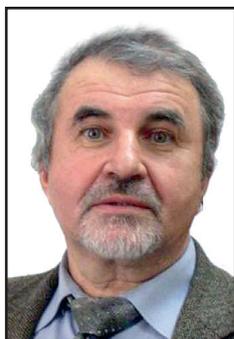




Mathematical Model of Spread of the Epidemic Inside a Railway Compartment Coach



Alexander S. BRATUS



Alexandra S. OCHERETYANAYA

Bratus, Alexander S., Russian University of Transport, Moscow, Russia.

Ocheretyanaya, Alexandra S., Russian University of Transport, Moscow, Russia.*

ABSTRACT

This article discusses an aspect of the most pressing problem of 2020, that of the spread of infectious diseases. The work considers a railway compartment coach as a particular object of spread of infectious diseases. The objective is to describe spread of the epidemic in a railway coach using a stochastic model. The model of the coach is represented as a network. The processes occurring on the network are considered to

be Markov processes. In this paper, two methods of stochastic modelling are applied: modelling based on Kolmogorov equations and Gillespie algorithm. Kolmogorov equations are used to test applicability of Gillespie algorithm, which, in turn, is used to simulate the model of the coach. The obtained data were analysed, and based on that analysis it is possible to make a conclusion about applicability of the model to the case of a typical passenger train.

Keywords: transport, railways, SIS model, stochastic modelling, railway coach, spread of infections, Markov random process, Kolmogorov equations, Gillespie algorithm.

*Information about the authors:

Bratus, Alexander S. – D.Sc. (Physics and Mathematics), Professor at the Department of Mathematical Modelling and System Analysis of the Institute of Management, Control and Digital Technologies of Russian University of Transport, Moscow, Russia, alexander.bratus@yandex.ru.

Ocheretyanaya, Alexandra S. – Ph.D. student at the Department of Mathematical Modelling and System Analysis of the Institute of Management, Control and Digital Technologies of Russian University of Transport, Moscow, Russia, sandra.och@yandex.ru.

Article received 16.06.2020, accepted 22.10.2020.

For the original Russian text of the article please see p. 6.

In late 2019 and early 2020, the world was shocked by massive infections caused by the new coronavirus infection COVID-19. In this regard, mathematical models, and modelling of spread of infections can be used to build stable systems for forecasting and counteracting such natural disasters.

The first mention of an epidemiological model was formulated by Daniel Bernoulli in 1760 with the aim of assessing the effect of smallpox (variola) vaccination on a person's life expectancy. However, the lack of global work in epidemiological modelling had persisted until the beginning of 20th century. In 1927, William Ogilvy Kermack and Anderson Gray McKendrick developed the famous limit theorem, which predicts, depending on the potential of transmission of infection, a critical proportion of vulnerable populations that must be exceeded in the event of an epidemic¹. This was followed by the work of Maurice S. Bartlett, who explored models and data to identify factors that determine disease resistance in large populations. The first landmark book on the mathematical modelling of epidemiological systems was published by Norman T. J. Bailey, and that resulted particularly in recognition of importance of modelling in public health systems. Given diversity of infectious diseases studied since the mid-1950s, an impressive variety of epidemiological models have been developed [1].

Transport is one of the main channels for spread of infections that cause disease. Studies have shown that air travelling [2; 3] and water transport [4; 5] play a huge role in global epidemics. In a recent work on spread of COVID-19, it was found that the first case, recorded in Wuhan, China, in mid-November 2019, quickly spread to the rest of China through «air travel and high-speed railway networks» [6].

The article deals with a typical railway coach as a subject of research. In our case that was a passenger coach used within the network of the JSC Russian Railways.

The *objective* of this work is to build a stochastic model to describe spread of the epidemic in a typical compartment coach depending on the source of infection.

¹ See, e.g., Breda, D., Diekmann, O., de Graff, W. F., Pugliese, A., Vermiglio, R. On the formulation of epidemic models (an appraisal of Kermack and McKendrick). *Journal of Biological Dynamics*, 2012, Vol. 6, Iss. 2, pp. 103–117. DOI: 10.1080/17513758.2012.716454.

To achieve this objective, a model of a railway coach was developed based on a network approach, where the nodes of the network are the elements of the compartment coach, between which ribs are installed according to the coach structure. The network is implemented in Python using *NetworkX* package [7].

Events occurring on the network are based on Markov random processes. The dynamics of spread of infections in a coach is realized using the method of stochastic modelling, namely Gillespie simulation algorithm [8]. To test applicability of this algorithm, a model with explicit constraints was developed based on a special type of differential equations namely on Kolmogorov equations.

As a result of numerical calculations, dependencies were obtained showing that spread of the epidemic in a train car is influenced not only by the number of initially infected persons and the infection rate, but also by the location of infected passengers.

In addition, measures were proposed that could slow down the dynamics of spread of infection along the coach through isolation of the infected compartment.

Statement of the problem

Now there are two main approaches to modelling epidemics: the deterministic approach [9, pp. 157–182] and the stochastic one [10, pp. 8–11]. Deterministic models do not consider movement along the coach, which has a primary effect on spread of infection. However, at the same time, the results of calculations within the framework of these models make it possible to identify the main regularities: whether an epidemic will occur, how long it will last, and how large it will be.

Stochastic models allow you to consider uncertainty, they are more accurate, but at the same time cumbersome and difficult to implement. However, this approach is increasingly used with the development of computational capabilities [11].

There are many classical deterministic models that describe the dynamics of spread of epidemics. One of them is SIS model [9, pp. 157–163; 10, pp. 6–7], which is based on division of people into two groups: $S(t)$ – individuals susceptible to the disease at time t ; $I(t)$ – infected disease vectors at time t . Moreover, the total number of people ($N = S(t) + I(t)$) is



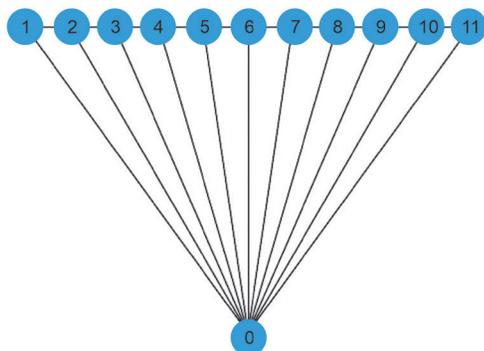


Pic. 1. Scheme of a typical corridor compartment coach used on the network of Russian railways.
 Source: <https://www.rzd.ru/>.

fixed. This model is most suitable for analysing spread of infection in a train coach because a person spends on average about a day in this type of transport [data for Russian long-distance trains, see below – ed. note]. This time is not enough to fully recover, but it is sufficient to get infected. It is assumed that the infection rate β is proportional to the size of groups S and I , while the recovery rate γ is proportional to group I only. Then the process of transition of individuals from one group to another is described using a system of differential equations (1):

$$\begin{cases} \frac{dS(t)}{dt} = \gamma I(t) - \beta S(t)I(t); \\ \frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t). \end{cases} \quad (1)$$

To consider the connections between people, the deterministic SIS model in this work is modified and reduced to stochastic one. The train coach is selected as the system. The number of people who can be either in the group S or I according to the previously purchased seats is considered as the state at the current moment of time. It is assumed that the infection rate of a susceptible individual S depends on the infection coefficient τ , and the number of infected neighbours k . Being in a confined space with a large percentage of sick people makes it more likely to become infected



Pic. 2. Type of the network, where 0 – common zone, 1, 11 – vestibules, 2–10 – compartments (compiled by the authors).

than if there was just a single infected person. The recovery rate for a person from group I depends only on the recovery rate γ . If an infected individual infects a susceptible individual, it does not matter how that person has been infected before. The state of the system in the future depends only on its current state. Thus, the problem is reduced to a Markov random process with continuous time and a finite number of states. The assumption in this model is that the circulation through inter-car walkways (gangways) is not considered, therefore the system is closed, and the number of people is equal to $N = S + I$. Therefore, if the system at time t was in a state with the number of people (S, I), then the following transitions are possible (2–3) [10, pp. 8–11]:

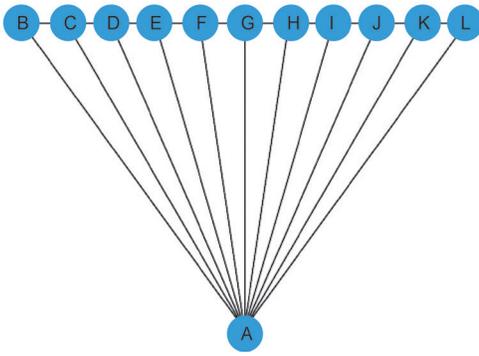
$$(S, I) \cdot \tau \cdot k \cdot (S-1, I+1), \quad (2)$$

$$(S, I) \cdot \bar{\gamma} \cdot (S+1, I-1). \quad (3)$$

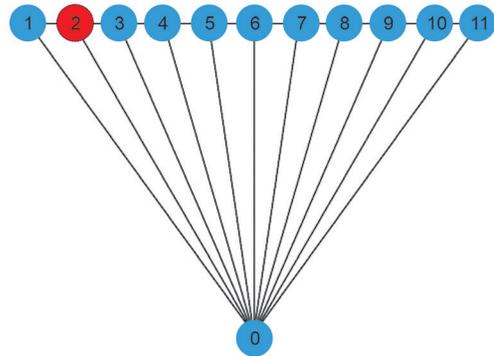
In this paper, long-distance trains are considered, so it is assumed that in most cases, compartment coaches will be selected for a more comfortable trip.

Let us consider a typical corridor coach. The scheme is taken from the ticket booking section of the Russian Railways website [12]. Tickets are sold for seats 1 to 36. There are no tickets on sale for seats 37 and 38. These are the places of the train attendants.

Thus, each coach consists of the elements: nine compartments, a conductor’s seat, two toilets and two vestibules. The model is built using the following assumptions. If an infected passenger is in a compartment, then it is highly likely that he will infect all his neighbours. Therefore, it is considered that the compartment is either in group S or in group I . It is necessary to distinguish a common area where the attendant, who is in contact with all the passengers, moves, as well as the passengers themselves who go to the vestibule or toilet. Passengers for their own purposes go to the vestibule and can come across each other there. Therefore, vestibules can be distinguished as separate zones.



Pic. 3. The system, in the state $S_1 = ABCDEFGHIJKL$ (compiled by the authors).



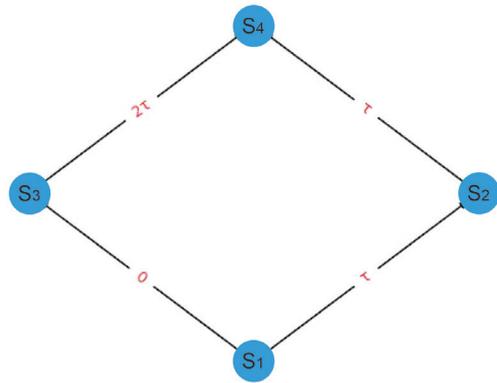
Pic. 4. State $S_1 = SSISSSSSSSSS$, where the vertices in group S are marked in blue (lighter colouring in black-and-white print version), and in group I – in red (compiled by the authors).

Thus, the train car can be represented as a network (Pic. 2), where the nodes are the common zone (0), vestibules (1, 11) and compartments (2–10), and the ribs are installed between each compartment and the common zone, between adjacent compartments, between extreme compartments and vestibules, as well as between vestibules and the common zone.

Each of the N nodes can have one of two statuses (S or I). That is, the network element is either infected or not. Thus, there are 2^N possible states. The state of a node changes over time. As noted earlier, the problem is reduced to a Markov random process with continuous time and a finite number of states. Thus, at any moment, it is assumed that the only factors that can affect the probability of a node's status change are its current state and the statuses of its nearest neighbours. A stream of events transfers the system from one state to another. The time between events is distributed exponentially [13, pp. 112–132]. The infection rate of a susceptible node (transition rate) depends only on how many neighbours are infected. The infected vertex is restored to the initial state at a rate that does not depend on the status of any neighbour.

Let the system be in a state $S_1 = ABCDEFGHIJKL$ (Pic. 3), where vertices A, B, C, D, E, F, G, H, I, J, K, L can take one of two statuses (S or I).

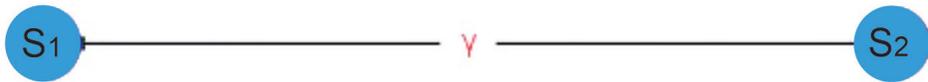
For example, it is known that there are infected passengers in the first (Pic. 2, vortex 2) compartment, but there are no infected passengers in all other parts of the coach, therefore, the system is in the state $S_1 = SSISSSSSSSSS$.



Pic. 5. Transition from state $S_1 = SSISSSSSSSSS$ to state $S_4 = SSIHSSSSSSS$, where $S_2 = SSIHSSSSSSS$ and $S_3 = SSISSSSSSSSS$ (compiled by the authors).

Let us consider the transition from state $S_1 = SSISSSSSSSSS$ to state $S_4 = SSIHSSSSSSS$. Note that you can change the status of only one vertex in a single step. That is, to go from S_1 state to S_4 state, you first need to get to $S_2 = SSIHSSSSSSS$ state, or to $S_3 = SSISSSSSSSSS$ state. Let us pay attention to the transition from S_1 to S_3 . The status changes the third compartment (Pic. 2, vertex 4) from S to I . According to the network shown in Pic. 2, the third compartment has a connection with the second and fourth compartments, as well as with the common area. Since the first compartment is infected, intensity of the transition from S_1 to S_3 is, according to (2): $0 \cdot \tau = 0$, that is, even though the first compartment is infected, it does not directly affect the third compartment. Moreover, intensity of the transition from S_3 to S_4 is equal to $2 \cdot \tau$, since the second compartment has two





Pic. 6. Transition from state $S_2 = SSISSSSSSS$ to state $S_1 = SSISSSSSSS$ with intensity γ (compiled by the authors).

infected neighbours. The transition from state S_1 to state S_4 is shown in Pic. 5.

In this case, from state S_2 to state S_1 one can pass according to (3) with the intensity γ .

Thus, a labelled state graph is compiled, where the vertices are the possible states of the entire system, and the edges are the transition intensities. A mathematical model is built directly from the marked state graph.

Each of the N vertices can have two possible statuses. The system has 2^N states. Let X_i be the probability that at time t the system is in state S_i . For any moment in time, the sum of all probabilities is $\sum_{i=0}^n X_i = 1$.

Kolmogorov equations are written based on the graphs of possible state. The derivatives of the probabilities \dot{X}_i of each S_i state are put on the left side. On the right-hand side there is the sum of the products of the transition intensities and the probabilities of states that can be reached from the current state minus the total intensity of all flows that take the system out of this state, multiplied by the probability of this S_i state [13, pp. 112–132].

The solution to the system of equations will be equal to the probabilities X_i of being in each state S_i at each moment of time t . The obtained probabilities are used to calculate the average number of infected elements I equal to the sum of the products of the number of sick persons

k by the obtained probabilities X_i with the number of sick persons k . Since the system is closed, the number of receptive elements is $S = N - I$.

In case of $N = 12$, the number of equations is $2^{12} = 4096$. Let us consider the case with the same network for $N = 7$ and $2^7 = 128$ equations, that is, the case with six compartments and one common zone to analyse the results obtained.

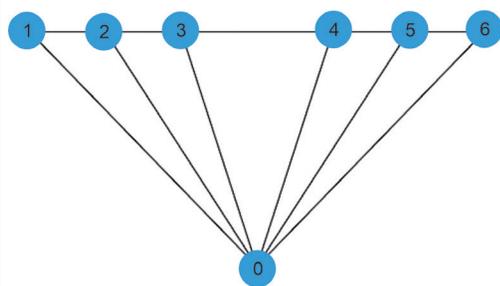
Numerical experiments

For this formulation of the problem calculations were carried out in Python programming language for a system of 128 Kolmogorov equations. Input data are initial states of the system, coefficients τ and γ . Assuming at the moment $t_0 = 0$ the initial state to be S_i , the probability X_i is taken to be equal to one, all the rest probabilities are deemed to be equal to zero. The output is the number of infected I and susceptible S persons.

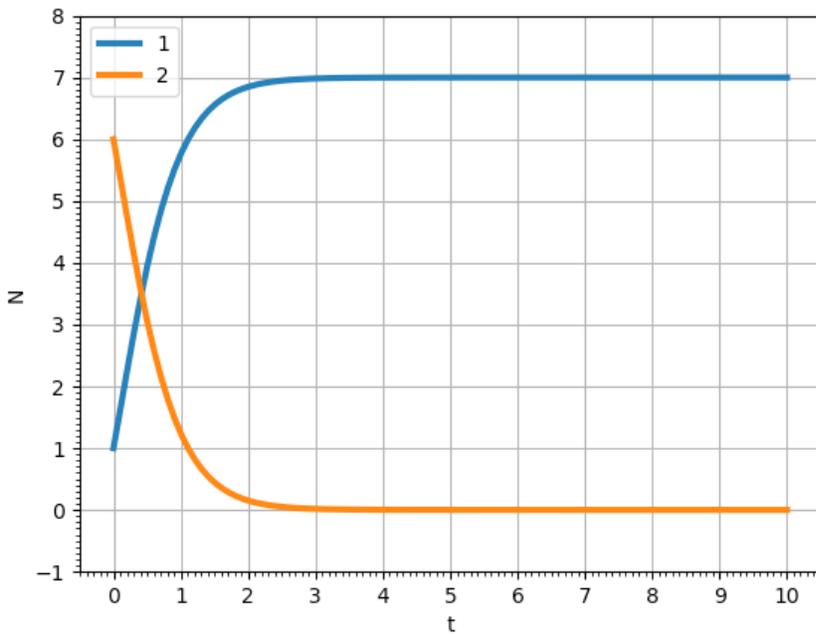
If vertex 0 is infected (Pic. 7), and all others have status S , then the initial state of the system is $S_i = ISSSSSS$. Let us take the recovery rate $\gamma = 0,0001$, the infection coefficient $\tau = 1$.

The dynamics of epidemic spread (Pic. 8) is consistent with the classical SIS model [10, pp. 6–7]. The results are interpreted as follows. If there is one infected person I , the recovery rate $\gamma = 0,0001$, and the infection rate $\tau = 1$, the epidemic will develop in such a way that after a while the entire network will potentially become infected. The examples below compare the time it takes for an entire coach population to become infected.

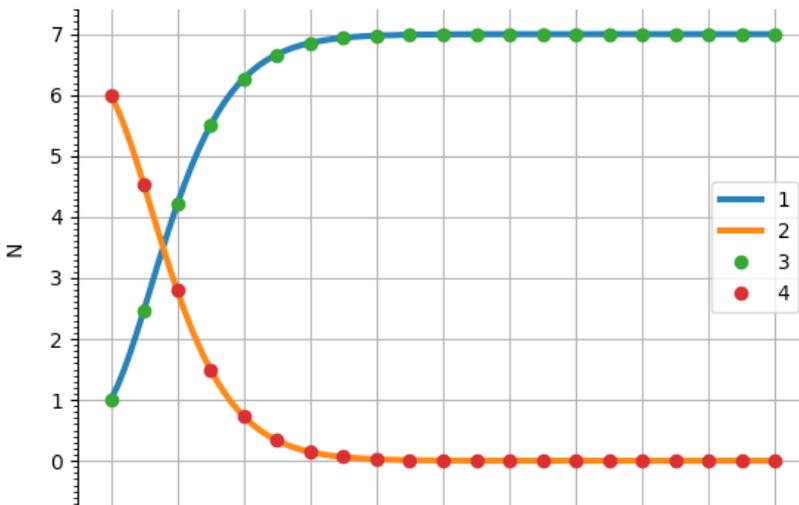
The stochastic model based on Kolmogorov equations is easy to be implemented and easy to be interpreted, however, when expanding the network from the considered case $N = 7$ to $N = 12$, it is necessary to take into account a larger number of interacting factors. The considered model can be used to check the results of Gillespie algorithm, which has no analytical solution. The work uses the implementation of this method for the case



Pic. 7. Network type with $N = 7$, where 0 – common zone, and 1–6 – compartments (compiled by the authors).



Pic. 8. The dynamics of epidemic development (calculation for $N = 7$), initial state $S_i = ISSSSSS$, recovery rate $\gamma = 0,0001$, infection rate $\tau = 1$, ordinate – number of people (N), abscissa – time (t), 1 – number of infected persons I , 2 – number of susceptible persons S (compiled by the authors).



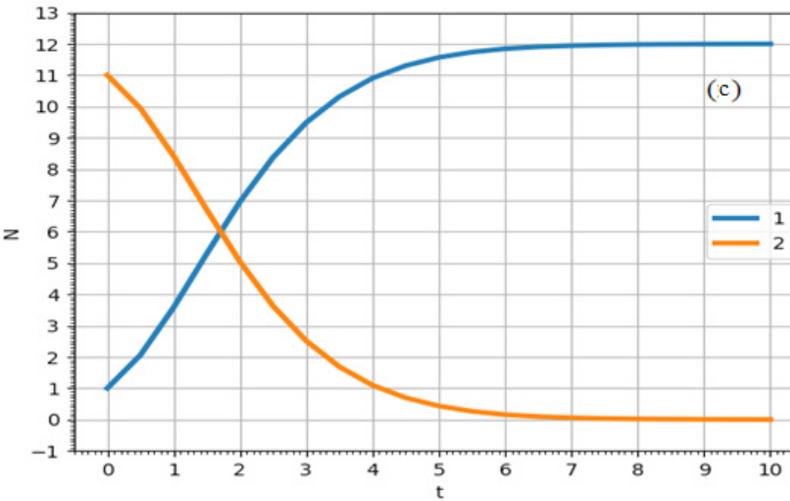
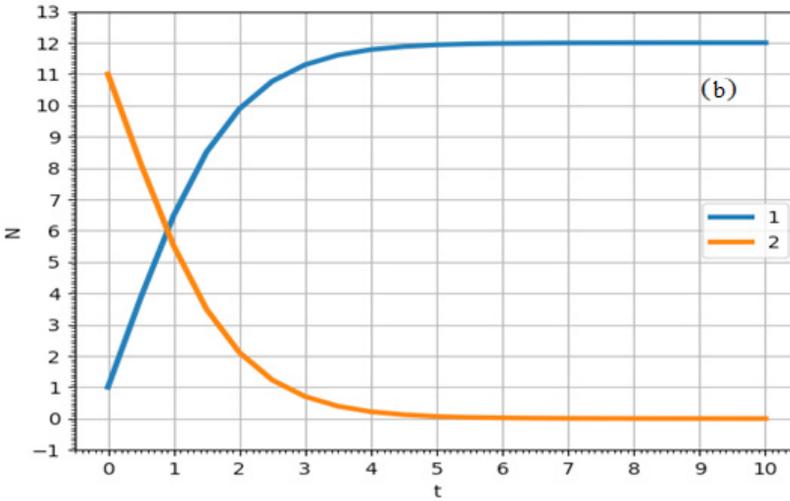
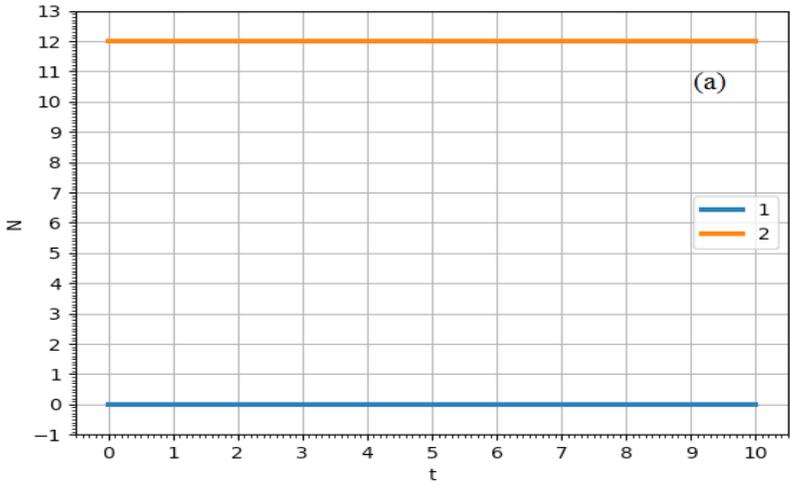
Pic. 9. Comparison of the results of Gillespie algorithm and the model based on Kolmogorov equations with $N = 7$, vertex in the status $I = 1$ and $S_i = SSSSSS$, recovery rate $\gamma = 0,0001$, infection rate $\tau = 1$, ordinate – number of people (N), abscissa – time (t), 1 – number of infected people I (Kolmogorov equations), 2 – number of people susceptible to disease S (Kolmogorov equations), 3 – number of infected people I (Gillespie algorithm), 4 – number of people susceptible to disease S (Gillespie algorithm) (compiled by the authors).

with networks, developed by a group of authors in Python programming language [10, pp. 381–384; 14].

The essence of the method is as follows: time until the next event (infection or restoration of one of the vertices to the initial state) is calculated based on total speed of all possible events. Time between events is

distributed exponentially, the parameter is the sum of all recovery and infection rates. Then it is calculated separately which event will happen. The steps are repeated until there are infected persons, and the maximum estimated time is reached. To achieve accuracy of results, calculations are performed on an iterative basis. Input data are elements in group I , coefficients





Pic. 10. Dynamics of epidemic development in the absence of initially infected persons (a), with infected common zone (b), with one infected compartment (c), recovery rate $\gamma = 0,0001$, infection coefficient $\tau = 0,5$, ordinate – number of people (N), abscissa – time (t), 1 – number of infected persons I, 2 – number of people susceptible to disease S (compiled by the authors).

τ and γ . The output is the number of infected I and susceptible S persons.

The Gillespie algorithm allows discrete and stochastic modelling of a system with a small number of elements, because each event is explicitly modelled. This method is widely used in modelling chemical reactions [15] and spread of diseases such as HIV [16].

Since Gillespie method considers all possible changes in events, its application is justified for systems of limited dimensions due to high computational costs. To solve the considered problem of spreading the epidemic in a train coach, the use of the algorithm is thus justified.

Let us compare the previously described model based on Kolmogorov equations with Gillespie algorithm for $N = 7$. Suppose that the first vertex is initially infected (Pic. 7, vertex 1): vertex in status $I = 1$, $S_i = S$ SSSSS, recovery rate $\gamma = 0,0001$, coefficient infection $\tau = 1$.

The solution based on Gillespie algorithm shows good coincidence with the solution based on Kolmogorov equations (Pic. 9), so this method can be applied to the extended network with $N = 12$ (Pic. 2), which is the train model in this article.

Results

In Pic. 2 compartments (2–10), a common area (0) and 2 vestibules (1, 11) are allocated as zones. Since the source of spread of infection is a person, the common zone (the conductor is taken into account) and the compartment can be initially infected. Let us consider and analyse the cases of spread of infection.

Below are the cases with the absence of infected passengers and a single infected person at initial time (Pic. 10). The rate of recovery is considered to be $\gamma = 0,0001$, and the infection rate $\tau = 0,5$.

Thus, the epidemic does not spread in the absence of infected passengers (Pic. 10a). The greatest risk of its spread occurs through the initially infected common zone (Pic. 10b). This is since the coach attendant is usually in contact with all the passengers. In addition, passengers move through the common area. Within the framework of this model, if any compartment becomes infected, the epidemic will develop in the same way (Pic. 10c). This is since it is assumed that people spend most of their time in their compartments, and each passenger spends the same amount of time on average as

compared with other passengers in public zones (toilets, vestibules). However, in subsequent works, these data will be specified.

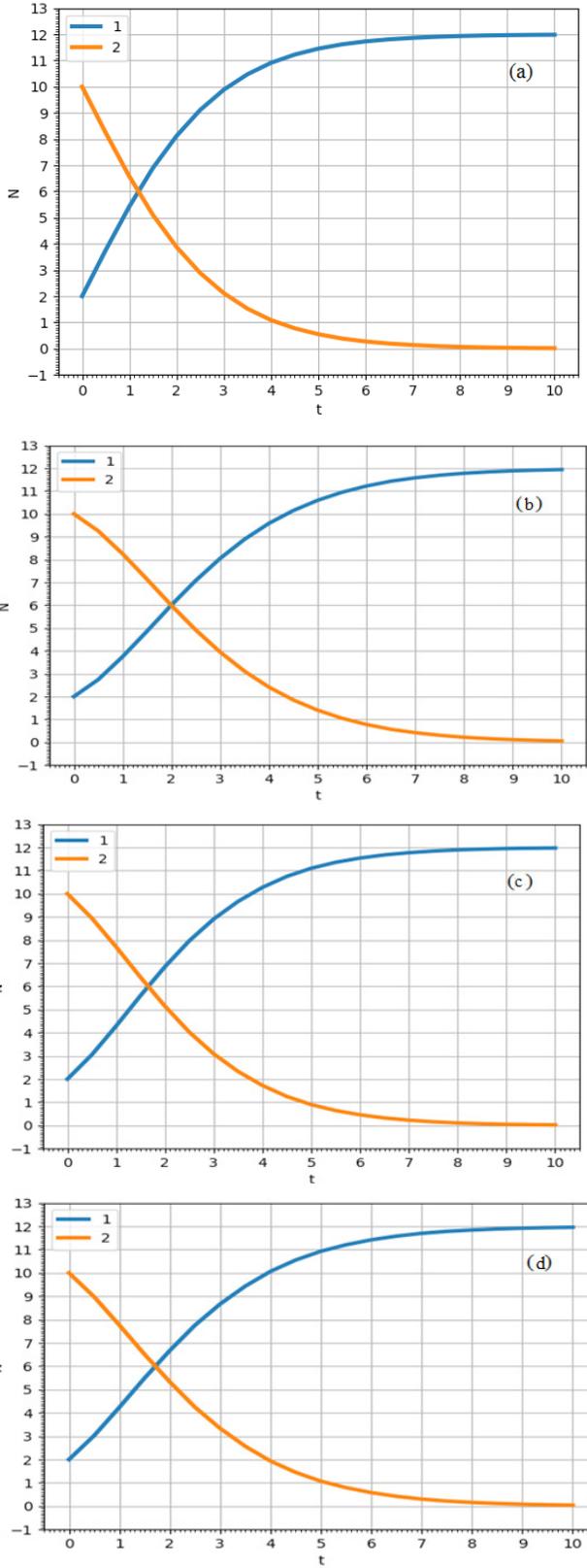
Let us consider four cases when initially there are two infected zones in order to analyse the influence of initial conditions on epidemic development. Since in this setting the calculations show that each of the compartments has an equal impact on the system, they are chosen arbitrarily. Let us suppose that in the first case the common zone and the first compartment were infected (Pic. 2, vertices 0 and 2). In the second case, let us consider any two adjacent compartments, for example, the second and the third (Pic. 2, vertices 3 and 4). In the third case, let us consider two infected compartments located at different ends: the first and the ninth (Pic. 2, vertices 2 and 10). In the fourth case, let the infected compartments be at close range, but not nearby: the fifth and seventh (Pic. 2, vertices 6 and 8). The results are shown in Pic. 11, the rate of recovery $\gamma = 0,0001$ and the infection rate $\tau = 0,3$.

Analysis shows that the epidemic develops most rapidly when the common area and any of all compartments are infected (Pic. 11a). In case of two initially infected compartments, their location matters. Therefore, with two infectious compartments, the most dangerous for spread is the case when the infected compartments are located at two different ends of the coach. This is because toilets and vestibules are located at two different ends, and, accordingly, the risk of infection upon contact with the outermost compartments is higher. The safest situation is when two infected compartments are side by side (Pic. 11b). The latter case, when two compartments are at a short distance (Pic. 11d), entails fewer consequences than when infected compartments are at opposite ends (Pic. 11c). However, this location is more dangerous than when two infected compartments are close (Pic. 11b).

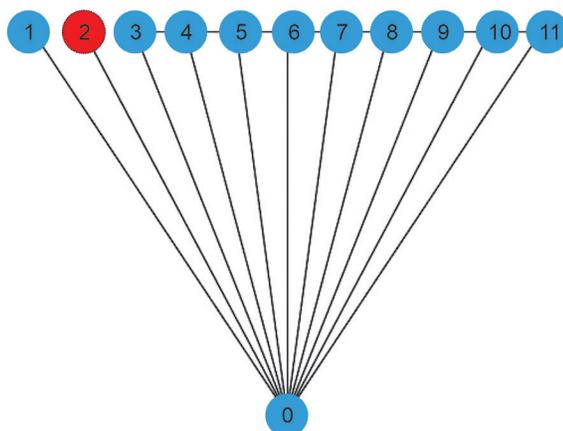
The cases considered are representative and represent a reasonable sample of infection cases. This approach can be extended both for the case of a larger number of infected areas and for a larger number of common areas.

Based on the results of calculations, it can be concluded that epidemic spread is influenced not only by the number of infected persons I , the infection coefficient τ and recovery rate γ , but also by the location of the initially infected

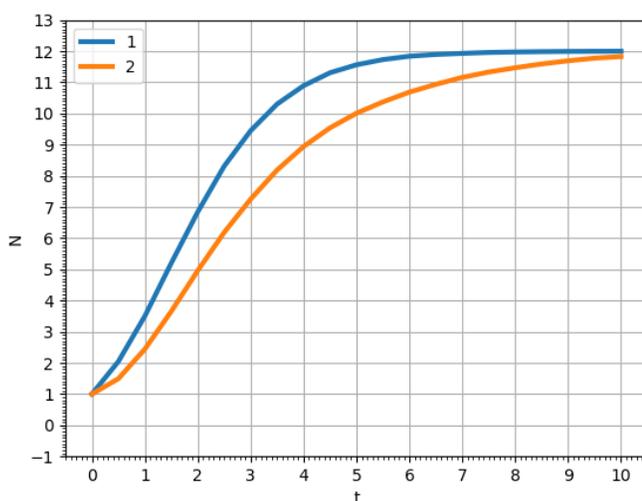




Pic. 11. Dynamics of epidemic development with infected common zone and the first compartment (a), infected second and third compartments (b), infected first and ninth compartments (c), infected fifth and seventh compartments (d), recovery rate $\gamma = 0,0001$, infection rate $\tau = 0,3$, 1 – number of people infected I, 2 – number of people susceptible to disease S (compiled by the authors).



Pic. 12. Type of the network, where 0 – common zone, 1, 11 – vestibules, 2–10 – compartment. Compartment under number 1 (vertex 2) is infected and isolated from others (compiled by the authors).



Pic. 13. Comparison of the results of spread of the epidemic in a coach operating normally and in a coach with an isolated infected compartment, recovery rate $\gamma = 0,0001$, infection rate $\tau = 0,3$, ordinate – number of people (N), abscissa – time (t), 1 – number of people infected I during normal operation of the coach, 2 – number of people infected I with isolation of the infected compartment (compiled by the authors).

passengers. The developed model allows considering the location of infected passengers, which is a key factor for the train.

This model can be extended to consider a train with a dining car.

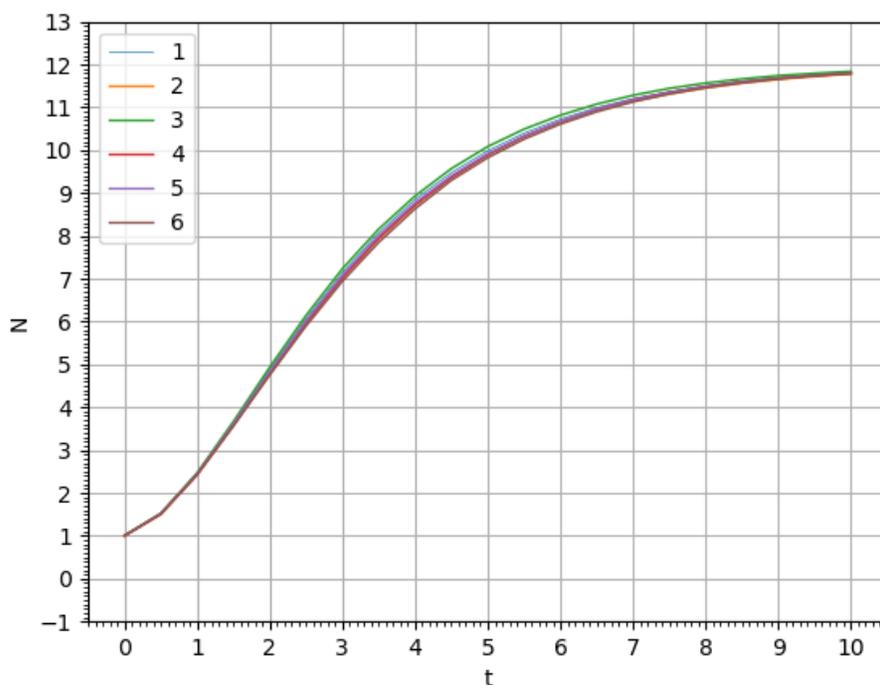
Numerical calculations have shown (Pic. 10b and Pic. 11a) that the coach attendant has the greatest risk of infection, therefore, the state of his health should be considered first. Also, special attention should be paid to common areas, they should be subject to regular sanitization.

Let us consider possible measures that can be taken in case of detection of infected passengers in a coach within the framework

of this model. Let one of the compartments be infected. The boarding is full, and there is no way to transfer passengers to empty compartments or seats. As a measure to prevent spread of the epidemic in this case, it is proposed among other steps to isolate the infected compartment from other passengers, and to evaluate the effectiveness of this assumption. Infected passengers have the opportunity to go to the common area, contact the attendant, observing safety measures, and visit the toilets at a time different from healthy passengers.

Let the first compartment be infected (Pic. 2, vertex 2), then, considering our





Pic. 14. Comparison of results of spread of the epidemic in a coach with different degrees of isolation, recovery rate $\gamma = 0,0001$, coefficient rate $\tau = 0,3$, ordinate – number of people (N), abscissa – time (t), 1 – number of people infected I when isolating the infected first compartment, 2 – number of people infected I when isolating the infected first and second compartments, 3 – number of people infected I when isolating the infected fifth compartment, 4 – number of people infected I when isolating the infected fifth and fourth compartments, 5 – number of people infected I when isolating the infected fifth and sixth compartments, 6 – number of people infected I when isolating fifth and neighbouring compartments (compiled by the authors).

assumptions, the model will take the following form (Pic. 12).

Let us compare the dynamics of spread of the epidemic following the previously described model (Pic. 2) but with its modification (Pic. 12) at the rate of recovery $\gamma = 0,0001$ and the infection rate $\tau = 0,3$.

Isolation of an infected compartment (Pic. 13) will slow spread of infection by almost 20 %. Thus, an important conclusion is that if an infected person is identified in a compartment, it is necessary to isolate him.

Let us further consider the dependence of the location of the infected compartment and the number of isolated compartments on the time of infection spread. Let us suppose that the first compartment is infected (Pic. 2, vertex 2), and to avoid dangerous situation, the second compartment is isolated along with the first one (Pic. 2, vertex 3). Also, by analogy, suppose that the fifth compartment is infected (Pic. 2, vertex 6). To prevent spread of the epidemic, as a preventive measure, the infected fifth compartment, or the fourth (Pic. 2, vertex 5) and the fifth, or sixth (Pic. 2, vertex 7)

and the fifth, or all three compartments at once, are isolated. In this case, the second compartment, like the fourth and sixth, are either healthy, or it is assumed that there are no passengers in them. Let us compare the results obtained, with the recovery rate $\gamma = 0,0001$, the infection coefficient $\tau = 0,3$.

Isolation of more than one compartment does not lead to significant improvements in this model. Thus, the main thing is to isolate the infected passengers. In case of such situations, this will significantly reduce the load on the attendants who are at risk, first of all, will bring less discomfort to other passengers, and will lead to better control of the situation.

Conclusion. The paper considers a model of spread of the epidemic in a railway compartment (corridor) coach.

The deterministic SIS model in this work is modified and reduced to a stochastic model based on Markov random processes with continuous time and a finite number of states. A graph was chosen to describe the spread of the epidemic inside the train coach.

For a simplified case with six compartments and one common zone ($N = 7$), a system with $2^7 = 128$ equations in the Python programming language was compiled and solved.

The model based on Kolmogorov equations was used to test the results of Gillespie algorithm, also implemented in Python. The consistency of the results made it possible to expand the network to the case with $N = 12$, which corresponds to the practically operated coaches in the trains used on the network of Russian Railways.

The results obtained allowed us to analyse the spread of the epidemic under various initial conditions and conclude that the location of the initially infected passengers affects the rate of its spread. It is shown that the greatest risk in the spread of the epidemic is represented by coach attendants and unregulated use of public areas. Measures are proposed in case of identifying a single infected compartment in the form of isolation of its passengers from other passengers. This measure showed an improvement in the dynamics of the spread of infection by 20%. Numerical calculations show that there is no need to isolate more than one compartment in this situation.

These results can be used in real transportation, as well as to track passengers who can be vectors of infection by processing data from CCTV cameras. These data are needed to modify the method used in the work to determine the influence of each of the compartments. For example, in [17], the authors conducted a study of the impact of public urban transport on the spread of COVID-19 infection in Singapore using transport cards. Data from travel cards were used to compile a mathematical model and identify passengers who need to be isolated at an early stage to prevent the spread of the epidemic.

REFERENCES

1. Choisy, M., Guégan, J.-F., Rohanil, P. Mathematical Modeling of Infectious Diseases Dynamics. Encyclopedia of Infectious Diseases: Modern Methodologies by Tibayrenc. M. John Wiley & Sons, Inc., 2007, pp. 379–403.
2. Barrat, A., Barthélemy, M., Colizza, V., Vespignani, V. The role of the airline transportation network in the prediction and predictability of global epidemics. *PNAS*, 14 February, 2006, Vol. 103 (7), pp. 2015–2020. DOI: www.pnas.org/cgi/doi/10.1073/pnas.051052103.
3. Balcan, D., Colizza, V., Gonçalves, B., Hu, H., Ramasco, J. J., Vespignani, A. Multiscale mobility networks and the spatial spreading of infectious diseases. *PNAS*, 22 December, 2009, Vol. 106 (51), pp. 21484–21489. DOI: <https://doi.org/10.1073/pnas.0906910106>.
4. Mari, L., Bertuzzo, E., Righetto L. [et al]. Modelling cholera epidemics: the role of waterways, human mobility and sanitation. *J. R. Soc. Interface*, 2012, Vol. 9 (67), pp. 376–388. DOI: 10.1098/rsif.2011.0304.
5. Gatto, M., Mari, L., Bertuzzo, E., Casagrandi, R., Righetto, L., Rodriguez-Iturbe, I., Rinaldo, A. Generalized reproduction numbers and the prediction of patterns in waterborne disease. *PNAS*, 27 November, 2012, Vol. 109 (48), pp. 19703–19708. DOI: 10.1073/pnas.1217567109.
6. Wu, J. T., Leung, K., Leung, G. M. Now casting and forecasting the potential domestic and international spread of the 2019-ncov outbreak originating in Wuhan, China: A modelling study. *The Lancet*, 29 February, 2020, Vol. 395 (10225), pp. 689–697. DOI: 10.1016/S0140-6736(20)30260-9.
7. Hagberg, A. A., Schult, D. A., Swart, P. J. Exploring network structure, dynamics, and function using NetworkX. Proceedings of the 7th Python in Science Conference (SciPy 2008). Eds.: G el Vároquaux, Travis Vaught, Jarrod Millman, Pasadena, CA, USA, August 2008, pp. 11–15.
8. Gillespie, D. T. A general method for numerically simulating the stochastic time evolution of coupled chemical reactions. *Journal of Computational Physics*, December, 1976, Vol. 22 (4), pp. 403–434.
9. Bratus, A. S., Novozhiov, A. S., Platonov, A. P. Dynamic systems of biology models [*Dinamicheskie sistemy i modeli biologii*]. Moscow, Fizmatlit publ., 2010, 400 p.
10. Kiss, I., Miller, J., Simon, P. *Mathematics of Epidemics on Networks: from Exact to Approximate Models*. Springer Math, 2007, 413 p.
11. Deng, Xiaomin; Wang, Xiaomeng. The Application of Gillespie Algorithm in Spreading. 3rd International Conference on Mechatronics Engineering and Information Technology (ICMEIT 2019), April 2019, pp. 688–695. DOI: 10.2991/icmeit-19.2019.110.
12. Official website of JSC Russian Railways. [Electronic resource]: <https://www.rzd.ru/>. Last accessed 15.06.2020.
13. Venttsel, E. S. Study of operations: tasks, principles, methodology: Study guide [*Issledovanie operatsii: zadachi, printsipy, metodologiya: Ucheb. posobie*]. 5th ed., ster. Moscow, Nauka publ.; Chief editorial board of physics-mathematical literature, 1980, 208 p.
14. EoN (Epidemics on Networks): a fast, flexible Python package for simulation, analytic approximation, and analysis of epidemics on networks. [Electronic resource]: <https://joss.theoj.org/papers/10.21105/joss.01731>. Last accessed 19.06.2020.
15. Gillespie, D. T. Exact stochastic simulation of coupled chemical reactions. *Journal of Computational Physics*, 01 December, 1977, Vol. 81 (25), pp. 2340–2361. DOI: 10.1021/j100540a008.
16. Kamina, K. M., Mwalili, S., Wanjoya, A. The Modeling of a Stochastic SIR Model for HIV/AIDS Epidemic Using Gillespie's Algorithm. *International Journal of Data Science and Analysis*, 2019, Vol. 5, No. 6, pp. 117–122. DOI: 10.11648/j.ijdsa.20190506.12.
17. Mo, Baichuan; Feng, Kairui; Shen, Yu; Tam, Clarence; Li, Daqing; Yin, Yafeng; Zhao, Jinhua. Modeling Epidemic Spreading through Public Transit using Time-Varying Encounter Network. [Electronic resource]: <https://arxiv.org/pdf/2004.04602.pdf>. Last accessed 19.06.2020.

This work was supported by the grant of the Russian Foundation for Basic Research 20-04-60157 «An integrative approach to mathematical modelling of the mechanisms of pathogenesis and development of a coronavirus infection pandemic».

