Laboratory exercise no. 3: Monte Carlo simulation of pandemic

Aim: The aim of the laboratory is to familiarize students with a simple Monte Carlo model simulating the development of a pandemic

Description:

A pandemic is a type of epidemic involving a significant proportion of the population, which is developing over a large area, often of a global nature. According to some sources, the cause of the pandemic may be the phenomenon of globalization, which greatly facilitates the spread of diseases. In order for a pandemic to have a chance to develop on a global scale, the disease responsible for it should have such characteristics as: (i) low mortality of infected people, (ii) high infectivity (each carrier must infect more than 1 person), (iii) long period of incubation , (iv) lack of resistance of the population to the pathogenic agent and (v) should not destroy their carriers (mild symptoms contribute to neglecting infections).

The pandemic development process depends on many factors, most of which are random (infection frequency, incubation length, mortality percentage). The Monte Carlo method is ideal for simulating such processes.

In frame of this exercise, a simple Monte Carlo model will be implemented describing the dynamics of the development of the number of infections for a specific population located in a limited area. The model assumptions are presented below:

1. The modeled phenomenon takes place in a limited rectangular area with dimensions specified in kilometers.
2. In the defined area there is a population of N persons, all of whom are initially healthy and one random individual is infected with a virus.
3. Periodic boundary conditions are applied in the area, and the movements of people are simulated as a process of random walking with a defined average speed dx, In each timestep only a part of the people specified by the MR parameter is moving.
4. The possibility of infection takes place through the contract of a healthy person with an infected or sick person, however, in order for an infection to occur, persons must be close enough (R_{inf}) for a certain period of time (T_{inf}).
5. The disease has two stages.
   a. In the first stage for the incubation period (T_{inc}) a person is treated as infected and can infect others, but has no symptoms, so he can move like a healthy person.
   b. In the second stage, symptoms occur and the person is immobilized for convalescence time (T_{rec}) and can still infect others.
6. After the recovery period, recovery or death of the person occurs (mortality rate is determined by the DR parameter). People who have recovered regain the ability to move and are resistant to subsequent infections. The deceased are removed from the simulation.

An example of model simulation presenting distribution of people and percentage of different disease stages is presented below:
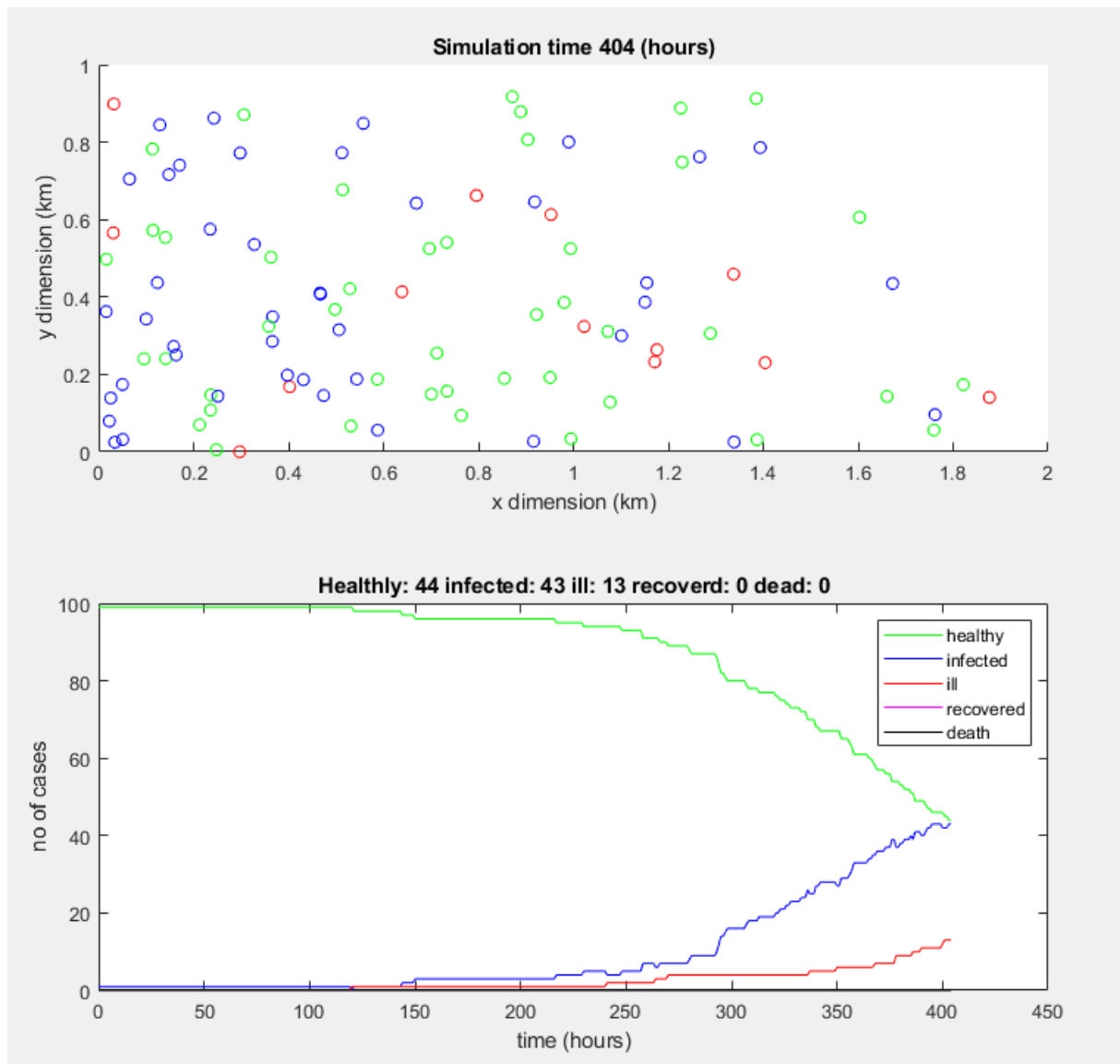
Laboratory programme:

The initial code of the model written in MATLAB is provided by a tutor. Students can freely develop the model by adding more mechanisms, like specified moving paths or statistical distribution of model parameters or isolation of infected individuals.

The first task is to check how the model parameters influence on overall statistics, like percentage of infected people or period required for infection of 25% of population.

In the second task, an isolation mechanism of infected peoples from others (only a limited access to infected peoples by medical personnel is applied) should be implemented in the model. The effect of quarantine will be compared with initial case.

Report outline:

1. The report must include the final model code, detailed description of modifications along with arguments for the changes introduced.

2. Presentation and discussion of obtained results presenting the contribution of different model parameters on the results.
3. Comparison of initial model configuration results with version having implemented quarantine mechanism.
4. Conclusions.