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**DEVELOPMENT AND IMPLEMENTATION OF
A MATHEMATICAL MODEL FOR HOSPITAL-ASSOCIATED
ANTIBIOTIC RESISTANCE**

Summary: The paper applies information technology and mathematical modeling to examine the epidemiological characteristics of a large-scale problem, known as antimicrobial resistance. It describes a mathematical model constructed to emulate the process of spread of resistant bacteria in a hospital environment using system dynamics. The model includes several key parameters such as the contact rate between the members of different observed groups, the rate of treatment with antibiotic drugs and others.

Key words: system dynamics, computer simulation, antimicrobial resistance, antibiotic resistance.

Introduction

Preserving and improving the health of the human population has always been a vital socio – economic issue for all over the world. In order to meet the health needs of citizens and provide public health services, the health care sector of each country monitors and controls the various operations starting from hospitalizations, patient treatments and research to vaccines and pharmaceuticals. The quality of the nation's health system is basically measured by the management of those processes, by how well they are organized and how fast they are performed.

Antibiotic resistance is one of the threats that is slowly devastating the weapons of humanity against infectious diseases. One of the main reasons why antibiotics lose their effectiveness lies behind the failure to appropriately conduct the treatment course with an antibiotic. The schedule of antibiotic usage during the treatment course has been accurately developed by pharmaceutical specialists. The course is usually designed so that the population of bacteria is effectively reduced with the medicine. The doses of the antibiotic are not too much to potentially harm the patient's organism and are not too little to result in adaptation of the bacteria. Adhering to the doctor's prescriptions in terms of timing and dosing is crucial for an effective and successful treatment of a disease. Individuals that do not adhere these rules and violate the prescription conditions are not only making their own treatment ineffective and even dangerous. They are also responsible for the process of antibiotic resistance. By exposing bacteria to insufficient amounts of the antibiotic, a patient stimulates the natural ability of the organisms to develop some immunity mechanisms against the killing medicine. This way, irresponsible patients are strengthening different dangerous microorganisms and reducing the power of the weapons that are used to fight against them.

This paper describes and analyzes a mathematical model of a hospital, in which we observe the populations infected with susceptible strains, resistant strains and the population uncolonized with the observed bacteria at all. The mentioned susceptibility and resistance of the bacteria are relative to a specific antibiotic drug.

Mathematical Modeling for Epidemiology

Modeling is one of the ways to solve problems that appear in the real world. In many cases we cannot afford finding the right solutions by experimenting with real objects: building, destroying, making changes may be too expensive, dangerous, or just impossible. If this is so, we leave the real

world and go up to the world of models. We build a model of a real system: its representation in a modeling language. This process assumes abstraction: we throw away the details that are irrelevant to the problem we are trying to solve and keep what we think is important. The model is always less complex than the real system. Having built the model (or sometimes even while building the model), we start to explore and understand the structure and behavior of the original system, test how the system will behave under various conditions, play and compare different scenarios, optimize. When we find the solution we are looking for, we map that solution back to the real world.

Simulation Model Development

We are going to implement a mathematical model that demonstrates the epidemiology of resistant bacteria strain in closed environment of a hospital. The differential equations that describe the change of every population group are the following: [3]

$$\frac{dS}{dt} = m + \beta SX - (\tau_1 + \tau_2 + \gamma + \mu)S$$

$$\frac{dR}{dt} = \beta(1 - c)RX - (\mu + \tau_2 + \gamma)R$$

$$\frac{dX}{dt} = (1 - m)\mu + (\tau_1 + \tau_2 + \gamma)S + (\tau_2 + \gamma)R - \beta SX - \beta(1 - c)RX - \mu X$$

S in the equations, denotes the individuals that are infected with the bacteria sensitive to drug A. R is correspondingly stands for the population infected with the bacteria resistant to drug A. By X we denote the people who are not carrying any type of these bacteria. Also, it is assumed that there are no any bacteria resistant to drug B in the system. A fraction m of people entering the bacteria is infected by a sensitive strain; the other 1-m of incoming people are not colonized with the bacteria at all (X).

The model was implemented on a computer simulation software AnyLogic, and its graphical representation looks as follows:

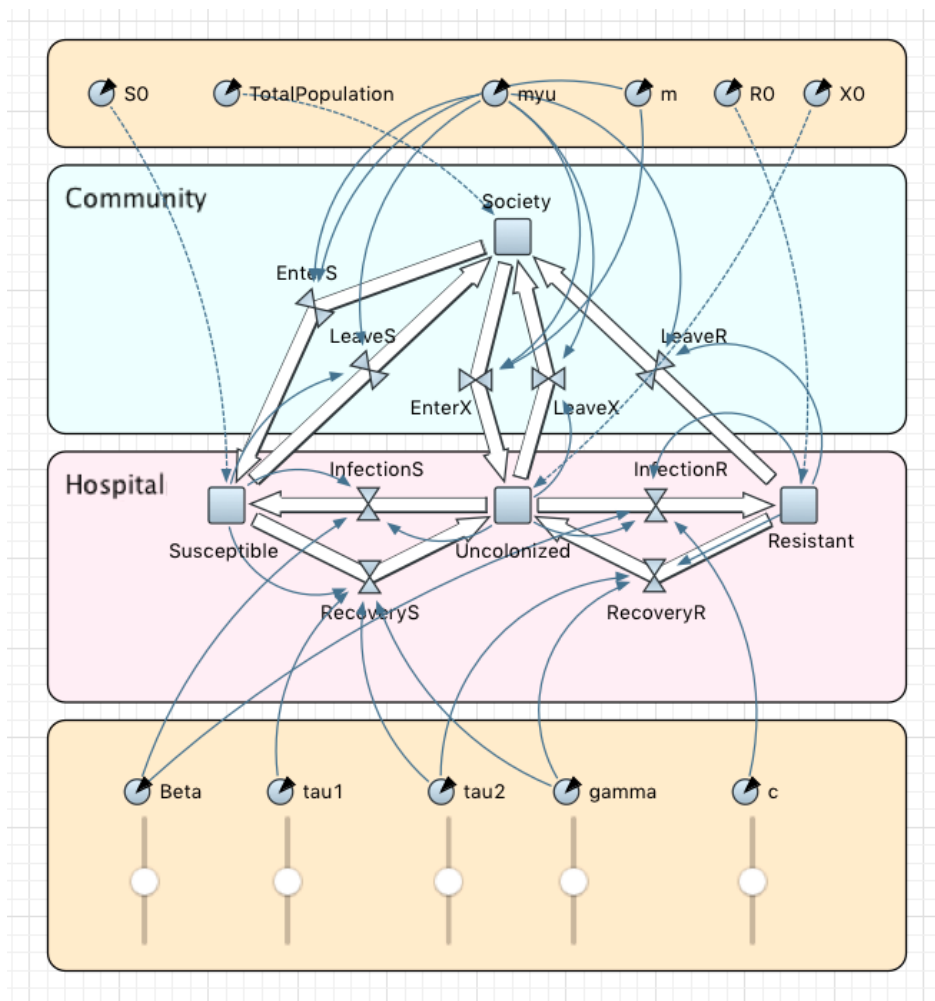


Figure 1. The simulation model of the antibiotic resistance spread in hospital.

Results and Discussion

The number of people colonized with resistant bacteria may fall to zero or stay positive. If the transmission probabilities of resistant and sensitive stains are equal, then the latter case happens under the following condition:

$$R_0 > \tau_1 / (\tau_1 - m\mu)$$

Here, $R_0 = \beta / (\tau_2 + \mu + \gamma)$ is a special value that indicates the rate of resistant strain reproduction in an ideal case when all of the individuals entering the hospital are not colonized with bacteria at all.

The execution of the described model shows how each population will change over time. We used a pie chart and a diagram to display the data in a convenient way.

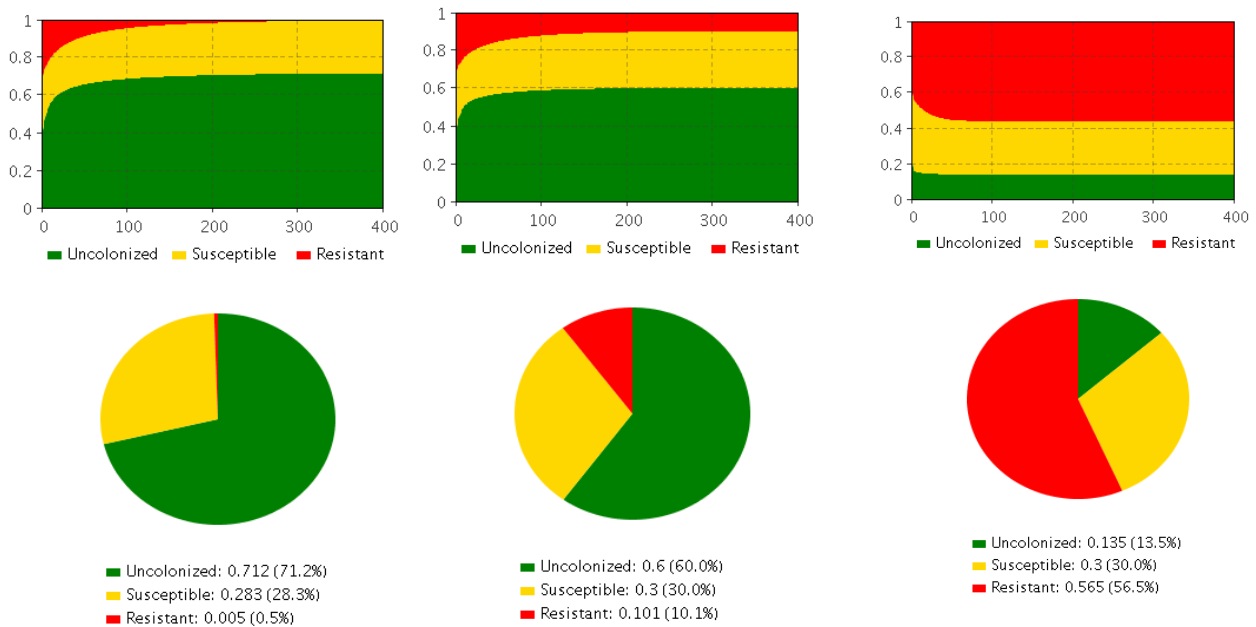


Figure 2. The simulation execution results, indicating the change of resistant population.

As it can be seen from the figures, when the basic reproductive rate of resistant bacteria strain is too small, the population will not manage to survive and eventually disappears. When the basic reproductive rate is large enough, the population will stay constant as it is in the second figure. Finally, if the basic reproductive rate is too big, then the resistant bacteria population flourishes over all others as it can be seen on the last figure.

References

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