemic infections

It's true that in our time, every year is more difficult to find an outbreak in the developed countries, but it isn't the same situation in the developing countries, in which the epidemics problems appear frequently (Porta, 2008).

Initially, human diseases began with the change of their way to live, the first change was when humans learnt the agriculture which made possible that more people could live in the same place, this situation produced problems on healthiness and then, the diseases started. The next step in the change of life was domesticating animals, which gave us some disease because of their genetic changes. Some of the diseases that we have thanks to animals are Measles, Tuberculosis, Smallpox, Influenza, Malaria, between others.

We introduce the *Bubonic Plague* who had his biggest spreading with the name *Black Death* in mid-fourteenth century, it received his name because of the black skin that people had when they were dying. This plague is spread by vectors that could be rats and other small mammals, and their fleas. Some cases of this plague were reported in Athens in the Peloponnesian War, and after the 14th century, in the World War II, Japan spread infected fleas over some cities in China (Christakos et al., 2005; Gottfried, 1983).

Now we talk about *Malaria* and *Yellow Fever*, both diseases are transmitted by flies and it for that reason that these diseases are very dangerous because his range of spread could be extremely wide. In the case of the *Malaria* the historians believe that its beginning was in the apes in Africa, this disease is also called *Burning Ague* because of intermittent painful fevers. The *Yellow Fever* is called "*Yellow Jack*", the name yellow is for the colour that people have with this illness. These diseases are described even in the bible, the old testament, Leviticus 26:16, "*then I will do this to you: I will visit you with panic, with wasting disease and fever that consume the eyes and make the heart ache...*" and Deuteronomy 28:22, "*The LORD will strike you with wasting disease and with fever, inflammation and fiery heat...*" And in present days still happen even more in countries near to the equatorial line because the mosquitoes find ideal conditions to survive, temperature between 20°C and 30°C, and humidity over 60%.

As a final example of infections, we bring the *Smallpox* and *Measles*, which are the most severe example of how humans appear the diseases, and these diseases have the highest fatality rate in the history, surpassing even the medieval *Black Death*. The *Smallpox* was widely used in the process of America's conquest with the intension of decimate the native population. With the last phrase we note the human intention to use biological weapons, and it's worrying to think in the biological weapon that we could have with the actual technologies (Bollet, 2004).

2.2 Models used

Now, we talk about some models used to predict the behaviour of the population along an infection. The models we show here are classical in epidemiology and they are differential equations systems (Stewart, 2002). We won't show the equations systems because they depend on the characteristics of the epidemic, but we will show some diagrams. If you want

to find the mathematical expressions, you can see the references (Brauer et al., 2008; Capasso, 2008; Ma & Xia, 2009; Daley & Gani, 2005). All these models have been formulated by great researchers who have contributed to the development of the techniques of diseases dynamics treatment, also it's important to note that the difficulty for the accuracy in these models is the obtaining of the parameters (Bellomo, 2008).

- **SIS Model**

This model is the simplest model in epidemiology because it has only two population groups the susceptible and the infected, which are related by λ and γ functions that could depend on time or be just a constant, these functions are named: λ is the infectious rate function and γ is the recovering rate function. Also, it is a model with a boucle or feedback. It could easily model a pneumonia disease (Ma & Xia, 2009).

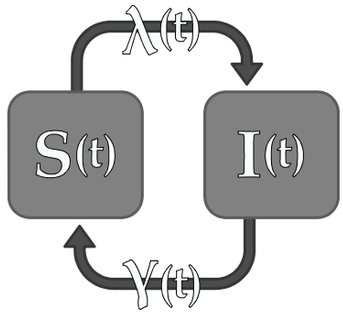

Fig. 1. Representation of the SIS Model

- **SIR Model**

Now, we present a model which has been widely used. In this model is included a new group, the Recovered group which is immune of the infection, in this chapter we are going to use a modified version of this model, with this system we can model a lot of diseases related to viruses such as Malaria, Influenza, Smallpox, Measles, Rubella, Yellow Fever, Dengue Fever, etc. (Castaño C., 2009; Ma & Xia, 2009).

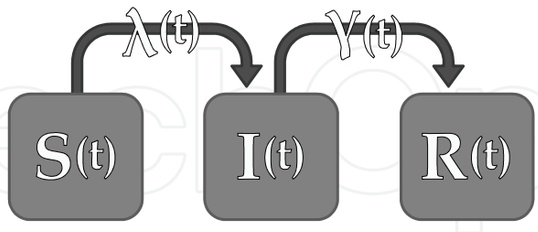

Fig. 2. Representation of the SIR Model

- **SIRS Model**

This model is basically the same SIR model except for the temporal immunity and the recovered people will be susceptible again after a time. In this model apart from the λ and γ functions is included a third relation function ξ which represent the susceptible creation rate. This model is used in the same cases of the SIS model such as Gonorrhoea, Typhoid Fever, Tuberculosis, Cholera, Meningitis, etc. The election depends on the person, if he wants to have in count the immunity time (Capasso, 2008).

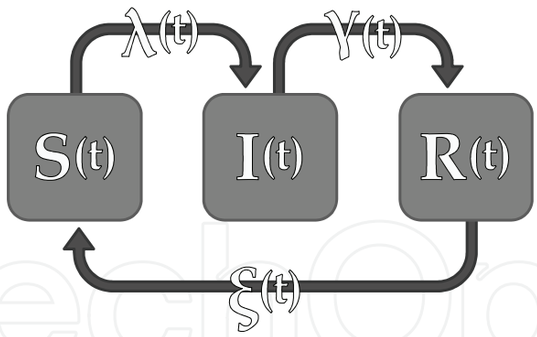

Fig. 3. Representation of the SIRS Model

- **SEIR and SEIRS Models**

These models are more elaborated because they included another group which is called the Exposed group that means; a person who has a contact with an infected person, he become exposed and passed certain time he become infected and start infecting too. The dynamics of the SEIR and SEIRS model is very similar to the SIR and SIRS models, respectively. Also, in these models appear a new function β that is the exposition rate.

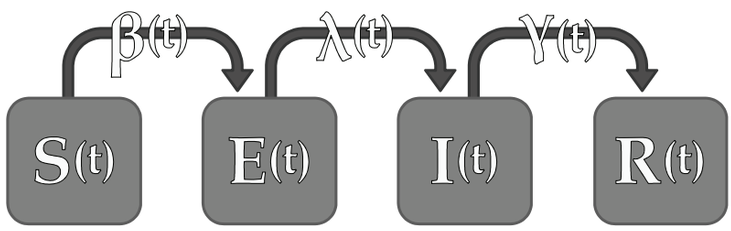

Fig. 4. Representation of the SEIR Model

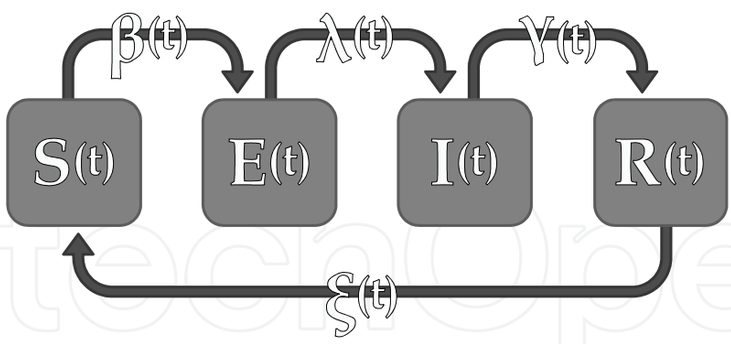

Fig. 5. Representation of the SEIRS Model

Apart from these models there are others like the M-Models which included in the M-group that is for the newborns who have a passive immunity in the moment of birth and after they will be part of the susceptible group (S-Group). If you want to clarify some concept of these models, we recommend reading the book of Basic Epidemiology (Bonita et al., 2006).

3. Malaria SIR coupled model

Now, we present the work we did based in the SIR model, which is coupled with other equal. These coupled models are for the human population and the vectors that allow model

the Malaria disease. We begin with a human group without inhomogeneities and after we start to include inhomogeneities for in the humans that are represented with the creation of different groups of humans, we begin with a single group until three groups of humans, and also, we present a generalization for the basic reproductive number. We introduce briefly the concept of Mechanized Reasoning too.

3.1 SIR model for one group of humans

For beginning we introduce the differential equations that describe the dynamics of the Malaria disease, apart from this, we introduce to Maple™ environment and show how to solve the model; showing the given instructions and the results.
We start presenting the differential equation system that describes the human population behaviour; this population is constant in time:

$$\frac{d}{dt}S_h(t) = \mu_h N_h - \frac{b\,\beta_{v,h}\,S_h(t)\,I_v(t)}{N_h} - \mu_h S_h(t) \tag{1}$$

$$\frac{d}{dt}I_h(t) = \frac{b\,\beta_{v,h}\,S_h(t)\,I_v(t)}{N_h} - (\gamma_h + \mu_h)\,I_h(t) \tag{2}$$

$$\frac{d}{dt}R_h(t) = \gamma_h\,I_h(t) - \mu_h\,R_h(t) \tag{3}$$

For inserting equation on Maple™ we write in a line the expression we want to have, like example for the equation (1), we write (note that *diff()* is the command for differential):

*diff(S[h](t),t)=mu[h]*N[h]-b*beta[v,h]*S[h](t)*I[v](t)/N[h]-mu[h]*S[h](t);*

The variables that appear in the equation system are:
μ_h : Natural death rate which is the same birth rate for keeping a constant population.
N_h : Total population of humans.
b : Susceptibility of the susceptible individuals.
$\beta_{v,h}$: Infection rate from the infected vectors to the susceptible humans.
γ_h : Recovering rate or Immunisation rate.
The subscript h is for referring to humans and the v is for the vectors.
Now, we introduce the analogue equations for the vector system:

$$\frac{d}{dt}S_v(t) = \mu_v N_v - \frac{b\,\beta_{h,v}\,S_v(t)\,I_h(t)}{N_h} - \mu_v S_v(t) \tag{4}$$

$$\frac{d}{dt}I_v(t) = \frac{b\,\beta_{h,v}\,S_v(t)\,I_h(t)}{N_h} - (\gamma_v + \mu_v)\,I_v(t) \tag{5}$$

$$\frac{d}{dt}R_v(t) = \gamma_v\,I_v(t) - \mu_v\,R_v(t) \tag{6}$$

For using the algorithm and obtaining an algebraic system, we exclude the time dependence in the functions:

$$S_h(t) = S_h \quad I_h(t) = I_h \quad R_h(t) = R_h \quad S_v(t) = S_v \quad I_v(t) = I_v \quad R_v(t) = R_v \tag{7}$$

These expressions, we introduce them:

S[h](t)=S[h],I[h](t)=I[h],R[h](t)=R[h],S[v](t)=S[v],I[v](t)=I[v],R[v](t)=R[v];

Taking the right hand side of the equation from (1) to (6), and replacing in them (7), we obtain a group of expressions:

$$\begin{gathered}
\mu_h\, N_h - \frac{b\,\beta_{v,h}\, S_h\, I_v}{N_h} - \mu_h\, S_h \\
\frac{b\,\beta_{v,h}\, S_h\, I_v}{N_h} - (\gamma_h + \mu_h)\, I_h \\
\gamma_h\, I_h - \mu_h\, R_h \\
\mu_v\, N_v - \frac{b\,\beta_{h,v}\, S_v\, I_h}{N_h} - \mu_v S_v \\
\frac{b\,\beta_{h,v}\, S_v\, I_h}{N_h} - (\gamma_v + \mu_v)\, I_v \\
\gamma_v\, I_v - \mu_v\, R_v
\end{gathered} \tag{8}$$

For taking the right hand side in Maple™ we use command *rhs()* and write as follow for obtaining the vector (command *Vector()*) of relations:

*Vector(subs(**(7)**,[rhs(**(1)**),rhs(**(2)**),rhs(**(3)**),rhs(**(4)**),rhs(**(5)**),rhs(**(6)**)]));*

In this command appears some number in bold, which indicate the reference, for making a link with the references we use *Ctrl+L*. For solving (8), we use the command *solve()* like the following line:

*solve(**(8)**,[S[h],I[h],R[h],S[v],I[v],R[v]]);*

Solving this group we find in the first place the trivial solution:

$$S_h(t) = N_h \quad I_h(t) = 0 \quad R_h(t) = 0 \quad S_v(t) = N_v \quad I_v(t) = 0 \quad S_v(t) = 0 \tag{9}$$

Continuing with the algorithm for finding the basic reproductive number, we build the Jacobian, for that we use the commands *Matrix()* and *jacobian()*, and also, we use (8):

*Matrix(jacobian(**(8)**,[S[h],I[h],R[h],S[v],I[v],R[v]]));*

We obtain the follow matrix:

$$\begin{bmatrix}
-\frac{b\beta_{v,h}I_v}{N_h} - \mu_h & 0 & 0 & 0 & -\frac{b\beta_{v,h}S_h}{N_h} & 0 \\
\frac{b\beta_{v,h}I_v}{N_h} & -\gamma_h - \mu_h & 0 & 0 & \frac{b\beta_{v,h}S_h}{N_h} & 0 \\
0 & \gamma_h & -\mu_h & 0 & 0 & 0 \\
0 & -\frac{b\beta_{h,v}\,S_v}{N_h} & 0 & -\frac{b\beta_{h,v}\,I_h}{N_h} - \mu_v & 0 & 0 \\
0 & \frac{b\beta_{h,v}\,S_v}{N_h} & 0 & \frac{b\beta_{h,v}\,I_h}{N_h} & -\gamma_v - \mu_v & 0 \\
0 & 0 & 0 & 0 & \gamma_v & -\mu_v
\end{bmatrix} \tag{10}$$

However, we replace (9) in (10), for that we use the command *subs()*:

*subs((**9**),(**10**));*

Obtaining the simplified matrix:

$$\begin{bmatrix} -\mu_h & 0 & 0 & 0 & -b\beta_{v,h} & 0 \\ 0 & -\gamma_h-\mu_h & 0 & 0 & b\beta_{v,h} & 0 \\ 0 & \gamma_h & -\mu_h & 0 & 0 & 0 \\ 0 & -\dfrac{b\beta_{h,v}\,N_v}{N_h} & 0 & 0-\mu_v & 0 & 0 \\ 0 & \dfrac{b\beta_{h,v}\,N_v}{N_h} & 0 & 0 & -\gamma_v-\mu_v & 0 \\ 0 & 0 & 0 & 0 & \gamma_v & -\mu_v \end{bmatrix} \tag{11}$$

From (11) we generate the characteristic polynomial (command *charpoly()*):

*factor(charpoly((**11**),lambda));*

We find:

$$(\lambda+\mu_v)^2(\lambda+\mu_h)^2\left(\lambda^2+(\gamma_h+\mu_h+\gamma_v+\mu_v)\lambda+(\mu_h+\gamma_h)(\mu_v+\gamma_v)-b^2\beta_{v,h}\beta_{h,v}\frac{N_v}{N_h}\right) \tag{12}$$

Now we take the larger term:

$$\lambda^2+(\gamma_h+\mu_h+\gamma_v+\mu_v)\lambda+(\mu_h+\gamma_h)(\mu_v+\gamma_v)-b^2\beta_{v,h}\beta_{h,v}\frac{N_v}{N_h} \tag{13}$$

From (13), we catch the lambda non-dependent term. For the infection-free equilibrium, this term should be major than zero.

$$0<(\mu_h+\gamma_h)(\mu_v+\gamma_v)-b^2\beta_{v,h}\beta_{h,v}\frac{N_v}{N_h} \tag{14}$$

Isolating N_v, we obtain (command *isolate()*):

$$N_v<\frac{(\mu_h+\gamma_h)(\mu_v+\gamma_v)N_h}{b^2\beta_{v,h}\beta_{h,v}} \tag{15}$$

Ordering (15), we define the basic reproductive number (Chowell et al., 2009):

$$R_0=\frac{b^2\beta_{v,h}\beta_{h,v}}{(\mu_h+\gamma_h)(\mu_v+\gamma_v)}\frac{N_v}{N_h} \qquad R_0<1 \tag{16}$$

Here we have obtained the condition for the infection-free equilibrium, if we have a system that satisfy $R_0<1$, then the population will be free of infection when the time lay to infinity (Ma et al., 2009).

For recapitulating the lines we put in Maple™, we present all the commands we used for obtain each equation presented before:

(1) *diff(S[h](t),t)=mu[h]*N[h]-b*beta[v,h]*S[h](t)*I[v](t)/N[h]-mu[h]*S[h](t);*
(2) *diff(I[h](t),t)=b*beta[v,h]*S[h](t)*I[v](t)/N[h]-gamma[h]*I[h](t)-mu[h]*I[h](t);*
(3) *diff(R[h](t),t)=gamma[h]*I[h](t)-mu[h]*R[h](t);*
(4) *diff(S[v](t),t)=mu[v]*N[v]-b*beta[h,v]*S[v](t)*I[h](t)/N[h]-mu[v]*S[v](t);*
(5) *diff(I[v](t),t)=b*beta[h,v]*S[v](t)*I[h](t)/N[h]-gamma[v]*I[v](t)-mu[v]*I[v](t);*
(6) *diff(R[v](t),t)=gamma[v]*I[v](t)-mu[v]*R[v](t);*
(7) *S[h](t)=S[h],I[h](t)=I[h],R[h](t)=R[h],S[v](t)=S[v],I[v](t)=I[v],R[v](t)=R[v];*
(8) *Vector(subs(**(7)**,[rhs(**(1)**),rhs(**(2)**),rhs(**(3)**),rhs(**(4)**),rhs(**(5)**),rhs(**(6)**)]));*
(9) *solve(**(8)**,[S[h],I[h],R[h],S[v],I[v],R[v]]);*
(10) *Matrix(jacobian(**(8)**,[S[h],I[h],R[h],S[v],I[v],R[v]]));*
(11) *subs(**(9)**,**(10)**);*
(12) *factor(charpoly(**(11)**,lambda));*
(13) *collect(expand(subs(lambda+mu[v]=1,lambda+mu[h]=1,**(12)**)),lambda);*
(14) *coeff(**(13)**,lambda,0)>0;*
(15) *solve(**(14)**,N[v]) assuming b>0,beta[h,v]>0,N[h]>0,beta[v,h]>0:%[1][1];*
(16) *R[0]=factor(lhs(**(15)**)*denom(rhs(**(15)**)))/numer(rhs(**(15)**)));*

It is vital to charge the package of linear algebra:

with(linalg);

For more information about this software, we recommend to you to see the reference that we have utilised for some command (Maplesoft, 2007).

3.2 SIR model for two groups of humans

Now we are concerned to a system that has an inhomogeneity in the humans, this could be thought as two different resistances against the infection or two different races. We present the constitutive equations, for the first group of humans we have:

$$\frac{d}{dt}S_{h,1}(t) = \mu_{h,1}\, N_{h,1} - \frac{b\,\beta_{v,h,1}\, S_{h,1}(t)\, I_v(t)}{N_{h,1}} - \mu_{h,1}\, S_{h,1}(t) \tag{17}$$

$$\frac{d}{dt}I_{h,1}(t) = \frac{b\,\beta_{v,h,1}\, S_{h,1}(t)\, I_v(t)}{N_{h,1}} - \left(\gamma_{h,1} + \mu_{h,1}\right) I_{h,1}(t) \tag{18}$$

$$\frac{d}{dt}R_{h,1}(t) = \gamma_{h,1}\, I_{h,1}(t) - \mu_{h,1}\, R_{h,1}(t) \tag{19}$$

For the second we have:

$$\frac{d}{dt}S_{h,2}(t) = \mu_{h,2}\, N_{h,2} - \frac{b\,\beta_{v,h,2}\, S_{h,2}(t)\, I_v(t)}{N_{h,2}} - \mu_{h,2}\, S_{h,2}(t) \tag{20}$$

$$\frac{d}{dt}I_{h,2}(t) = \frac{b\,\beta_{v,h,2}\, S_{h,2}(t)\, I_v(t)}{N_{h,2}} - \left(\gamma_{h,2} + \mu_{h,2}\right) I_{h,2}(t) \tag{21}$$

$$\frac{d}{dt}R_{h,2}(t) = \gamma_{h,2}\, I_{h,2}(t) - \mu_{h,2}\, R_{h,2}(t) \tag{22}$$

And for the vector or group of mosquitoes, we have:

$$\frac{d}{dt}S_v(t) = \mu_v\, N_v - \left(\frac{b_1\beta_{h,v,1}\, I_{h,1}(t)}{N_{h,1}} + \frac{b_2\beta_{h,v,2}\, I_{h,2}(t)}{N_{h,2}}\right) S_v(t) - \mu_v S_v(t) \tag{23}$$

$$\frac{d}{dt}I_v(t) = \left(\frac{b_1\beta_{h,v,1}\, I_{h,1}(t)}{N_{h,1}} + \frac{b_2\beta_{h,v,2}\, I_{h,2}(t)}{N_{h,2}}\right) S_v(t) - (\gamma_v + \mu_v)\, I_v(t) \tag{24}$$

$$\frac{d}{dt}R_v(t) = \gamma_v\, I_v(t) - \mu_v\, R_v(t) \tag{25}$$

Now, we need to change the notation from differential equation to algebraic expressions, we have to change the equations (17) to (25), following the next terms:

$$\begin{array}{ccc} S_{h,1}(t) = S_{h,1} & I_{h,1}(t) = I_{h,1} & R_{h,1}(t) = R_{h,1} \\ S_{h,2}(t) = S_{h,2} & I_{h,2}(t) = I_{h,2} & R_{h,2}(t) = R_{h,2} \\ S_v(t) = S_v & I_v(t) = I_v & R_v(t) = R_v \end{array} \tag{26}$$

With (26), and the right hand side of the equations (17) to (25), we make the change to algebraic expression, after that, we generate the Jacobian matrix which allow us analysing the stability of the system, in other words, seeing if the system will be free of infection. We continue showing the Jacobian we have made:

$$\begin{bmatrix} -\frac{b_1\beta_{v,h,1}I_v}{N_{h,1}} - \mu_{h,1} & 0 & 0 & 0 & 0 & 0 & 0 & -\frac{b_1\beta_{v,h,1}S_{h,1}}{N_{h,1}} & 0 \\ \frac{b_1\beta_{v,h,1}I_v}{N_{h,1}} & -\gamma_{h,1} - \mu_{h,1} & 0 & 0 & 0 & 0 & 0 & \frac{b_1\beta_{v,h,1}S_{h,1}}{N_{h,1}} & 0 \\ 0 & \gamma_{h,1} & -\mu_{h,1} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\frac{b_2\beta_{v,h,2}I_v}{N_{h,2}} - \mu_{h,2} & 0 & 0 & 0 & -\frac{b_2\beta_{v,h,2}S_{h,2}}{N_{h,2}} & 0 \\ 0 & 0 & 0 & \frac{b_2\beta_{v,h,2}I_v}{N_{h,2}} & -\gamma_{h,2} - \mu_{h,2} & 0 & 0 & \frac{b_2\beta_{v,h,2}S_{h,2}}{N_{h,2}} & 0 \\ 0 & 0 & 0 & 0 & \gamma_{h,2} & -\mu_{h,2} & 0 & 0 & 0 \\ 0 & -\frac{b_1\beta_{h,v,1}S_v}{N_{h,1}} & 0 & 0 & -\frac{b_2\beta_{h,v,2}S_v}{N_{h,2}} & 0 & A & 0 & 0 \\ 0 & \frac{b_1\beta_{h,v,1}S_v}{N_{h,1}} & 0 & 0 & \frac{b_2\beta_{h,v,2}S_v}{N_{h,2}} & 0 & B & -\gamma_v - \mu_v & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_v & -\mu_v \end{bmatrix} \tag{27}$$

Where *A* and *B* are:

$$A = -\frac{b_1\beta_{h,v,1}I_v}{N_{h,1}} - \frac{b_2\beta_{h,v,2}I_v}{N_{h,2}} - \mu_v \tag{28}$$

$$B = \frac{b_1\beta_{h,v,1}I_v}{N_{h,1}} + \frac{b_2\beta_{h,v,2}I_v}{N_{h,2}} \tag{29}$$

As the first model, we find that the trivial solution is:

$$\begin{array}{lll} S_{h,1}(t) = N_{h,1} & I_{h,1}(t) = 0 & R_{h,1}(t) = 0 \\ S_{h,2}(t) = N_{h,2} & I_{h,2}(t) = 0 & R_{h,2}(t) = 0 \\ S_v(t) = N_v & I_v(t) = 0 & R_v(t) = 0 \end{array} \tag{30}$$

Replacing the found results in the trivial solution (30) in (27), we find the simplified matrix which let us find the basic reproductive number.

$$\begin{bmatrix} -\mu_{h,1} & 0 & 0 & 0 & 0 & 0 & 0 & -b_1\beta_{v,h,1} & 0 \\ 0 & -\gamma_{h,1} - \mu_{h,1} & 0 & 0 & 0 & 0 & 0 & b_1\beta_{v,h,1} & 0 \\ 0 & \gamma_{h,1} & -\mu_{h,1} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\mu_{h,2} & 0 & 0 & 0 & -b_2\beta_{v,h,2} & 0 \\ 0 & 0 & 0 & 0 & -\gamma_{h,2} - \mu_{h,2} & 0 & 0 & b_2\beta_{v,h,2} & 0 \\ 0 & 0 & 0 & 0 & \gamma_{h,2} & -\mu_{h,2} & 0 & 0 & 0 \\ 0 & -\dfrac{b_1\beta_{h,v,1}N_v}{N_{h,1}} & 0 & 0 & -\dfrac{b_2\beta_{h,v,2}N_v}{N_{h,2}} & 0 & -\mu_v & 0 & 0 \\ 0 & \dfrac{b_1\beta_{h,v,1}N_v}{N_{h,1}} & 0 & 0 & \dfrac{b_2\beta_{h,v,2}N_v}{N_{h,2}} & 0 & 0 & -\gamma_v - \mu_v & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_v & -\mu_v \end{bmatrix} \tag{31}$$

With the matrix we find the characteristic polynomial,

$$\left(\lambda + \mu_{h,2}\right)^2 \left(\lambda + \mu_{h,1}\right)^2 (\lambda + \mu_v)^2 (\lambda^3 + C\lambda^2 + D\lambda + E) \tag{32}$$

Where *C*, *D* and *E*:

$$C = \gamma_{h,1} + \mu_{h,1} + \gamma_{h,2} + \mu_{h,2} + \gamma_v + \mu_v \tag{33}$$

$$D = \left(\gamma_{h,1} + \mu_{h,1}\right)\left(\gamma_{h,2} + \mu_{h,2}\right) + \left(\gamma_{h,1} + \mu_{h,1}\right)(\gamma_v + \mu_v) + \left(\gamma_{h,2} + \mu_{h,2}\right)(\gamma_v + \mu_v) - \left(\frac{b_1^2\beta_{h,v,1}\beta_{v,h,1}}{N_{h,1}} + \frac{b_2^2\beta_{h,v,2}\beta_{v,h,2}}{N_{h,2}}\right) N_v \tag{34}$$

$$E = \left(\gamma_{h,1} + \mu_{h,1}\right)\left(\gamma_{h,2} + \mu_{h,2}\right)(\gamma_v + \mu_v) - \left(\frac{b_1^2\beta_{h,v,1}\beta_{v,h,1}}{N_{h,1}}\left(\gamma_{h,2} + \mu_{h,2}\right) + \frac{b_2^2\beta_{h,v,2}\beta_{v,h,2}}{N_{h,2}}\left(\gamma_{h,1} + \mu_{h,1}\right)\right) N_v \tag{35}$$

From (32) we substrate the larger term:

$$\lambda^3 + C\lambda^2 + D\lambda + E \tag{36}$$

Here, we take the term lambda non-dependent, which should be major than zero, for accomplish the free-equilibrium condition:

$$0 < \left(\gamma_{h,1} + \mu_{h,1}\right)\left(\gamma_{h,2} + \mu_{h,2}\right)\left(\gamma_v + \mu_v\right) - \left(\frac{b_1^2 \beta_{h,v,1}\beta_{v,h,1}}{N_{h,1}}\left(\gamma_{h,2} + \mu_{h,2}\right) + \frac{b_2^2 \beta_{h,v,2}\beta_{v,h,2}}{N_{h,2}}\left(\gamma_{h,1} + \mu_{h,1}\right)\right) N_v \tag{37}$$

For the free-equilibrium, the population of mosquitoes should be:

$$N_v < \frac{\left(\gamma_{h,1} + \mu_{h,1}\right)\left(\gamma_{h,2} + \mu_{h,2}\right)\left(\gamma_v + \mu_v\right)}{\left(\frac{b_1^2 \beta_{h,v,1}\beta_{v,h,1}}{N_{h,1}}\left(\gamma_{h,2} + \mu_{h,2}\right) + \frac{b_2^2 \beta_{h,v,2}\beta_{v,h,2}}{N_{h,2}}\left(\gamma_{h,1} + \mu_{h,1}\right)\right)} \tag{38}$$

Where the basic reproductive number R_0 is:

$$R_0 = \frac{b_1^2 \beta_{h,v,1}\beta_{v,h,1}}{\left(\gamma_{h,1} + \mu_{h,1}\right)\left(\gamma_v + \mu_v\right)}\frac{N_v}{N_{h,1}} + \frac{b_2^2 \beta_{h,v,2}\beta_{v,h,2}}{\left(\gamma_{h,2} + \mu_{h,2}\right)\left(\gamma_v + \mu_v\right)}\frac{N_v}{N_{h,2}} \tag{39}$$

If you notice the equation (16) and (39) are similar in their structure.

3.3 SIR model for three groups of humans

In this subsection we just present another model where it's included a third inhomogeneity, so we have now three groups of humans. We commence with the systems of humans, which are represented by nine equations, every group with three equations, for the first group:

$$\frac{d}{dt}S_{h,1}(t) = \mu_{h,1}\, N_{h,1} - \frac{b\, \beta_{v,h,1}\, S_{h,1}(t)\, I_v(t)}{N_{h,1}} - \mu_{h,1}\, S_{h,1}(t) \tag{40}$$

$$\frac{d}{dt}I_{h,1}(t) = \frac{b\, \beta_{v,h,1}\, S_{h,1}(t)\, I_v(t)}{N_{h,1}} - \left(\gamma_{h,1} + \mu_{h,1}\right) I_{h,1}(t) \tag{41}$$

$$\frac{d}{dt}R_{h,1}(t) = \gamma_{h,1}\, I_{h,1}(t) - \mu_{h,1}\, R_{h,1}(t) \tag{42}$$

For the second one:

$$\frac{d}{dt}S_{h,2}(t) = \mu_{h,2}\, N_{h,2} - \frac{b\, \beta_{v,h,2}\, S_{h,2}(t)\, I_v(t)}{N_{h,2}} - \mu_{h,2} S_{h,2}(t) \tag{43}$$

$$\frac{d}{dt}I_{h,2}(t) = \frac{b\, \beta_{v,h,2}\, S_{h,2}(t)\, I_v(t)}{N_{h,2}} - \left(\gamma_{h,2} + \mu_{h,2}\right) I_{h,2}(t) \tag{44}$$

$$\frac{d}{dt}R_{h,2}(t) = \gamma_{h,2}\, I_{h,2}(t) - \mu_{h,2}\, R_{h,2}(t) \tag{45}$$

And for the third system:

$$\frac{d}{dt}S_{h,3}(t) = \mu_{h,3}\, N_{h,3} - \frac{b\, \beta_{v,h,3}\, S_{h,3}(t)\, I_v(t)}{N_{h,3}} - \mu_{h,3} S_{h,3}(t) \tag{46}$$

$$\frac{d}{dt}I_{h,3}(t) = \frac{b\, \beta_{v,h,3}\, S_{h,3}(t)\, I_v(t)}{N_{h,3}} - \left(\gamma_{h,3} + \mu_{h,3}\right) I_{h,3}(t) \tag{47}$$

$$\frac{d}{dt}R_{h,3}(t) = \gamma_{h,3}\, I_{h,3}(t) - \mu_{h,3}\, R_{h,3}(t) \tag{48}$$

Now we show in the same direction, the system for the vectors:

$$\frac{d}{dt}S_v(t) = \mu_v\, N_v - \left(\sum_{i=1}^{3} \frac{b_i \beta_{h,v,i}\, I_{h,i}(t)}{N_{h,i}}\right) S_v(t) - \mu_v S_v(t) \tag{49}$$

$$\frac{d}{dt}I_v(t) = \left(\sum_{i=1}^{3} \frac{b_i \beta_{h,v,i}\, I_{h,i}(t)}{N_{h,i}}\right) S_v(t) - (\gamma_v + \mu_v)\, I_v(t) \tag{50}$$

$$\frac{d}{dt}R_v(t) = \gamma_v\, I_v(t) - \mu_v\, R_v(t) \tag{51}$$

Now, with all the equations from our system we can start replacing the time dependent functions for variables:

$$\begin{array}{ccc} S_{h,1}(t) = S_{h,1} & I_{h,1}(t) = I_{h,1} & R_{h,1}(t) = R_{h,1} \\ S_{h,2}(t) = S_{h,2} & I_{h,2}(t) = I_{h,2} & R_{h,2}(t) = R_{h,2} \\ S_{h,3}(t) = S_{h,3} & I_{h,2}(t) = I_{h,3} & R_{h,2}(t) = R_{h,3} \\ S_v(t) = S_v & I_v(t) = I_v & R_v(t) = R_v \end{array} \tag{52}$$

Where the trivial solution is:

$$\begin{array}{ccc} S_{h,1}(t) = N_{h,1} & I_{h,1}(t) = 0 & R_{h,1}(t) = 0 \\ S_{h,2}(t) = N_{h,2} & I_{h,2}(t) = 0 & R_{h,2}(t) = 0 \\ S_{h,3}(t) = N_{h,3} & I_{h,2}(t) = 0 & R_{h,2}(t) = 0 \\ S_v(t) = N_v & I_v(t) = 0 & R_v(t) = 0 \end{array} \tag{53}$$

With this information and following the algorithm that we have been following in this section, we build the Jacobian matrix:

$$\begin{bmatrix} 12\ x\ 12\ Matrix \\ Data\ Type: anything \\ Storage: rectangular \\ Order: Fortran\_order \end{bmatrix} \tag{54}$$

We just put in (54) the information that Maple™ give us about the matrix, and also, we just put this because the matrix is too big for the paper size.

If the matrix is big, you can imagine the characteristic polynomial, for that reason for this model, we just write the basic reproductive number.

$$R_0 = \frac{b_1^2 \beta_{h,v,1} \beta_{v,h,1}}{(\gamma_{h,1} + \mu_{h,1})(\gamma_v + \mu_v)} \frac{N_v}{N_{h,1}} + \frac{b_2^2 \beta_{h,v,2} \beta_{v,h,2}}{(\gamma_{h,2} + \mu_{h,2})(\gamma_v + \mu_v)} \frac{N_v}{N_{h,2}} + \frac{b_3^2 \beta_{h,v,3} \beta_{v,h,3}}{(\gamma_{h,3} + \mu_{h,3})(\gamma_v + \mu_v)} \frac{N_v}{N_{h,3}} \tag{55}$$

Again, we can see that this result is similar to the others (16) and (39). With that it's easy to introduce the next section.

4. Generalized malaria SIR coupled model

As we will show in this section, it is possible in an intuitive way to start generalizing some part of the model, we start resuming the equation for the n groups of humans:

$$\frac{d}{dt} S_{h,i}(t) = \mu_{h,i} N_{h,i} - \frac{b \beta_{v,h,i} S_{h,i}(t) I_v(t)}{N_{h,i}} - \mu_{h,i} S_{h,i}(t) \tag{56}$$

$$\frac{d}{dt} I_{h,i}(t) = \frac{b \beta_{v,h,i} S_{h,i}(t) I_v(t)}{N_{h,i}} - (\gamma_{h,i} + \mu_{h,i}) I_{h,i}(t) \tag{57}$$

$$\frac{d}{dt} R_{h,i}(t) = \gamma_{h,i} I_{h,i}(t) - \mu_{h,i} R_{h,i}(t) \tag{58}$$

And the group of vectors or mosquitoes:

$$\frac{d}{dt} S_v(t) = \mu_v N_v - \left(\sum_{i=1}^{n} \frac{b_i \beta_{h,v,i} I_{h,i}(t)}{N_{h,i}} \right) S_v(t) - \mu_v S_v(t) \tag{59}$$

$$\frac{d}{dt} I_v(t) = \left(\sum_{i=1}^{n} \frac{b_i \beta_{h,v,i} I_{h,i}(t)}{N_{h,i}} \right) S_v(t) - (\gamma_v + \mu_v) I_v(t) \tag{60}$$

$$\frac{d}{dt} R_v(t) = \gamma_v I_v(t) - \mu_v R_v(t) \tag{61}$$

The complete system is described for $3(n+1)$ equations, which is condensed in the last six expressions. For solving these systems for large values of n, it becomes in a computational problem; for that reason the idea of a computer that with the simplest forms of the problem could obtain generalized results. This foundation is called Mechanized Reasoning and in this direction is thought this section (Castaño C, 2009).

With the results that we have obtained in the three studied cases, we could intuitively try to discover de general rule or expression for our generalized system.

Could see the results (16), (39) and (55), with this results we can build a logical general result, it's important to note that we rewrite the basic reproductive number with the intension to show easily the behaviour of the result between the different values for n. We note $R_{0,n}$ for each model where n is the number of the groups of humans.

$$R_{0,1} = \frac{b^2\beta_{v,h}\beta_{h,v}}{(\mu_h + \gamma_h)(\mu_v + \gamma_v)}\frac{N_v}{N_h} \tag{62}$$

$$R_{0,2} = \frac{b_1^2\beta_{h,v,1}\beta_{v,h,1}}{(\gamma_{h,1} + \mu_{h,1})(\gamma_v + \mu_v)}\frac{N_v}{N_{h,1}} + \frac{b_2^2\beta_{h,v,2}\beta_{v,h,2}}{(\gamma_{h,2} + \mu_{h,2})(\gamma_v + \mu_v)}\frac{N_v}{N_{h,2}} \tag{63}$$

$$R_{0,3} = \frac{b_1^2\beta_{h,v,1}\beta_{v,h,1}}{(\gamma_{h,1} + \mu_{h,1})(\gamma_v + \mu_v)}\frac{N_v}{N_{h,1}} + \frac{b_2^2\beta_{h,v,2}\beta_{v,h,2}}{(\gamma_{h,2} + \mu_{h,2})(\gamma_v + \mu_v)}\frac{N_v}{N_{h,2}} + \frac{b_3^2\beta_{h,v,3}\beta_{v,h,3}}{(\gamma_{h,3} + \mu_{h,3})(\gamma_v + \mu_v)}\frac{N_v}{N_{h,3}} \tag{64}$$

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$$R_{0,n} = \sum_{i=1}^{n} \frac{b_i^2\beta_{h,v,i}\beta_{v,h,i}}{(\gamma_{h,i} + \mu_{h,i})(\gamma_v + \mu_v)}\frac{N_v}{N_{h,i}} \tag{65}$$

This is how we have found the generalized result, which could be used in lot of cases in where the Malaria is the main actor, with this generalization we can find the basic reproductive number for whatever inhomogeneities we have or whatever information we obtain in the real world.

5. Future work

The work in epidemiology never ends because every day there is the possibility that a new virus or infective form could appear in the society, for that reason we have to be prepared for finding the way to remain alive. Also, there are a lot of difficulties in the sense of recovering the information of the world and adapting to the models that exist. In first place, it is necessary to think in a new form to obtain this information, and for the other side it is important to find models that can used the information that exist until now.

If we talk to the generated models in this chapter, there is other thing we can improve and that is to create a mosquito's population with inhomogeneities, in other words, to generate a model with n-groups of humans and m-groups of vectors, and finding the basic reproductive number for this new general model. This could be used without the restriction of grouping the people and the varieties of mosquitoes in some. However, we consider that the mechanized reasons foundation should be developed for the benefit of all scientific community.

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7. References

Baker, Robert (2007). *EPIDEMIC: The Past, Present and Future of the Diseases that Made Us.* Satin Publications Ltd, ISBN 978-1-905745-08-1, London.

Bellomo, Nicola (2008). *Mathematical Modeling of Biological Systems, Volume II*. Birkhäuser, ISBN 978-0-8176-4555-7, Berlin.

Bollet, Alfred J. (2004). *Plagues & Poxes: The Impact of Human History on Epidemic Disease.* Demos, ISBN 1-888799-79-X, New York.

Bonita, Ruth; Beaglehole, Robert & Kjellström, Tord (2006). *Basic Epidemiology 2ed*. World Health Organization, ISBN 978-92-4-154707-9, Geneva.

Brauer, Fred; Wu, Jianhong & van den Driessche, Pauline (2008). *Mathematical Epidemiology*. Springer, ISBN 978-3-540-78910-9, Berlin.

Capasso, Vincenzo (2008). *Mathematical Structures of Epidemic Systems*. Springer, ISBN 978-3-540-56526-0, Berlin.

Castaño C., Davinson (2009). World Congress on Engineering and Computer Science. *Proceedings of the World Congress on Engineering and Computer Science 2009 Vol I*. pp. 36-40, ISBN 978-988-17012-6-8, San Francisco USA, October 2009.

Chowell, Gerardo; Hyman, James M.; Bettencourt, Luis M. A. & Castillo-Chavez, Carlos (2009). *Mathematical and Statistical Estimation Approaches in Epidemiology.* Springer, ISBN 978-90-481-2312-4, London.

Christakos, George; Olea, Ricardo A.; Serre, Marc L.; Yu, Hwa-Lung & Wang, Lin-lin (2005). *Interdisciplinary Public Health Reasoning and Epidemic Modelling: The Case of Black Death.* Springer, ISBN 3-540-25794-2, New York.

Daley, D.J. & Gani, J. (2005). *Epidemic Modelling: An Introduction.* Cambridge University Press, ISBN 978-0-521-64079-4, New York.

Gottfried, Robert S. (1983). *The Black Death: Natural and Human Disaster in Medieval Europe.* Fress Press, ISBN 978-0029123706, New York.

Ma, Stefan & Xia, Yingcun (2009).*Mathematical Understanding of Infectious Disease Dynamics*. World Scientific, ISBN 978-981-283-482-9, London.

Ma, Zhien; Zhou, Yicang; Wu, Jianhong (2009). *Modeling and Dynamics of Infectious Diseases*. World Scientific, ISBN 978-7-04-024757-2, China.

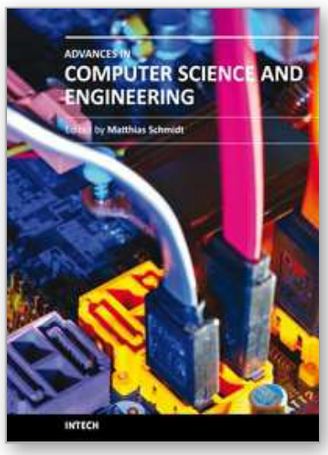
Magal, Pierre & Ruan Shigui (2008). *Structured Population Models in Biology and Epidemiology*. Springer-Verlag, ISBN 978-3-540-78272-8, Berlin.

Maplesoft (2007). *Maple User Manual*. Maplesoft, ISBN 978-1-897310-20-5, Canada.

Perthame, Benoît (2007).*Transport Equations in Biology*. Birkhäuser Verlag, ISBN 978-3-7643-7841-7, Berlin.

Porta, Miquel (2008). *A Dictionary of Epidemiology.* Oxford University Press, ISBN 978–0-19–531449–6, New York.

Stewart, Antony (2002). *Basic Statistics and Epidemiology: A practical guide*. Radcliffe Medical Press, ISBN 1-85775-589-8.



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InTech Europe
University Campus STeP Ri
Slavka Krautzeka 83/A
51000 Rijeka, Croatia
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