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MATHEMATICAL MODELING OF THE SPREAD OF THE EPIDEMIC

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Relevance: studying the spread limit of the epidemic through the Kermak-McKendrick model and studying the mathematical expression of the breeding trend.

The purpose of the study: to study the limits of the spread of the epidemic based on the Kermak-McKendrick model.

Methods and techniques: mathematical analysis and modeling methods were used in the research process. In describing the epidemiological process, the Kermack-McKendrick model was taken as a basis. The population was divided into three groups - the healthy, infected and those who recovered from the disease (isolated) - and their processes of mutual transition were expressed using equations

Results: this article examined the limits of an epidemic that could spread in a single population. We include the designation of organisms in the population in which the epidemic is spread into 3 groups. – the number of healthy (uninfected) people, – the number of infected people, – the number of people who have recovered from the disease or have been isolated. The number of healthy individuals in the observation period is determined as follows:

$$x_{n+1} = (1-p)^{y_n} x_n$$

Further developing the Model, we get the following conclusions: In this case-there will be a chance that every healthy person will avoid contact with infected people. Now we assume that the observation interval is not exactly compatible with the infectious period. Those who leave the state of Health will go directly to the state of the infected, and at the end of each period, the part of the infected will continue to transmit the disease. So:

$$x_{n+1} = e^{-ay_n} x_n \qquad y_{n+1} = (1-e^{-ay_n})x_n + by_n \qquad z_{n+1} = z_n + (1-b)y_n$$

This formula follows from the conclusions. This is the Kermak-McKendrick model.

Conditions for the spread of the epidemic Suppose there is only one infected person in the initial state

$$y_0 = 1 \quad y_1 - 1 = b - 1 + (1-e^{-a})x_0$$

If this expression is **positive**, it means that those infected manage to reproduce themselves. $x_0 > (1-b)/(1-e^{-a}) \equiv x^*$

Simulations based on models:

The Kermack-McKendrick model shows three cases:

1. A condition in which infection is impossible (below the limit) – the epidemic does not begin.
2. Moderate condition-the disease spreads widely, but some survive.
3. A very strong epidemic-all healthy people get the disease in 3 periods.

If we compare the population as $u_n = x_n / 5 \;\; v_n = y_n / 5$, then:

$$u_{n+1} = e^{-5av_n} u_n \qquad v_{n+1} = (1-e^{-5av_n})u_n + bv_n$$

For the three cases in this case, the A values were 0.02; 0.07 and 0.149. Their corresponding P values are 0.1; 0.3 and 0.5.

As a result: in case 1 there is no epidemic, in case 2 there is a moderate epidemic,

And in case 3, we will observe a strong epidemic.

Conclusions: mathematical models are important in the study of epidemics. Through them, it is possible to predict the spread of the disease, develop effective measures against it. The kermack-McKendrick model is a basic model widely used in the analysis of the dynamics of infectious diseases.