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MODELING EPIDEMIOLOGY OF ANTIMICROBIAL RESISTANCE IN HOSPITALS

Summary: The article studies a mathematical model for understanding the epidemiology of antimicrobial resistant bacteria in hospital. The model provides division of the population on three different groups relatively to the susceptible and resistant strains of a hypothetical bacteria and corresponding antibiotic drug. The differential equations are analyzed and simulated using AnyLogic 7 simulation software, which brings to the discussion of results.

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

Introduction

Antimicrobial resistance is an increasing problem among the whole humanity. A solution for it still has not been discovered yet, therefore the optimal usage of the antibiotics is very important for our population. Antibiotics are very special type of medicine, which is used against bacterial diseases and often can be considered as the only possible treatment for a patient. The chemical structure of antibiotics let them effectively devastate exponentially growing populations of bacteria. In order to treat a disease effectively, doctors prescribe a specific antibiotic with specific course of usage. The antibiotics are usually needed to be used in specific doses within specific periods of time. The exact timing of treatment and accurate dosing of the medicine is very important for the right effect of the antibiotic. When patients do not adhere the prescribed conditions and rules of antibiotic usage, they allow the bacteria to develop immunity against the antibiotic medicine. This is in fact an amazing biological property, which shows how living creatures are able to adapt to different murderous enemies and conditions.

The prevention of antibiotic / antimicrobial resistance is a global process. This can't be done by a single person or organization, but rather by the collaboration of many institutions and organizations of the world. It is important to understand, how can we and should we handle this global problem and find a solution for the better future. There are many complexities involved in antimicrobial resistance. Different bacteria may be resistant or susceptible to different types of antibiotics, can infect various human populations and etc. In order to understand the problem better, we are considering the mathematical model behind this complex process. The mathematical model can be used to predict ongoing changes in the process as well as understand the key variables involved in the process. Mathematical models can be computed using computer simulations, in order to produce more detailed outcomes.

Epidemiological Modeling

The most epidemic models are designed by SIR concept, which was developed by W. O. Kermack and A. G. McKendrick. They considered a fixed population with only three classes: susceptible, S(t); infected, I(t); and recovered, R(t)[1]. The compartments used for this model consist of three classes.

S(t) - individuals who are susceptible to the disease, it represents the number of people who are not yet infected with the disease at time t [1];

I(t) - individuals who have been infected with the disease at time t and are able to spread the disease to those in the susceptible category [1];

R(t) - people who have recovered from the disease after being infected. Those in this category are not able to be infected again or to transmit the infection to others [1].

The flow of this model may be considered as follows:

$$S \rightarrow I \rightarrow R$$

Considering that the total population is N and $\mathrm{N} = \mathrm{S(t)} + \mathrm{I(t)} + \mathrm{R(t)}$, the following equations can be derived [2]:

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

There has recently been conducted a study that examined the case of transmission of resistant and susceptible bacteria in hospitals. The research of such processes is particularly important for understanding the nosocomial transmission rates of the bacteria. It is significant for the healthcare workers to be able to control the spread of resistant bacteria and reduce their antimicrobial resistance. The model may predict whether the usage of an antibiotic, which does not have corresponding resistant bacteria present in the hospital will be useful to decrease the level of resistance in the examined bacteria.

Mathematical Model Description

We are going to observe a mathematical model proposed by [3], which describes the epidemiology of antimicrobial resistant infections in hospitals. The model examines a population of people in a closed environment, where new patients come into the system at some rate and go out of the system respectively. The model can be applied for the diseases that are transmitted through the skin, respiratory or digestive organs. A few examples of such bacteria are Escherichia coli, Staphylococcus, Enterococcus, Klebsiella pneumoniae and others. The mentioned bacteria are dangerous enough to cause a painful or even lethal infection. The hospital environment was chosen because the transmission of these bacteria often takes place inside the hospitals. Different patients may accidentally contact with each other and spread their infections to one another, as well as to medical personnel. The medical workers are also often responsible for the spread of infections inside the hospital, since they may pass the bacteria between their patients. This might happen as a result of insufficient hygiene with respect to their hands and inventory items. The bacteria in the system are continuously encountering the antibiotics that are used in the hospital. As a result, the patients may always get infected accidentally and the bacteria can pass their antibiotic resistant plasmids to other strains.

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

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

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

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).

Results and Discussion

The number of people that are colonized with sensitive bacteria is always non-zero, i.e. such people are always present in the system. This happens because such individuals are constantly entering the hospital. The population that is free from bacteria colonization is also present, since this kind of people are constantly entering from outside, too, and infected people is cured. 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.

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