IRSTI 27.35.47 DOI: https://doi.org/10.26577/JMMCS131320266

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MATHEMATICAL MODELING OF THE SPREAD OF EPIDEMICS ACROSS THE TERRITORY

The process of epidemic spread across a territory is considered. Among the many mathematical models of epidemiology, compartmental models are most commonly used. They identify groups of people in a given epidemiological state, describe the transitions of people from one group to another over time, and represent systems of ordinary differential equations. Studies devoted to the mathematical modeling of epidemic spread across a territory typically employ the concept of reaction-diffusion systems, which involves adding appropriate diffusion terms to the standard equations of compartmental models. This paper demonstrates that such an approach is ineffective in the situation under consideration. As an alternative, an equation for the change in the infection rate of the territory is derived based on known information about the course of the epidemic. This equation is a first-order partial differential equation with variable coefficients, belonging to the class of transport equations. The resulting equation, with appropriate boundary conditions and a particular method for choosing the law of change in the area of infection, can be used as a mathematical model of the system under consideration to predict the spread of the epidemic across a territory.

Key words: epidemiology, mathematical model, spatio-temporal system, infection, transport equation.

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Эпидемиялардың аумақта таралуын математикалық модельдеу

Эпидемиялық таралу процесі аумақ бойынша қарастырылады. Эпидемиологияның көптеген математикалық модельдерінің ішінде компартменттік модельдер жиі қолданылады. Олар берілген эпидемиологиялық жағдайдағы адамдар тобын анықтайды, адамдардың уақыт өте келе бір топтан екінші топқа ауысуын сипаттайды және қарапайым дифференциалдық теңдеулер жүйелерін ұсынады. Аумақ бойынша эпидемияның таралуын математикалық модельдеуге арналған зерттеулер әдетте реакция-диффузиялық жүйелер тұжырымдамасын қолданады, бұл компартменттік модельдердің стандартты теңдеулеріне тиісті диффузиялық терминдерді қосуды қамтиды. Бұл мақалада мұндай тәсіл қарастырылып отырған жағдайда тиімсіз екендігі көрсетілген. Балама ретінде, аумақтың инфекциялану жылдамдығының өзгеруіне арналған теңдеу эпидемияның барысы туралы белгілі ақпарат негізінде шығарылады. Бұл теңдеу тасымалдау теңдеулері класына жататын айнымалы коэффициенттері бар бірінші ретті дербес дифференциалдың теңдеу болып табылады. Тиісті шекаралық шарттармен және инфекция аймағының өзгеру заңын таңдаудың белгілі бір әдісімен алынған теңдеу эпидемияның аумақ бойынша таралуын болжау үшін қарастырылып отырған жүйенің математикалық моделі ретінде пайдаланылуы мүмкін.

Кілт сөздер: эпидемиология, математикалық модель, кеңістіктік-уақыттық жүйе, инфекция, трансферттік теңдеу.

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Математическое моделирование распространения эпидемии по территории

Рассматривается процесс распространения эпидемии по территории. Среди множества математических моделей эпидемиологии чаще всего используются compartmental models, выделяющие группы людей, находящихся в том или ином эпидемиологическом состояния, описывающие переходы со временем людей из одной группы в другую и представляющие собой системы обыкновенных дифференциальных уравнений. Среди исследований, посвященных математическому моделированию распространения эпидемии по территории обычно используют концепцию систем реакция-диффузия, подразумевающую добавление к стандартным уравнениям compartmental models соответствующих диффузионных членов. В настоящей работе показывается, что подобный подход в рассматриваемой ситуации не является эффективным. В качестве альтернативы на основе известной информации о ходе развития эпидемии получается уравнение относительно изменения зараженности территории. Оно представляет собой уравнение в частных производных первого порядка с переменными коэффициентами, относящееся к классу уравнений переноса. Полученное уравнение с соответствующими краевыми условиями с тем или иным способом выбора закона изменения области заражения может быть использовано в качестве математической модели рассматриваемой системы для прогнозирования распространения эпидемии по территории.

Ключевые слова: эпидемиология, математическая модель, пространственно-временная система, зараженность, уравнение переноса.

1 Introduction

The COVID-19 epidemic has significantly updated research in the field of mathematical epidemiology. The overwhelming majority of studies in this field are based on mathematical models classified as *compartmental models*. These models divide the entire population into groups of people (compartments) that differ in their epidemiological status (healthy, ill in one form or another, recovered, vaccinated, etc.) and describe the transitions of people from one group to another over time. These models (SIR, SEIR, and their various generalizations) are systems of nonlinear ordinary differential equations for the numbers of people in the corresponding groups (see, for example, [1], [2], [3]).

Models describing the spread of an epidemic across a territory are significantly less represented. At first glance, the most natural approach to deriving the corresponding equations here is to use the idea of *reaction-diffusion systems*, which goes back to the problems of chemical kinetics [4]. Specifically, if any chemical reactions occur, then this process, in accordance with the law of mass action, is described by a system of ordinary differential equations relative to the concentrations of all reactants. On the other hand, if there is a substance that is unevenly distributed over a certain territory, then, in accordance with Fick's law, diffusion flows arise, and the process itself is described by a parabolic partial differential equation relative to the concentration of this substance. If the reaction and diffusion occur simultaneously, then the concentrations of the reactants change due to both of these factors, and the mathematical model of this process is based on a system of partial differential equations obtained from a system of ordinary differential equations characterizing the existing reactions, by adding the appropriate diffusion terms. Although the main object of application of this approach is chemical processes, it finds application in physics (diffusion of neutrons associated with nuclear reactions), biology (migration of animals of different species somehow interacting with each other), economics (commercial activities of several economic entities associated with the transportation of goods), etc.

The idea behind this approach to describing the spread of an epidemic across a territory is that infection is transmitted from sick people to healthy people in much the same way as heat spreads from a hot body to a cold one; a substance moves from an area where it is abundant to an area where it is scarce; animals migrate from an overcrowded area where food is scarce to a relatively free area where food is plentiful; merchants transport goods from where they are abundant, and therefore cheap, to where they are scarce, and therefore can be sold profitably. Indeed, many well-known models of epidemic spread across a territory are obtained from standard compartmental models of the SIR type by adding appropriate diffusion terms (see, for example, [5], [6], [7]). However, there are serious reasons to doubt the validity of using reaction-diffusion systems to describe the considered processes.

Indeed, what happens if we formally add the appropriate diffusion terms to the standard epidemiological equations, thereby transforming them from ordinary differential equations into the class of parabolic partial differential equations? Naturally, as a result, they will acquire the properties of heat conduction or diffusion-type equations, i.e., in addition to intergroup transitions (healthy people become infected and sick, sick people recover or die, etc.), they will also describe transfer processes, i.e., the movement of people from an area where they are numerous to one where they are few. In real life, we typically have a significantly unevenly populated area, with cities with millions of people (whose residents during an epidemic include large numbers of healthy, sick, and recovered individuals), and places where virtually no one lives. If we now attempt to solve the corresponding equations, we will inevitably encounter (in addition to the development of the epidemic) the migration of people from cities to uninhabited areas. In reality, we need to describe the spread of an epidemic from its source deep into an initially uninfected area. This means that the unevenness of infection is the only important factor, not the unevenness of population distribution. This means that adding diffusion terms to each equation of SIR-type models is clearly not going to yield the desired results. We also note that transmission processes can only include the infection of healthy individuals through contact with sick individuals, and not other intergroup transitions characteristic of epidemiological models. The occurrence of disease in individuals who have been in contact with sick individuals, the vaccination of the population, the hospitalization of sick individuals, their recovery or death, and so on are in no way influenced by the number of other individuals nearby or distantly located in the same or any other epidemiological state.

There is another additional reason why reaction-diffusion systems, in our opinion, are fundamentally inapplicable to the situation under consideration. When a hot body comes into contact with a cold one, the hot one cools down and the cold one heats up. Here, we observe a redistribution of heat, i.e., the action of the corresponding conservation law. A similar situation is observed in the processes of diffusion of matter, electrical conductivity, animal migration, and the transport of goods. However, when healthy people come into contact with sick people, some of the healthy ones do become ill, but none of the sick people will ultimately become healthy. Consequently, the process of infection transfer is fundamentally different from the process of heat transfer and, therefore, must be described differently.

This paper proposes an equation describing the spread of an epidemic across a territory.

2 Main results

Let us attempt to provide a mathematical description of the spread of an epidemic across a territory. As noted above, of all the processes associated with the development of an epidemic, only infection transmission is associated with spatial effects. Therefore, we can limit our consideration to a single function u, which characterizes the infection rate of the territory. Let us try to understand what equation, in principle, describes the process under study. In doing so, we start from the general principle of the theory of inverse problems: if information is insufficient to obtain a complete mathematical model, then we should use the additional information about the state of the system that can be determined. However, inverse problems typically assume the existence of equations describing the process under study, with only certain parameters included in the formulation of the direct problem being unknown [8]. Here, we are attempting to establish an equation itself describing the spread of the epidemic across a territory. To do this, we first select a function with the desired properties, and then the simplest possible equation for which this function is a solution. In doing so, we are essentially also solving an inverse problem, only of a different type.

First, we assume that initially (at $t = 0$) there is a relatively small (compared to the total area under consideration) infected area, in the center of which infection is highest, decreasing with distance from it, and being absent altogether beyond the infection territory. We select the infection center as the origin of coordinates, and assume the value of the function u at this point to be equal to one, and equal to zero outside the infected area. Then, assuming for simplicity that the territory under consideration is homogeneous, we establish that the desired function depends only on time t and on a unique spatial variable x, expressing the distance to the infection center. We assume that at the initial time $t = 0$, the function u is equal to one at $x = 0$, then decreases with increasing x to zero at some point $x = L$, corresponding to the depth of the initial infected area, after which (in the infection region) it is equal to zero everywhere. Let φ be an arbitrary function with the above properties.

We are interested in how events unfold over time. There is reason to believe the infected area is gradually expanding, and at any moment in time t, the function $u_t = u_t(x) = u(x,t)$, which characterizes the distribution of infection across the territory, has practically the same form as φ, but over a wider area, increasing with increasing t. This assumes that the equality $u(x,t) = \varphi(\omega(t)x)$ holds. The function ω included in this equality is equal to unity at $t = 0$, since at the initial moment of time the state of the system should be described by the function φ. In addition, it decreases monotonically (the epidemic gradually spreads into the territory). Finally, it tends to zero with an unlimited increase in time, since over time the epidemic front can spread arbitrarily far. Thus, the function $\omega = \omega(t)$ must satisfy the following conditions:

$$\omega(0) = 1,\ \omega'(t) < 0\ \forall t > 0,\ \omega(t) \to 0 \text{ if } t \to \infty.$$

Note that for $x = \omega(t)^{-1}$, based on the properties of the function φ, the equality $u(x,t) = 0$ follows. Thus, the function $L = L(t) = \omega(t)^{-1}$ characterizes the size of the infected area at time t.

Now we need to find the simplest possible equation for which this function is a solution. Since this function depends on two arguments, it is natural to determine its rate of change with respect to each of these variables, i.e., the corresponding partial derivatives. We have

$$u_x(x,t) = \omega(t)\varphi'(\omega(t)x),\ u_t(x,t) = \omega'(t)x\varphi'(\omega(t)x).$$

Comparing these values, we obtain the equality

$$\omega(t)u_t = \omega'(t)xu_x,$$

which is reduced to the form

$$\frac{\partial u}{\partial t} - x\frac{d}{dt}\ln\omega(t)\frac{\partial u}{\partial x} = 0.$$

Note that, due to the negativeness of the derivative of the function ω, the coefficient in front of the spatial derivative of the function u is positive. The resulting ratio is chosen as the equation for the spread of the epidemic across the territory.

3 Examples and discussion

The subject of this paper is a mathematical model of the spread of an epidemic across a territory. Unlike most works in this area, which use the idea of reaction-diffusion systems implemented by adding appropriate diffusion terms to standard compartmental models, the system under consideration is described by a first-order partial differential equation with variable coefficients. It should be noted that an equality

$$u_t + a(x,t)u_x = 0$$

is called the *transport equation* and has important applications in physics [9]. The function a is called the transport velocity. Interestingly, in the article [10], a similar equation, but with a constant transport velocity and an additional term directly proportional to the desired function, is used to describe the movement of infected passengers on public transport.

The method used to obtain this equation may seem somewhat unusual. However, it was precisely this method that was used to establish, for example, the Schrödinger equation, the most important equation in quantum mechanics [11]. Specifically, it was first assumed that a quantum-mechanical system is described by a function ψ (the wave function). It was then noted that it must necessarily possess certain specific properties. After this, a relatively simple equation was selected for which it is a solution. We followed exactly the same approach for the considered system.

Now, knowing the general form of the equation for the spread of an epidemic across a territory, we can attempt to derive it directly. Let us assume that we need to find the infection rate of a territory $u = u(x,t)$, corresponding to the number of patients per unit length at a distance x from the center of the infection center at time t. Then the number of patients in an arbitrarily small area dx is equal to $dN = udx$. Then the number of patients located in an extended area $[x, x+\Delta x]$ is equal to the integral

$$N = \int_x^{x+\Delta x} udx.$$

The change in the number of patients in the specified area over time from t to $t+\Delta t$ is equal to

$$N_1 = \int_x^{x+\Delta x} [u(x,t+\Delta t) - u(x,t)]dx.$$

Let v be the rate of infection spread. Then, in an arbitrarily small time dt, the infection travels a distance vdt. On a section of the corresponding length, the number of patients is equal to $dN = uvdt$. Then, the number of patients corresponding to an extended time interval $[t, t + \Delta t]$ is equal to the integral

$$N = \int_{t}^{t+\Delta t} uvdt.$$

We are interested in the change in the number of patients due to the spread of infection in the selected area $[x, x + \Delta x]$. Since the rate of spread of infection is directed from the center of the infection source into the territory, i.e., in the direction of increasing coordinate x, the change in the number of patients in a given area due to the spread of infection will be equal to

$$N_2 = \int_{t}^{t+\Delta t} (uv|_x - uv|_{x+\Delta x})dt.$$

It is assumed that the change in the number of patients is due solely to the spread of infection, which corresponds to the equality $N_1 = N_2$. Applying the mean value theorem, we arrive at the equality

$$[u(\xi, t + \Delta t) - u(\xi, t)]\Delta x = (uv|_x - uv|_{x+\Delta x})|_\tau \Delta t,$$

where $\xi \in [x, x + \Delta x]$, $\tau \in [t, t + \Delta t]$. Dividing the resulting formula by $\Delta x \Delta t$ and passing to the limit as $\Delta x \to 0$ and $\Delta t \to 0$, we obtain the equality

$$\frac{\partial u}{\partial t} = -\frac{\partial (uv)}{\partial x},$$

valid at any point x at any time t.

It is natural to assume that the rate of infection spread at a given point is proportional to the population density ρ at that point, since the larger the population in a given area, the greater the number of contacts between healthy people and sick people, and therefore, the higher the rate of infection spread. A similar idea (the rate of change in the number of infected is directly proportional to the number of both healthy and sick people) is present in well-known lumped models of epidemic spread [1-3]. As a result, we arrive at the equality $v = c\rho$, where the proportionality coefficient c depends on the specific disease and characterizes the contagiousness (the degree of infectiousness of the disease): the higher the contagiousness, the faster the infection spreads. As a result, we arrive at the equation

$$\frac{\partial u}{\partial t} + c\frac{\partial (\rho u)}{\partial x} = 0,$$

which describes the spread of the epidemic across the territory and is consistent with the result obtained earlier.

4 Conclusions

This paper examines mathematical modeling of the spread of an epidemic across a territory. To describe this process, we propose a first-order partial differential equation with a variable coefficient, which belongs to the class of transport equations. Note that it was obtained first on the basis of an assumption about the probable behavior of the function characterizing the infection rate of the territory, and then directly. The resulting equation, with certain boundary conditions can be used to predict the spread of an epidemic across a territory.

In a specific situation, it is of interest to determine the transfer rate in the epidemic spread equation by solving an inverse problem, for example, using information on the change in the infection rate over time at individual points in the territory under consideration or the size of the infected area. It is also possible, in principle, to imagine a situation where the transfer rate depends on the function u, and the equation itself is nonlinear.

I would like to thank A. Shakir for participating in the discussion of the presented materials.

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Received: May 18, 2026
Accepted: August 06, 2026