Miniproject

Modelling malaria epidemy using deterministic and stochastic methods

Beräkningsvetenskap II

February 26, 2020

1 Motivation

We consider an extended epidemic model to simulate the dynamics of malaria epidemy, involving the demography of both humans and malaria mosquitoes.

Malaria is a communicable disease and can lead to a dramatical decrease of the human population. Even though the disease has been investigated for hundreds of years, it still remains a major public health problem with 109 countries declared as endemic to the disease in 2008. There were then 243 million malaria cases reported, and nearly a million deaths - primarily of children under 5 years. In 2018, according to the World Health Organization, there have been 228 million cases of malaria and 405 000 death cases. Hence, malaria is responsible for the fifth greatest number of deaths due to infectious diseases and is the second leading cause of death in Africa behind AIDS. Therefore, a significant effort is put into constructing adequate mathematical models that will enable us to simulate the development of this epidemy and to study the mechanisms by which such malaria spread, to predict the future course of an outbreak and to evaluate strategies to control it.

Already in 1927, Kermack and McKendrick ([2]) created an epidemic model (also known as SIR model) for the following three compartments (seen as corresponding densities):

- susceptibles (S)- who have yet to contract the disease and become infectious,

- infectives (I) - who can pass on the disease to others,

- removed (R)- who have been infected but cannot transmit the disease for some reason.

The SIR model is of the form of a system of three coupled ordinary differential equations, as described in Lab1, Exercise 3.

We consider a different type of model, referred to as 'host-vector-host' model, where the disease spreads indirectly through an intermediary ('vector'), a typical example of which is malaria.

Malaria is caused by infection with single-celled parasites of genus Plasmodium. The parasites are transmitted to humans through the bites of infected female mosquitoes (the vectors). The so-called Ross-MacDonald model, developed in 1910 ([3]) is the earliest attempt to quantitatively describe the dynamics of malaria transmission at a population level. We consider a more advanced model, described in [1]. It is again a deterministic differential

equation model of malaria, however it better differentiates the various groups in the human and mosquito populations, and is expected to enable a better description of the processes during the development and seise of a malaria epidemy.

The model divides the two population into the following groups:

S_h susceptible humans

I_h infected humans

E_h exposed humans, i.e., in a transition state, when the individuals who are infected are not able to pass on the infection to others

R_h recovered humans

S_m susceptible mosquitoes

I_m infectious mosquitoes

E_m exposed mosquitoes

(There are no 'recovered' mosquitoes due to their short life time.)

The model parameters are the following:

Λ_h Birth number of humans

Λ_m Birth number of mosquitoes

b Biting rate of the mosquito

β_h Probability that a bite by an infectious mosquito results in transmission of disease to human

β_m Probability that a bite results in transmission of parasite to a susceptible mosquito

μ_h Per capita rate of human mortality

μ_m Per capita rate of mosquito mortality

δ_h Disease induced death rate of human

δ_m Disease induced death rate of mosquito

α_h Per capital rate of progression of humans from the exposed state to the infectious state

α_m Per capital rate of progression of mosquitoes from the exposed state to the infectious state

r Recovery rate of humans

ω Per capital rate of loss of immunity in humans

ν_h Proportion of an antibody produced by human in response to the incidence of infection caused by mosquito

ν_m Proportion of an antibody produced by mosquito in response to the incidence of infection caused by human

The detailed description of the deterministic model is given in Section 2.

As in many cases, a deterministic model of the above type can be converted into a stochastic model in terms of *reactions*, as shown in Section 3.

Major aim

The major task of the miniproject is to compare the deterministic and the stochastic models from Sections 2 and 3 - their performance and sensitivity to certain parameters.

2 Description of the deterministic model

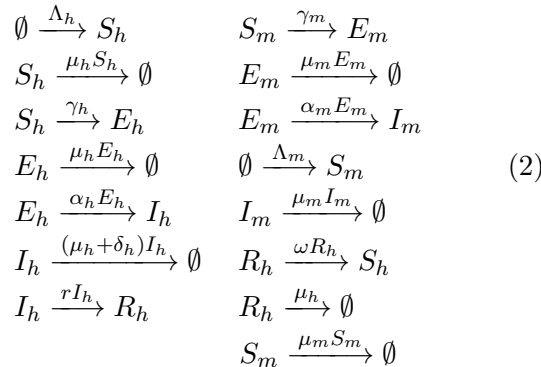The deterministic model consists of the following coupled nonlinear ODEs:

$$
\begin{aligned}
\frac{d\,S_h}{d\,t} &= \Lambda_h - \frac{b\beta_h S_h I_m}{1+\nu_h I_m} - \mu_h S_h + \omega R_h \\
\frac{d\,E_h}{d\,t} &= \frac{b\beta_h S_h I_m}{1+\nu_h I_m} - (\alpha_h + \mu_h)E_h \\
\frac{d\,I_h}{d\,t} &= \alpha_h E_h - (r + \mu_h + \delta_h)I_h \\
\frac{d\,R_h}{d\,t} &= rI_h - (\mu_h + \omega)R_h \\
\frac{d\,S_m}{d\,t} &= \Lambda_m - \frac{b\beta_m S_m I_h}{1+\nu_m I_h} - \mu_m S_m \\
\frac{d\,E_m}{d\,t} &= \frac{b\beta_m S_m I_h}{1+\nu_m I_h} - (\alpha_m + \mu_m)E_m \\
\frac{d\,I_m}{d\,t} &= \alpha_m E_m - (\mu_m + \delta_m)I_m
\end{aligned}
\tag{1}
$$

The initial conditions and the parameter values are as follows

$$
\begin{array}{lll}
S_h(0) = 900 & \Lambda_h = 20 & \delta_h = 0.05 \\
I_h(0) = 50 & \Lambda_m = 40 & \delta_m = 0.15 \\
E_h(0) = 30 & b = 0.075 & \alpha_h = 0.6 \\
R_h(0) = 20 & \beta_h = 0.3 & \alpha_m = 0.6 \\
S_m(0) = 900 & \beta_m = 0.5 & \nu_h = 0.5 \\
I_m(0) = 270 & \mu_h = 0.015 & \nu_m = 0.5 \\
E_m(0) = 330 & \mu_m = 0.02 & \omega = 0.02 \\
 & r = 0.05 &
\end{array}
$$

3 Description of the stochastic model

The ODE model (2) is converted to a system of reactions as follows:

$$
\begin{array}{ll}
\emptyset \xrightarrow{\Lambda_h} S_h & S_m \xrightarrow{\gamma_m} E_m \\
S_h \xrightarrow{\mu_h S_h} \emptyset & E_m \xrightarrow{\mu_m E_m} \emptyset \\
S_h \xrightarrow{\gamma_h} E_h & E_m \xrightarrow{\alpha_m E_m} I_m \\
E_h \xrightarrow{\mu_h E_h} \emptyset & \emptyset \xrightarrow{\Lambda_m} S_m \\
E_h \xrightarrow{\alpha_h E_h} I_h & I_m \xrightarrow{\mu_m I_m} \emptyset \\
I_h \xrightarrow{(\mu_h+\delta_h)I_h} \emptyset & R_h \xrightarrow{\omega R_h} S_h \\
I_h \xrightarrow{rI_h} R_h & R_h \xrightarrow{\mu_h} \emptyset \\
 & S_m \xrightarrow{\mu_m S_m} \emptyset
\end{array}
\tag{2}
$$

where $\gamma_h = \frac{b\beta_h S_h I_m}{1+\nu_h I_m}$ and $\gamma_m = \frac{b\beta_m S_m I_h}{1+\nu_n I_h}$. The values of the parameters are the same as in the ODE model.

4 Tasks

4.1 Perform numerical simulations using the ODE model

(ODE 1) Implement the ODE solver. You can use the uploaded Matlab script `MalariaSym_ODE_0.m`, edit it correspondingly and use as a solver your implementation of Ralston's method.

(ODE 2) Run simulations for the time interval $[0, 100]$.

(ODE 3) Plot the solutions (say, in Figure 1) on one and the same plot (each curve in a different color or line type) and add a legend.

(ODE 4) In a separate figure (say, Figure 2) plot the total amount of humans and mosquitoes as a function of time.

(ODE 5) Repeat the simulation with new values of the parameters, $\Lambda_m = 0.5$ and $\nu_m = 0.15$. These values can be thought as a result of measures to distinguish the mosquitoes.

4.2 Perform numerical simulations using the SSA model

(SSA 1) Implement the SSA solver. The functions `Malaria_stoch.m` and `Malaria_prop.m` that define the reactions and the corresponding propensities, are given. You can use the uploaded Matlab script `MalariaSym_SSA_0.m` and edit it correspondingly. When determining the next reaction, use the code you have written in Assignment 3 (or some other suitable Matlab commands).

(SSA 2) Run simulations for the time interval $[0, 100]$.

(SSA 3) Plot the solutions (say, in Figure 3) on one and the same plot (each curve in a different color or line type) and add a legend.

(SSA 4) In the same figure used for the ODE simulations, Figure 2, plot the total amount of humans and mosquitoes as a function of time.

(SSA 5) Repeat the simulation with parameters, changed as given in Section 4.1.

5 Writing the report

5.1 Structure

The final report should have the following predefined structure:

R 1 Title and authors

R 2 Introduction, problem description

R 3 Mathematical models used

    R 3.1. Deterministic model (include a brief description of the model)

    R 3.2. Stochastic model (include a brief description of the model)

R 4 Numerical methods

R 4.1. Numerical methods to simulate the deterministic model
Short description of the method(s) using course terminology

R 4.2. Numerical method to simulate the stochastic model
Short description of the method using course terminology

R 5 Numerical experiments
Describe the experiments, include plots, information regarding execution time, step length, etc.

Note that when you plot curves that are close to zero, it may be better to plot using `semilogy`.

Compare the simulations using the two sets of parameter values, given above and try to discuss the differences. What do the simulations show? Are there some mosquitoes left towards the end of the simulation? Comment on possible advantages or disadvantages of the two types of simulation methods, deterministic and stochastic.

Note: To ease your effort to write a good-looking report, the attached .tex file contains the descriptions of the two models in LaTex. Feel free to use it.

References

[1] Farago I., Dorner F.: Two epidemic propagation models and their properties, 2019

[2] Kermack, W.O., McKendrick, A.G.: A contribution to the mathematical theory of epidemics. I. Proc. Roy. Soc. Lond. Series A, 700-721, (1927)

[3] Ross, R.:The Prevention of Malaria, J. Murray, London (1910)

[4] Olaniyi, S., Obabiyi, O.S.: Mathematical models for malaria transmission dynamics in human and mosquito populations with nonlinear forces of infection. Int. J. Pure and Appl. Math., 88 125-156 (2013)

[5] World Health Organisation(WHO) and WHO Global Malaria Program, `https://www.who.int/malaria/en/`