

# The Framework of Estimation of the Impact of the Russian War on the Infectious Diseases Spreading

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## Abstract

This paper presents a framework for assessing the impact of the Russian war in Ukraine on the dynamics of the epidemic process of infectious diseases. The framework involves developing a machine learning model to predict the dynamics of morbidity and mortality from an infectious disease in a selected area, verifying the model, and assessing factors influencing the epidemic process. The results obtained from the simulation provide valuable lessons for improving the functioning of healthcare systems during extreme situations, including times of war. Mathematical modeling is essential for assessing the dynamics of the epidemic process and making timely adjustments to preventive and anti-epidemic measures. The proposed framework can help identify changes in the spread of morbidity and introduce timely control measures to prevent the spread of the disease.

## Keywords

Epidemic model, simulation, epidemic process, artificial intelligence, infectious disease modeling

## 1. Introduction

Infectious diseases continue to significantly threaten public health, causing millions of deaths and illnesses worldwide each year [1]. Despite advances in medicine and technology, the emergence and spread of new infectious diseases and the re-emergence of previously controlled diseases continue to challenge healthcare systems and economies globally [2]. This persistent problem underscores the need for continued research and development of effective strategies for controlling infectious diseases.

One of the recent most significant infectious disease outbreaks is the COVID-19 pandemic, caused by the novel coronavirus SARS-CoV-2 [3]. Since its emergence in late 2019, COVID-19 has rapidly spread to virtually every country worldwide, leading to a massive global health crisis. The pandemic has highlighted the urgent need for effective prevention and control measures and has exposed weaknesses in healthcare systems worldwide. As such, COVID-19 has spurred a surge of research efforts to develop strategies to combat infectious diseases [4].

Simulation models have emerged as a powerful tool for studying infectious diseases and evaluating the effectiveness of different intervention strategies [5]. These models can simulate the spread of diseases under various conditions and help researchers and policymakers identify the most effective approaches for controlling outbreaks. Moreover, simulation models can enable researchers to investigate the potential impact of future outbreaks, such as those caused by emerging infectious diseases or bioterrorism [6]. As such, developing and refining infectious disease simulation models are critical for improving public health and global preparedness.

The COVID-19 pandemic has significantly accelerated research efforts in infectious diseases simulation, as the situation's urgency has highlighted the critical need for effective disease control

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strategies. Such studies were aimed at creating complex models for studying epidemic processes [7], automated diagnostics [8], analysis of medical data [9], processing of medical images [10], identification of factors affecting the epidemic process [11], organization of public health systems [12], systems for warning the public about the risks of infection [13], etc. With the rapid spread of COVID-19 and the high mortality rate, researchers have been motivated to develop simulation models that can accurately predict the spread of the disease and evaluate the effectiveness of various interventions, such as social distancing, mask-wearing, and vaccination. Furthermore, the pandemic has highlighted the importance of proactive preparedness and the need for simulation models that can forecast potential outbreaks and evaluate the impact of different intervention strategies. As a result, there has been a surge in research into infectious disease simulation, focusing on developing more accurate and sophisticated models to provide policymakers with the insights needed to control infectious diseases effectively.

On February 24, 2022, Russia launched a full-scale invasion of Ukraine. In addition to tens of thousands of deaths and injuries, the escalation of the Russian war in Ukraine has also brought a massive humanitarian crisis that has affected public health [14].

Thus, this study aims to develop a framework for assessing the impact of the Russian war in Ukraine on the dynamics of the spread of infectious diseases.

## 2. Current research analysis

The use of mathematical models to study infectious diseases dates back to the early XX century. In the 1920s, Ronald Ross, a Nobel laureate in medicine, developed a mathematical model to study the transmission of malaria, which helped inform malaria control efforts [15]. In the 1940s, William Hamer and colleagues developed a mathematical model to simulate the spread of infectious diseases, which they applied to the study of measles [16]. Since then, infectious disease modeling has grown significantly, with advancements in computing power and data collection enabling more sophisticated and accurate models. In the 1970s, models were developed to study the transmission of HIV/AIDS [17], and in the 1990s, models were used to evaluate control strategies for tuberculosis [18]. Today, infectious disease models study various diseases, including COVID-19. They have become an essential tool for public health officials and policymakers in the fight against infectious diseases.

Compartment models are mathematical models commonly used in infectious disease modeling [19]. These models divide the population into different compartments based on their disease status, such as susceptible, infected, and recovered. The dynamics of disease transmission are then modeled through the movement of individuals between these compartments. Compartment models can be simple, with only a few compartments and assumptions, or more complex, with multiple compartments and subpopulations. The simplest compartment model is the SIR model, which stands for susceptible, infected, and recovered and assumes that individuals move sequentially through these compartments. The SIR model has been widely used to study the spread of infectious diseases, including COVID-19.

The paper [20] presents a mathematical model that incorporates the effect of testing and contact tracing on the transmission dynamics of a SIR epidemic in a homogeneous community. The model is analyzed using large population approximations, which enable quantifying the impact of testing and contact tracing on adequate reproduction numbers, the probability of a significant outbreak, and the final fraction of infected individuals. The authors demonstrate, through numerical illustrations, that the Test-and-Trace strategy effectively reduces the epidemic's reproduction number. Interestingly, the reproduction number for the branching process of components is not monotonically decreasing in the tracing probability, but the individual reproduction number is expected to be monotonic. The paper also explores the influence of the tracing probability and screening rate on the epidemic outcome when individuals self-report for testing. The findings of this study provide insights into the effectiveness of testing and contact tracing strategies in controlling the spread of infectious diseases. The drawback of the model is that it assumes a homogeneous population, which may not accurately reflect the heterogeneity of real-world populations and their behavior.

The authors of [21] present a refined epidemiological model called the fractional susceptible-exposed-infected-removed (SEIR) model, which utilizes the Caputo-Hadamard fractional derivative to account for the concealed transmission of the Omicron variant of COVID-19. The model is calibrated using fractional physics-informed neural networks to infer the fractional order, time-dependent

parameters, and unobserved dynamics of the fractional SEIR model and is used to make short-term predictions of the COVID-19 dynamics caused by the Omicron variant. The findings suggest that the fractional SEIR model can provide reliable short-term predictions of COVID-19 dynamics caused by the Omicron variant. However, the slow increase in reported cases at the pandemic's beginning may challenge accurate predictions. The drawback of the model is that it assumes that the transmission dynamics of the Omicron variant will remain constant over the short-term prediction period, which may not hold if there are significant changes in public health interventions, social behaviors, or the virus itself.

The paper [22] proposes a modified SEIR model with a time-varying parametric strategy to fit better the actual situation of the COVID-19 epidemic and account for the utility of intervention strategies, which may cause abrupt changes in the trend of the parameters. A model selection algorithm based on the information criterion is also suggested to detect the jump in the transmission parameter. The proposed method is demonstrated through accurate data analysis of the COVID-19 epidemic in Wuhan and a simulation study, showing its plausibility and validity. The limitation of the proposed model is that it assumes that the time-varying parameters change abruptly, which may only sometimes be the case in real-world situations. In some cases, the parameter changes may be more gradual or continuous, limiting the proposed method's applicability.

The study [23] proposes a compartment model called SVEIHRM to simulate the COVID-19 pandemic, considering multiple vaccinations and mutant viruses of COVID-19 and investigates the effects of adjusting the daily vaccination rate and timing of vaccination on the number of infected individuals, showing that starting vaccinations is critical to reducing the number of infected individuals and delaying the start date requires a substantial increase in the vaccination rate, with a sensitivity analysis demonstrating that a 10% increase (decrease) in vaccination rates can reduce (increase) the number of confirmed cases by 35.22% (82.82%), respectively. The drawback of the SVEIHRM model proposed in the paper is that it may only partially capture some of the complex and dynamic factors that influence the spread of COVID-19, such as changes in human behavior, environmental factors, and public health policies.

This paper [24] presents a fractional-order differential mathematical model of HCV infection dynamics, incorporating virus-to-cell and cell-to-cell modes of transmission of the infection along with a cure rate of infected cells. The model includes four compartments, each involving a long memory effect modeled by a Caputo fractional derivative. The paper starts by introducing some preliminaries about the needed fractional calculus tools and then establishes the well-posedness of the mathematical model. The paper presents the different problems of steady states depending on some reproduction numbers and moves to the stage of proving the global stability of the three steady states. To evaluate the theoretical study of global stability, the paper applies a numerical method based on the fundamental theorem of fractional calculus and a three-step Lagrange polynomial interpolation method. The numerical simulations show that the free-endemic equilibrium is stable if the basic reproduction number is less than unity. In addition, the numerical tests demonstrate the stability of the other endemic equilibria under some optimal conditions.

While helpful in modeling infectious diseases and predicting their spread, the compartment approach has several drawbacks. One major drawback is the assumption of homogeneity within each compartment, meaning that individuals within a given compartment are considered identical regarding their disease progression and transmission potential. This assumption ignores individual-level differences in susceptibility, contact patterns, and behavior, which can significantly affect the dynamics of the disease. Additionally, compartment models can be limited by their complexity and lack of flexibility, as they typically require pre-defined compartments and parameters and may only be able to capture some relevant factors influencing disease spread. Finally, the compartment approach may not account for spatial heterogeneity or time-varying dynamics, which can be important in understanding and controlling epidemics in different settings.

Machine learning (ML) techniques have recently shown great potential in infectious disease modeling and simulation [25]. These approaches allow for analyzing large and complex data sets, identifying patterns, and predicting outcomes that would be difficult to achieve through traditional modeling methods. Machine learning models can be trained on real-world data to estimate the parameters of a model, which can then be used to simulate the spread of infectious diseases. Additionally, machine learning algorithms can help optimize intervention strategies by predicting the

impact of various control measures on disease transmission. However, one challenge in using machine learning in infectious disease simulation is the need for extensive and diverse data sets, which may be challenging to obtain for emerging or rare diseases. Furthermore, there is a risk of overfitting the data and losing generalizability, and transparency in model decisions and interpretations may be challenging.

This paper [26] proposes a novel edge-centric healthcare framework that integrates wearable sensors and advanced machine learning models to detect and prevent infectious diseases like COVID-19. The authors collect a set of features through wearable sensors, which are preprocessed to prepare a valuable dataset. Due to the limited resource capacity of edge devices, the authors introduce an advanced ML technique called Deep Transfer Learning (DTL) for data analysis. DTL transfers the knowledge from a well-trained model to a new lightweight ML model that can support the resource-constrained nature of distributed edge devices. The authors validate their framework using a benchmark COVID-19 dataset consisting of 11 features and 2 million sensor data, achieving 99.8% accuracy in disease prediction. The proposed framework has the potential to provide timely decisions with minimum delay, even in resource-constrained environments where PCR test kits are not available. The limitation of the proposed approach is that it relies on the availability and accuracy of wearable sensor data. In some settings, particularly in low-resource areas or among vulnerable populations, access to such technology may be limited or nonexistent, which could prevent the widespread implementation of this approach. Additionally, there may be concerns about privacy and data security when using wearable sensors to collect personal health information.

Authors of [27] present a statistical study and a machine learning model developed to triage COVID-19 patients based on their medical records and test results. The study identifies features with a more pronounced effect on the patient outcome, which constitutes the inputs of four machine learning models. The accuracy of the models is tested when the number of input features is varied, demonstrating their stability. The Random Forest and Gradient Boosting classifiers are shown to be highly accurate in predicting patients' mortality and categorizing patients into four distinct risk classes for the severity of COVID-19 infection. The approach presented in this paper combines statistical insights with various machine learning models, which can pave the way forward in the AI-assisted triage and prognosis of COVID-19 cases. One potential drawback of the study is that it was conducted during the height of the COVID-19 pandemic in Hong Kong, which could limit the generalizability of the findings to other locations or future outbreaks with different characteristics. Additionally, the study only considers hospitalized patients, so the results may not apply to patients with less severe cases of COVID-19 who were not hospitalized.

The paper [28] aims to predict the duration of emergency evacuation following a hospital fire using machine learning algorithms. The study analyzed the emergency evacuation duration of 190 patients admitted to a hospital-based on eight factors. Statistical machine learning models were used to design and validate the model, including Support Vector Machines Random Forest, Naive Bayes Classifier, and Artificial Neural Network. Results showed that the Random Forest model outperformed other models with an AUC of 99.5%, a precision of 92.4%, and a sensitivity of 92.1%. The study concludes that predicting evacuation duration can provide managers with accurate information for developing appropriate plans using machine learning models to promote preparedness and responsiveness during the fire. The drawback of this study is that the simulation was based on a single hospital and may not necessarily apply to other hospitals with different layouts or patient populations. Therefore, further studies may be needed to validate the model in different hospital settings.

Machine learning approaches have shown great potential for infectious disease simulation and prediction, providing accurate and timely insights to help prevent and control outbreaks. One advantage of using machine learning for infectious diseases is the ability to handle and analyze large amounts of data from different sources, allowing for the identification of patterns and trends that traditional methods may miss. Additionally, machine learning can adapt and learn from new data, making it useful for ongoing monitoring and prediction. However, there are also some drawbacks to using machine learning for infectious diseases. One primary concern is the potential for bias and inaccuracy in the algorithms, which can lead to incorrect predictions and ultimately compromise public health efforts.

Additionally, machine learning models may be complex and difficult to interpret, making it challenging to understand how decisions are being made. Finally, there may be limitations in the data available for training and testing these models, which can impact their accuracy and generalizability.

Overall, while machine learning has the potential to be a powerful tool for infectious disease management, caution must be taken to ensure that models are accurate, unbiased, and transparent.

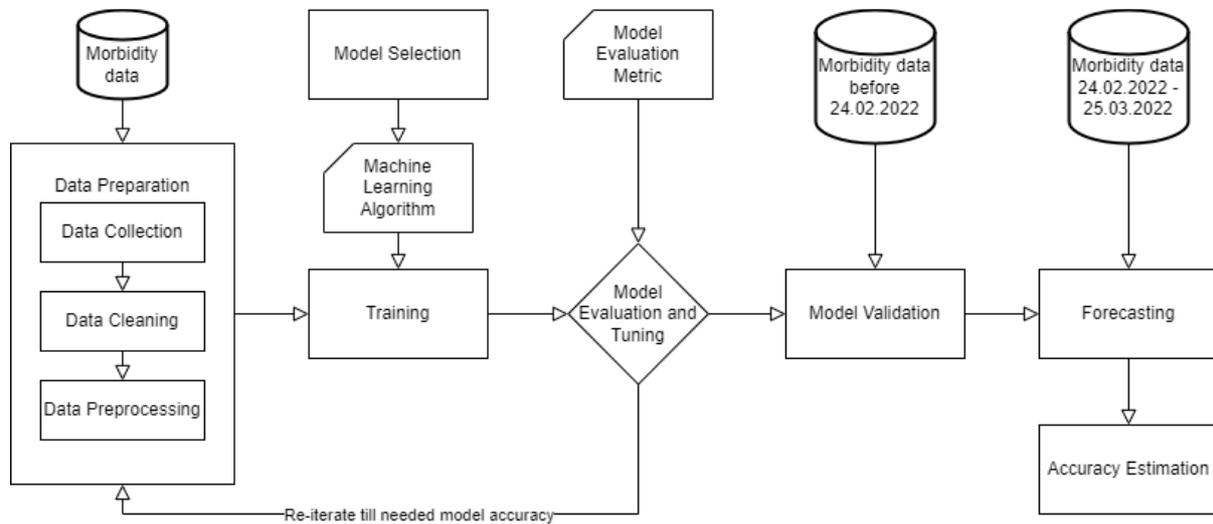
Nevertheless, an analysis of existing approaches to modeling epidemic processes has shown that machine learning methods provide the highest accuracy. Therefore, the methodology proposed in this article is based on machine learning methods.

### 3. Methodology

This paper proposes a methodology for assessing the impact of Russia's war in Ukraine on the dynamics of epidemic processes. For this, the following steps are proposed:

1. Develop a machine learning model of the epidemic process to predict the dynamics of morbidity and mortality from an infectious disease in a selected area.
2. Verify the model by assessing the accuracy of the retrospective forecast of morbidity and mortality from an infectious disease in the selected area from January 25, 2022, to February 23, 2022, i.e. 30 days before the escalation of the Russian war in Ukraine.
3. Calculate the predicted morbidity and mortality from an infectious disease in the selected territory on February 24, 2022, to March 25, 2022, i.e. 30 days after the start of the escalation of the Russian war in Ukraine.
4. Calculate the deviation of actual morbidity and mortality from an infectious disease in the selected area from the constructed forecast.
5. Assess the factors influencing the epidemic process depending on the infectious disease, the nature of its distribution, and the selected territory.
6. Based on the simulation results, identify public health risks and necessary measures to control the spread of infectious diseases.

The framework for assessing the impact of the Russian war in Ukraine on the dynamics of epidemic processes of infectious diseases is shown in Figure 1.



**Figure 1:** The framework for assessing the impact of the Russian war in Ukraine on the dynamics of epidemic processes of infectious diseases

To evaluate the performance of the model, it is proposed to apply mean absolute percentage error (MAPE):

$$MAPE = \frac{100\%}{n} \sum_{t=1}^n \left| \frac{A_t - F_t}{A_t} \right|, \quad (1)$$

where  $A_t$  is the actual value,  $F_t$  is the forecasted value.

One of the main advantages of using MAPE is its ability to provide a standardized measure of the prediction accuracy, which can be easily understood and compared across different datasets and models.

Additionally, MAPE has a clear interpretation as a percentage error, which allows for a more intuitive understanding of the prediction errors. Another advantage of MAPE is its sensitivity to large errors, which means that it can capture outliers or extreme values that may be missed by other metrics like mean squared error. Overall, the use of MAPE can provide a useful and transparent way to evaluate the performance of machine learning models and other predictive algorithms.

To assess the impact of the Russian war in Ukraine on the dynamics of the epidemic process of infectious diseases, it is proposed to calculate the deviation of the forecast calculated for February 24, 2022 to March 25, 2022 from the actual incidence:

$$D = |F_t - A_t|, \quad (2)$$

where  $A_t$  is the actual value, and  $F_t$  is the forecasted value.

Another critical aspect of applying the proposed methodology is the use of data. For example, the Johns Hopkins University & Medicine Coronavirus Resource Center is the most popular dataset for analyzing the COVID-19 epidemic process [29]. It is a widely used online platform that provides up-to-date information and visualizations on the global COVID-19 pandemic. It was launched in early 2020 to track and report the spread of the virus and has since become a trusted source of information for the public, policymakers, and healthcare professionals. The dashboard features real-time data on confirmed cases, deaths, recoveries, and testing, with breakdowns by country, state/province, and county. It also includes interactive maps, charts, and graphs that allow users to visualize the data in various ways. The Johns Hopkins team collects the data from various sources, including the World Health Organization, the Centers for Disease Control and Prevention, and national health ministries. The dashboard has been praised for its accessibility, accuracy, and transparency and has played a crucial role in shaping public health policies and informing the public during the pandemic.

However, after February 24, 2022, it does not contain any data regarding the epidemic process of COVID-19 in Ukraine.

Therefore, in the case of modeling the epidemic process of COVID-19, we recommend using the WHO Coronavirus (COVID-19) Dashboard of World Health Organization data [30]. It is an online platform provided by the World Health Organization (WHO) that provides up-to-date information on the COVID-19 pandemic. The dashboard includes global and country-level data on confirmed cases, deaths, and recoveries, as well as data on testing and vaccination rates. The data is presented as interactive maps, graphs, and tables, and users can filter the data by country, region, and date. The dashboard also includes links to WHO guidance and resources related to COVID-19 and news and updates on the pandemic. Overall, the WHO Coronavirus Dashboard provides a comprehensive and authoritative source of information on the global COVID-19 situation.

In analyzing other infectious diseases, it is necessary to pay attention to the availability of data in Ukraine after the start of the escalation of the Russian war in Ukraine. The lack of data may be due to the termination of cooperation with the Ukrainian public health authorities and the concealment of incident data from public access.

## 4. Experimental Study

For the experimental study, the Polynomial regression model was applied [31].

Polynomial regression is a regression analysis in which the relationship between the independent variable (in this case, time) and the dependent variable (the forecasted variable) is modeled as an  $n$ -degree polynomial function. Polynomial regression aims to find the best-fitting curve that passes through the data points.

In time-series forecasting using polynomial regression, the historical data is plotted on a graph with time on the  $x$ -axis and the dependent variable on the  $y$ -axis. Using a polynomial function, a regression line is then fitted to the data points. The degree of the polynomial is chosen based on the data's complexity and the forecast accuracy required. A higher degree polynomial may fit the data more accurately but also overfit it, resulting in poor forecast performance on new data.

The first step is to choose the polynomial degree to fit a polynomial regression model to the time-series data. This is done by selecting a value of  $n$  that produces the best tradeoff between the model's complexity and ability to fit the data. Once the degree is chosen, the next step is to fit the polynomial

function to the data using least-squares regression. The polynomial coefficients are determined by minimizing the sum of the squared errors between the predicted and actual values.

Once the polynomial function is fitted to the data, it can forecast the dependent variable's future values. This is done by extrapolating the polynomial function into the future. However, it is essential to note that the accuracy of the forecast will depend on how well the polynomial function fits the historical data. If the polynomial overfits the historical data, the forecast will perform poorly on new data.

In summary, polynomial regression is a method for time-series forecasting in which the relationship between time and the dependent variable is modeled using a polynomial function. The degree of the polynomial is chosen based on the data's complexity and the forecast accuracy required. Once the polynomial function is fitted to the historical data, it can forecast the dependent variable's future values. However, ensuring that the polynomial does not overfit the data is essential, as this will result in poor forecast performance.

Advantages of the polynomial regression method for time-series forecasting:

- Can model nonlinear relationships between variables.
- Can capture curvilinear trends in time series data.
- Can be used to forecast over multiple periods.
- Can handle missing data points and outliers effectively.
- Allows for interpretation of the relationship between predictor and response variables.

Disadvantages of the polynomial regression method for time-series forecasting:

- Overfitting can occur if the model is too complex or lacks enough data to support the complexity.
- Extrapolation outside the range of the training data can lead to unreliable forecasts.
- Polynomial regression assumes a fixed degree of the polynomial, which may not be appropriate for all data.
- The method does not consider seasonal or cyclical patterns in the data, which may be necessary for time series forecasting.
- Requires careful feature selection and engineering to avoid including irrelevant or redundant predictors.

A machine learning model based on polynomial regression method was applied to estimate the impact of the Russian war in Ukraine on the dynamics of COVID-19 epidemic process in Ukraine. The model was implemented in Python. To verify the model, a retrospective forecast of morbidity and mortality from COVID-19 in Ukraine from January 25, 2022 to February 23, 2022 was built.

Table 1 shows model accuracy rates for cumulative new cases and deaths of COVID-19 in Ukraine for a sample from January 25, 2022 to February 23, 2022.

**Table 1**

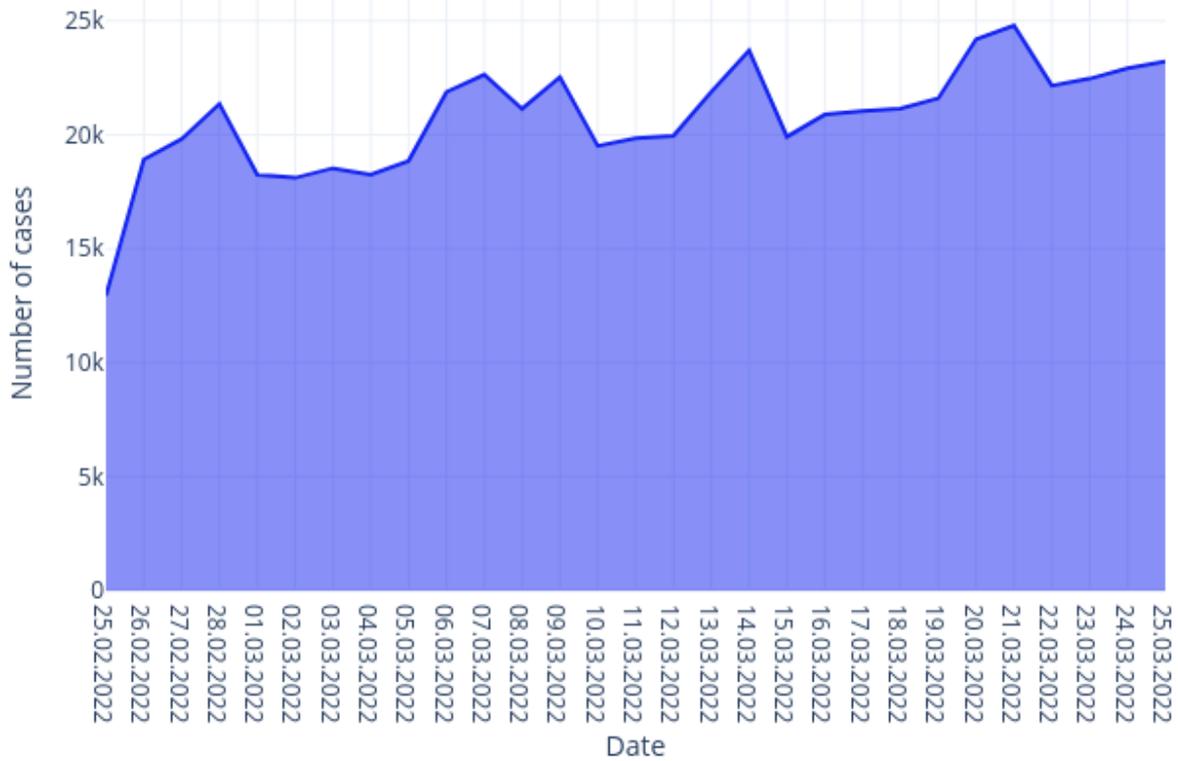
MAPE of forecast from January 25, 2022 to February 23, 2022

Duration of forecast (days)	New cases	Death cases
7 days	0,84 %	0,12 %
10 days	0,97 %	0,09 %
20 days	1,78 %	0,09 %
30 days	2,12 %	0,17 %

To evaluate the impact of the Russian war in Ukraine on the COVID-19 epidemic process dynamics in Ukraine, we have applied the developed model to the data sample from February 24, 2022, to March 25, 2022.

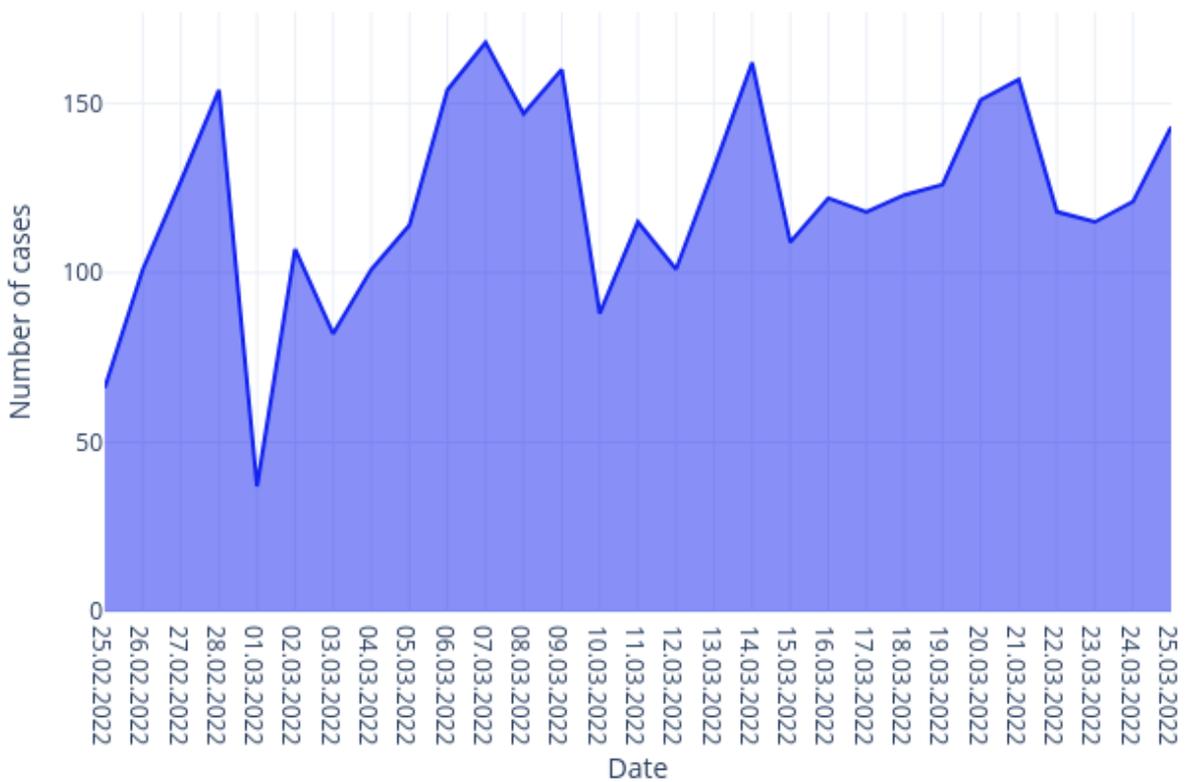
Table 2 shows model accuracy rates for cumulative new cases and deaths of COVID-19 in Ukraine for a sample from February 24, 2022, to March 25, 2022.

Figure 2 shows the deviation of daily reported new cases of COVID-19 in Ukraine from the predicted values for the period from February 24, 2022, to March 25, 2022.



**Figure 2:** Deviation of COVID-19 daily new cases from forecasted values (24.02.22 – 25.03.2022)

Figure 3 shows the deviation of daily reported death cases of COVID-19 in Ukraine from the predicted values for the period from February 24, 2022, to March 25, 2022.



**Figure 3:** Deviation of COVID-19 daily death cases from forecasted values (24.02.22 – 25.03.2022)

**Table 2**

MAPE of forecast from February 24, 2022, to March 25, 2022.

Duration of forecast (days)	New cases	Death cases
7 days	285,07 %	89,04 %
10 days	283,96 %	89,06 %
20 days	423,01 %	165,08 %
30 days	497,09 %	204,28 %

## 5. Conclusions

Russia's military intervention in Ukraine in February 2022 has resulted in a humanitarian crisis and has exacerbated the COVID-19 situation in the country. The war has made it difficult to identify, diagnose, and register COVID-19 cases, and hospitalization of severely ill patients is limited due to the overcrowding of hospitals with wounded military and civilians. The electronic system for recording COVID-19 incidence is also limited, leading to a significant decrease in reported cases compared to real ones. Anti-epidemic measures, such as social distancing and mask-wearing, are not observed due to the introduction of martial law and the need for people to hide from artillery and airstrikes in bomb shelters and basements.

The vaccination campaign against COVID-19 in Ukraine began on February 24, 2021, exactly one year before the Russian war in Ukraine escalated. Only 36.93% of the population had been vaccinated with two doses. However, vaccination has been completely stopped in temporarily occupied by Russia territories of Ukraine and territories where active hostilities are taking place. The chaos of war and accompanying psychological factors have also forced the problem of infectious diseases out of people's minds. The pandemic is no longer the top priority of Ukraine's healthcare system.

The Russian war in Ukraine is a critical factor in the new infectious disease outbreaks and exacerbates the country's humanitarian catastrophe caused by Russia's military intervention. The situation highlights the importance of ensuring access to medical facilities and supplies, maintaining and improving public health infrastructure, and ensuring that humanitarian crises are not ignored during the war.

The framework proposed in this study for assessing the impact of the Russian war in Ukraine on the dynamics of the epidemic process of infectious diseases makes it possible to identify changes like the spread of morbidity and introduce timely control measures.

The results obtained from the simulation have highlighted several problems that exist in healthcare systems. These results provide valuable lessons that can be used to improve the functioning of healthcare systems during extreme situations, including times of war. Mathematical modeling is essential for assessing the dynamics of the epidemic process and understanding the factors that influence the spread of the disease. Doing this makes it possible to make timely adjustments to the structure and scope of preventive and anti-epidemic measures that can help prevent the spread of the disease. When epidemiological surveillance and response systems are weakened and conditions worsen, mathematical modeling and adequate models can help minimize the consequences of any disruption in the public health system. They can also help adjust the activities of relevant services and reduce the burden on the healthcare system caused by a growing incidence, disease severity, and mortality.

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