Application of a Kinetic Model for Studying the Spatial Spread of COVID-19

V. V. Aristov\textsuperscript{a, *}, A. V. Stroganov\textsuperscript{b, **}, and A. D. Yastrebov\textsuperscript{b, ***}

Presented by Academician Yu.G. Evtushenko March 4, 2021

Received March 17, 2021; revised March 17, 2021; accepted March 30, 2021

Abstract—A one-dimensional model based on a kinetic-type equation is proposed for studying the dynamic distribution density of virus carriers in time and space while taking into account their distribution from a dedicated center. This model is new and fundamentally different from known models of the diffusion–reaction type. The analytical solution is built; for obtaining a series of calculations, numerical methods are also used. The model and real data from Italy, Russia, and Chile are compared. In addition to the rate of infection, the “rate of recovery” is considered. When the wave of recovery passes through a territory with the greater part of the commonwealth, a conclusion is made about the onset of global recovery, which corresponds to real data. The predictions are proved to have been accurate also for the second wave of the pandemic in Russia. The model is expected to be able also to describe adequately subsequent epidemics instead of only the development of COVID-19.

Keywords: mathematical modeling, COVID-19 pandemic, kinetic-type equation

DOI: 10.1134/S1028335821050013

Scientific groups around the world are working on the study of the COVID-2019 pandemic using various mathematical methods including very complex ones, which require powerful computing devices. But even simple models capable of identifying the characteristics of the current epidemic can detect regularities that escape due to the abundant data. Such identification would enable one to make certain predictions and, possibly, prevent more dangerous scenarios of the spread of the epidemic. In the articles based on the well-known model SIR and its modifications with a large number of parameters, the solutions are built, as a rule, for studying the development of disease only in time [1–3]. The spatial distribution of viruses is usually studied with the diffusion–reaction model [4–7]; see also [8]. This approach is used in the study of complex autowave processes [9]. However, it is also possible to use kinetic equations, which, in fact, are based on a different physical and mathematical model: such methods are used for describing the traffic streams in [10] and for modelling the sociohistorical processes (model of aggression) in [11, 12].

This study is similar to [11, 12]; however, the model turned out to be simpler due to the linearity of the equation. We emphasize that this is a fundamental difference from the models with diffusion, where the movement of infected people from an area with a large level of infection to an area with a lower level of infection always occurs. It is possible to imagine a situation in which people from an area with a lower level of infection in transport move to an area with a higher level, where quarantine is declared, and the exit is closed.

We use an inhomogeneous transport equation with a kinetic right-hand side. There are two parameters in the equation. The first corresponds to the averaged (over different vehicles) speed of the epidemic. The second corresponds to the value of “resistance” to the spread of virus carriers, which is modeled by the kinetic term describing a decrease in the number of infected passengers, which is associated with their return to places of residence or to places of temporary stay upon leaving the nidus of infection.

Two phases of the spread of infection were distinguished: portable and contact; the first phase lays the foundations for the contact phase. In our study, we investigate the transferential mechanism associated
with the migration of infected carriers from the center of infection. The contact mechanism is secondary: after the appearance of infected carriers, the infections occur locally. The superposition of the two factors gives the sum of all those infected. The contact infections are clearly manifested themselves when the measures of quarantine isolation of individual regions are introduced. The assumptions about isolation and the course of disease in such areas for approximately the same period of time enable us to show that the recovery process is “symmetric” to the infection process: the recovery begins earlier in the places where the infection earlier occurred.

We studied the processes in Russia, Italy, and Chile, where the main sources of the epidemic were associated with the capital centers (Moscow, Milan—the capital of Lombardy, and Santiago), which were visited by passengers from other countries, where the epidemic had already begun. The spread of infection occurred mainly in one direction, which was facilitated by the geographical extent of the countries, which allows us to consider a one-dimensional equation (the absence of infection from the “lateral borders” was taken into account, for example, from the Tyrrhenian and Adriatic seas, the Pacific Ocean, and the Andes, the northern and southern border sparsely populated territories in Russia)—only the areas to the east of Moscow were considered. The data on infections were taken from [13–16].

(2) By analogy with [12], for determining the density of infected passengers disembarking at a certain place at a certain moment of time, the following non-uniform transfer equation is used:

\[
\frac{dn}{dt} + U \frac{dn}{dx} = -\sigma n(t, x),
\]

where \( t \) is the time, \( x \) is the distance, \( n(t, x) \) is the density of moving carriers of the virus in a vehicle, \( U \) is the vehicle velocity, and \( \sigma \) is the coefficient of “resistance” to the motion of infected elements (mainly due to the disembarkation of passengers at their places of residence), which has the dimension of frequency. The initial condition for the Cauchy problem is taken in the form

\[ n_0(x) = H(-x), \]

where \( H(x) \) is the Heaviside function. This formulation of the problem means that, in fact, the carriers of virus enter the area under study \( x > 0 \) through the boundary \( x = 0 \). Using standard methods for solving linear partial differential equations, we obtain the following solution:

\[ n(t, x) = n_0(x - U t) \times e^{-\frac{\sigma x}{U}}. \]

We denote the density of virus carriers that landed at a given point as \( n_M(t, x) \). It is clear that this density grows as \( n(t, x) \) decreases; therefore, we can write

\[ \frac{dn}{dt} + \frac{dn_M}{dt} = 0; \]

\[ \frac{dn}{dt} = \frac{dn}{dt} + U \frac{dn}{dx}; \]

\[ \frac{dn_M}{dt} = \frac{dn_M}{dt}. \]

With taking into account Eq. (1), the equation for \( n_M(t, x) \) takes the following form:

\[ \frac{\partial n_M}{\partial t} = \sigma n. \]  

The solution of this equation is written as follows:

\[ n_M(t, x) = n_{M0}(x) + \int_0^t \sigma n(\tau, x) d\tau. \]

The substitution of expression (2) and the initial conditions \( n_{M0}(x) = 0 \) and \( n_0(x) = H(-x) \) permits us to obtain the expression for \( n_M(t, x) \):

\[ n_M(t, x) = \frac{\sigma}{U} (U t - x) \times H(U t - x) \times e^{-\frac{\sigma x}{U}}. \]

The parameter \( \sigma \) may depend on \( t \) and \( x \) (\( U \) may also be a dependent value, but we assumed it as constant). One of the options for the dependence of \( \sigma \) on the coordinate can be obtained by taking into account the density of the population

\[ \sigma(x) = \sigma_i \rho(x), \]

where \( \rho(x) \) is the linear population density, which has a dimension of \( 1/\text{km} \), and \( \sigma_i \) is a certain constant, which has the dimension of \( \text{km/day} \).

Substituting Eq. (5) into formula (2), we obtain the following expression:

\[ n(t, x) = n_0(x - U t) \times e^{-\frac{\sigma_i}{U} \int_0^t \rho(\zeta) d\zeta}. \]

A similar substitution in formula (4) results in the following:

\[ n_M(t, x) = \frac{\sigma_i \rho(x)}{U} (U t - x) \times H(U t - x) \times e^{-\frac{\sigma_i}{U} \int_0^t \rho(\zeta) d\zeta}. \]

The parameter \( \sigma_i \) is acquired as follows: \( t \) is fixed in formula (6) and the known data for two values of \( x \) are substituted.

The territory of the country is divided into regions along the selected direction of the spread of infection. For approximating the information from known sources in the selected regions, we summarized the values in the regions included in the region with the corresponding weights.

(3) In Italy, the territory was divided into nine regions. The \( U \) parameter, which determines the rate
of virus spread, can be estimated from the data on the first infections in each region. We fixed the first day in which there were at least five cases. By setting the points corresponding to these days, we plot the corresponding straight line using the least squares method. From the tangent of the slope of this straight line in the upper graph in Fig. 1, we find $U$. The lower graph in Fig. 1 corresponds to the spread of recovery. The onset of recovery for the selected region was determined when the peak infections per day were achieved. The least squares method was used with an approximation by the second-order polynomial. For each parabola, we determined the peak, which was taken as the date of the onset of recovery for this region. An example of the application of the least squares method is shown in Fig. 2 for Russia. For Italy, the infection rate was 53 km/day and the recovery rate was 52 km/day.

In Russia, the territory was divided into seven regions to the east of Moscow and similar methods were used for finding the infection rate of 87 km/day and the recovery rate of 52 km/day.

In Chile, the territory was divided into four regions to the north of Santiago and three regions to the south of the capital. These two directions were considered independently of each other. For Chile, infection rates were 44 and 97 km/day for the north and south, respectively. The recovery rates are 23 and 96 km/day.

The comparison of the solution according to the model equations (the lower graph in Fig. 3) with real data (the upper graph in Fig. 3) is shown for the first 18 days of observations (starting from February 24). It can be seen that the nature of the real and theoretical distributions is similar, but the values of the real data are higher than the theoretical ones, since the second contact factor begins to play an important role. Moreover, although the positions of the peaks of the number of infected peoples according to the calculated and real data approximately correspond to the positions of the local peaks of the population density (the middle graph in Fig. 3), the second peaks of infected peoples are lower than the first peaks (and, for the density, the second peak is higher). This fact shows that the model corresponds to reality: in Italy, the rapid decrease in space is associated both with the fact that many people sought to leave Lombardy and with quarantine barriers. Subsequently, with the effect of population density on the contact infections, the second peak...
becomes gradually higher than the first peak (these data after 18 days of infection are not shown).

The proximity of the values of the rates of spread and recovery (this proximity turned out to be true with a certain error for both Russia and Chile) enables us to predict the peak of infections per day in the country using information about the peak infections in the center of spread of the epidemic. For example, on the bases of the data from the first wave of COVID-19 in Russia, it was found that the peak infection in Russia is achieved from two to three weeks after achieving a similar peak in Moscow.

(4) Nowadays, a new wave of the pandemic continues and such clear conditions for the development and spread of COVID-19 are no longer observed. The autumn wave of the pandemic is of a more complex nature, which was facilitated by many factors; in particular, there was no strict isolation such as in the spring. Nevertheless, for Russia, the situation in which is of the greatest interest to us, it can be assumed that Moscow was the main center for spreading the virus to the east. Therefore, the peak infection in Moscow is achieved approximately two—three weeks earlier than in the whole of Russia. The predictions made at the end of December (see Fig. 2), were confirmed with taking into account the real data at the end of January (see Fig. 4). In Figs. 2 and 4, the upper graphs correspond to the nature of infection in Moscow and Russia as a whole, respectively. In Fig. 2, which shows the data for December 30, the peak for Moscow corresponds to December 10—12; for Russia, it is achieved approximately by December 28—30. It can be expected that, from this moment of time, the morbidity rate began to decrease in Russia. The data obtained...
at the end of January confirmed this prediction of the model. The plotted graphs in Fig. 4 show the above-noted lag in Russia as compared to Moscow. However, in accordance with the accepted method for determining the peaks, there was a slight shift of them to somewhat previous dates, but the indicated difference of about two weeks remains. In Fig. 4, the peak corresponds to December 4–5 for Moscow and to December 20–21 for Russia.

The results obtained may have predictive potential for the expected subsequent waves of the pandemic, in particular, for those associated with the emergence of new strains of the virus. For further use of a more detailed two-dimensional model with many centers of infection, it would be necessary to carry out more complex numerical calculations.

CONFLICT OF INTEREST
The authors confirm that they have no conflicts of interest.

REFERENCES
1. W. O. Kermack and A. G. McKendrick, Proc. R. Soc. London, Ser. A 115, 1098 (1927). https://doi.org/10.1098/rspa.1927.0118
2. B. Ivorra, M. R. Ferrandez, M. Vela-Perez, and A. M. Ramos, Commun. Nonlin. Sci. Numer. Simul. 88, 105303 (2020). https://doi.org/10.1016/j.cnsns.2020.105303
3. N. T. J. Bailey, Mathematical Theory of Epidemics (Griffin, London, 1957).
4. A. N. Kolmogorov, I. G. Petrovskii, and N. S. Piskunov, Byull. Mosk. Univ., Ser. Mat. Mekh. 1, 1 (1937)
5. J. V. Noble, Nature (London, U.K.) 250, 1038 (1974). https://doi.org/10.1038/250726a0
6. B. Gross, Z. Zheng, S. Liu, X. Chen, A. Sela, and J. Li, Europhys. Lett. 131, 1209 (2020). https://doi.org/10.1209/0295-5075/131/58003
7. H. Ramaswamy, A. A. Oberai, and Ya. C. Yortsos, Sci. Eng. 233, 116347 (2021). https://doi.org/10.1016/j.sce.2020.116347
8. S. E. Pastukhova and O. A. Evseeva, Ros. Tekhnol. Zh. 5 (5), 60 (2017). https://doi.org/10.32362/2500-316X-2017-5-5-60-69
9. V. A. Vasil’ev, Yu. M. Romanovskii, D. S. Chernavskii, and V. G. Yakhno, Autowave Processes in Kinetic Systems (Nauka, Moscow, 1987; Springer, Berlin, 1987).
10. I. Prigogine and R. Herman, Kinetic Theory of Vehicular Traffic (Am. Elsevier, New York, 1971).
11. V. V. Aristov and O. V. Il’in, Komp’yut. Issled. Model. 6 (5), 165 (2014). https://doi.org/10.20537/2076-7633-2014-6-5-829-838
12. V. V. Aristov and O. V. Ilyin, Phys. Rev. E 91, 042806 (2015). https://doi.org/10.1103/PhysRevE.91.042806
13. Coronavirus Distribution Map in Russia and the World. https://yandex.ru/web-maps/covid19.
14. Coronavirus in Italia, Data and Map. http://lab24.ilsole24ore.com/coronavirus.
15. Rospotrebnadzor, On Confirmed Cases of the New COVID-2019 Corona Infection in Russia. http://www.rospotrebnadzor.ru/about/info/news/news_details.php?ELEMENT_ID=16253&sphrase_id=2989389.
16. Ministerio de Salud. Casos Confirmados en Chile COVID-19. http://www.minsal.cl/nuevo-coronavirus-2019-ncov/casos-confirmados-en-chile-covid-19/.