https://www.sworldjournal.com/index.php/swj/article/view/swj33-02-112
DOI: 10.30888/2663-5712.2025-33-02-112

A METHOD FOR PREDICTING THE SPREAD OF EPIDEMIOLOGICAL THREATS BASED ON THE TELEGRAPH EQUATION

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Abstract. *Mathematical modeling of epidemic dynamics plays a crucial role in understanding, predicting, and controlling the spread of infectious diseases. Traditional approaches are often based on diffusion-type equations, which assume instantaneous propagation of changes in infection density. However, such models may oversimplify real transmission processes, as the spread of infection among the population usually occurs at a finite rate and exhibits wave-like behavior. To overcome these limitations, this article presents a method for predicting epidemiological threats based on the telegraph equation.*

The telegraph equation, being a second-order hyperbolic differential equation, allows the terminal velocity of propagation and inertial effects to be included in the model. This makes it possible to reflect both diffusion and wave-like modes of epidemic propagation, depending on the balance between diffusion and transport mechanisms. The proposed model describes the spatial-temporal distribution of infection cases and provides insight into the dynamics of epidemic fronts.

Analytical methods make it possible to obtain solutions and analyze them under complex initial and boundary conditions. The results confirm that the approach based on the telegraph equation provides a more realistic description of the spread of the epidemic wave compared to classical diffusion models. Moreover, this method allows identifying critical thresholds, predicting infection peaks, and estimating the time required for the epidemic to spread in specific regions.

The proposed approach can be applied both in theoretical research and as a practical forecasting tool for healthcare systems. It provides a flexible and physically consistent mathematical framework for predicting the spread of epidemiological threats, assisting in decision-making regarding epidemic preparedness and response strategies.

Keywords: *telegraph equation, epidemic spread, epidemiological threats, mathematical modeling, wave propagation, forecasting, partial differential equations.*

Problem Statement.

The problem of predicting the spread of epidemiological threats is one of the key issues in modern mathematical biology and medical statistics. Classical diffusion models based on the heat conduction equation describe the spread of infection as an instantaneous propagation of changes in space. However, real epidemic processes are characterized by finite transmission rates and wave propagation. As a result, classical models do not take into account inertial effects and can distort the results of forecasting.

The telegraph equation, which is a second-order hyperbolic differential equation, allows the mechanisms of diffusion and wave propagation to be combined. In the context of epidemiology, it provides a more realistic description of the process, as it takes into account both local fluctuations in infection density and the wave propagation of the epidemic front.

Thus, the task is to develop a method for predicting the spread of epidemiological threats based on the telegraph equation, which allows:

1) adequately describe the dynamics of infections in space and time;

2) identify critical modes of epidemic development;

3) determine the speed of spread of infectious waves;

4) predict the timing of reaching certain regions and peak incidence values.

Solving this problem will contribute to the construction of more effective mathematical models for healthcare needs and rapid response to epidemiological threats.

Analysis of recent studies and publications. Every healthcare project, whether it involves introducing new medical technology, modernizing a hospital, implementing an electronic health system, or launching a disease prevention program, requires careful planning, coordination, and monitoring. This includes clearly defining goals, managing resources, monitoring deadlines, assessing risks, and monitoring results. The success of healthcare projects is often determined by the team's ability to achieve a balance between service quality, financial constraints, and regulatory compliance.

Modeling the spread of an epidemic is an important tool in managing healthcare projects, especially when projects are aimed at overcoming or mitigating the effects of infectious disease outbreaks. This not only allows for the prediction of the development of an epidemic, but also provides project managers with scientifically sound data for making critical decisions.

Infection spread models allow us to assess possible scenarios for the development of an epidemic under various conditions: the rate of infection spread, the number of cases, the peak of the epidemic, and possible ways to contain it. This enables project managers to plan resources, infrastructure, logistics of medical supplies, and hospital beds based on actual needs. Modeling can be used to analyze where and when resources such as medicines, vaccines, or medical personnel will be needed. This helps to allocate financial and material resources efficiently to avoid shortages or surpluses in certain regions or healthcare facilities.

Modeling allows for the analysis of various measures, such as quarantine restrictions, vaccination, or social distancing. This helps to assess the effectiveness of these measures in different scenarios and select the optimal strategy to reduce the rate of infection spread.

Epidemics create a high level of uncertainty and risk for healthcare projects. Modeling allows you to identify key risks (such as excessive strain on medical facilities or lack of resources) and create plans for different scenarios, improving the flexibility and resilience of the project to external threats. Data obtained from modeling provides the basis for evidence-based decisions at all levels of management. This is particularly important for strategic decisions such as scaling countermeasures, prioritizing medical supplies, or preparing health systems for future waves of the epidemic.

Managing medical projects during epidemics requires flexible and informed decisions that balance effectiveness with cost minimization. Modeling becomes a key tool for ensuring predictable and controlled management in such a complex situation.

One of the fundamental approaches in epidemiology and mathematical biology for analyzing the dynamics of infectious diseases in a population is the construction of models based on differential equations [1]. Incorporating parameters such as the transmission rate, recovery time, and interactions between population groups makes it possible not only to predict future outbreaks but also to evaluate the effectiveness of preventive measures, including quarantine, vaccination, and social distancing.

Classical epidemic models, such as the SIR (Susceptible–Infected–Recovered) framework, remain among the most fundamental tools in mathematical epidemiology. The SIR model employs systems of ordinary differential equations to capture the temporal evolution of three essential population groups: individuals susceptible to infection, individuals currently infected, and those who have recovered and acquired immunity. Its formulation relies on calculating the proportion of the population within each of these categories and on defining the rates of transition between them. In particular, the model requires the estimation of two key epidemiological parameters: the infection transmission rate, which reflects the probability of disease spread during contact between susceptible and infected individuals, and the recovery rate, which characterizes the average duration of infection before recovery. Despite its relative simplicity, the SIR model provides valuable insights into the mechanisms of epidemic spread and serves as the basis for numerous extensions and generalizations in modern epidemiological modeling.in following form

Let us consider SIR model

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

where *S(t)* denotes the number of individuals susceptible to infection, *I(t)* represents the number of infected individuals, and *R(t)* corresponds to the number of recovered individuals [2, 3]. Mathematical modeling of the development of an epidemic process, taking into account the specific features of COVID-19 transmission, has been presented in [4] using a system of differential equations.

Mathematical models of disease transmission provide a powerful framework for analyzing both the temporal evolution of the number of infected individuals and their spatial distribution within a population. While classical models, such as the SIR (Susceptible–Infected–Recovered) framework, describe the dynamics of infection in terms of time-dependent changes in the size of three key compartments, they often neglect the impact of spatial heterogeneity. To address this limitation, extended models have been developed that incorporate diffusion or transport terms, thereby allowing for the representation of spatial mobility and local clustering of individuals. Such spatially explicit models are particularly relevant in the study of modern epidemics, as they capture processes such as regional transmission, population density effects, and spatially dependent interventions (e.g., localized quarantines or vaccination campaigns). These extensions significantly enhance the predictive and explanatory power of mathematical epidemiology, making it possible to model not only the overall course of an epidemic but also its spatial patterns and spread across different regions [5].

To model the process of epidemic spread more realistically, diffusion terms are incorporated into the classical SIR equations [6]. These terms account for the spatial mobility of both susceptible and infected individuals, thereby extending the traditional time-dependent formulation of the model. The inclusion of diffusion reflects the natural movement of people across different locations, which directly influences local infection dynamics and the geographical progression of an epidemic. By doing so, the model not only tracks the evolution of population groups over time but also captures spatial interactions, such as clustering of cases or wave-like propagation of disease. This spatially extended approach thus provides a more comprehensive representation of epidemic processes and offers valuable insights for designing region-specific control measures.

$$\frac{\partial S(t,x,y)}{\partial t} = -\beta S(t,x,y)I(t,x,y) + D_s \nabla^2 S(t,x,y), \beta$$

$$\frac{\partial I(t,x,y)}{\partial t} = \beta S(t,x,y)I(t,x,y) - \gamma I(t,x,y) + D_i \nabla^2 I(t,x,y),$$

$$\frac{\partial R(t,x,y)}{\partial t} = \gamma I\left(t,x,y\right) + D_r \nabla^2 R(t,x,y), .$$

where β is the transmission rate, γ is the recovery rate, D_s, D_i, D_r are the diffusion coefficients for the susceptible and infected compartments, ∇^2 denotes the Laplace operator.

Reference [6] presents an epidemic model formulated in terms of a second-order differential equation with respect to time (spatial diffusion).

$$a_2 \frac{d^2 X(t)}{dt^2} + \left(1 + a_1 X(t) \frac{dX(t)}{dt}\right) + \left(a_0 X(t) - \varphi\right) v X^0(t) = 0,$$

where $X(t)$ denotes the number of infected individuals at time *t*, φ represents the rate of growth of the infected population, and $\{a_0, a_1, a_2\}$ are coefficients that serve as epidemic parameters (a_0 is the proportion of individuals susceptible to infection; a_1 is the asymmetry coefficient of the flow; a_2 is the level of population susceptibility to the virus).

Contemporary challenges in epidemiology, including globalization, spatial interactions, and complex socioeconomic factors, require more sophisticated approaches that take into account both the spatial and temporal aspects of disease spread. In this regard, epidemic modeling using partial differential equations is used to describe the spatial and temporal processes of infection spread [7]. Such models, which include elements of diffusion or wave propagation, provide a more accurate reflection of the real dynamics of diseases, especially in conditions of heterogeneous population distribution and human mobility.

For models based on wave or diffusion equations with specified conditions at two points in time, using the differential-symbol method [8, 9], it is possible to write down an analytical solution that makes it possible to predict the spread of the process at any point in time at any point in the region.

Purpose of the work: the purpose of this study is to develop a mathematical model of the spread of epidemiological threats based on the telegraph equation, which takes into account both the temporal dynamics of the disease and the spatial characteristics of its spread, and to develop a method for finding analytical solutions to the problem, which makes it possible to study the influence of key model parameters on the course of the epidemic. the aim of this study is to develop a mathematical model of the spread of epidemiological threats based on the telegraph equation, which accounts for both the temporal dynamics of the disease and the spatial characteristics of its propagation, as well as to investigate the impact of key model parameters on the course of the epidemic.

Presentation of main material.

This article discusses approaches to modeling the spread of epidemics using second-order differential equations, in particular, wave equations and diffusion equations.

If we model the spread of an epidemic using second-order differential equations over time, it may resemble a wave equation or a diffusion equation that takes into account inertial effects. The second order in time indicates the effect of acceleration or inertia in the dynamics of the epidemic spread. This approach can be useful for modeling situations where there are delays in the system's response to changes, for example, due to the incubation period or other time delays.

The equation describing the state of the infected population looks like a modified wave equation that takes into account both spatial and temporal effects

$$\frac{\partial^2 I(t,x,y)}{\partial t^2} = c^2\nabla^2 I(t,x,y) - \alpha\frac{\partial I(t,x,y)}{\partial t} - \gamma I(t,x,y), \quad (1)$$

where $\frac{\partial^2 I(t,x,y)}{\partial t^2}$ denotes acceleration of the change in infected individuals over time, $c^2\nabla^2 I(t,x,y)$ is spatial distribution of infected individuals (c is rate of spread of infection in space), $\alpha\frac{\partial I(t,x,y)}{\partial t}$ is a term that takes into account attenuation or damping (interpreted as a resistance coefficient, for example, due to isolation), $\gamma I(t,x,y)$ is the process of recovery or exit from infection (roughly analogous to the classic SIR model). These models provide a deeper understanding of the mechanisms of transmission between different regions and population groups, as well as an assessment of the impact of external factors on the dynamics of the epidemic.

When forecasting the spread of epidemiological threats, the telegraph equation is proposed to be used to model the wave-like spread of epidemics. Unlike diffusion models (which are based on heat conduction equations and describe the gradual spread of infections), the telegraph equation has its own characteristics and allows for a number of components of the project environment to be taken into account (Fig. 1).

In particular, the spatial-temporal delay in the spread of infection. Infection does not spread instantly. That is, it takes time for the wave of spread to reach new territories or regions. The model also takes into account the presence of a wave of spread. During an epidemic, waves of infection can be observed, when after the first outbreak of the disease there is a wave of decrease in the number of patients, followed by a new outbreak. This is due to repeated contacts or other factors of the project environment. The telegraph equation describes such oscillatory processes well. In addition, the proposed method takes into account the speed of infection spread.

The telegraph equation assumes that the infection spreads in waves at a rate of c . These waves are dampened by attenuation α, which describes the natural processes of epidemic decay or implemented measures (e.g., quarantine). At the beginning of an epidemic, the function $I(t,x,y)$ describes a sharp outbreak when the number of infected people increases rapidly in the center of the epidemic and gradually spreads to other regions.

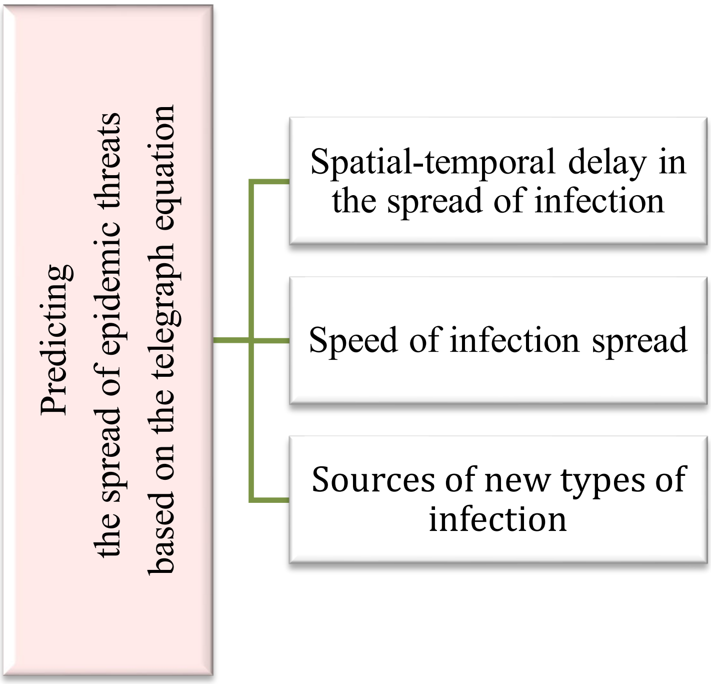

Figure 1. Taking into account the characteristics of the project environment when forecasting the spread of epidemiological threats based on the telegraph equation

For example, if the epidemic started at point x_0, the wave of infection will spread from this point at a rate of c. After a certain time, infected people will appear at points $(x_1,y_1),(x_2,y_2),...(x_n,y_n)...$. The change in the intensity of infection of the population with infectious diseases in different regions depends on the attenuation coefficient α.

When forecasting epidemiological threats, the initial number of infected people at a given point x_0, time $t=0$, level of population mobility, and the impact of quarantine are specified. Quarantine or vaccination affect the parameter α, increasing or decreasing the rate at which the epidemic subsides. This makes it possible to model the spread of infection in different regions with given initial conditions, as well as to assess how the infection spreads within a hospital district. Let $I(0,x,y)$ and $I(l,x,y)$ are functions that describe the epidemic process at two points in time, according to the differential-symbol method [10, 12], it is possible to find the solution to this problem, i.e., a function that analytically describes the process of the spread of the epidemic at any point and at any point in time. In the case when the absence of sources of new infections or external influences leading to the appearance of additional infected individuals in the region, equation (1) is homogeneous.

Let us find analytical solution of the equation (1), which satisfies two-point condition

$$I(0,x,y)=\varphi(x,y),\ I(l,x,y)=\phi(x,y). \tag{2}$$

According to the differential-symbol method, the solution of the two-point problem (1), (4) can be found in the following form

$$I(t,x,y)=\varphi\left(\frac{\partial}{\partial\nu}\right)\frac{\sinh\left[(l-t)R(\nu)\right]}{\sinh\left[lR(\nu)\right]}e^{-\frac{1}{2}\alpha t+\nu_1x_1+\nu_2x_2}\Bigg|_{\nu=0}+$$
$$+\phi\left(\frac{\partial}{\partial\nu}\right)\frac{\sinh\left[tR(\nu)\right]}{\sinh\left[lR(\nu)\right]}e^{-\frac{1}{2}\alpha t+\nu_1x_1+\nu_2x_2}\Bigg|_{\nu=0},$$

where $R(\nu)=\frac{1}{2}\sqrt{\alpha^2+4c^2\|\nu\|-4\gamma}$, $\frac{\partial}{\partial\nu}=\left(\frac{\partial}{\partial\nu_1},\frac{\partial}{\partial\nu_2}\right)$. The functions $\varphi\left(\frac{\partial}{\partial\nu}\right)$ and $\phi\left(\frac{\partial}{\partial\nu}\right)$ are obtained by replacing (x,y) with $\left(\frac{\partial}{\partial\nu_1},\frac{\partial}{\partial\nu_2}\right)$ in the functions $\varphi,\ \phi$.

Note that if the functions $\varphi,\ \phi$ are constants ($\varphi(x,y)=c_1,\ \phi(x,y)=c_2,$), i.e., only the number of infected individuals at two points in time is considered, then the solution to the problem $I(t,x,y)$ depends only on t, i.e., we obtain the dependence of the change in the number of infected individuals over time

$$I(t,x,y)=$$
$$=\frac{e^{-\frac{1}{2}\alpha t}}{\sinh\left[\frac{1}{2}l\sqrt{\alpha^2-4\gamma}\right]}\left(c_1\sinh\left[\frac{1}{2}\sqrt{\alpha^2-4\gamma}(l-t)\right]+c_2\sinh\left[\frac{1}{2}t\sqrt{\alpha^2-4\gamma}\right]\right).$$

Knowing the number of infected individuals at different spatial points of the region at two distinct time moments, the differential-symbol method can be applied to construct solutions of the telegraph equation that describe the spatiotemporal dynamics of the epidemic spread. This approach allows not only the prediction of overall trends in the infection process but also the identification of characteristic features, such as peak incidence periods and subsequent phases of decline.

The telegraph equation allows for an accurate description of the wave-like dynamics of infection spread in a given region, taking into account time delays, the speed of infection spread, and the sources of new outbreaks. Based on the proposed method, forecasts are made for peaks in population morbidity, the spread of infection to new territories, and assessments of the overall burden on medical facilities during an epidemic.

Let us consider correlation of the telegraph equation with the classic SIR model. This makes it possible to expand the spatio-temporal approach to modeling the spread of epidemiological threats. Combining these two approaches allows us to simultaneously take into account both the dynamics of infectious disease transmission among the population of a given region and the spatial distribution of the infection.

The classical SIR (Susceptible-Infectious-Recovered) model describes the dynamics of infectious disease in a population by dividing the population into three groups:

– S (susceptible) – the population of the region that can be infected;

– I (infected) – the population of the region that is infected and can transmit the infection to others;

– R (recovered) – the population of the region that has recovered or become immune, i.e., can no longer transmit the disease.

The model is described by a system of differential equations:

$$\frac{dS}{dt}=-\beta\frac{SI}{N},\quad \frac{dI}{dt}=\beta\frac{SI}{N}-\gamma I,\quad \frac{dR}{dt}=\gamma I, \tag{3}$$

where $S(t)$ is number of vulnerable individuals over time; $I(t)$ is number of infected individuals over time; $R(t)$ is number of recovered individuals; β denotes rate of infection among the region's population; γ is rate of recovery among the region's population; N is total population living in the region.

The model (3) is the basis for calculating the dynamics of infectious diseases. However, it does not take into account spatial features such as changes in different regions, human migration, or delays in the spread of infection. Combining it with the telegraph equation makes it possible to eliminate these shortcomings.

The SIR model describes the general dynamics of infection within a population well, but does not take into account the spatial aspect of the spread of infection. To simulate not only the temporal but also the spatial-temporal dynamics of infection, the telegraph equation (1) is introduced. This equation allows us to model the spread of infection in the form of waves that propagate at a certain speed c in space x and time t.

Let us consider the relationships between the models. The telegraph equation (1) for spatial propagation is refined as follows. The SIR model is extended by introducing a dependence on spatial coordinates. For this purpose, the telegraph equation is used, which describes the processes of how the infection spreads from one region to another at a rate (the rate of infection spread).

Thus, for each of the parameters $S(x,t)$, $I(x,t)$ and $R(x,t)$, it is proposed to use the telegraph equation (1) to describe the spatio-temporal dynamics.

The classical SIR framework presumes that the infection is transmitted instantaneously across the entire population. In contrast, real-world epidemic dynamics exhibit a gradual expansion, whereby the infection front advances progressively into new geographic regions. The telegraph equation (1) provides a more realistic description of this process by incorporating a finite propagation velocity ccc. Furthermore, empirical observations indicate that the spread of infection is characterized by a temporal delay τ\tauτ, during which the epidemic wave propagates outward from the initial epicenter to surrounding areas. This inherent delay is rigorously accounted for in the telegraph equation (1) through the inclusion of the second-order time derivative.

The proposed method incorporates population mobility between regions, thereby enabling the modeling of infection spread into new territories. This feature is of particular importance for assessing epidemiological threats across large hospital districts. Spatial differentiation enhances the accuracy of predictions, since infections propagate unevenly across regions, directly influencing the distribution of resources among hospitals and healthcare facilities. Based on this approach, it becomes possible to anticipate hospital loads in different areas and ensure their more balanced allocation.

The telegraph equation (1) provides a framework for predicting epidemic waves and periods of decline, which is critical for identifying the timing of new outbreaks and implementing timely response measures. Moreover, by introducing a source function, the model captures the emergence of new outbreaks in distinct regions or the effects of interventions (e.g., vaccination campaigns or quarantine measures), thus offering a more reliable basis for planning preventive strategies.

The integration of the classical SIR model with the telegraph equation enables the modeling of not only the temporal dynamics of infection within a population, but also its spatial propagation. Such an approach allows for the development of a more accurate and effective decision-support system for forecasting epidemiological threats and optimizing the allocation of healthcare resources across hospital districts.

An important feature of the proposed framework is the incorporation of potential intervention scenarios, such as quarantine measures and vaccination campaigns. Within our method, these scenarios are explicitly embedded in the modeling of epidemic dynamics, thereby allowing the simulation of the impact of public health interventions on the spread of infection. This provides valuable insights for designing preventive strategies and improving the preparedness of healthcare systems in the face of future outbreaks.

Vaccination introduces an additional term that modifies the number of susceptible individuals *S(t)* available for infection, with the rate of vaccination ν directly influencing the dynamics. This leads to modifications of the equations (3):

$$\frac{dS}{dt} = -\beta \frac{SI}{N} - \nu S, \quad \frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I, \quad \frac{dR}{dt} = \gamma I + \nu S \tag{4}$$

where ν denotes the vaccination rate, which directly decreases the number of susceptible individuals *S(t)* and correspondingly increases the number of recovered individuals *R(t)*.

Based on the spatio-temporal modeling framework, the impact of the spread of infectious diseases on the healthcare resources of hospital districts can be evaluated. To account for the hospital load, we introduce a variable *H(t),* representing the occupancy of hospitals over time. The maximum hospital load within a given period can be expressed through the integral of the number of infected individuals within a specific territory:

$$H(t)=\iint\limits_{\Omega} I\left(x,t\right)dS$$

where Ω denotes the boundary of the hospital district.

The hospital load depends on the number of infected individuals within a given region. If the number of infected individuals *I(t)* at time *t* exceeds the hospital capacity $H_{\max}$, this leads to a critical overload of healthcare facilities.

The proposed method for predicting the spread of epidemiological threats, which incorporates spatio-temporal dynamics, makes it possible to forecast the following indicators (Fig. 2):

1. the peak period of morbidity, corresponding to the maximum number of infected individuals $I_{\max}$, which is determined as the maximum of $I\left(x,t\right)$ over all values of *t*;
2. the duration of the epidemic, defined as the time interval after which the number of infected individuals becomes less than one;
3. the hospital load, determined from the predicted hospital occupancy $H\left(t\right)$ and its correspondence to the maximum available bed capacity $H_{\max}$.

4. The proposed epidemiological model, which combines the classical SIR framework with spatial dynamics, leads naturally to the telegraph equation as a governing relation for the spatio-temporal spread of infection. Unlike the diffusion equation, the telegraph equation accounts for both finite propagation speed and time delay in the transmission of the infection, reflecting more realistic epidemic dynamics. Its solutions, expressed through damped traveling waves, describe the spread of infection from an epicenter to new regions, the attenuation of epidemic waves, and the emergence of new outbreaks under the influence of source terms. These solutions,

adapted to the initial and boundary conditions of the model, form the mathematical basis for forecasting epidemic waves and evaluating hospital load in different regions.

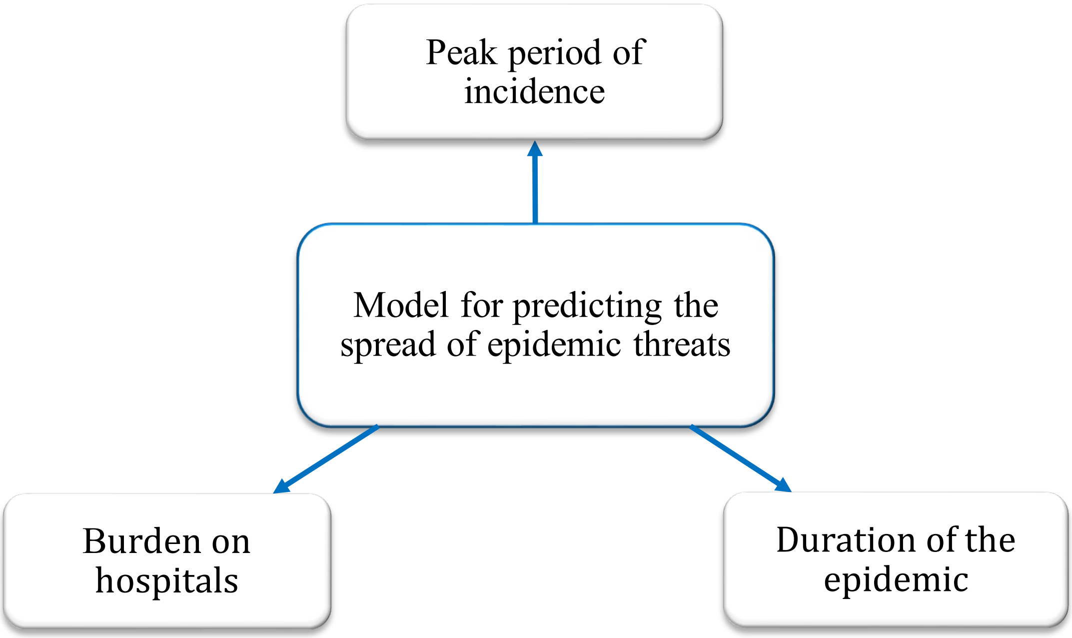

Fig. 2. Diagram of indicators that can be quantitatively assessed based on the proposed method for forecasting the spread of epidemiological threats

The proposed method for predicting the spread of epidemiological threats based on the telegraph equation makes it possible to account for both the temporal and spatial dynamics of infection transmission. This is of particular importance for assessing hospital load and supporting appropriate management decisions by healthcare project managers.

Conclusion.

In this study, a method for predicting the spread of epidemiological threats based on the telegraph equation has been proposed. The approach integrates classical SIR-type epidemiological models with spatial-temporal dynamics, allowing for a more accurate assessment of infection propagation across regions. By incorporating diffusion and delay effects, the method captures both the temporal evolution and spatial distribution of infected and susceptible populations. This enables the prediction of key indicators such as peak incidence periods, epidemic duration, and hospital load. The differential-symbol method provides a systematic way to construct solutions to the telegraph equation using data from two distinct time points, facilitating the identification of epidemic peaks, attenuation phases, and potential new outbreaks. Overall, the proposed framework supports effective decision-making for resource allocation and preventive measures in hospital districts, improving preparedness and response to epidemiological threats.

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