

COVID-19 Spread Modeling Considering Vaccination and Re-Morbidity

Aleksey I. Borovkov¹, Marina V. Bolsunovskaya¹, Aleksei M. Gintciak^{1*}, Valeriya V. Rakova¹, Marina O. Efremova¹, Ruslan B. Akbarov¹

¹Peter the Great St. Petersburg Polytechnic University, 29 Polytechnicheskaya st., St. Petersburg, 195251, Russian Federation

Abstract. To effectively counter the COVID-19 spread, using scientifically based decision-making methods in this area is required. The disease characteristics and the methods applied to stem it are constantly changing, so it is necessary to update existing methods for predicting the COVID-19 spread in light of new trends. The present paper deals with developing a new SVEIRS model from the SEIR class, taking into account the vaccination campaign and the possibility of recurrent morbidity cases. These improvements make it possible to increase the accuracy of the disease spread prediction due to a more direct correspondence to reality. The developed SVEIRS model was verified when predicting the COVID-19 spread in Moscow in July-September of 2022 and showed higher prediction accuracy compared to the SEVIS reference model. Based on the developed model, it is possible to predict the COVID-19 spread in various regions to form an optimal vaccination campaign strategy.

Keywords: COVID-19; Epidemiology; Infection spread; Simulation modeling; System dynamics

1. Introduction

At the end of 2019, the pandemic of the new coronavirus infection SARS-CoV-2 swept the world. The COVID-19 pandemic became geographically widespread; the virus rapidly affected the world's population in every corner of the globe (Rothan & Byrareddy, 2020). For more than two years, humanity has been countering this disease. Several waves of increase and decrease in COVID-19 spread were observed.

Regarding the frequent cases of the population's recurrent morbidity, vaccination and revaccination remain the most effective measures to counter infection (Pilz et al., 2021). Due to these measures, the virus's contagiousness is reduced and the number of death cases among the vulnerable proportion of the population. From the economic perspective, vaccination is the most effective measure to stem coronavirus infection, since the vaccinated part of the population has the right to return to their usual lifestyle, earn and consume, which causes the country's economy to grow (Berawi, 2021). To fully restore the global economy and prevent the emergence of new variants of coronavirus infection, it is required to vaccinate at least 70% of the world population. Thus, the development of a proper vaccination groups, is a complex and time-consuming process, implementing such a

^{*}Corresponding author's email: gintsyak_am@spbstu.ru, Tel.: +7-911-157-74-26 doi: 10.14716/ijtech.v13i7.6186

strategy makes it possible to form collective immunity, reduce the economic burden (Polyanin et al., 2020), increase the vaccination attractiveness.

Traditional approaches to modeling the infectious disease spread have a significant disadvantage in the form of "uncertainty" parameters that are difficult to measure. These are indicators of mobility and population homogeneity, which also assumes a proportional infection spread among the entire population. It is generally incorrect. In the early stages of the pandemic, the incubation period, the infectivity period, the patient isolation period, the time and effectiveness of immunity after the disease, and later the effect of vaccination was considered as uncertain indicators. In this connection, such predictions were approximate, short-term, requiring a scenario approach (Klyushin, 2022). Models do not only predict events but also describe possible outcomes and scenarios for the pandemic development. The use of simulation modeling, machine learning, and interpolation methods make it possible to solve this problem due to the principle of trainability on samples and data obtained as a result of experiments. Moreover, it is worth noting that with the course of the COVID-19 infection, several additional factors affecting the modeling results accuracy have appeared, in particular, the population recurrent morbidity, revaccination which requires current models calibration.

The above determines the relevance of the current study and the urgent need to develop a simulation model considering the above factors and generating highly accurate realistic predictions on coronavirus infection spread based on the methodology of mathematical modeling and dynamic prediction of the COVID-19 spread.

This research aims to develop a new SVEIRS ("Susceptible – Vaccinated – Exposed – Infected – Recovered – Susceptible") model from the SEIR ("Susceptible – Exposed – Infected – Recovered") class (Li et al., 2021), taking into account the vaccination campaign and the possibility of recurrent morbidity cases. Within the present study, simulation modeling tools were considered from the perspective of applicability for predicting the infectious diseases spread, taking into account recurrent morbidity and vaccination.

2. Methods

2.1. Infectious disease spread modeling

Simulation modeling is a quantitative method of making and supporting decisions. A digital model of the system under study is created to evaluate and predict its effectiveness in real-world conditions. System analysis is used as the methodological basis for simulation modeling, classifying it as system modeling. The method's main feature is the possibility of reproducing the system under study without losing the dynamics of the system element's interaction. The research method is based on simulation and an experimental approach, which enables distinguishing it from mathematical modeling based on a computational approach.

Mathematical modeling provides possibilities for studying systems that change under the influence of random factors. At the same time, simulation models are widely used in the study of stochastic and deterministic systems and are applicable to solving complex problems under uncertainty (Lychkina, 2005). For managers and health services, simulation modeling is of key importance when making decisions since it allows studying and evaluating the effect of various alternative solutions, situations and conditions (Borovkov et al., 2020).

The modeling method selection should be based on the requirements, problems, and complexity of the system under study. Currently, the following methods of simulation modeling are widely used (Currie et al., 2020).

System dynamics based on creating simultaneous differential equations that reflect resources (human, material), the connections between them, and the importance (criticality) of these connections for the system. The most essential elements of system dynamics are the feedback loops and delays, which make it possible to explain the system's behavior. The SIR (suspected-infected-recovered) model is the most widely used in predicting the spread of infectious diseases. The SIR model and models based on it are designed to support strategic decisions that have consequences for the entire population of a country or region (Branding, 2022).

Agent-based modeling (agent-based approach) simulates the interaction of individuals in society and allows for determining how small changes in their behavior can affect the entire population in the area under study. Modeling social ties and population mobility becomes critically important in the need's context to ensure high accuracy in predicting the spread of infectious disease (Makarov et al., 2020). Agent models are stochastic because they assume and consider many human behavior scenarios. Due to this, the models can predict the effectiveness of management decision-making, even under the impermanence (changeability) of the population's behavior.

Discrete-event approach (simulation) involves using stochastic models that consider the spread (delay and variability) of time between the measures taken by the authorities and the onset of their impact on the system (epidemiological situation). The discrete-event approach is widely used to simulate the operation of systems in time, in which such system elements as people, agents, tasks, and messages (information) undergo the procedures of queues and operations. A typical application area of such models is the assessment of the medical resources (e.g., doctors and nurses) availability impact for the waiting time and the number of items in the queue (for example, patients).

Having studied the existing paradigms of simulation modeling, a group of authors of the present research concluded that the system dynamics methods application is the most appropriate, particularly SIR class models. They are possible to take into account a large number of factors without significantly reducing the modeling accuracy. This approach is applicable under incomplete information and uncertainty. Moreover, it gives the opportunity of dynamically changing environment and the possibility of simulating numerous scenarios. The key argument for the system dynamics selection was the possibility of taking into account a large number of causality chains and identifying functional dependencies between various factors, which makes it possible to accurately simulate the system's behavior (Yusoff & Izhan, 2020).

The analysis of existing methods of modeling and predicting the spread of infectious diseases and the distinctive features of the coronavirus infection progress allowed us to determine a mechanistic Kermack-McKendrick SEIR model as a basis for the experimental model development. It appears to be the most valid model that provides sufficient prediction accuracy in the medium term.

The current study proposes an extension of the SEIR model to the SVEIRS model by adding appropriate elements and interconnections between them. The model considers a significant number of factors affecting the dynamics of the COVID-19 spread for the complete simulation of a real system.

2.2. Model description

The SVEIRS model developed within the current study is based on the system dynamics principles and are simultaneous differential equations linking reserves (categories of the population to the COVID-19 morbidity process) via flows (infection, vaccination, and recovery processes) and converters (the morbidity process parameters).

In addition to the basic population categories for SEIR class models (S - Susceptible, E - Exposed, I - Infected, R - Recovered), the SVEIRS model includes an additional type: V - Vaccinated.

The developed SVEIRS model is described by the following simultaneous differential equations (1)-(5):

$$\frac{dS(t)}{dt} = -\beta \times S(t) \times I(t) + \alpha \times R(t) - v(t) + \sigma \times V(t)$$
(1)

$$\frac{dV(t)}{dt} = v(t) - \sigma \times V(t)$$
(2)

$$\frac{dE(t)}{dt} = \beta \times S(t) \times I(t) - \gamma \times E(t)$$
(3)

$$\frac{dI(t)}{dt} = \gamma \times E(t) - \delta \times I(t)$$
(4)

$$\frac{dR(t)}{dt} = \delta \times I(t) - \alpha \times R(t)$$
(5)

where S(t) is the number of susceptible individuals at time t; V(t) is the number of vaccinated individuals with artificial immunity (acquired via vaccination) at time t; E(t) is the number of exposed individuals at time t; I(t) is the number of infected individuals at time t; R(t) is the number of recovered individuals with natural immunity (acquired as a result of a previous disease) at time t; v(t) is the absolute rate of vaccination campaign, people per day; β - the relative frequency of effective (leading to disease transmission) contacts of individuals - the value is determined during calibration; α - the relative frequency of individual's transition from the Recovered (R) category to the Susceptible (S) category - the value inversely proportional to the natural immunity duration; σ - the relative frequency of individual's transition from the Exposed (E) category to the Infected (I) category - the value inversely proportional to the incubation period duration; δ - the relative frequency of individual's transition from the Exposed (E) category to the Recovered (R) category to the universely proportional to the incubation period duration; β - the relative frequency of individual's transition from the Exposed (E) category to the Recovered (I) category - the value inversely proportional to the incubation period duration; δ - the relative frequency of individual's transition from the Exposed (E) category to the Recovered (R) category - the value inversely proportional to the incubation period duration; δ - the relative frequency of individual's transition from the Infected (I) category to the Recovered (R) category - the value inversely proportional to the incubation period duration; δ - the relative frequency of individual's transition from the Infected (I) category to the Recovered (R) category - the value inversely proportional to the disease duration.

Figure 1 shows the block diagram of the developed SVEIRS model.



Figure 1 Block diagram of the developed SVEIRS model

In addition to the dependencies widely used in SEIR class models, there are two critical features in the developed SVEIRS model.

Firstly, the model considers the vaccination campaign as a way to reduce morbidity by minimizing the number of susceptible individuals at risk. Vaccinated individuals are identified as a separate category linked by flows only to the category of susceptible individuals. The absolute rate of vaccination campaign determines the rate of this category of individuals replenishment, depends on government measures to vaccinate the

population and the propensity of the people to vaccinate, therefore, within the model, it is an external parameter. The rate of this category of individuals withdrawals is determined by the rate of termination of artificial immunity acquired via vaccination. The relative rate of individuals transitioning into the category of susceptible is inversely proportional to the duration of the artificial immunity effect obtained via vaccination.

Secondly, the model considers the possibility of recurrent morbidity as an additional source of susceptible individuals. Unlike traditional SEIR models, in this case, recovered individuals are susceptible to the recurrence of the same disease not forever, but for a certain period equal to the duration of the natural immunity acquired due to the previous disease. Considering the recurrent COVID-19 cases, this model extension makes it more realistic. The recurrent morbidity possibility is implemented as a result of combining an additional flow between the Recovered (R) and Susceptible (S) categories, the rate of individuals transition which is determined by the rate of termination of the natural immunity acquired as a result of the previous disease. The relative rate of individuals growth into the category of susceptible is inversely proportional to the duration of the natural immunity acquired due to the previous disease.

The main reference model for the developed SVEIRS model is the SEVIS ("Susceptible – Exposed – Vaccinated – Infected – Susceptible") model (Li et al., 2021), which is described by the following simultaneous differential equations:

$$\frac{dS(t)}{dt} = -\beta \times S(t) \times I(t) - \upsilon \times S(t) + (1-\omega) \times \delta \times I(t)$$
(6)

$$\frac{dE(t)}{dt} = \beta \times S(t) \times I(t) - \gamma \times E(t)$$
(7)

$$\frac{dV(t)}{dt} = v \times S(t) + \omega \times \delta \times I(t)$$
(8)

$$\frac{dI(t)}{dt} = \gamma \times E(t) - \delta \times I(t)$$
(9)

where ω - the proportion of the disease cases ending with the immunity acquisition. The other symbols were described in formulas (1)–(5).

Figure 2 shows the block diagram of the SEVIS reference model.



Figure 2 Block diagram of the SEVIS reference model

The SEVIS reference model is also an extension of the SEIR model. It was created by adding a vaccination campaign and the recurrent morbidity possibility to the model. However, this extension is implemented differently than in the developed SVEIRS model. The vaccination process is one-sided, i.e., once vaccinated against COVID-19, an individual receives permanent immunity to the disease. At the same time, individuals fall into the Vaccinated (V) category not only after vaccination but also with some probability after the

disease. Thus, the Vaccinated (V) category in the SEVIS model contains individuals with the artificial and natural immunity. In addition, both types of immunity are indefinite, which is contrary to the actual dynamics of the disease spread.

Table 1 compares the SEVIS and SVEIRS models regarding vaccination features and the possibility of recurrent morbidity.

Table 1	Comparison	of SEVIS and	SVEIRS	models
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SEVIS reference model (Li et al., 2021)		Developed SVEIRS model	
Vaccination campaign	A separate category of Vaccinated (V) individuals. A flow from the Susceptible (S) category, depending on the relative rate of the vaccination campaign. No reverse flow is provided.	A separate category of Vaccinated (V) individuals. A flow from the Susceptible (S) category, depending on the total rate of the vaccination campaign. The reverse flow into the Susceptible (S) category, depending on the duration of the immunity acquired via vaccination.	
Recurrent morbidity	Some individuals are transferred to the Susceptible (S) category after the disease. Another part of individuals after the disease is assigned to the Vaccinated (V) category.	All individuals after the disease are moved to the Recovered (R) category and receive natural immunity. The flow from the Recovered (R) category to the Susceptible (S) variety depends on the duration of the immunity acquired due to the previous disease.	

Even though both models are SEIR class model extensions and additionally consider the same set of disease features and ways to stem its spread, these features are implemented in different ways in the models, which affects the simulation experiments with these models.

Within the present research, both models are verified on the same data set to assess their functional features. Moscow is chosen as the modeling object. For the model calibration historical data on the number of infected (I, Infected individuals) in Moscow from 07/01/2022 to 07/30/2022 (30 days) will be used. The prediction accuracy estimation will be carried out on the relevant data from 07/31/2022 to 09/28/2022 (60 days), which corresponds to the medium-term prediction horizon.

The parameters of the models are deduced from historical data on the COVID-19 incidence in Moscow and modern publications studying the COVID-19 features (Table 2).

3. Mathematical Model

For the selection the relative frequency of effective contacts the calibration of models based on historical data on the number of infected (I, Infected individuals) in Moscow from 07/01/2022 to 07/30/2022 (30 days) has been performed. Figure 3 shows the data series of the SVEIRS and SEVIS models at the calibration time interval to the actual data at the same time interval.

Table 2 Model parameters

Parameter	Value in the SEVIS reference model	Value in the developed SVEIRS model
The initial number of susceptible individuals, S(0), people (Stopkoronavirus.rf, 2022)	10,958,609	
The initial number of vaccinated individuals, V(0), people (Stopkoronavirus.rf, 2022)	1,500,649	782,616
The initial number of exposed individuals, E(0), people (Stopkoronavirus.rf, 2022)	29,368	
The initial number of infected individuals, I(0), people (Stopkoronavirus.rf, 2022)	146,840	
The initial number of infected individuals, R(0), people (Stopkoronavirus.rf, 2022)	-	718,033
Relative frequency of effective contacts, 1 / (people * day)	it is determined during the calibration process	
The absolute rate of vaccination campaign, v, people per day (Stopkoronavirus.rf, 2022)	-	386
Relative rate of the vaccination campaign, 1 / day (Stopkoronavirus.rf, 2022)	1 / 28,390	-
Relative frequency of individual's transition from the Recovered (R) category to the Susceptible (S) category, 1 / day (Dan et al., 2021)	-	1 / 180
Relative frequency of individual's transition from the Vaccinated (V) category to the Susceptible (S) category, 1 / day (Lopez Ledesma et al., 2021)	-	1 / 180
Relative frequency of individual's transition from the Exposed (E) category to the Infected (I) category, 1 / day (Hay et al., 2022)	1/2	
The relative frequency of an individual's transition from the Infected (I) category to other categories, 1 / day (Hay et al., 2022)	1/	10
The proportion of the disease cases ending with immunity acquisition. (Li et al., 2021)	0.8	-



Figure 3 Data series of the SVEIRS and SEVIS models with real data in the interval from 07/01/2022 to 07/30/2022

Table 3 demonstrates calibration results. As part of the calibration, a value of the relative frequency of effective contacts has been selected for both models. The same parameter value has been chosen for both models as a result of the calibration. The chosen value minimizes the mean percentage absolute error (MAPE) to the nearest thousandths. Table 3 also provides the value of the square root of the root-mean-square error for the calibration accuracy (and further prediction) interpretability.

	SEVIS reference model	Developed SVEIRS model
Relative frequency of effective contacts, 1 / (people * day)	0	.064
MAPE	0.300%	0.299%
RMSE, people	573.340	571.647

Table 3 Models calibration results in the interval from 07/01/2022 to 07/30/2022

The calibration accuracy of the SEVIS and SVEIRS models using data series from 07/01/2022 to 07/30/2022 is comparable. It makes possible to evaluate the accuracy of prediction models using data series in the interval from 07/30/2022 to 09/28/2022 compared to actual data (Figure 4).



Figure 4 Prediction data series of the SVEIRS and SEVIS models with real data in the interval from 07/31/2022 to 09/28/2022

Table 4 shows indicators of the prediction accuracy of the COVID-19 spread in Moscow from 07/31/2022 to 09/28/2022 using SEVIS and SVEIRS models.

Table 4 Indicators of the SEVIS and SVEIRS models	s prediction accuracy
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	SEVIS reference model	Developed SVEIRS model
MAPE	6.309%	3.329%
RMSE, people	14,374.837	7,772.028

The results of the COVID-19 spread modeling using SEVIS and SVEIRS models allow us to claim a higher prediction accuracy of the developed SVEIRS model in this case.

4. Discussion

For a more reliable SEVIS and SVEIRS models accuracy assessment, it is required to simulate the COVID-19 spread on data corresponding to other regions and time intervals. Within the present paper, the application of the SEVIS reference model and the developed SVEIRS model to modeling the COVID-19 spread in one region (Moscow) in the interval of 90 days (30 days for calibration and 60 days for evaluation) has been considered.

Prediction accuracy depends not only on the model and the features of the modeling object, but also on the prediction horizon. Thus, particular models may have high accuracy in short term prediction, but may be inappropriate for long-term prediction, and vice versa. Although the developed SVEIRS model has shown higher prediction accuracy in the considered case, during its development, assumptions were made, the elimination of which can bring the model behavior closer to the conduct of the real system.

Firstly, in the SVEIRS model, only one disease variant is constantly active. In contrast, the SARS-CoV-2 virus that causes COVID-19 has several thousand variants (Koyama et al., 2020), some of which cause mutually independent morbidity waves. It shows that the natural immunity obtained from one virus variant disease does not always prevent infection with another virus variant (Tang et al., 2020). In addition, vaccines' effect is often directed at particular virus variants (Callaway, 2021).

Secondly, in the SVEIRS model, it is assumed that vaccination is available only to susceptible individuals, and the possibility of vaccination of individuals with natural or artificial immunity is not considered, although such cases are undoubtedly encountered in real life. However, this assumption is inherent in most SEIR class models that consider the vaccination campaign (Johnston et al., 2022).

Thirdly, the SVEIRS model assumes that all recovered individuals acquire natural immunity, and all vaccinated individuals acquire artificial immunity. At the same time, there are cases of individuals recurrent morbidity shortly after the disease. In addition, none of the existing COVID-19 vaccines has absolute efficacy (Huang et al., 2022). The correction for the probability of acquiring natural immunity and the effectiveness of vaccines can be made in the SVEIRS model extensions.

5. Conclusions

The paper describes the developed SVEIRS model, the SEIR class model extension created by considering the vaccination campaign and the possibility of recurrent morbidity. The developed model makes it possible to predict the spread of infectious diseases (including COVID-19) characterized by the prospect of acquiring natural immunity due to the previous disease and artificial immunity via vaccination. The developed SVEIRS model was verified when predicting the COVID-19 spread in Moscow in July-September of 2022 compared to the SEVIS reference model. SVEIRS model showed higher prediction accuracy. Based on the developed model, it is possible to predict the COVID-19 spread in various regions to form an optimal vaccination campaign strategy.

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