

Determination of parameters of a mathematical model of bacterial infection development taking into account antimicrobial resistance

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Motivation and Aim: Bacteria that cause certain diseases sooner or later develop resistance to antibiotics used during treatment. This is a natural adaptation process called antimicrobial resistance (AMR). Its development means that the duration of the effectiveness of antibiotics is limited, and their improper and unjustified use contributes to the emergence and spread of antibiotic-resistant bacteria. More and more infectious diseases, such as pneumonia, tuberculosis, gonorrhea and salmonellosis, are becoming more difficult to treat due to the reduced effectiveness of antibiotics. The consequence of antibiotic resistance is longer hospitalizations, increased medical costs and mortality. AMR is today one of the most serious threats to human health, food security and development.

Results: We apply mathematical modeling to study the development of AMR [1]. We investigate a mathematical model [2] based on a system of nonlinear ODEs that describes the development of populations of sensitive and resistant bacteria under the action of an antibacterial drug and the immune response of body cells.

However, some parameters of the model cannot be measured experimentally, and therefore an important task is to identify the parameters of the mathematical model.

The inverse problem is to identify the parameters of the mathematical model of AMR, such as the intensity of bacteria that destroy immune cells, the growth rate of resistant bacteria, the constant intensity of conjugation, the frequency of mutations of susceptible bacteria, according to additional information about the population of sensitive and resistant bacteria in the human body.

Conclusion: The result of the study is the developed method for solving the inverse problem, which is reduced to minimizing the cost functional by the method of particle swarm optimization and differential evolution.

References

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