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VARIANTS OF THE STOCHASTIC SIR MODELS AND VACCINATION STRATEGIES*

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Abstract. *Several options of the stochastic SIR epidemics model with limited treatment are proposed. For these methods, the efficiency of different vaccination strategies is demonstrated, and a method for obtaining the optimal vaccination strategy minimizing the cost functional is proposed.*

Keywords: *stochastic model, epidemic, optimal strategy.*

INTRODUCTION

The COVID-19 pandemic is remaining a global challenge. Although the number of infections is reduced compared to the peaks of the last year, it is still high because of the emerging new strains and the incomplete vaccination of the population. There is also the threat of emergence of future epidemics of different diseases.

Thus, forecasting the development of epidemics remains an important problem, and solving it allows us to forecast the future pressure on the medical facilities, to reserve medicine in advance, to implement quarantine measures, to estimate the impact of the partial vaccination of the population on the infection distribution dynamics, and to find the optimal of vaccination strategy.

One of the most widely used epidemics models is SIR [1] where the population is divided into the following groups depending on their state of health:

— the individuals prone to sickness, but not sick;

— the individuals who are ill and can infect those who are prone to sickness;

— the individuals who recovered and developed an immunity to the sickness.

This model presents variants of stochastic SIR models with limited treatment [2]. Here, a couple of model versions are proposed depending on the epidemic type and the vaccination strategies. Moreover, the search for the optimal vaccination strategy to minimize the cost functional is considered, which depends on the forecast number of patients and expenses on vaccine introduction.

STOCHASTIC SIR MODEL WITH LIMITED TREATMENT

Consider the stochastic SIR model with limited treatment [2]. Let $S(t)$ be the number of individuals prone to sickness at the moment in time t and $I(t)$ be the number of infected. Under usual circumstances, the third component of the model is R, i.e., the number of individuals who recovered. However, in the model variants presented in what follows, the immunity that is obtained after recovery is considered to be constant and absolutely efficient; thus, the variable R does not influence the future epidemic development and the dynamics of this variable is not considered separately.

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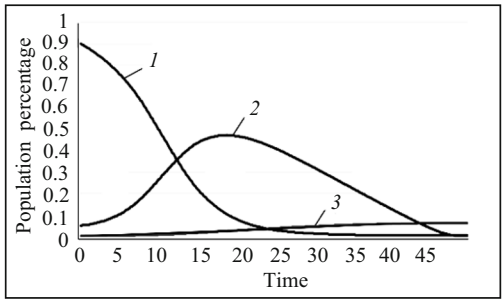

Fig. 1. The model variant without vaccine introduction where curve *1* is the number of individuals prone to getting the disease, curve *2* is the number of ill individuals, and curve *3* is the number of fatal cases.

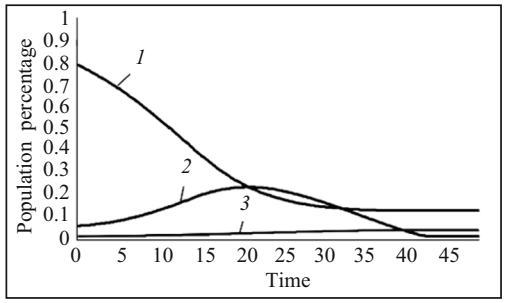

Fig. 2. The model variant with vaccination before the start of the epidemic where curve *1* is the number of individuals prone to getting the disease, curve *2* is the number of ill individuals, and curve *3* is the number of fatal cases.

First, let us consider the course of the epidemic in a comparatively constant number of the population in a short timeframe when the appearance of new infected individuals in the environment under study is not an important factor. In this case, changes in the variables $S(t)$ and $I(t)$ solely depend on the epidemic development, and their dynamics is described by the equations

$$dS(t) = \{-\beta S(t)I(t) - Y(S(t), I(t))\}\, dt - \varepsilon S(t)I(t)dW_1(t), \tag{1}$$

$$dI(t) = \left\{ \beta S(t)I(t) - \mu I(t) - \frac{rI(t)}{a + I(t)} \right\} dt + \varepsilon S(t)I(t)dW_2(t), \tag{2}$$

where β is the speed of the infection spread, which depends on the virulence of the infectious disease, the number of contacts within the population, quarantine measures, etc., Y is the speed with which vaccination is implemented, and it is the guiding parameter of this problem, ε is the diffusion, μ is the number of fatal cases caused by the disease, r is the maximum feasible number of recovered individuals in a certain timeframe, and a is the number of disease cases, under which a half of the maximum number of recovered individuals is reached in a certain amount of time. The growth of the number of disease cases $I(t)$ puts medical facilities under exceeding stress, and the ratio of recovered individuals to the number of disease cases decreases.

As we can see, except for the diffusion $\varepsilon S(t)I(t)\,dW_1(t)$, the variable $S(t)$ monotonically decreases. Depending on the ratio of the speed of infection spread to the recovery speed or the existence of fatal cases, the number of infection cases can grow at the beginning of the epidemic and gradually decline only through the decrease in the number of infected individuals. That is why this model is very well forecast under a not very high diffusion as here $S(t)$ monotonically decreases to a certain level, at which the epidemic spreads slower than the rate of treatment, and the number of infections decreases to zero.

A Model Variant without Vaccine Introduction. In the variant under consideration, the model does not have the summand $Y(S(t), I(t))$. Then, Eq. (1) transforms into

$$dS(t) = -\beta S(t)I(t)dt - \varepsilon S(t)I(t)\,dW_1(t).$$

The number of disease and fatal cases can be estimated using a computer simulation depending on the given model parameters. Figure 1 presents the simulation results of the model variant without vaccine introduction with the parameters $\beta = 0.5$, $\varepsilon = 0.3$, $\mu = 0.005$, $r = 0.02$, $a = 0.01$, $S_0 = 0.9$, and $I_0 = 0.05$.

A Model Variant with Vaccine Introduction. Consider the impact of vaccination on the reduction of number of the infected individuals. Vaccination can take place both before the start and during an epidemic. If vaccination of the population is performed before the epidemic starts, then the number of individuals prone to getting the disease is lower.

Figure 2 presents the simulation results of the model variant with vaccination before the start of the epidemic. Here, the same parameters are used as in the case of the model variant in Fig. 1, except $S_0 = 0.8$.

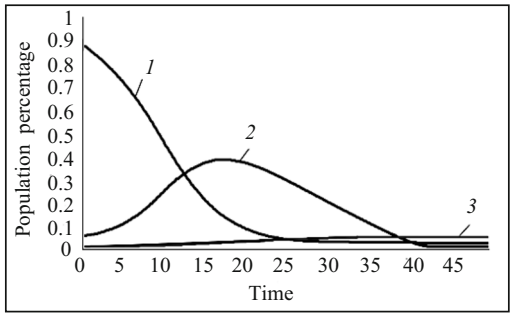

Fig. 3. The model variant with vaccination after the start of the epidemic where curve *1* is the number of individuals prone to getting the disease, curve *2* is the number of ill individuals, and curve *3* is the number of fatal cases.

As we can see (see Fig. 2), despite the low value of S_0, the number of ill persons and of fatal cases is significantly lower compared to the model variant without vaccine introduction.

Consider the model with vaccination after the start of the epidemic. We consider the vaccination speed to be a constant Y. Then, Eq. (1) take the form

$$dS(t) = \{-\beta S(t) I(t) - Y\} dt - \varepsilon S(t) I(t) dW_1(t).$$

Figure 3 presents the simulation results of the model variant with vaccination after the start of the epidemic with the set of parameters that were used for the model variant in Fig. 1, as well as the vaccination speed $Y = 0.005$.

Normally, compared to the vaccination before the start of the epidemic, the delay in vaccinating leads to its lessened efficiency. In the considered model variant, double as many vaccination doses were used compared to the model variant with vaccination before the start of the epidemic; yet, the number of disease and fatal cases was much higher.

A Model Variant with a More Dynamic Population. Here, either a population of animals with a short lifespan can be considered, or a lengthy epidemic, in the process of which it is impossible to talk about a stable population.

To model dynamic population changes, the logistic function [3] is used. Equations (1) and (2) take the form

$$dS(t) = \{\gamma S(t)(K - S(t)) - \beta S(t) I(t) - Y(S(t), I(t))\} dt - \varepsilon S(t) I(t) dW_1(t), \quad (3)$$

$$dI(t) = \left\{ \beta S(t) I(t) - \mu I(t) - \frac{r I(t)}{a + I(t)} \right\} dt + \varepsilon S(t) I(t) dW_2(t), \quad (4)$$

where γ is the coefficient of the population growth speed and K is the environmental capacity. Under comparatively small to K values of $S(t)$, the logistic function $S(t)(K - S(t))$ grows approximately exponentially. In the case where $S(t)$ is approaching to K, their difference exponentially falls.

Together with the random diffusion, the above brings additional uncertainty into the model. In the case when a full vaccination is impossible, there arises a need to search for optimal vaccination strategy, which depends on the current cause of epidemic, i.e., the number of persons prone to sickness and of the infected individuals. Thus, the vaccination level is the function $Y(S(t), I(t))$.

Using (3) and (4), we can formulate the stochastic vector equation in the form

$$dx(t) = b(x(t), Y(t)) dt + \sigma(x(t)) dW(t), \quad (5)$$

where

$$b_1(x(t), Y(x(t))) = \gamma x_1(t)(K - x_1(t)) - \beta x_1(t) x_2(t) - Y(x(t)),$$

$$b_2(x(t), Y(x(t))) = \beta x_1(t) x_2(t) - \mu x_2(t) - \frac{r x_2(t)}{a + x_2(t)},$$

$$\sigma_{11}(x(t)) = -\varepsilon x_1(t)x_2(t),$$

$$\sigma_{22}(x(t)) = \varepsilon x_1(t)x_2(t),$$

$$\sigma_{12} = \sigma_{21} = 0.$$

The epidemic continues while there are the infected or prone to sickness individuals. From there, it follows that the values x_1 and x_2 are lower-bounded. At the same time, the population number cannot exceed the environmental capacity, and as such, we have an upper bound. Thus, let us consider the process x on the set

$$V = \{x \in \mathbb{R}^2 : 1 \le x_i \le 2K;\ i = 1, 2\}.$$

Here, we have the cost functional [2]

$$\Psi_Y(x) = E_x \int_0^\tau f(x(t), Y(x(t)))dt = E_x \int_0^\tau \{m_1 x_1(t) + m_2 x_2(t) + rY^2(x(t))\}\, dt,$$

where m_1 and m_2 are certain parameters and τ is the moment when the epidemic ends or when the process x leaves the domain V.

The problem statement is to find the control function $Y(x)$ that minimizes the cost functional $\Psi_Y(x)$.

A characteristic operator of the process determined in (5) has the form [4]

$$L = \sum_{i,j=1}^{2} a_{ij}(x) \frac{\partial^2}{\partial x_i \partial x_j} + \sum_{i=1}^{2} b_i(x, Y(x)) \frac{\partial}{\partial x_i},$$

where

$$a_{ij}(x) = \frac{1}{2}(\sigma(x)\sigma^{\mathrm{T}}(x))_{ij},$$

$$\sigma(x)\sigma^{\mathrm{T}}(x) = \begin{pmatrix} -\varepsilon x_1 x_2 & 0 \\ 0 & \varepsilon x_1 x_2 \end{pmatrix}^2 = \begin{pmatrix} \varepsilon^2 x_1^2 x_2^2 & 0 \\ 0 & \varepsilon^2 x_1^2 x_2^2 \end{pmatrix}.$$

Then,

$$L = \frac{1}{2}\varepsilon^2 x_1^2 x_2^2 \left\{ \frac{\partial^2}{\partial x_1^2} - 2\frac{\partial^2}{\partial x_i \partial x_j} + \frac{\partial^2}{\partial x_2^2} \right\} + \sum_{i=1}^{2} b_i(x, Y(x)) \frac{\partial}{\partial x_i}.$$

Let us write certain properties of Eq. (5).

Property 1. The functions $a_{ij}(x)$ are bounded on V.

Property 2. The Lipschitz functions $a_{ij}(x)$ are continuous on V. Indeed,

$$\left| \frac{\partial a_{ii}}{dx_1} \right| = \varepsilon^2 x_1 x_2^2 \le \varepsilon^2 8K^3,$$

$$\left| \frac{\partial a_{ii}}{dx_2} \right| = \varepsilon^2 x_1^2 x_2 \le \varepsilon^2 8K^3,$$

$$|a_{ii}(x_1, x_2) - a_{ii}(x_1^*, x_2^*)| \le |a_{ii}(x_1, x_2) - a_{ii}(x_1^*, x_2)| + |a_{ii}(x_1^*, x_2) - a_{ii}(x_1^*, x_2^*)|$$

$$\le |x_1 - x_1^*| \max_V \left| \frac{\partial a_{ii}}{dx_1} \right| + |x_2 - x_2^*| \max_V \left| \frac{\partial a_{ii}}{dx_2} \right| \le 8\varepsilon^2 K^3 (|x_1 - x_1^*| + |x_2 - x|) \le 16\varepsilon^2 K^3 |x - x^*|.$$

Property 3. For any x, $\lambda_i \in \mathbb{R}$, we obtain

$$\mu \sum_{i=1}^{2} \lambda_i^2 \le \sum_{i,j=1}^{2} a_{ij}(x) \lambda_i \lambda_j \le \frac{1}{\mu} \sum_{i=1}^{2} \lambda_i^2, \ \mu = \text{const} > 0.$$

Indeed,

$$\sum_{i,j=1}^{2} a_{ij}(x) \lambda_i \lambda_j = \frac{1}{2} \varepsilon^2 x_1^2 x_2^2 (\lambda_1^2 + \lambda_2^2).$$

For $\varepsilon \ge 1$, we have

$$\frac{1}{16K^4 \varepsilon^2} (\lambda_1^2 + \lambda_2^2) \le \frac{1}{2} \varepsilon^2 x_1^2 x_2^2 (\lambda_1^2 + \lambda_2^2) \le 16K^4 \varepsilon^2 (\lambda_1^2 + \lambda_2^2),$$

and, for $\varepsilon \le 1$, we obtain

$$\frac{1}{16K^4} \varepsilon^2 (\lambda_1^2 + \lambda_2^2) \le \frac{1}{2} \varepsilon^2 x_1^2 x_2^2 (\lambda_1^2 + \lambda_2^2) \le \frac{16K^4}{\varepsilon^2} (\lambda_1^2 + \lambda_2^2).$$

Let the feasible strategies $Y(x)$ belong to a certain interval $[0, c]$ (as the maximum number of vaccine doses is limited). Let us denote by $\mathfrak{N}$ a class of such feasible strategies. Then, we obtain the following property.

Property 4. The functions $b_i(x, Y)$ are bounded and continuous on $V \times C$.

The following theorem is introduced in [5] for the equations with Properties 1–4.

THEOREM 1. In the domain V, there is a unique solution $u^*(x)$ to the equation

$$\sum_{i,j=1}^{2} a_{ij}(x) \frac{\partial^2 u}{\partial x_i \partial x_j} + \max_{y \in [0, c]} \left\{ \sum_{i=1}^{2} b_i(x, y) \frac{\partial u}{\partial x_i} - f(x, y) \right\} = 0 \tag{6}$$

with zero boundary conditions where $f(x, y) = m_1 x_1 + m_2 x_2 + r y^2$.

The optimal feasible strategy $Y^*(x)$ exists as well, i.e., the one that

$$Y^*(x) \ge Y(x), \ Y \in \Upsilon, \ x \in V,$$

and for which $\Psi_{Y^*}(x) = u^*(x)$ exists.

Any feasible strategy $Y(x)$, which maximizes the expression

$$\sum_{i=1}^{2} b_i(x, Y(x)) \frac{\partial u^*}{\partial x_i} - f(x, Y(x))$$

for all $x \in V$, is optimal.

Consider expression (6). Here, we obtain

$$\frac{1}{2} \varepsilon^2 x_1^2 x_2^2 \left(\frac{\partial^2 u}{\partial x_1^2} + \frac{\partial^2 u}{\partial x_2^2} \right) + \max_{y \in [0, c]} \left\{ [(\gamma x_1 (K - x_1) - \beta x_1 x_2 - y] \frac{\partial u}{\partial x_1} \right.$$

$$\left. + \left[\beta x_1 x_2 - \mu x_2 - \frac{r x_2}{a + x_2} \right] \frac{\partial u}{\partial x_2} - m_1 x_1 - m_2 x_2 - r y^2 \right\}$$

$$= \frac{1}{2} \varepsilon^2 x_1^2 x_2^2 \left(\frac{\partial^2 u}{\partial x_1^2} + \frac{\partial^2 u}{\partial x_2^2} \right) + \max_{y \in [0, c]} \{ g(x, y, u(x)) \} = 0, \tag{7}$$

$$\frac{\partial g}{\partial y} = -2ry - \frac{\partial u}{\partial x_1}, \ \frac{\partial^2 g}{\partial y^2} = -2r < 0. \tag{8}$$

From (8) it follows that $\max_{y \in [0, c]} \{ g(x, y, u(x)) \}$ is reached for $y = -\frac{1}{2r} \frac{\partial u}{\partial x_1}$ if $\frac{\partial u}{\partial x_1} \in [-2cr, 0]$, for $y = 0$ if $\frac{\partial u}{\partial x_1} > 0$, and for $y = c$ if $\frac{\partial u}{\partial x_1} < -2cr$.

Thus, through (7) and (8), Eq. (6) takes the form

$$\frac{1}{2}\varepsilon^2 x_1^2 x_2^2\left(\frac{\partial^2 u}{\partial x_1^2}+\frac{\partial^2 u}{\partial x_2^2}\right)+[(\gamma x_1(K-x_1)-\beta x_1 x_2]\frac{\partial u}{\partial x_1}$$

$$+\left[\beta x_1 x_2-\mu x_2-\frac{r x_2}{a+x_2}\right]\frac{\partial u}{\partial x_2}-m_1 x_1-m_2 x_2$$

$$+\left(-c\frac{\partial u}{\partial x_1}-rc^2\right)1_{\left\{\frac{\partial u}{\partial x_1}<-2cr\right\}}+\frac{1}{4r}\left(\frac{\partial u}{\partial x_1}\right)^2 1_{\left\{\frac{\partial u}{\partial x_1}\in[-2cr,0]\right\}}=0. \quad (9)$$

Let us substitute the approximation of derivatives through the finite differences in this equation as follows:

$$\frac{\partial u}{\partial x_1}=\frac{u(x_1,x_2)-u(x_1-h,x_2)}{h},$$

$$\frac{\partial u}{\partial x_2}=\frac{u(x_1,x_2)-u(x_1,x_2-h)}{h},$$

$$\frac{\partial^2 u}{\partial x_1^2}=\frac{u(x_1,x_2)-2u(x_1-h,x_2)+u(x_1-2h,x_2)}{h^2},$$

$$\frac{\partial^2 u}{\partial x_2^2}=\frac{u(x_1,x_2)-2u(x_1,x_2-h)+u(x_1,x_2-2h)}{h^2}.$$

Thus, as we can see, that Eq. (9) allows us to calculate the value $u(x_1,x_2)$ from the previous values u. Using zero boundary conditions $u(S(0),I(t))=u(S(t),I(0))=0$ (which result from Theorem 1), we can estimate the approximation of the optimal vaccination strategy for each pair $x_1=S(t)$ and $x_2=I(t)$ on the plane $V\times V$ starting from $u(S(0),I(t))=u(S(t),I(0))=0$.

CONCLUSIONS

Several options of the stochastic SIR epidemics model with limited treatment are considered in this paper. For the model with a stable population, the model simulation results are presented, as well as the impact of different vaccination strategies on the average number of infected individuals and fatal cases. For the model with a variable population, equations are obtained, as well as the search algorithm for finding the optimal vaccination strategy, which minimizes the cost functional.

REFERENCES

1. O. V. Bogdanov and P. S. Knopov, "Stochastic models in the problems of predicting the epidemiological situation," Cybern. Syst. Analysis, Vol. 58, No. 1, 58–64 (2022). https://doi.org/10.1007/s10559-022-00435-4.
2. M. Ishikawa, "Optimal vaccination strategy under saturated treatment using the stochastic SIR model," Trans. Inst. of Systems, Control and Information Eng., Vol. 26, No. 11, 382–388 (2013). https://doi.org/10.5687/iscie.26.382.
3. R. Pearl, The Biology of Population Growth, A. A. Knopf, New York (1925).
4. B. Øksendal, Stochastic Differential Equations: An Introduction with Applications, 6th ed., Springer, Berlin–Heidelberg (2010). https://doi.org/10.1007/978-3-642-14394-6.
5. W. H. Flemming, "Some Markovian optimization problems," J. Math. Mech., Vol. 12, No. 1, 131–140 (1963).