

# Graphical User Interface With Applications In Epidemic Mathematical Models

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**Abstract**—The mathematical study of the dynamics of infectious diseases has a long history. By incorporating computer-based simulations in dynamic epidemiological models, it could be possible for modeling methods and theoretical analyses to be more realistic and reliable, allowing a more detailed understanding of the rules governing epidemic spreading. To provide the basis for a disease transmission, the population of a region is often divided into various compartments, and the model governing their relation is called the compartmental model. The graphical interface shown in this paper is performed using the Matlab software version 7.6.0. To achieve it, I had to make three separate files, one for defining the mathematical model and two for the interface itself. Considering a fixed population, it is observed that the number of susceptible individuals diminishes along with an increase in the number of infectious individuals so that in about ten days the number of individuals infected and susceptible, respectively, has the same value. If the epidemic is not controlled, it will continue for an indefinite period of time. By changing the global parameters specific of the SIS model and SIR epidemic model, a more rapid increase of infectious individuals is noted. Using the graphical user interface shown in this paper helps achieving a much easier interaction with the computer, simplifying the structure of complex instructions by using icons and menus, and, in particular, programs and files are much easier to organize. Some numerical simulations have been presented to illustrate theoretical analysis

**Keywords**—Infectious diseases; SIS epidemic model; Gui; Matlab

## I. INTRODUCTION

Classical research of Kermack and McKendrick (1927) laid the foundations of mathematical modelling in the field of epidemic dynamics. Variables indicate the number of host individuals in various stages -

susceptible, infectious and recovered. This formality is the current basis of dynamics modelling and evolution of infectious diseases. To prevent and control their spread, epidemic dynamics has played an essential part in investigating their transmission, predicting trends of development, estimating key parameters from the data published by health departments, understanding the characteristics of transmission and implementing prevention and control measures. Both history and reality show that, while people are faced with the threat of several infectious diseases, the importance of the investigation concerning transmission mechanism, spreading rules and strategy for prevention and control have increased rapidly, and such studies are a critical mission to be dealt with as quickly as possible.

In general, the mathematical models applicable in epidemiology divide the population into three compartments [1-2]:

- a susceptible one (marked S), in which all individuals are susceptible to the disease;
- an infected one, marked I, in which all individuals are infected by disease and are infectious;
- an "isolated" one, marked R (removed) in which all individuals are removed from the infected compartment, where S(t), I(t), R(t) denote the number of individuals of the three compartments at the point of time t .

## II. MATERIAL AND METHODS

The Susceptible-Infected- Susceptible model with vital dynamics (births and deaths) is characterized by the following system of differential equations (1):

$$\begin{cases} \frac{dS}{dt} = \mu N - \mu S - \frac{\beta IS}{N} + \gamma I \\ \frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I - \mu I \end{cases} \quad (1)$$

With initial conditions :  $S(0) = S_0 > 0$ ,  $I(0) = I_0 > 0$  and  $S(t) + I(t) = N$ , where  $N$  is the total number of individuals and  $\beta$  is the total number of contacts. The SIS model shows an increased number of newborn babies in the susceptible compartment at a  $\mu N$  rate and a  $\mu S$  death rate,  $\mu I$ , respectively, where  $\frac{1}{\mu}$  is the average life expectancy and  $\frac{1}{\gamma}$  is the infectious period [1-3]. Deaths and births are balanced in such a way that total population  $N$  remains constant. This model is the simplest epidemiological model and is used for diseases, which do not confer immunity after infection. Susceptible individuals become infected and then become susceptible again after recovery. The model is an endemic one as the disease persists, and it is used in diseases such as gonorrhoea, meningitis or streptococcal infections [1-4]. The SIR model is dynamic in the sense that the number of individuals in the compartment can fluctuate over time. The SIR epidemic model is characterized by the following system of differential equations (1):

$$\begin{cases} \frac{ds}{dt} = -\beta i s \\ \frac{di}{dt} = \beta i s - \gamma i \end{cases} \quad (2)$$

Where:  $s(0) = s_0 \geq 0$ ,  $i(0) = i_0 \geq 0$ , and  $r(t) = 1 - s(t) - i(t)$ , with  $s(t)$ ,  $i(t)$  and  $r(t)$  representing class fractions. This model uses standard indices and has a  $\gamma$  recovery rate, which corresponds to an exponential waiting time of  $e^{-\gamma t}$ . The model does not have vital dynamics (births and deaths) because it is used in the case of short-term epidemic outbreaks. The  $\sigma = \frac{\beta}{\gamma}$  number of contacts represents the  $\beta$  contact rate in the time unit,

multiplied by  $\frac{1}{\gamma}$  average infectious period. SIR

epidemic model has been intensely studied, resulting in various generalizations. The studies examined stability of equilibrium solutions, global asymptotic stability and provided sufficient conditions for global existence of solutions. Some of the variations of the basic model are: SIRS model with vital dynamics, SIRS model with fatality, SIRS model with fatality and immigration. A graphical interface (Graphical User Interface) is an interface located between the user and electronic devices such as computers, hand-held devices (mp3 players, portable media players), electronic appliances and some office equipment. To present all available information and actions, a GUI provides icons and visual indicators, in contrast to

text-based user interfaces, which provide names of commands to be typed in or text navigation [1-5]. This is intended to facilitate the user's work by eliminating the process of writing the software code.

### III.RESULTS

The graphical user interface consists of a panel for displaying different graph views, a panel for controlling graphs and a panel for introducing and controlling parameters (Figure 1).

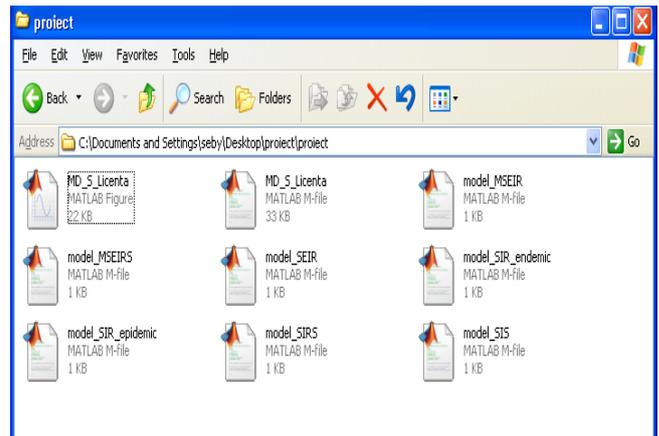


Fig. 1. Files contained by GUI

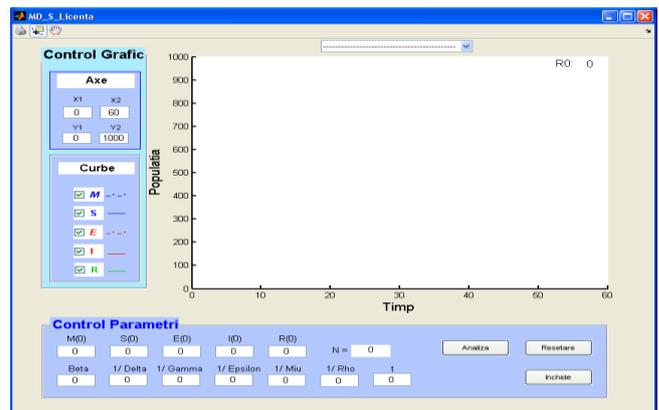


Fig. 2. Graphical user interface with applications in epidemiology

- **Graph display panel:** This area defines the "axes of coordinates" (abscissa and ordinate) required in graphic view of curves of solutions:  $S(t)$ ,  $I(t)$ .
- **Parameter control panel:** In this panel, values of each and every parameter can be changed. To choose the relevant model, one of the models that can be accessed from the top of the graph display panel is selected, as shown in Figure 3.

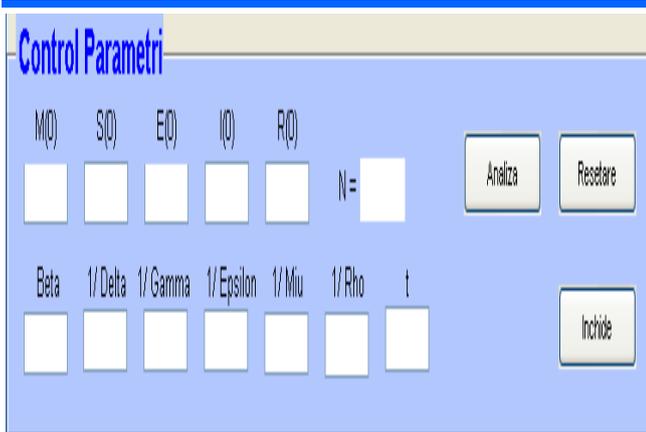


Fig. 3. Parameter control panel

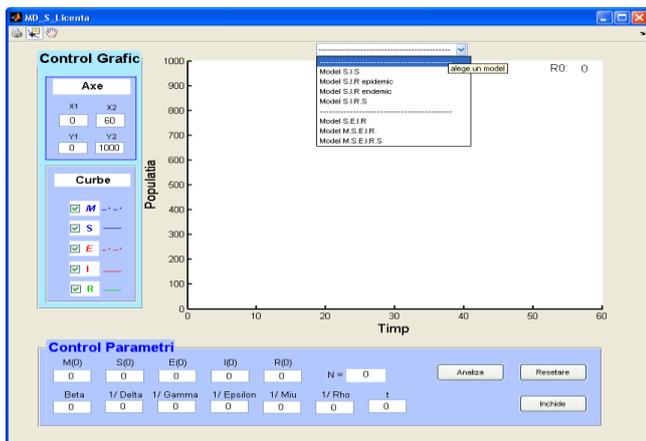


Fig. 4. Example of choosing a model

After having selected a model, the parameter values specific of the models under analysis must be introduced, and parameters that are not specific of the model analyzed will be set to zero. The "Reset" button is pressed to re-enter parameter values and the "Analysis" button is pressed to display the graph. To exit the program, the "Close" button is pressed.

- **Graphic control panel:** At the top, specific values to view the graph obtained will be introduced. Initially, these values are automatically set to the values displayed. Subsequently, according to the user's needs, these values can be modified. The selection buttons to display curves resulting from the analysis are placed at the bottom. Subsequent simulations have been made using epidemiological databases and considering an early time of the epidemic onset.

The SIS model described by the system of equations (1) is characteristic of diseases caused by bacteria. Infected individuals automatically move to susceptible class after recovery. In Figure 4 considers a number of contacts of  $\beta=5$  during the given time period and

an infectious period of  $\frac{1}{\gamma} = 3$  days. The initial number

of susceptible individuals is  $S(0) = 1000$ , while the initial number of infectious individuals is  $I(0) = 10$ . Life expectancy has an average value of  $\frac{1}{\mu} = 75$ , while birth and death rate is  $\mu = 0.013$ .

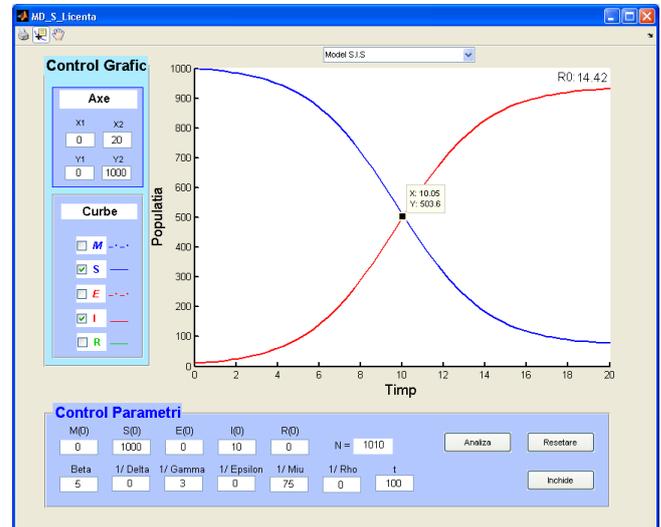


Fig. 5. SIS model analysis for  $\beta = 5$  and  $\frac{1}{\gamma} = 3$

I assumed that each contact of an infected individual was with a non-infected, or susceptible. It is more realistic to assume that the number of susceptible contacts is a function of the number of susceptible persons in the population. We also need to specify an initial fraction of the infected population. Disease transmission is a process driven by the interaction between the susceptible and the infective. Should we change the global parameters characteristic of the SIS model,  $\beta$  and  $\frac{1}{\gamma}$ , we can see a more rapid increase

of infectious individuals, corresponding to a lower point of balance reported to the S/I curves (approximately four days). It is also noted that a great variation of the infectious period (from three to ten days) causes a proportional variation of the basic reproductive number, from a value of

$$R_0 = \frac{\beta}{\gamma + \mu} \approx 29 \text{ in the case of a small infectious}$$

period, to a higher value, i.e.  $R_0 \approx 88$  for a

incubation period of  $\frac{1}{\gamma} = 10$ . This number  $R_0$  is

critical in the beginning of an epidemic (Figure 5 and Figure 6).

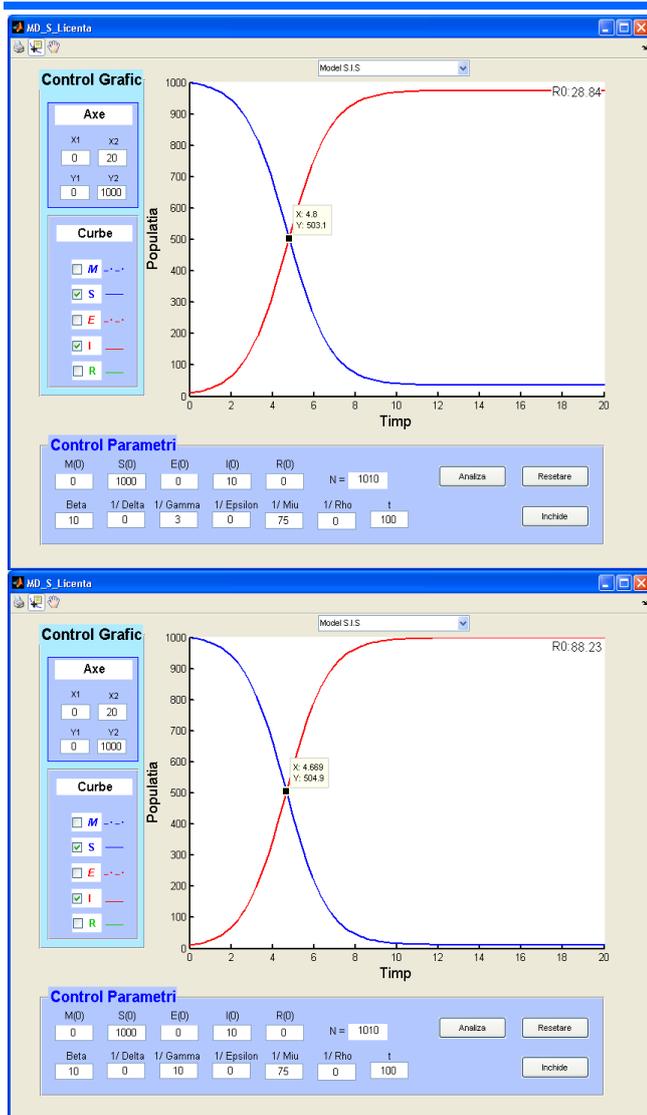


Fig. 6. SIS model analysis a.(up)  $\beta = 10$  and  $\frac{1}{\gamma} = 3$ ;  
 b.(down)  $\beta = 10$  and  $\frac{1}{\gamma} = 10$ ;

The lack of susceptible individuals slows the epidemic when there are many infective individuals; and many susceptible individuals increase the spread of the epidemic when there are few infective individuals. Because an epidemic usually begins with a small set of infected individuals, let us choose this value to  $I_0$ . When  $R_0 > 1$ , the disease can enter a totally susceptible population and the number of cases will increase. The SIR epidemic model described by the equation system (2) is associated to diseases such as measles, herpes, HIV, SARS. Theoretical results simulated in this chapter refer to measles, in which we have considered an infectious period of  $\frac{1}{\gamma} = 4$  days and a  $\beta = 10$  contact number.

The simulation revealed that a single infectious case will produce other 40 infected cases [ $R_0 = 40$  (Figure7)]. Birth and death rates are disregarded.

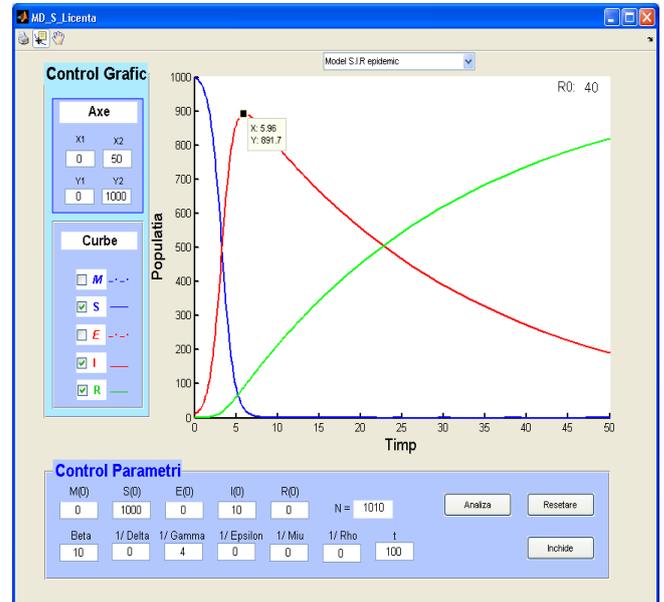


Fig.7 SIR epidemic model analysis for:  $\beta = 10, \frac{1}{\gamma} = 4$

We ignore any subdivisions of the population by age, sex, mobility, or other factors. One would like to precisely determine what parameters would control or prevent the epidemic. When the disease induced death rate is high the infective population drops gradually. When  $R_0 < 1$ , the disease will always fail to spread. Global parameters of this model are  $\beta$  number of contacts and  $\frac{1}{\gamma}$  infectious period, similar to the SIS model. In addition to the above model (SIS), there is the recovered compartment and  $\frac{1}{\mu}$  life expectancy is neglected. We have noted that for  $\frac{1}{\gamma} = 4$ , the susceptible compartment shows a rapid decrease to zero, with a maximum value of infection occurred after about 6 days and a  $R_0 = 40$  coefficient, while a 5-day infectious period will produce a maximum of 910 infectious individuals with an  $R_0 = 50$  value. Therefore, an increase of the infectious period will lead to an increase in infected cases, which is specific of diseases such as rubella, mumps.

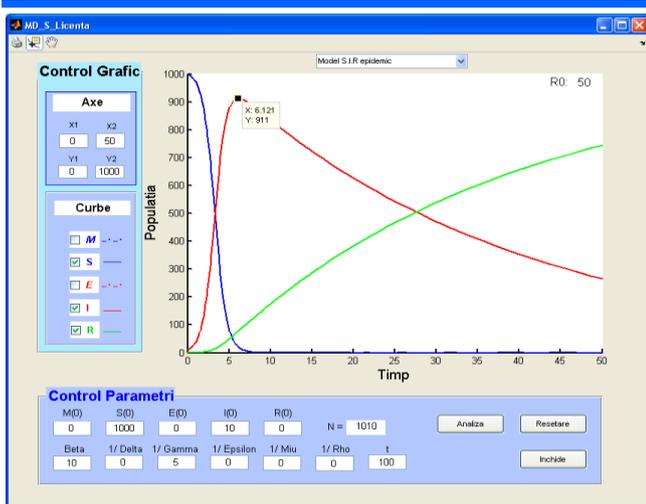


Fig.8 SIR epidemic model analysis for:  $\beta = 10, \frac{1}{\gamma} = 5$ .

We also assume that the whole event is of sufficiently short duration that we may ignore natural births and deaths during the epidemic. When the disease induced death rate is low the infectious population increases. A small number of contacts ( $\beta = 2$ ), while keeping the same conditions for the infectious period, will lead to a more latent increase in time of the epidemic (after approximately 27 days of its occurrence) in conjunction with a slow decrease of susceptible category, with a maximum of recovered individuals of  $I = 667$ , as is the case of rubella (Figure 7).

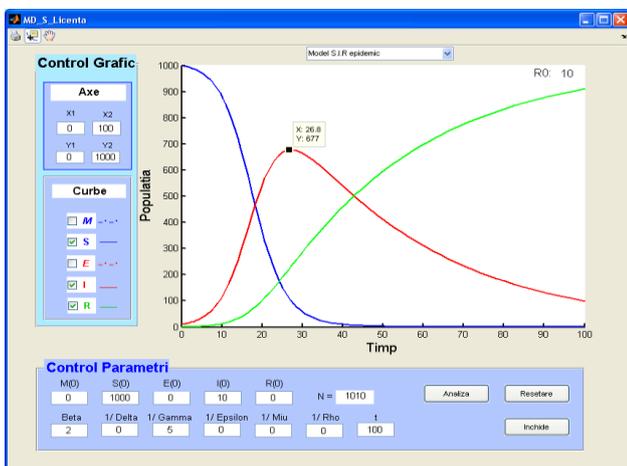


Fig.9. SIR epidemic model analysis for:  $\beta = 2, \frac{1}{\gamma} = 5$ .

The populations will be modeled by two differential equations. The three populations versus time give the output. We found how varied the number of infected and susceptible individuals is during a broadcast of an epidemic.

#### IV. CONCLUSIONS

Infectious diseases have always been a fierce opponent. In our study, the use of a graphical user interface provides a much easier interaction with the computer, simplifies the structure of complex instructions, using icons and menus. To prevent and control their spread, numerical and mathematical modeling of epidemic dynamics has played an essential part in investigating their transmission, estimating key parameters from the data published by the departments of health, understanding the characteristics of transmission and implementing prevention and control measures. Using the graphical user interface suggested by this paper, detailed calculation experiments may be carried out, that may help planning the response of authorities in case of a pandemic situation. I have not considered a mathematical model to represent a specific disease in this paper, because my main objective was to demonstrate the idea that the infection transmission can easily be studied using graphical user interfaces.

#### REFERENCES

- [1] M.Ilea, M.Turnea, D.Arotăriței, M.Popescu, M.Rotariu, "Graphical user interface with applications in susceptible-infectious-susceptible models", *The Medical-Surgical Journal*, vol.119, pp 610-614, 2015.
- [2] R. M. Anderson, R.M. May, *Infectious Diseases of Humans: Dynamics and Control*, Oxford University Press: Oxford, England, 1991.
- [3] L. J. S Allen, "Some discrete-time SI, SIR, and SIS epidemic models", *Math. Bioscience*, vol. 124, pp. 83–105. 1994.
- [4] D.J.Daley, J.Gani, *Epidemic modeling an introduction*, Cambridge, 1999.
- [5] A. De Vries, *Course in Mathematical Biology: Quantitative Modeling with Mathematical and Computational Methods*, Society for Industrial Mathematics, SIAM, 2006.