4-бөлім **Раздел 4** **Section 4**

Қолданбалы математика **Прикладная математика** **Applied Mathematics**

IRSTI 27.39.21 DOI: https://doi.org/10.26577/JMMCS.2021.v112.i4.14

S.Ya. Serovajsky[1*], O.N. Turar[2]
[1]Al-Farabi Kazakh National University, Kazakhstan, Almaty
[2]Astana IT University, Kazakhstan, Nur-Sultan
*e-mail: serovajskys@mail.ru

MATHEMATICAL MODEL OF THE EPIDEMIC PROPAGATION WITH LIMITED TIME SPENT IN EXPOSED AND INFECTED COMPARTMENTS

A discrete nonlinear mathematical model of the epidemic development is proposed. It involves dividing the population into eight compartments (susceptible, exposed, asymptomatic, easily sick, hospitalized, critically ill, recovered and deceased). At the same time, the time spent in compartments of exposed and all forms of patients is considered limited. Thus, any person who has been in contact with an infected person, after a while, either gets sick or does not, leaving the exposed compartment, and any patient, over time, for sure, either goes to the group of more severe patients, dies or recovers. This deterministic model is presented in a discrete form and simulates the quantitative change of various groups by day during the spread of the epidemic. It is a transformation of the SEIR model. The article also presents a numerical analysis of the proposed model. The development of the COVID epidemic in Kazakhstan is considered as an example. At the end, forecasts are given based on preliminary data from the first months of quarantine. Various parameters of the model when starting numerical experiments were found based on computational experiments. At the same time, for a given deterministic one, the effect of wavelike changes in the number of infected is observed.

Key words: epidemic, mathematical model, COVID.

С.Я. Серовайский[1*], О.Н. Тұрар[2]
[1]Әл-Фараби атындағы Қазақ ұлттық университеті, Қазақстан, Алматы қ.
[2]Astana IT University, Қазақстан, Нұр-Сұлтан қ.
*e-mail: serovajskys@mail.ru

ЭПИДЕМИЯНЫҢ ДАМУЫНЫҢ КОНТАКТ ЖӘНЕ ЖҰҚТЫРҒАН ТОПТАРДА ШЕКТЕУЛІ УАҚЫТ БОЛАТЫН МАТЕМАТИКАЛЫҚ МОДЕЛІ

Эпидемиялық дамудың дискретті емес сызықтық математикалық моделі ұсынылған. Ол халықты сегіз топқа бөлуді қамтиды (сезімтал, жанаспалы, асимптоматикалық, жеңіл ауру, ауруханаға түскен, ауыр науқас, айыққан және қайтыс болған). Сонымен қатар, науқастардың барлық формаларында және байланыс түрлерінде өткізілген уақыт шектеулі болып саналады. Осылайша, кез-келген адам жұқтырған адаммен байланыста болғаннан кейін, біраз уақыттан кейін немесе ауырады, немесе байланыс тобынан шықпайды және кез-келген пациент уақыт өте келе неғұрлым ауыр пациенттер тобына барады, қайтыс болады немесе қалпына келеді. Бұл детерминирленген модель дискретті түрде ұсынылған және эпидемияның таралуы кезінде әр түрлі топтардың сандық згеруін имитациялайды. Бұл SEIR моделін жаңарту. Мақалада ұсынылған модельдің сандық талдауы да келтірілген. Қазақстандағы COVID эпидемиясының дамуы мысал ретінде қарастырылады. Соңында, карантиннің алғашқы айларындағы алдын-ала мәліметтер негізінде болжамдар жасалады. Есептік тәжірибелер негізінде сандық эксперименттерді бастаған кезде модельдің әр түрлі параметрлері табылды, ол параметрлер негізінен әр үрлі топтар арасында адамдар алмасуды, науқастардың ауру жұқтыру жылдамдықтарын сипаттайды. Сонымен бірге, берілген детерминирленген үшін, жұқтырғандар санының толқын тәрізді өзгеруінің әсері байқалады.

Түйін сөздер: эпидемия, математикалық модель, COVID.

С.Я. Серовайский[1*], **О.Н. Турар**[2]
[1]Казахский национальный университет имени аль-Фараби, Казахстан, г. Алматы
[2]Astana IT University, Казахстан, г. Нур-Султан *e-mail: serovajskys@mail.ru

МАТЕМАТИЧЕСКАЯ МОДЕЛЬ РАЗВИТИЯ ЭПИДЕМИИ С ОГРАНИЧЕННЫМ ВРЕМЕНЕМ ПРЕБЫВАНИЯ В ГРУППАХ КОНТАКТНЫХ И ИНФИЦИРОВАННЫХ

Предлагается дискретная нелинейная математическая модель развития эпидемии. Она предполагает разбиение популяции на восемь групп (восприимчивые, контактные, бессимптомные, легко больные, госпитализированные, критические больные, выздоровевшие и умершие). При этом время пребывания в группах контактных и всех форм больных считается ограниченным. Таким образом, любой человек, бывший в контакте с зараженным, через некоторое время либо заболевает, либо нет, покидая группу контактных, а любой больной со временем наверняка, либо переходит в группу более тяжелый больных, умирает или выздоравливает. Данная детерминистическая модель представлена в дискретном виде и моделирует количественное изменение различных групп по дням во время распространения эпидемии. Она является модернизацией SEIR модели. Так же в статье представлен проведенный численный анализ предложенной модели. В качестве примера рассматривается развитие эпидемии COVID в Казахстане. В конце даются прогнозы, полученные на основе предварительных данных первых месяцев карантина. Различные параметры модели при запусках численных экспериментов находились на основе вычислительных экспериментов. При этом для данной детерминированной наблюдается эффект волнообразных изменений количества инфицированных.
Ключевые слова: эпидемия, математическая модель, COVID.

1 Introduction

Modern mathematical models of epidemiology originate from the SIR model developed by W. Kermak and A. Mackendrick about a hundred years ago [1]. It involves dividing the entire population under consideration into susceptible, infected and recovered compartments. The mathematical model of the process is a system of differential or difference equations describing the change in the size of each of the indicated population groups. Its simplest modifications are the SIRD model, which adds a compartment of deceased (deceased) [2] and the SIS model of a disease to which immunity is not produced [3]. We also note the SIRS model, in which the recovered lose their immunity over time [4].

The disadvantage of the described models is the lack of an incubation period, i.e. the assumption that a person who had contact with a sick person immediately falls ill. As a result, the SEIR model was proposed, to which the exposed compartment was added, see, for example, [5]. Thus, in the process of infection, a person susceptible to the disease first becomes exposed and only then becomes infected.

2 Literature review

The overwhelming majority of mathematical models of the development of the epidemic that are currently used are modifications of the SEIR model. In particular, the SEIS model differs from it only in that immunity is not produced [6]. The SEIRD model additionally includes a group of deceased [7, 8], the MSEIR model additionally includes a group of people

who are maternally derived immunity [9, 10], and the SEIRHCD model includes a group of hospitalized and critical patients. [8, 11]. In a number of cases, models with a variable frequency of contacts are also considered [12], which take into account the spread of the epidemic over a certain territory and are described by partial differential equations [13], models that take into account vaccination [14], as well as stochastic models in which the transition from one group to another is a random event [3]. A significant number of models are also given in monographs [15–19] devoted to mathematical models of epidemiology.

In these models, one significant circumstance is not taken into account, namely, the limited stay in a compartment of exposed and different groups of patients. In particular, any person who has been in contact with a patient, after some time, will probably either get sick or not get sick, which means that he will certainly leave the exposed compartment. Anyone sick after some time will probably either recover or die, i.e. will definitely leave the group of infected.

In this paper, we propose a discrete dynamic model of the development of the epidemic, which assumes the division of the entire population into eight groups and considers the limited stay in groups of contact and various forms of patients. Based on this model, some calculations are made on the spread of the COVID-19 epidemic in Kazakhstan.

3 Method: Description of the model

A certain isolated population under the conditions of an epidemic is considered. The entire population is divided into the following compartments:

S: susceptible (healthy, but potentially sick);

E: exposed (healthy, in contact with sick);

A: asymptomatic (infected, asymptomatic);

I: easily sick (mild patients undergoing treatment at home);

H: hospitalized (seriously ill, hospitalized);

C: critically il (patients in critical condition);

R: recovered (recovered, who have no signs of illness);

D: deceased.

Further through S_k, E_k etc. denotes, respectively, the number of susceptible, exposed, etc. at time k. In this case k is understood as the k-th day from the moment of the start of the study. We do not take into account the natural fertility and mortality of the population, i.e. we consider the sum N of all the above mentioned compartments of the population constant.

As with the SEIR models, it is assumed that the susceptible person becomes infected by going through the exposed compartment stage. At the same time, only asymptomatic and easily sick people are sources of infection. In addition, it is assumed that all who have recovered are immunized, i.e. are not susceptible to disease.

When building a model, the following intergroup transitions are taken into account:

- es: the exposed person may not get sick and become susceptible again;

- ea: the exposed person may become asymptomatic;
- ei: the exposed person can become easily sick;
- eh: the exposed person may become hospitalized;
- ar: asymptomatic can become recovered;
- ae: asymptomatic can become easily sick;
- ih: easily sick patient can be hospitalized;
- ic: easily sick patient can become critically ill;
- ir: easily sick patient can become recovered;
- hc: the hospitalized person may become critically ill;
- hr: a hospitalized person can recover;
- cr: the critically ill can recover;
- cd: critically ill patient may die;
- se: susceptible can become exposed.

Moreover, let's indicate the proportions of exposed (e), passing over time into compartments of susceptible (s), asymptomatic patients (a), etc. δ_{es}, δ_{ea} etc. All these quantities lie between zero and one, and the obvious equalities $\delta_{es} + \delta_{ea} + \delta_{ei} + \delta_{eh} = 1$, etc. are fulfilled, i.e. any exposed will either not get sick at all, or get sick in one form or another.

The fundamental difference between the proposed model and the known ones is the assumption about the limited presence of a person in compartments of exposed and any form of patients. Further we indicate etc. the time (number of days) of being in the compartment of exposed (e), asymptomatic (a), etc. as n_e, n_a, and indicate the number of exposed on j-th day since contact, the number of asymptomatic j-th day since the start of the disease, etc. at time k as e_k^j, a_k^j, etc. Moreover, the following obvious equalities hold:

$$E_k = \sum_{j=1}^{n_e} e_k^j,\ A_k = \sum_{j=1}^{n_a} a_k^j,\ I_k = \sum_{j=1}^{n_i} i_k^j,\ H_k = \sum_{j=1}^{n_h} h_k^j,\ C_k = \sum_{j=1}^{n_c} c_k^j, \tag{1}$$

the number of exposed E_k at the moment of time k is the sum of the number of exposed of the first day, the second day, ..., n_e day at this moment of time, etc.

Note that the exposed of the j-th (previous) day at the previous moment of time becomes exposed of the $(j+1)$-th (subsequent) day at the subsequent moment of time, i.e.

$$e_{k+1}^{j+1} = e_k^j,\ j = 1, \ldots, n_e - 1. \tag{2}$$

Following equalities have a similar meaning

$$a_{k+1}^{j+1} = a_k^j,\ j = 1, \ldots, n_a - 1;\ i_{k+1}^{j+1} = i_k^j,\ j = 1, \ldots, n_i - 1; \tag{3}$$

$$h_{k+1}^{j+1} = h_k^j,\ j = 1, \ldots, n_h - 1;\ c_{k+1}^{j+1} = c_k^j,\ j = 1, \ldots, n_c - 1; \tag{4}$$

In accordance with the assumptions made earlier, the number of susceptible at the next moment in time is equal to the number of susceptible at the previous moment of time minus newly exposed at this moment of time plus the number of uninfected exposed of the last day at the previous moment in time:

$$S_{k+1} = S_k - e_{k+1}^1 + \delta_{es} e_k^{n_e}. \tag{5}$$

The number of exposed at the next moment in time is equal to the number of exposed at the previous moment in time plus the number of new exposed at this moment in time minus the number of exposed on the last day at the previous moment in time, i.e. who have left the exposed compartment at the moment:

$$E_{k+1} = E_k + e_{k+1}^1 - e_k^{n_e}. \tag{6}$$

Similarly, we have the following equalities

$$A_{k+1} = A_k + a_{k+1}^1 - a_k^{n_a}. \tag{7}$$

$$I_{k+1} = I_k + i_{k+1}^1 - i_k^{n_i}. \tag{8}$$

$$H_{k+1} = H_k + h_{k+1}^1 - h_k^{n_h}. \tag{9}$$

$$C_{k+1} = C_k + c_{k+1}^1 - c_k^{n_c}. \tag{10}$$

Further, the number of recovered at the next time point is equal to the number of recovered at the previous point in time plus all recovered patients of the last day of illness at this point in time:

$$R_{k+1} = R_k + \delta_{ar} a_k^{n_a} + \delta_{ir} i_k^{n_i} + \delta_{hr} h_k^{n_h} + \delta_{cr} c_k^{n_c}. \tag{11}$$

Finally, the number of deaths at the next time point is the sum of the number of deaths at the previous time point and the number of new deaths, i.e. critically ill of the last day of illness at this point in time who died:

$$D_{k+1} = D_k + \delta_{cd} c + k^{n_c}. \tag{12}$$

It remains to indicate the formulas for calculating the number of exposed and various patients on the first day at the next moment in time. In particular, the number of exposed on the first day, i.e. newly exposed at a later point in time is determined by the formula

$$e_{k+1}^1 = (\beta_a A_k + \beta_i I_k)\frac{S_k}{N}, \tag{13}$$

where $\beta_a,\ \beta_i$– positive constants characterizing the infectivity of asymptomatic and easily sick. The number of asymptomatic first day, i.e. newly ill at the next time point is equal to the number of those who left the exposed compartment at the previous time point who fell ill in an asymptomatic form, i.e.

$$a_{k+1}^1 = \delta_{ea} e_k^{n_e}. \tag{14}$$

The number of easily sick on the first day, i.e. newly ill at the next time point is equal to the number of those who left the exposed and asymptomatic compartments at the previous time point and fell ill in a mild form, i.e.

$$i_{k+1}^1 = \delta_{ei} e_k^{n_e} + \delta_{ai} a_k^{n_a}. \tag{15}$$

The following formulas have a similar meaning

$$h_{k+1}^1 = \delta_{eh} e_k^{n_e} + \delta_{ih} i_k^{n_i}. \tag{16}$$

$$c_{k+1}^1 = \delta_{hc} h_k^{n_e} + \delta_{ic} i_k^{n_i}. \tag{17}$$

Relations (1) – (17) with the corresponding initial conditions constitute a mathematical model of the considered process.

4 Results and Analysis

As an example, we consider one variant of the COVID epidemic forecasting in Kazakhstan for the period from August 1, 2020. The model parameters were selected partly on the basis of official data from the Ministry of Health of the Republic of Kazakhstan, partly on the basis of expert assessments of epidemiologists. The following figures show graphs of the change over time in the total number of all cases, recovered and deaths, as well as daily increases in these characteristics.

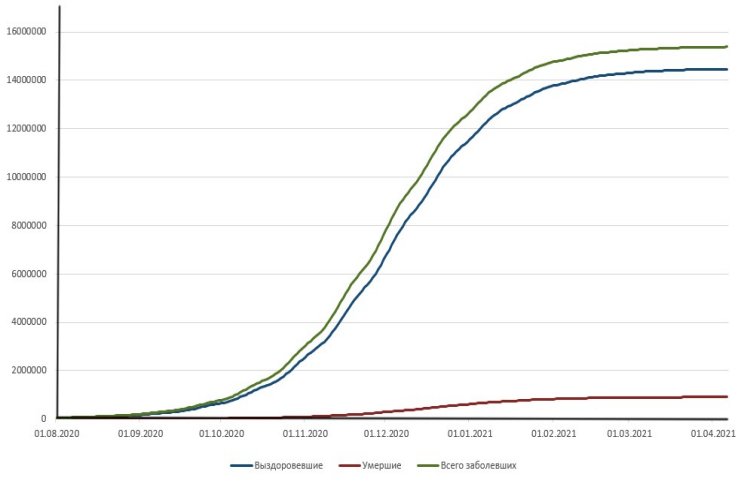

Fig. 1: The total number of cases, recovered and deaths.

The obtained results of the numerical analysis are of a preliminary nature, since the information used to determine the parameters of the model is insufficiently complete and not accurate enough. Nevertheless, the established qualitative results indicate the sufficient effectiveness of the proposed model. In particular, we see that initially the epidemic develops exponentially. Then its growth slows down, reaches its maximum, declines and in the end the epidemic ends. It is characteristic that the development of the epidemic is not monotonous,

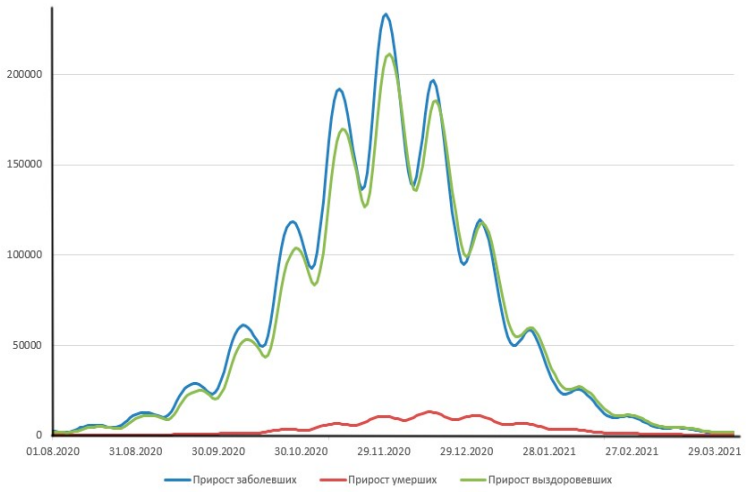

Fig. 2: Daily increase in the total number of cases, recovered and deaths.

but wavy, which is consistent with the known data on the development of the epidemic both in Kazakhstan and in other countries. In addition, it was found that the introduction of a stricter quarantine, which is associated with a decrease in infection rates β_a and β_i leads to a shift in the time of the peak of the epidemic. Thus, the resulting model, subject to its more accurate identification, can be used for long-term forecasting of the development of epidemics.

5 Discussion and conclusion

The results of numerical analysis confirm the viability of the proposed model. In particular, comparing the results obtained with the actual development of COVID-19 in Kazakhstan in late summer and autumn 2020, a relatively high forecast accuracy can be noted. An important circumstance is the wave-like development of the epidemic obtained as a result of model calculations, which is not typical for most of the currently used mathematical models of epidemiology.

The model can be refined by taking into account the random nature of its individual parameters. This applies primarily to the time spent in the compartments. In addition, we can remove the restriction on the isolation of the population, considering the course of the epidemic in the system of regions, we can take into account the possibility of virus mutation, the emergence of a vaccine, the spread of the epidemic over a certain territory, etc.

6 Acknowledgments

The authors are grateful to Academician of NAS RK G.M. Mutanov, who initiated this study, Corresponding Member of the Russian Academy of Sciences S.I. Kabanikhin, who kindly provided the authors with research materials of the Siberian Branch of the Russian Academy of Sciences in this direction, and Professor S.D. Akilbekov for consultations in the

field of epidemiology. This research was funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan (Grant No. AP09260317).

References

[1] Kermack, W.O. and McKendrick, A.G. A Contribution to the Mathematical Theory of Epidemics. – Proc. Roy. Soc. Lond. A, 1927, 115, 700–721.

[2] Bailey, N. The mathematical theory of infectious diseases and its applications (2nd ed.). London, Griffin, 1975.

[3] Bacaer, N. Le Modele Stochastique SIS pour une Epiddmie dans un Environnement Aleatoire. – J. of Mathematical Biology, 2016, v. 73, 847–866.

[4] Wang, X. An SIRS Epidemic Model with Vital Dynamics and a Ratio-Dependent Saturation Incidence Rate. – Discrete Dynamics in Nature and Society. 2015. https://doi.org/10.1155/2015/720682

[5] Mwalili, S., Kimathi, M., Ojiambo, V. et al. SEIR model for COVID-19 dynamics incorporating the environment and social distancing. – BMC Res Notes 13, 352,2020. https://doi.org/10.1186/s13104-020-05192-1

[6] Wang, J. Analysis of an SEIS Epidemic Model with a Changing Delitescence. – Abstract and Applied Analysis, 2012, 4. https://www.hindawi.com/journals/aaa/2012/318150/

[7] R. Sameni Mathematical Modeling of Epidemic Diseases; A Case Study of the COVID-19 Coronavirus. – arXiv:2003.11371. 2020.

[8] Криворотько О.И., Кабанихин С.И., Зятьков Н.Ю., Приходько А.Ю., Прохошин Н.М., Шишленин М.А. Математическое моделирование и прогнозирование COVID-19 в Москве и Новосибирской области. – 2020 https://arxiv.org/pdf/2006.12619.pdf

[9] Hethcote, H.W. The Mathematics of Infectious Diseases. – SIAM Review 42, 599–653, 2000.

[10] Almeida, R., Cruz, A., Martins, N., and Monteiro N. An epidemiological MSEIR Model Described by the Caputo Fractional Derivative. – Int. J. of Dynamics and Control, 2019, 7, 776–784.

[11] Unlu, E., Leger, H. Motornyi, O. et al Epidemic Analysis of COVID-19 Outbreak and Counter-Measures in France. – 2020. medRxiv. 2020.04.27.20079962. DOI: 10.1101/2020.04.27.20079962.

[12] Greenhalgh, D. and Das R. Modeling Epidemics with Variable Contact Rates. – Theoretical Population Biology, 1995, 2 (47), 129-179.

[13] Huang, H. and Wang, M. The Reaction-Diffusion System for an SIR Epidemic Model with a Free Boundary. – Discrete and Continuous Dynamical Systems. Series B, 2015, 20(7), 2039-2050.

[14] Gao, S., Teng, Z., Nieto, J. and Torres, A. Analysis of an SIR Epidemic Model with Pulse Vaccination and Distributed Time Delay. – Journal of Biomedicine and Biotechnology. 2007, 64870. doi:10.1155/2007/64870. PMC 2217597. PMID 18322563.

[15] May, R. and Anderson, R. Infectious diseases of humans: dynamics and control. – Oxford: Oxford University Press, 1991.

[16] Brauer, F. et al. Mathematical Epidemiology. Eds. – Springer, 2008.

[17] Capasso, V. Mathematical Structures of Epidemic Systems. 2nd Printing. – Heidelberg, Springer, 2008.

[18] Vynnycky, E. and White, R.G., eds. An Introduction to Infectious Disease Modelling. – Oxford: Oxford University Press, 2010.

[19] Diekmann, O., Heesterbeek, H. and Britton, T. Mathematical Tools for Understanding Infectious Disease Dynamics. – Princeton Series in Theoretical and Computational Biology. Princeton University Press, Princeton, 2013.