Article

Epidemiological Implications of War: Machine Learning Estimations of the Russian Invasion's Effect on Italy's COVID-19 Dynamics

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Abstract: Background: The COVID-19 pandemic has profoundly transformed the global scenario, marked by overwhelming infections, fatalities, overburdened healthcare infrastructures, economic upheavals, and significant lifestyle modifications. Concurrently, the Russian full-scale invasion of Ukraine on 24 February 2022, triggered a severe humanitarian and public health crisis, leading to healthcare disruptions, medical resource shortages, and heightened emergency care needs. Italy emerged as a significant refuge for displaced Ukrainians during this period. Aim: This research aims to discern the impact of the Russian full-scale invasion of Ukraine on the COVID-19 transmission dynamics in Italy. Materials and Methods: The study employed advanced simulation methodologies, particularly those integrating machine learning, to model the pandemic's trajectory. The XGBoost algorithm was adopted to construct a predictive model for the COVID-19 epidemic trajectory in Italy. Results: The model demonstrated a commendable accuracy of 86.03% in forecasting new COVID-19 cases in Italy over 30 days and an impressive 96.29% accuracy in estimating fatalities. When applied to the initial 30 days following the escalation of the conflict (24 February 2022, to 25 March 2022), the model's projections suggested that the influx of Ukrainian refugees into Italy did not significantly alter the country's COVID-19 epidemic course. Discussion: While simulation methodologies have been pivotal in the pandemic response, their accuracy is intrinsically linked to data quality, assumptions, and modeling techniques. Enhancing these methodologies can further their applicability in future public health emergencies. The findings from the model underscore that external geopolitical events, such as the mass migration from Ukraine, did not play a determinative role in Italy's COVID-19 epidemic dynamics during the study period. Conclusion: The research provides empirical evidence negating a substantial influence of the Ukrainian refugee influx due to the Russian full-scale invasion on the COVID-19 epidemic trajectory in Italy. The robust performance of the developed model affirms its potential value in public health analyses.

Keywords: epidemic model; epidemic simulation; machine learning; XGBoost; simulation; war

1. Introduction

The COVID-19 pandemic, caused by the SARS-CoV-2 virus, has had a profound impact on the world's health, economy, and social fabric. Since the first cases were reported in Wuhan, China, in December 2019, the virus has rapidly spread across the globe, resulting in millions of infections and deaths [1]. The disease primarily spreads through respiratory

droplets, and symptoms can range from mild to severe, including fever, cough, and shortness of breath [2]. The pandemic has prompted widespread public health interventions, including lockdowns, travel restrictions, and the widespread use of personal protective equipment [3]. The development of effective vaccines has been a critical milestone in the fight against COVID-19, but the emergence of new variants of the virus and vaccine hesitancy pose ongoing challenges [4].

Countermeasures against the COVID-19 pandemic have been diverse and multifaceted, encompassing public health interventions, clinical management, and vaccination strategies. Non-pharmaceutical interventions, such as social distancing, wearing face masks, and hand hygiene practices, have been widely implemented to reduce the transmission of the virus [5]. Clinical management of COVID-19 patients has involved a range of approaches, including the use of antiviral drugs, corticosteroids, and oxygen therapy, depending on the severity of the illness [6]. The development and deployment of effective vaccines against SARS-CoV-2 have been a critical component of the response, with multiple vaccines being authorized for emergency use globally. Mass vaccination campaigns are ongoing, but challenges remain, including vaccine hesitancy, equitable distribution, and the emergence of new variants of the virus. Continued surveillance, testing, and genomic sequencing of the virus are essential for monitoring the efficacy of countermeasures and adapting to the evolving pandemic situation.

The development of the pandemic has stimulated research groups around the world to direct their efforts to develop data-driven approaches aimed at combating COVID-19. Such studies included the analysis of medical data [7], the search for the informativeness of medical factors [8], methods of automated diagnostics [9], complex models of the dynamics of the epidemic process [10], methods of medical computer vision [11], assessment of factors affecting the epidemic process [12], the formation of strategies to stop the epidemic spread of morbidity [13], etc.

Simulation is a valuable tool for decision-making in the context of the COVID-19 pandemic. Simulation models can provide insights into the potential impact of various interventions and policies, including non-pharmaceutical interventions and vaccination strategies, on the spread of the virus and the burden on healthcare systems. These models can take into account various factors, such as demographic characteristics, healthcare capacity, and the characteristics of the virus itself [14]. By using simulations, decision-makers can explore different scenarios and assess the potential outcomes of their decisions before implementation [15]. However, it is crucial to acknowledge the limitations of simulation models, such as the assumptions made and the uncertainties involved, and to use multiple models and sensitivity analyses to evaluate the robustness of the results. Overall, simulation can be a powerful tool for informing evidence-based decision-making in the context of the COVID-19 pandemic.

On 24 February 2022, Russia began the escalation of the war in Ukraine. The full-scale invasion caused thousands of victims and started a humanitarian crisis in Ukraine [16]. Hundreds of medical institutions and other infrastructure facilities were destroyed [17]. In addition, Russia's full-scale invasion of Ukraine has caused mass migration of the population. These and other factors have a negative impact on the spread of COVID-19 both in Ukraine and in countries that have received a large number of refugees.

During the year of a full-scale war, more than 8 million refugees were registered in Europe, and more than 5 million became internally displaced persons [18]. As of April 2023, Italy received 173 thousand people from Ukraine, and became the fourth country in the world in terms of the number of Ukrainian refugees. In addition, Italy ranks eighth in the world in terms of the number of cases of COVID-19. The highest dynamics of the spread of the new coronavirus in the world after China characterized the beginning of the pandemic in Italy. This has attracted many research groups to study the COVID-19 pandemic in Italy. Therefore, the situation with COVID-19 in Italy was chosen as a pilot study of the impact of a full-scale Russian invasion of Ukraine on the dynamics of infectious diseases.

Thus, the aim of this study is to assess the impact of Russia's full-scale war in Ukraine on the dynamics of the COVID-19 epidemic process in Italy using machine learning tools.

To achieve the goal, the following tasks were set:

1. To analyze the methods and patterns of COVID-19 in Italy.
2. To analyze COVID-19 incidence data in Italy.
3. To develop a methodology for assessing the impact of Russia's full-scale war in Ukraine on the dynamics of the epidemic process.
4. To develop a model of the COVID-19 epidemic process based on the XGBoost method.
5. To adjust the developed model on the data on morbidity and mortality from COVID-19 in Italy from 25 January 2022 to 23 February 2023 (30 days before the start of the escalation of the Russian war in Ukraine).
6. To calculate the forecast dynamics of the COVID-19 epidemic process in Italy from 24 February 2022 to 25 March 2022 (30 days after the start of the escalation of the Russian war in Ukraine).
7. To analyze the results of the experimental study.

The respective contribution of the study is three-fold. Firstly, the application of a model based on the XGBoost method will allow us to evaluate the effectiveness of using ensemble machine learning methods for simulating the COVID-19 epidemic process. Secondly, the use of real data on the dynamics of COVID-19 in Italy will allow us to investigate the nature of the epidemic process of COVID-19 in Italy. Thirdly, the methodology proposed in the paper will allow us to assess the impact of Russia's full-scale war in Ukraine on the dynamics of the COVID-19 epidemic process in Italy.

The structure of the paper is the following: Section 2, Current Research Analysis, provides an overview of models and methods of epidemic process simulation in Italy and provides a brief description of the COVID-19 pandemic in Italy and the factors influencing the infectious diseases epidemic process by the Russian full-scale invasion of Ukraine. Section 3, Materials and Methods, describes the methodology of the study, the XGBoost model of COVID-19 epidemic process, and the model's evaluation metrics. Section 4, Results, describes the results of the model's performance, and estimation of the developed model's adequacy and forecasting accuracy. Section 5, Discussion, discusses the impact of the Russian full-scale invasion of Ukraine on the COVID-19 epidemic process in Italy. The conclusion describes the outcomes of the research.

2. Current Research Analysis

2.1. Simulation of COVID-19 Spreading in Italy

Simulation of the epidemic process is an approach that has been used extensively to study the dynamics of infectious diseases, including the COVID-19 pandemic. The development of mathematical models to simulate the spread of infectious diseases dates back to the early 20th century, with the first models developed for the study of the transmission of malaria. Over time, these models have become more sophisticated, incorporating more complex epidemiological dynamics and demographic factors. With the emergence of the COVID-19 pandemic, simulation models have played a critical role in understanding the potential impact of various interventions and policies on the spread of the virus and the burden on healthcare systems. These models have been used to evaluate the effectiveness of non-pharmaceutical interventions, such as social distancing and the use of face masks, and to inform the development of vaccination strategies. The ongoing development of simulation models for COVID-19 is essential for guiding evidence-based decision-making and informing public health policy in the face of an evolving pandemic.

In the study [19], the authors introduce a novel model, SIDARTHE, to predict the trajectory of the COVID-19 epidemic in Italy, thus facilitating the formulation of efficacious containment strategies. This model consists of eight infection phases, distinguishing between identified and unidentified cases, as well as varying symptom severities. SIDARTHE elucidates misconceptions regarding case fatality rates and the spread of the epidemic by matching simulated outcomes with empirical data from Italy's COVID-19 situation. The

study posits that a synergy of social distancing, testing, and contact tracing is imperative to control the ongoing pandemic. Moreover, the model can simulate the epidemic's progression, assess potential misjudgments of its scope based on prevailing statistics, and forecast the repercussions of implementing disparate guidelines and protocols. However, the predictions are contingent upon parameter values, which are uncertain and susceptible to fluctuations owing to multiple factors.

The paper [20] examines the efficacy of community quarantine measures in halting the spread of COVID-19 within Italian towns under lockdown. The authors ascertain that strict adherence to stay-home policies and reduced household sizes is crucial to controlling the epidemic in enclosed areas. They deduce that absent rigorous community quarantine protocols encompassing a near-total cessation of communal activities, viral transmission will persist. Furthermore, smaller household or quarantine groups correlate with decreased secondary infections. These insights are pivotal for policymakers formulating lockdown strategies to preclude further incursions and dissemination of the virus within confined regions.

In the paper [21], an SEIR model was employed to project the number of infections and fatalities due to the COVID-19 epidemic in Northern Italy, mainly focusing on the Lombardy region. By modifying parameters and initial conditions and calibrating the model with actual data, the authors estimate approximately 15,600 fatalities and 2.7 million infections by the epidemic's conclusion. They highlight the contingent nature of the fatality rate and other parameters on the precision of available data. The study underscores the vital role of isolation, social distancing, and comprehension of diffusion conditions in grasping the epidemic's dynamics and assessing lockdown efficacy.

The study [22] evaluates the initial stage of the SARS-CoV-2 outbreak in Italy, determining the basic reproduction number (R_0) of the virus. The research focuses on nine cities with the highest infection rates, applying the SIR model to data from 25 February to 12 March 2020. Results indicate R_0 values for the Italian outbreak ranging between 2.43 and 3.10, aligning with prior research. The study emphasizes the SIR model's efficacy in elucidating virus transmission and ascertaining pivotal epidemiological parameters such as R_0.

In paper [23], the ramifications of Italy's lockdown on COVID-19's proliferation and the potential case and recovery numbers with a 60-day lockdown extension are evaluated. Utilizing case data from mid-February to March's end, the study employed a seasonal ARIMA forecasting model, achieving 93.75% and 84.4% accuracy for predicted cases and recoveries, respectively. The findings indicate that an extended lockdown could diminish registered cases by 35% and bolster recoveries by 66% by May's conclusion. The study underscores the crucial role of lockdown and self-isolation in mitigating disease transmission.

Paper [24] introduces a mathematical model assessing lockdown measures' efficacy in curbing COVID-19 transmission, considering potential contagion from deceased individuals and social distancing impacts. Findings reveal comprehensive lockdowns and social distancing can decrease fatalities, carriers, and infections. The study emphasizes the importance of prompt testing and results to enhance disease control. Developed using Italian data, the authors recommend integrating differential and integral operators to incorporate non-locality into the mathematical formulations.

Paper [25] investigates the regional disparities in Italy's COVID-19 epidemic, introducing a regional-level modeling approach. The study employs early outbreak data to parameterize the model for each region, validating the national lockdown's regional efficacy. Furthermore, the authors recommend synchronized regional strategies to avert future national lockdowns while minimizing costs and precluding regional healthcare system overload. They assert the adaptability of their methodology to various granular levels to aid policymakers and decision-makers.

Paper [26] introduces a novel statistical modeling methodology to explore the relationship between COVID-19's regional spread in Italy and various regional factors, diverging from the predominant focus on epidemic forecasting and spread pattern analysis. This approach utilizes a patterned Poisson regression model for longitudinal counts to delineate

regional spread patterns of daily confirmed COVID-19 cases. Subsequently, it correlates these regional regression parameters with regional factors to accurately assess their influence on spread patterns. The study demonstrates that this methodology adeptly identifies diverse growth and decline patterns and regional turning points and evaluates the impact of regional factors on the spread of daily confirmed COVID-19 cases.

Paper [27] presents a novel methodology for approximating the magnitude of Italy's early-stage COVID-19 outbreak, employing the cumulative and weighted average daily growth rate (WR) to analyze an epidemic curve. The study utilizes an exponential decay model (EDM) to calculate the WR across four-time intervals from 27 February to 7 April 2020, comparing its efficacy to the Gompertz model. Results indicate that the EDM, when applied to WR, surpasses the Gompertz model in short-term epidemic prediction. Additionally, the study offers credible interval-inclusive estimates of cumulative infection cases in Italy based on data up to March 31. The authors conclude that an EDM applied to WR is a valuable tool for estimating COVID-19 case numbers and outbreak peaks in Italy.

Paper [28] evaluates diverse time-series forecasting methodologies to project COVID-19's spread during Italy's second wave, concentrating on hospitalization rates for mild cases and intensive care unit patients. The study discerns that hybrid models, amalgamating multiple forecasting methods, outperform singular models in encapsulating the pandemic's linear, nonlinear, and seasonal tendencies. The hybrid models forecast a substantial surge in COVID-19 hospitalizations from October to mid-November 2020, predicting a bed requirement doubling in 10 days and tripling in approximately 20 days. These projections align with observed trends, underscoring hybrid models' utility in informing public health authority decisions, particularly in the short term.

Paper [29] introduces an epidemic multi-group model composed of SEIR-like structures to investigate the dynamics of COVID-19 and assess the efficacy of non-pharmaceutical interventions in Italy. The model, tailored to evaluate inter-regional mobility's impact, is applied to epidemiological data from three Italian macro-areas between March and October 2020, encompassing the summer holiday exodus. The simulation results, aligning well with the data, reveal that while unrestricted mobility alone did not instigate the second wave, it, in conjunction with the resumption of production, trade, and educational activities, homogenized the infection's spatial distribution nationwide, fueling contagion from September 2020 onwards. The model proves beneficial for forecasting containment measures' effects on potential future pandemics.

Paper [30] investigates the risk factors influencing COVID-19 patient Length of Stay (LoS) in Bologna, Italy, analyzing data from February 2020 to May 2021 and employing various statistical models such as Poisson, negative binomial, and Hurdle. Findings show significant LoS predictors include the Intensive Care Unit (ICU) setting and long-term hospitals, while age group, epidemic wave, and hospital type variably impact average LoS. Additionally, quantile regression is utilized to explore conditional heterogeneity and account for unobserved individual characteristics. The study offers valuable insights into factors contributing to prolonged LoS for COVID-19 patients and is a benchmark for future model-based analyses.

Paper [31] introduces an augmented version of the SUIHTER epidemiological model to analyze COVID-19 progression in Italy, considering vaccination efforts and emerging viral variants. The model incorporates clinical evidence-based characteristics of the variants and vaccines, including transmission rates and preventative efficacy against hospitalization and death. Validation is performed by juxtaposing the model's projections with other models' projections and evaluating various scenarios.

Paper [32] presents a deterministic compartmental model to analyze COVID-19's spread in Italy, factoring in vaccination efforts, new variant emergence, and mobility restrictions. The model considers waning immunity and examines the influence of behavioral changes, population mobility, seasonal virus infectivity variability, and new variants on the epidemiological curve. The study identifies seasonal virus stability variation as the most significant mechanism, with awareness following closely. The Delta variant and mobility

shifts have negligible impacts. The paper anticipates the emergence and dominance of the more contagious Omicron variant by January 2022, highlighting the potentially catastrophic scenario without vaccines, marked by a significant increase in total infections and deaths.

Paper [33] introduces a fractional order SEIQRD compartmental model utilizing the Caputo approach to explore COVID-19 transmission dynamics in Italy, establishing findings on existence, uniqueness, non-negativity, and solution boundedness. The Routh-Hurwitz criteria and La-Salle invariant principle analyze equilibrium dynamics, while fractional-order Taylor's approach approximates the model's solution. The study also evaluates the effectiveness of consistent mask-wearing in mitigating COVID-19 spread, validating the model through real-world data comparison.

The overview of the COVID-19 models in Italy is presented in Table A1.

Despite that most models applied to Italian data are based on compartmental models, the machine learning approach shows higher accuracy [34]. Machine learning approaches have shown great promise in the simulation and prediction of epidemic processes due to their ability to automatically learn and adapt to complex and dynamic systems. Unlike traditional mathematical models, which rely on pre-defined assumptions and parameters, machine learning models can learn from large and heterogeneous datasets, including demographic, social, and environmental factors, and incorporate non-linear and high-order interactions among different variables. Moreover, machine learning models can handle missing or noisy data and make real-time predictions, making them particularly useful in the context of fast-spreading and evolving epidemics such as COVID-19. The use of machine learning approaches can provide valuable insights into epidemic dynamics, identify risk factors and intervention strategies, and ultimately support decision-making for public health policies and resource allocation.

2.2. Background on COVID-19 in Italy

Italy was one of the first countries outside Asia to be severely affected by the COVID-19 pandemic. The first cases of COVID-19 in Italy were officially registered at the end of February 2020 in the Lombardy region [35]. Since this initial discovery, there has been a rapid spike in cases, and the virus has spread throughout Lombardy and neighboring regions. By early March 2020, Italy had the highest number of confirmed COVID-19 cases outside of China, making it the global epicenter of the virus. Several factors contributed to this rapid escalation. Italy's population is among the oldest in the world, making it especially vulnerable to the virus, disproportionately affecting the elderly. In addition, the spread of the virus was facilitated by high population density in cities and high mobility within and between regions [36].

At the same time, Italy's early status as an epicenter was also affected by the country's proactive approach to testing [37]. Unlike other countries that initially tested only those with symptoms, Italy has conducted extensive testing, including asymptomatic contacts with confirmed cases. While this approach helped increase the number of reported cases, it also gave a more accurate picture of the spread of the virus.

At the same time, the death rate from COVID-19 in Italy was notably high. Early in the pandemic, Italy reported a higher case fatality rate than most other countries [38]. Factors such as a higher prevalence of comorbidities in the elderly, including cardiovascular disease, diabetes, and respiratory disease, exacerbated the risk of severe illness and mortality [39]. In addition, the sudden and rapid surge in cases early in the pandemic overwhelmed the healthcare system, especially in the hardest-hit northern regions [40]. This significantly affected the ability to provide adequate care to all critically ill patients, contributing to the higher mortality rate.

The dramatic increase in cases has required a corresponding increase in healthcare capacity. In some regions, hospitals operated at or near full capacity, with additional makeshift facilities to accommodate the influx of patients. Despite these efforts, resources have been depleted, and numerous reports of overcrowded hospitals and malnourished medical workers have been reported. In response to these challenges, the Italian healthcare

system has taken numerous measures to increase capacity, provide essential equipment and protect healthcare workers. However, the strain on the system had significant implications for patient care and outcomes, especially during the peak periods of the pandemic.

In response to the exponential rise in COVID-19 cases and the resulting strain on the healthcare system, the Italian government has implemented one of Europe's earliest and most stringent national lockdowns [41]. The sequence of interventions clearly illustrated the scale and speed with which the government had to respond to the escalation of the crisis.

The effectiveness of the lockdown in reducing the spread of the virus and reducing the burden on the healthcare system is a complex issue. Early research suggests that lockdown helped reduce transmission and lower infection rates. However, more comprehensive assessments are needed to fully understand the implications, including indirect effects on mental health, social structures, and economic conditions. The acceptability and sustainability of these interventions also raise important questions for current and future pandemic strategies.

The vaccination campaign in Italy, as in other countries, was an important component of the strategy to control the spread of COVID-19 and mitigate its impact [42]. Italy launched the vaccination campaign on 27 December 2020 as part of a coordinated effort by the European Union. Initial doses of the vaccine were provided by Pfizer-BioNTech (mRNA, BNT162b2), and other vaccines, such as those from Moderna (mRNA-1273) and AstraZeneca (recombinant vaccine ChAdOx1-S), have subsequently been added to the portfolio. The first vaccines were given to healthcare workers and nursing home residents, given their high risk of infection and severe illness. The vaccination campaign prioritized certain groups based on risk. After healthcare workers and residents of nursing homes, priority was given to the elderly and people with certain high-risk diseases. As vaccine supplies increased, the vaccination program expanded to reach younger age groups and a wider population.

At the beginning of May 2022, 25.8 million cases were registered in Italy, of which 190.2 thousand were fatal [43]. Moreover, 80.46% of the population was vaccinated, 79.6% received a full vaccination, and 78.02% received a booster course [44].

2.3. Impact of Russian War on Infectious Diseases Spreading

Russia's war in Ukraine, launched on 24 February 2022, has had a profound impact, resulting in significant loss of life and exacerbating a grave humanitarian crisis. According to estimates, as of 2 May 2023, civilian casualties in Ukraine currently stands at 23,375 people: 8709 killed and 14,666 injured [45]. The actual figures are considerably higher, as the receipt of information from some locations where intense hostilities have been going on has been delayed, and many reports are still pending corroboration. These concern, for example, Mariupol (Donetsk region), Lysychansk, Popasna, and Sievierodonetsk (Luhansk region), where there are allegations of numerous civilian casualties. However, the consequences go beyond the direct destruction and suffering caused by the conflict. Notably, Russia's military intervention came amid a wave of the COVID-19 pandemic caused by the Omicron strain, further exacerbating the situation.

To understand the impact of the war on the situation with COVID-19 in Ukraine, it is crucial to take into account various factors [46]. The analysis of six key aspects influencing the spread of infection provides valuable information.

First, detecting cases of COVID-19 is very difficult in occupied territories and areas affected by hostilities. The collapse of medical facilities and the shortage of medical staff prevent people from seeking the necessary medical care, forcing them to rely on online consultations with family doctors.

Secondly, diagnostic problems arise in connection with combat operations. In the areas temporarily occupied by Russian troops, medical institutions practically do not function, and there are no laboratory facilities for diagnostic purposes. Therefore, PCR and rapid tests are not available. In the eastern and southern regions of Ukraine, controlled by Ukraine but still affected by the conflict, only a small proportion (2.5–3%) of diagnostic laboratories operate, mainly diagnosing severe cases requiring hospitalization.

Thirdly, the registration of COVID-19 cases is severely limited throughout Ukraine. The electronic case registration system is limited, and data transmission mainly depends on telephone service in areas where connectivity is available. As a result, the number of reported cases of COVID-19 is significantly lower than the actual numbers. The lack of data for Ukraine on the Johns Hopkins University dashboard further highlights the problem of underreporting. Consequently, only severe cases requiring hospitalization are recorded [47].

Fourth, treating patients with COVID-19 is facing significant difficulties due to the overwhelming number of wounded military personnel and civilians in hospitals. Repurposing medical facilities to provide emergency care to the wounded significantly reduces the availability of dedicated COVID-19 beds and limits access to vital resources such as oxygen. Intense fighting and occupation make getting medical supplies to the affected areas even more difficult. In addition, the growing number of deaths makes post-mortem diagnosis of COVID-19 impossible, as autopsies are not performed. Providing medical assistance to internally displaced persons is also tricky, as family doctors assigned to them remain in other regions of Ukraine. Access to medical care without an established declaration is possible only through ambulances in severe cases requiring hospitalization.

Fifth, anti-epidemic activities are facing significant obstacles due to the war. People living in the territories temporarily not controlled by Ukraine and in areas affected by hostilities are forced to take shelter in bomb shelters, basements, and subways to protect themselves from artillery shelling and air strikes. These shelters typically have a high population density and lack social distancing measures, mask-wearing rules, and adequate ventilation, which increases the risk of virus transmission. In addition, the imposition of martial law prevents compliance with the rules for wearing masks. The nature of military conditions makes contact tracing, testing, and isolation measure impractical, making it difficult to identify epidemic chains. Self-isolation becomes challenging in combat, allowing symptomatic people to continue spreading the virus. The evacuation process also contributes to the increased circulation of the virus due to the high population density in trains and stations, with many evacuees being children, primarily unvaccinated.

Sixth, the war in Ukraine has seriously undermined preventive measures, particularly the COVID-19 vaccination campaign. Prior to the outbreak of the conflict, Ukraine launched a vaccination campaign on 24 February 2021, exactly one year before the start of the war [48]. However, vaccination coverage remained relatively low, with only 36.93% of the population receiving two doses. Russia's active anti-vaccination information campaign partly explains this low coverage.

Thus, the Russian war in Ukraine has far-reaching consequences, including significant loss of life and a severe humanitarian crisis. In addition to the immediate destruction and suffering caused by the conflict, the war has exacerbated the COVID-19 situation in Ukraine. Problems in detecting, diagnosing, reporting, and treating cases of COVID-19 have arisen due to the destruction of medical infrastructure and lack of resources. The need for shelter hampered the adoption of anti-epidemic measures during hostilities and the impossibility of contact tracing and isolation. The disruption of the vaccination campaign, fueled by anti-vaccination propaganda and logistical difficulties, further exacerbated the situation. The chaotic nature of the war and shifting priorities have pushed COVID-19 out of the spotlight, leading to the virus's rapid spread. Overall, Russia's war in Ukraine has contributed significantly to exacerbating the country's COVID-19 crisis and the existing humanitarian catastrophe.

According to the United Nations, more than 8.2 million refugees are registered in Europe as of May 2023 [49], and 5.9 million are internally displaced persons at the end of 2022 [50]. The massive population migration carries with it the risk of changing the nature of the epidemic process in the territories that have received many refugees [51]. Therefore, this study tests the hypothesis about the impact of migration from Ukraine on the dynamics of the COVID-19 epidemic process in Italy.

3. Materials and Methods

3.1. Methodology

Figure 1 presents a framework for assessing the impact of the Russian war in Ukraine on the dynamics of the epidemic process of infectious diseases.
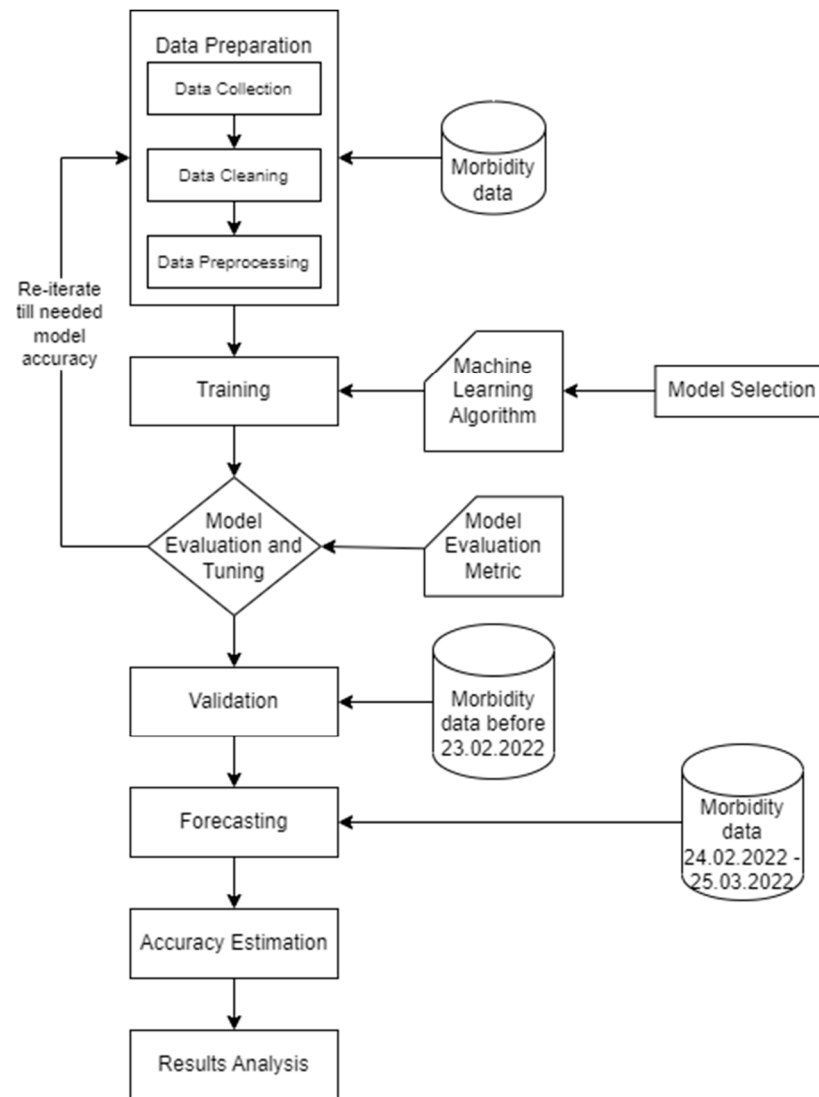

Figure 1. The framework for assessing the impact of the Russian war in Ukraine on the dynamics of the epidemic process of infectious diseases.

This study proposes a methodology to assess the impact of the Russian war in Ukraine on the dynamics of infectious diseases consisting of the following steps:

1. To develop a machine learning model for the dynamics of the epidemic process in the selected area.
2. To verify the constructed model on the data of morbidity and mortality from infectious diseases from 25 January 2022 to 23 February 2022, i.e., 30 days before the start of a full-scale Russian invasion of Ukraine.
3. To calculate the predicted incidence and mortality from an infectious disease in the study area from 24 February 2022 to 25 March 2022, i.e., 30 days after the start of a full-scale Russian invasion of Ukraine.
4. To calculate the deviation of actual morbidity and mortality from infectious disease from the estimated forecast in the study area.

5. To assess the factors that affect the epidemic process, depending on the specifics of the infectious disease and the study area.
6. To analyze the results, identify risks for the public health system, and determine the necessary measures to control the epidemic spread of an infectious disease.

Most studies of the dynamics of COVID-19 use morbidity and mortality data provided by the John Hopkins Coronavirus Resource Center [47]. However, this dashboard does not provide data on COVID-19 in Ukraine starting from 24 February 2022. In addition, the data presented in the dashboard for periods earlier do not correspond to the official statistics on the incidence of COVID-19 in Ukraine. Therefore, this study is based on data from the World Health Organization COVID-19 Dashboard [48].

3.2. XGBoost Model

Machine learning has become a valuable tool in recent years for predicting the spread of infectious diseases. An essential application is to build sophisticated predictive models that can analyze vast amounts of data from various sources, including medical records, social media feeds, and global transportation patterns, to predict future cases. Machine learning-based predictive models use algorithms trained on historical data to identify patterns and correlations that may indicate an impending outbreak.

Machine learning has shown significant promise in the early detection of epidemics. In traditional epidemiological models, outbreaks are usually detected after a significant number of reported cases. However, machine learning models can detect subtle changes in population behavior and public health patterns to detect an outbreak much earlier. Such early warning systems can help public health officials take preventive action before an epidemic spreads widely, saving lives and resources. Similarly, machine learning algorithms can also predict the spread of a disease by analyzing factors that influence its transmission, such as population density, climatic conditions, and vaccination rates, and predicting how changes in these factors might affect the spread of the disease in the future.

Ensemble machine learning methods are designed to improve the accuracy and stability of predictions by combining the output of multiple models. They can be especially effective in forecasting problems where the forecasting problem is complex, and no single model can efficiently account for all relevant factors.

There are three main types of ensemble methods: bagging, boosting, and stacking.

In bagging, multiple models are trained independently on different subsets of the training data, and their predictions are averaged (in regression) or accepted as a majority vote (in classification). This method is designed to reduce the forecast variance without increasing the bias. Random Forest is a classic example of an ensemble model based on bags.

Boosting builds a sequence of models, where each model tries to correct the errors of the previous ones. It aims to reduce systematic error as well as the variance in order to increase the prediction accuracy. Unlike bagging, models in boosting are not independent; each model learns from its predecessor and updates misclassified instances to improve the next model. Gradient Boosting and AdaBoost are typical examples of boosting methods.

Stacking involves training several different models and then combining them by training a meta-model to make a final prediction based on the predictions of the individual models. Individual model predictions are treated as "meta-features", and the meta-model is trained to use these features for the final prediction best.

Ensemble methods are widely used in disease prediction due to their reliability and excellent predictive performance. They can handle complex relationships and interactions between variables, which is especially useful in epidemiology, where many factors can influence the spread of disease [52]. It is important to note that ensemble models can also provide some uncertainty in their predictions, which can be critical in decision-making processes during an outbreak.

XGBoost, short for eXtreme Gradient Boosting, is an extended implementation of the gradient boosting algorithm [53]. In the context of forecasting the dynamics of COVID-19, XGBoost is used to predict future case numbers, death rates, and more.

The first step in using XGBoost for prediction is feature selection. Relevant features could include information about the pandemic's current state, such as infection rates and deaths, as well as other potentially important variables, such as population density, vaccination rates, mobility data, and social distancing measures. Then historical data about these features are collected and prepared for input into the model.

During the training phase, XGBoost creates a set of decision trees that predict the outcome (for example, the future number of cases). Initially, all instances are assigned the same weight. However, in each subsequent iteration, XGBoost adds a new tree to correct the errors made by the current ensemble of trees. This is achieved by defining a differentiable loss function and using gradient descent to minimize the loss. At each step, the algorithm calculates the gradient of the loss function concerning the current model's prediction and uses it to update the model.

XGBoost includes several regularization methods to help avoid overfitting. This is especially important in forecasting, where overfitting can cause predictions to be overly influenced by noise in the training data, reducing their accuracy on unseen data. XGBoost uses L1 (lasso regression) and L2 (ridge regression) regularization to prevent overfitting.

Once trained, the XGBoost model can predict future COVID-19 dynamics by inputting relevant feature data and generating a forecast. This can be done periodically, with the model continually retraining on the most recent data to keep the predictions accurate.

Uncertainty in forecasts can be estimated using bootstrapping, a technique that involves creating multiple resamples of the data, training a separate model for each one, and then using the variation in the forecasts to estimate the uncertainty. Bootstrap is built directly into the XGBoost platform, providing a powerful predictive tool for quantifying uncertainty. It is often used for classification and regression problems and has gained popularity due to its efficiency and performance.

In Gradient Boosting, we construct an additive model in a form of a sum of simple base models. Mathematically, if we denote our prediction model at step i by $F_i(x)$, and our base model by $h(x)$, the model at step i + 1 is given by

$$F_{i+1}(x) = F_i(x) + h_i(x). \tag{1}$$

The function $h_i(x)$ is chosen to minimize the loss function $L(y, F_i(x) + h_i(x))$, where y is the true label.

In the case of XGBoost, the specific form of the base model $h_i(x)$ and the loss function $L(y, F)$ depend on the task and the specific settings of the XGBoost method.

The power of XGBoost comes from the fact that it introduces an additional layer of complexity to the boosting procedure by considering a regularized learning objective. The objective function to be minimized in XGBoost at each step includes both a differentiable loss function L and a regularization term Ω. It is given by:

$$\sum(L(y_i, F(x_i))) + \Omega(F). \tag{2}$$

where

$$\Omega(F) = \gamma T + \frac{1}{2}\lambda \|w\|^2, \tag{3}$$

T is the number of leaves in the tree, w are the leaf weights, y is the parameter that controls the complexity of the model, λ is the L2 regularization on the leaf scores.

The addition of the regularization term helps to control the complexity of the model, reducing overfitting and making XGBoost more robust to noise in the data.

Advantages of the XGBoost method:

- XGBoost can handle numeric and categorical variables and be used for binary, multiclass classification problems, and regression problems. This allows for a wide range of data types and problems that can arise in infectious disease prediction.

- XGBoost includes regularization options to prevent overfitting, making the data more robust to noise and outliers. This is especially important in epidemiology, where data are often noisy or incomplete.
- XGBoost consistently demonstrates superior predictive performance across a wide range of tasks. In infectious disease forecasting, this can lead to more accurate and timely forecasts to aid in decision-making processes.
- XGBoost has a built-in procedure for handling missing values. This ability can be critical when dealing with public health data that often contain missing or incomplete records.
- XGBoost implements parallel processing, which makes it significantly faster than other gradient boosting algorithms. This can be critical in a pandemic situation where timely forecasts are needed.

Disadvantages of the XGBoost method:

- Like other ensemble methods, XGBoost models can be difficult to interpret. This lack of interpretability can be a barrier to understanding the underlying dynamics of the disease and communicating the results to stakeholders.
- XGBoost requires careful parameter tuning for optimal performance. Customization needs can take a long time and a certain level of expertise.
- Despite built-in regularization, XGBoost can still overfit if the data are too noisy or the hyperparameters are set incorrectly.
- Although XGBoost is faster than many other gradient boosting algorithms, it is still computationally intensive, especially when working with large datasets. This can be a problem in resource-constrained settings or where real-time forecasts are required.

However, despite these shortcomings, XGBoost is well suited to the task of this study.

3.3. Evaluation Metrics

To assess the adequacy of the constructed model, it is proposed to use Mean Absolute Percentage Error (MAPE). MAPE is a common metric used to evaluate the accuracy of forecasting models. It measures the average magnitude of errors in a set of predictions, without considering their direction. It does this by averaging the absolute percentage difference between the actual and the predicted values. The formula for MAPE is:

$$MAPE = \frac{100\%}{n} \sum_{t=1}^{n} \left| \frac{A_t - F_t}{A_t} \right|, \tag{4}$$

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

One of the main advantages of MAPE is that it is easy to interpret, as it gives the error rate as a percentage. However, it can lead to issues when the actual values are close to zero, as the error can approach infinity in those cases. Moreover, it tends to put a heavier penalty on forecasts that exceed the actual values compared to those that are below the actual values.

To assess the impact of the Russian war in Ukraine on the dynamics of the COVID-19 epidemic process in Italy, it is proposed to calculate the deviation of the forecast calculated for 24 February 2022 to 25 March 2022 from the actual incidence:

$$D = |F_t - A_t|, \tag{5}$$

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

4. Results

4.1. Model Tuning

The model based on the XGBoost method was implemented using Python. Forecasts for new cases and deaths from COVID-19 in Italy were calculated to tune the model. The forecast was built for 3, 7, 10, 20, and 30 days. To verify the model, we used data on

morbidity and mortality from COVID-19 in Italy from 25 January 2022 to 23 February 2022, i.e., for the period 30 days before Russia's full-scale invasion of Ukraine.

During data cleaning for time-series data concerning daily incidence and fatality rates of COVID-19, one of the primary concerns revolves around handling missing values. Missing data can arise due to delays in reporting or errors during data entry. One strategy is to propagate the last valid observation forward to the next valid data point or utilize the subsequent valid observation to bridge the gap, a technique known as forward-fill or backward-fill. Another sophisticated method is interpolation, especially pertinent to time-series data where trends are discernible. Alternatively, one might consider omitting records with missing values altogether, though this decision should be approached with caution to ensure significant data are not lost. However, data on COVID-19 incidence and mortality in Italy obtained from the WHO dashboard did not contain missing data. However, such a step may be necessary for other epidemic processes and study areas.

After cleaning, preprocessing time-series data is imperative for refining the dataset and making it suitable for modeling. Initially, data normalization or standardization plays a crucial role. This ensures that the model does not unduly prioritize variables with inherently larger magnitudes. However, in our case, the XGBoost method includes regularization and makes the data robust to noise and outliers. On the other hand, smoothing is a critical step, especially for time-series data like the daily incidence and fatality rates of COVID-19, which might exhibit volatility when using other machine learning techniques.

Forecasting over varying time horizons, such as 3, 7, 10, 20, and 30 days, plays a vital role in evaluating a predictive model for several interconnected reasons.

One of the most significant reasons is understanding short-term versus long-term trends. In the context of epidemiological data, there can be a clear distinction between these two. Daily case counts may show considerable volatility due to reporting anomalies, testing rate changes, or transient events. In contrast, the overall trajectory of the epidemic often follows more stable, longer-term trends. By using different time horizons, we can capture both these short-term fluctuations and long-term patterns.

Evaluating the model's predictions over different periods allows us to assess its stability and resilience to temporal variability. A model that can deliver consistent predictive accuracy over different time frames demonstrates its ability to adapt to changes in the data pattern over time. This is a key aspect of model robustness.

The effect of external interventions also plays a role in why we need different time horizons. Changes in government policies or other interventions to control the disease's spread may have different impacts over short and long periods. For instance, the effects of a lockdown might not be immediately apparent in the three-day forecast but may significantly influence the 30-day trend. Therefore, different time horizons can help us understand and account for the potential effects of such interventions.

Using multiple time horizons, we also estimate the time shifts between the date migrants came to the country and the infection was registered.

We incorporated a rigorous verification process to ascertain the model's robustness and prevent overfitting. Rather than merely training the model on the most recent data and risking the capture of transient noise, we leveraged data on morbidity and mortality rates of COVID-19 in Italy from 25 January 2022 to 23 February 2022. This 30-day period, which precedes the onset of Russia's full-scale military invasion of Ukraine, provided us with a stable and relevant historical dataset.

By training our model on this specific dataset and testing its forecasting capabilities on subsequent data, we ensured that our model was generalizing patterns from the historical data rather than memorizing them. This methodological diligence gives us confidence in the model's predictions, as it demonstrates resilience against overfitting and positions it to provide reliable forecasts in diverse scenarios.

In our study, hyperparameter optimization was conducted through a structured methodology, amalgamating both grid search and cross-validation techniques. The grid search protocol comprehensively explores a predefined hyperparameter domain, examin-

ing each potential combination therein. To enhance the model's generalization capabilities and circumvent potential overfitting during tuning, we incorporated k-fold cross-validation. The training dataset is systematically segmented into 'k' uniform partitions in this procedure. Subsequent training transpires on k-1 partitions, while the singular remaining partition is the validation set. This iterative process continues until every individual fold functions as the validation subset. The resultant performance metrics across all iterations are aggregated to furnish a holistic and resilient assessment of the model's efficacy.

Table 1 presents model accuracy rates for cumulative new and fatal cases of COVID-19 in Italy from 25 January 2022 to 23 February 2022.

Table 1. MAPE of cumulative cases retrospective forecast for 25 January 2022–23 February 2022.

Duration of Forecast (Days)	New Cases	Fatal Cases
3 days	2.69%	0.56%
7 days	5.49%	1.09%
10 days	7.05%	1.45%
20 days	11.18%	2.67%
30 days	13.97%	3.71%

Figure 2 presents the results of a retrospective forecast of daily new cases of COVID-19 in Italy from 25 January to 23 February 2022.
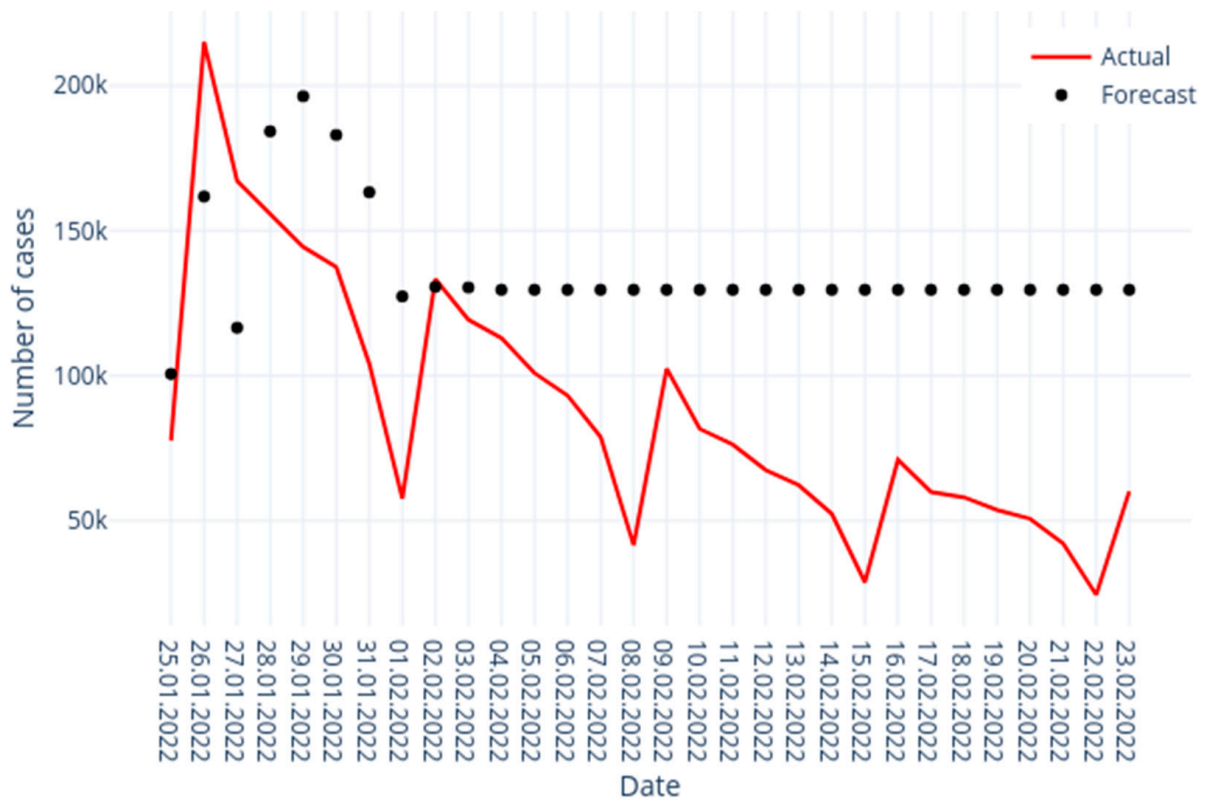

Figure 2. Retrospective forecast of confirmed COVID-19 cases in Italy (25 January 2022–23 February 2022).

Figure 3 presents the results of a retrospective forecast of daily fatal cases of COVID-19 in Italy from 25 January to 23 February 2022.
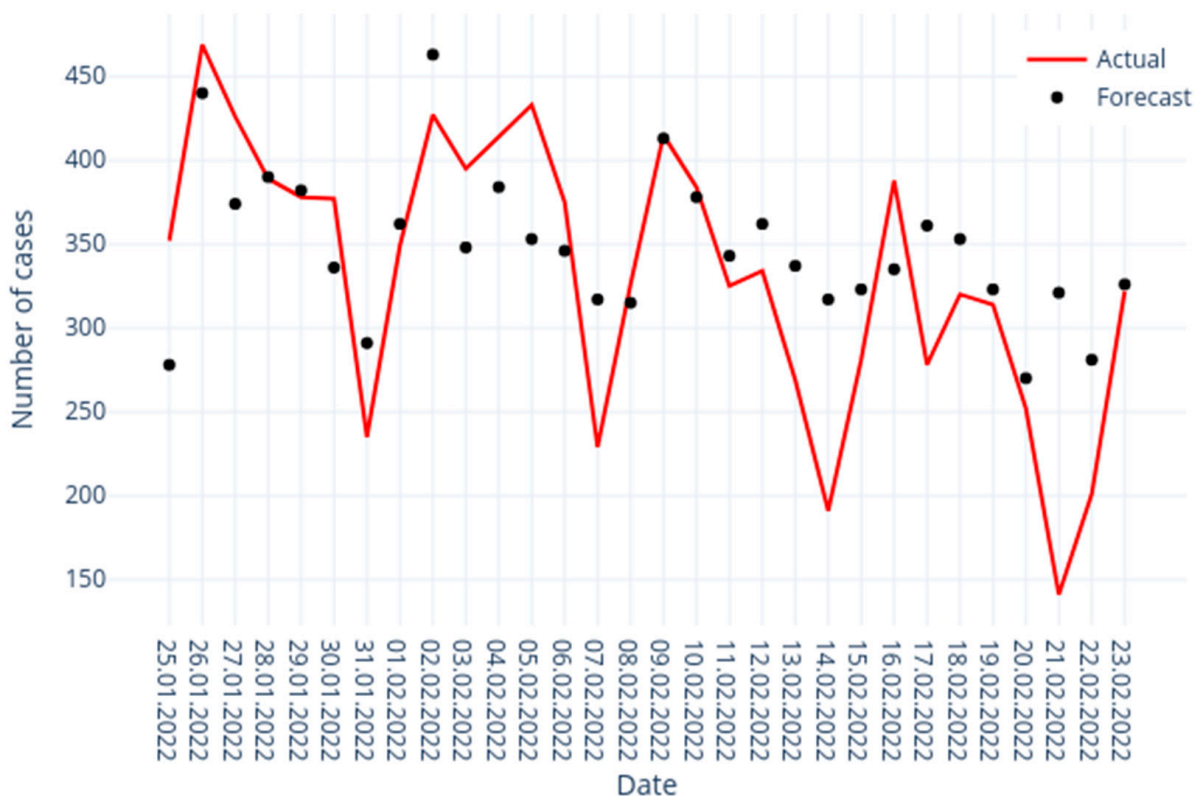
Figure 3. Retrospective forecast of fatal COVID-19 cases in Italy (25 January 2022–23 February 2022).

Adjustment of the COVID-19 dynamics model in Italy for the data sample from 25 January 2022 to 23 February 2022 shows sufficient accuracy to use the model in public health practice.

4.2. Experimental Study

Forecasts for new cases and deaths from COVID-19 in Italy were calculated to assess the impact of the Russian military invasion of Ukraine on the dynamics of the COVID-19 epidemic process in Italy. The forecast was built for 3, 7, 10, 20, and 30 days. To verify the model, we used data on morbidity and mortality from COVID-19 in Italy from 24 February 2022 to 25 March 2022, i.e., for 30 days after the start of a full-scale Russian invasion of Ukraine.

Table 2 presents model accuracy rates for cumulative new and fatal cases of COVID-19 in Italy from 24 February 2022 to 25 March 2022.

Table 2. MAPE of cumulative cases retrospective forecast for 24 February 2022–25 March 2022.

Duration of Forecast (Days)	New Cases	Fatal Cases
3 days	0.75%	0.31%
7 days	1.32%	0.57%
10 days	1.75%	0.76%
20 days	3.28%	1.31%
30 days	5.23%	1.77%

Figure 4 presents the results of a retrospective forecast of daily new cases of COVID-19 in Italy from 24 February to 25 March 2022.
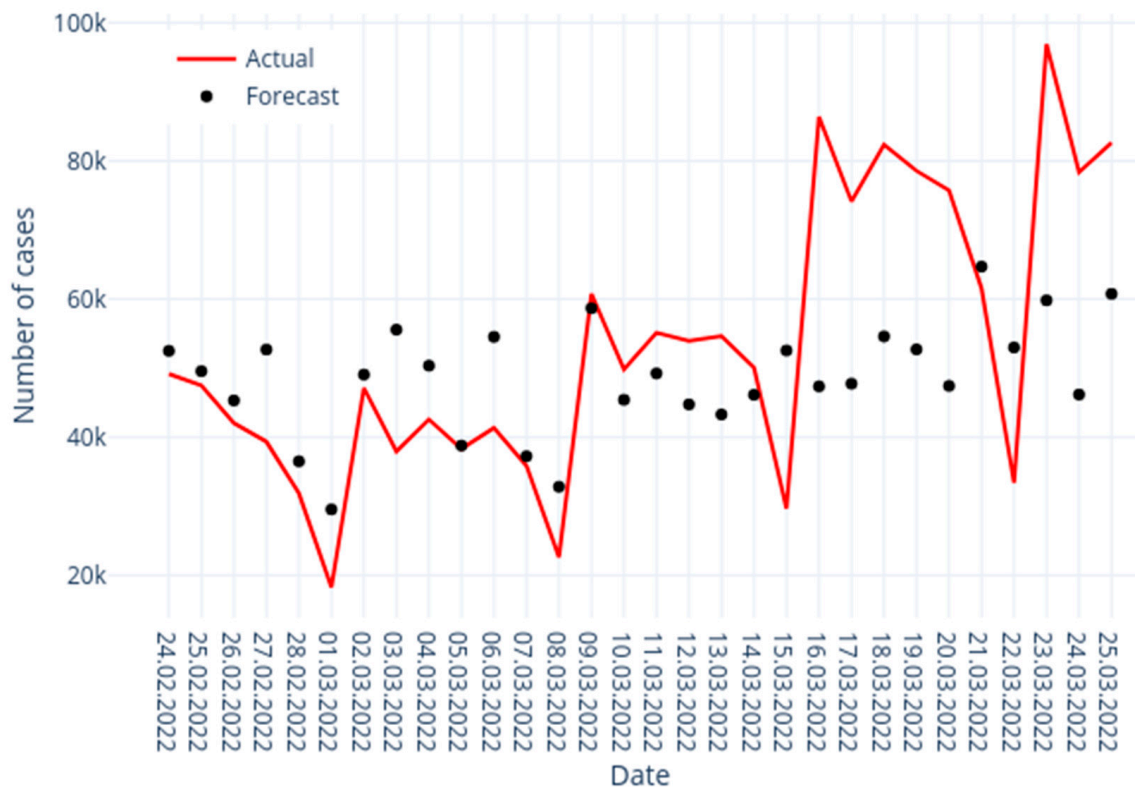
Figure 4. Retrospective forecast of daily COVID-19 cases in Italy (24 February 2022–25 March 2022).

Figure 5 presents the results of a retrospective forecast of daily fatal cases of COVID-19 in Italy from 24 February to 25 March 2022.
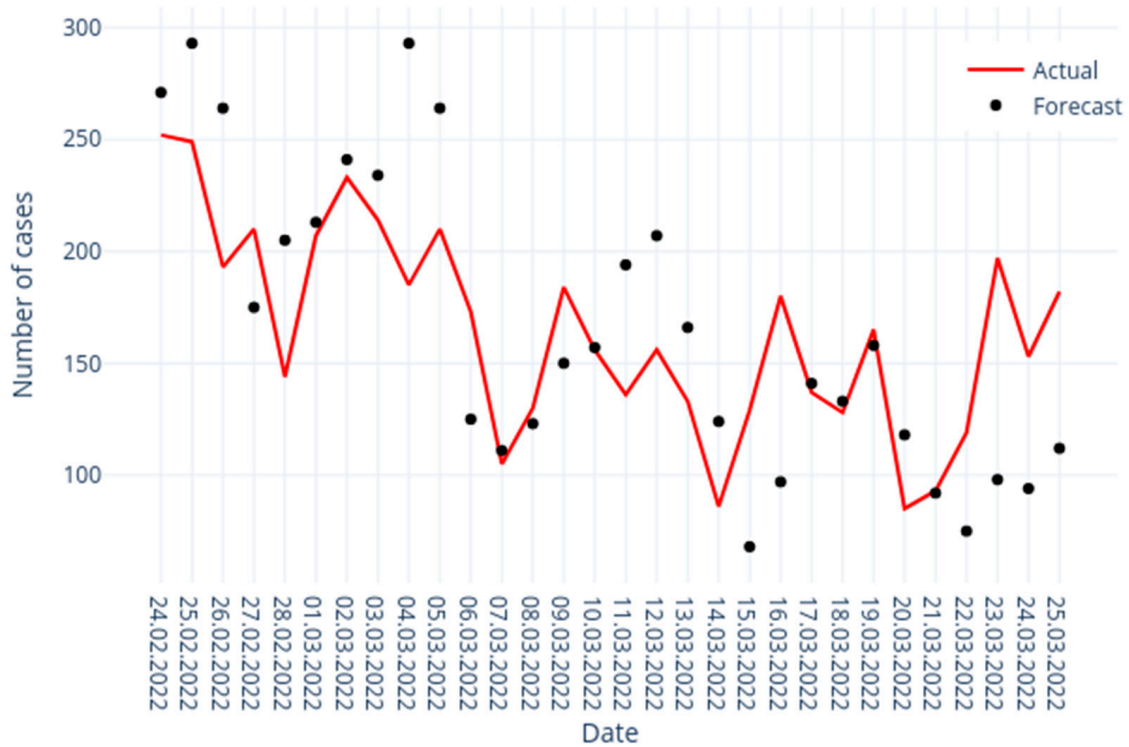

Figure 5. Retrospective forecast of fatal COVID-19 cases in Italy (24 February 2022–25 March 2022).

Figure 6 presents the deviation of daily confirmed COVID-19 cases in Italy from 24 February 2022 to 25 March 2022.
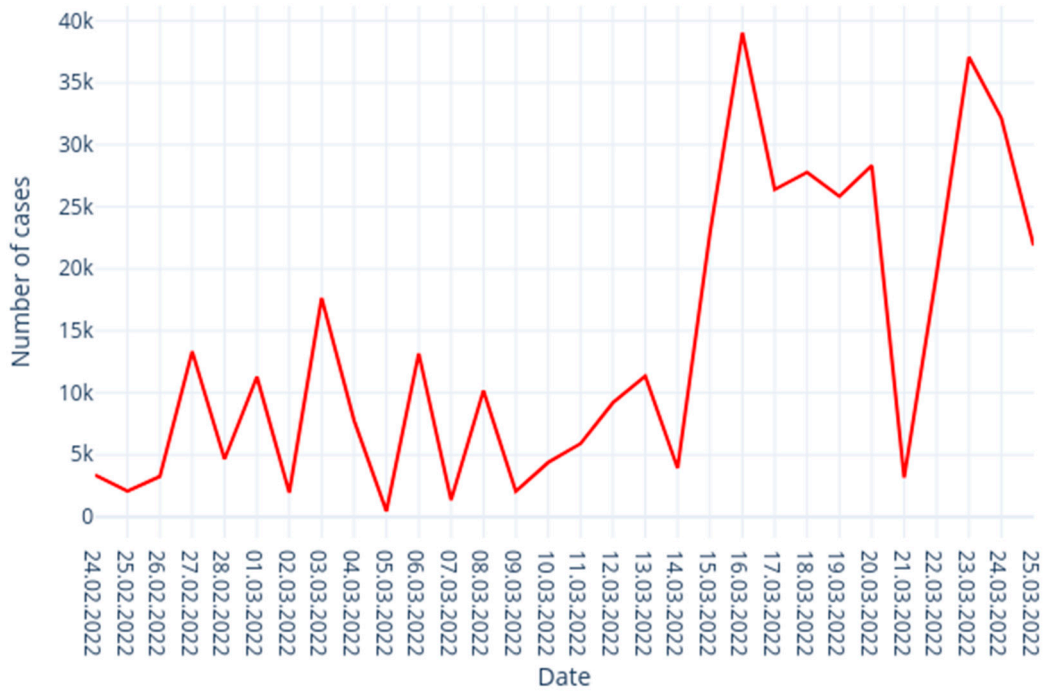

Figure 6. Deviation of COVID-19 daily new cases from forecasted values in Italy (24 February 2022–25 March 2022).

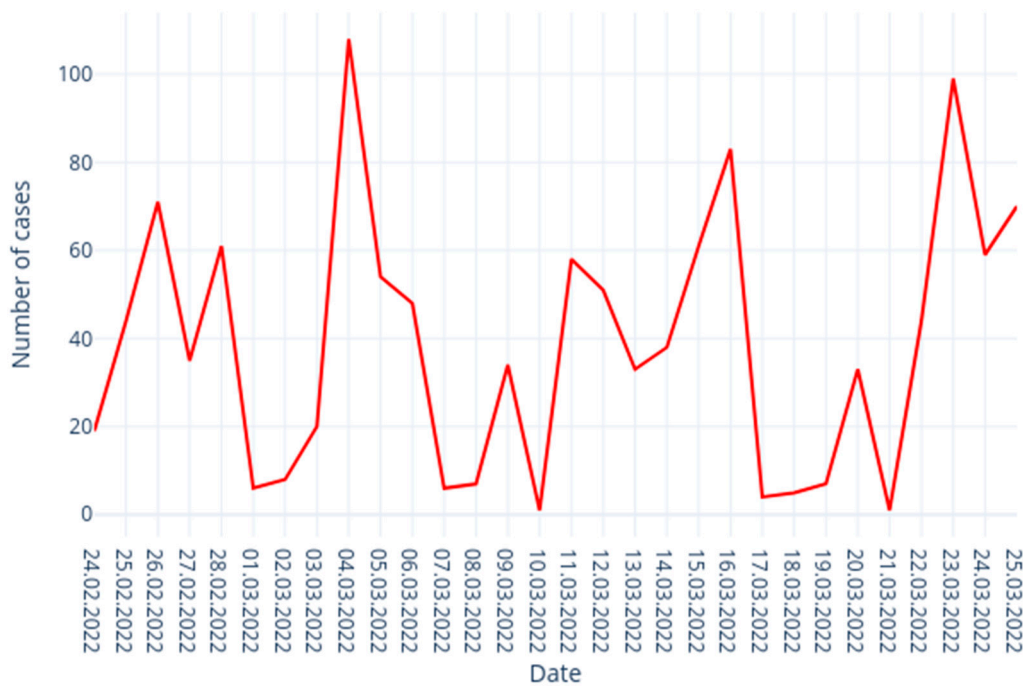Figure 7 presents the deviation of daily fatal COVID-19 cases in Italy from 24 February 2022 to 25 March 2022.

Figure 7. Deviation of COVID-19 fatal new cases from forecasted values in Italy (24 February 2022–25 March 2022).

Following the calculated forecasts assessing the potential impact of the Russian military invasion of Ukraine on the dynamics of the COVID-19 epidemic process in Italy, engaging in a more profound interpretation and analysis of these results in the broader epidemiological context is imperative. Within the 30 days post the onset of the Russian invasion, the available morbidity and mortality data from COVID-19 in Italy served as a crucial backdrop against which our forecasts were validated. The selected timeframes for the forecast—spanning 3, 7, 10, 20, and 30 days—provided a comprehensive short- to medium-term outlook, allowing for nuanced observations and variances that might have arisen during the study period.

As we transition into the discussion, we will delve into a granular epidemiological analysis of these findings. This will facilitate a comprehensive understanding of how external geopolitical events, such as the military invasion, can potentially intersect with public health scenarios in a globalized world. The data over the one-month window serve as a foundation for deriving critical insights on the spread patterns, potential externalities influencing transmission rates, and the broader implications of these results for both policymakers and the public health community. The epidemiological lens will further elucidate potential correlations, causations, and anomalies, ensuring a holistic interpretation of the impact of the invasion on Italy's COVID-19 landscape, if any.

5. Discussion

The COVID-19 pandemic has become a severe challenge for all of humanity, forcing health systems to work with significant overload and necessitating the development of effective measures to control and prevent the spread of infection. Scientists managed to create several effective vaccines for the prevention of COVID-19 quickly. However, the emergence of new strains of the pathogen reduces the effectiveness of vaccine prevention and requires the implementation of new vaccine doses. At the same time, limited resources and insufficient capacities for producing vaccines do not allow for achieving the required high vaccination coverage against COVID-19 in all countries of the world. As of early May 2023, 69.9% of the world population has received at least one dose of a COVID-19 vaccine. Moreover, 13.37 billion doses have been administered globally, and 209,759 are now administered daily and 29.5% of people in low-income countries have received at least one dose [54]. Non-drug measures such as social distancing, face masks, and hand sanitizers have also been used to prevent the spread of COVID-19.

With Russia's full-scale invasion of Ukraine, additional risks of a worsening COVID-19 epidemic situation in European countries, including Italy, have arisen. This is due, first of all, to a large influx of refugees from Ukraine, who, saving their lives, moved mainly to European countries. As of 28 June 2022, the number of immigrants from Ukraine to Italy amounted to 141.6 thousand people. Italy became the fourth number on the list of countries accepting refugees from Ukraine [55].

On the eve of the full-scale Russian invasion of Ukraine in February 2022, the COVID-19 epidemic was severe. By 23 February 2022, 4,783,835 cases of COVID-19 were registered. In just one day, 24 February, 2022, 25,789 cases were registered. At the same time, vaccination coverage against COVID-19 was 36.96% of the population, which is not enough to stop the circulation of the virus. Rocket attacks and artillery attacks forced people to hide in shelters; in cities with a metro, people moved there and stayed in the metro for a long time in crowded conditions, with limited air ventilation, and did not observe the mask regime and distancing. These living conditions facilitated the spread of the SARS-CoV-2 virus among humans. However, the dominant fear for their lives and their children's lives forced the population to leave their homes and move to other countries. At the same time, people with symptoms of the disease did not seek medical help but, along with other refugees, were sent to overcrowded trains and buses and left the country. Thus, significant quantities of sources of COVID-19 infection poured into European countries. A sharp increase in the incidence was to be expected. However, Italy, one of the first European countries to meet the coronavirus and where there was a high incidence and mortality from

COVID-19, effectively implemented preventive measures in practice. Vaccination against the coronavirus in Italy began on 27 December 2020. By 15 February 2022, the mandatory vaccination requirement for people over 50 was introduced. Before a comprehensive population migration from Ukraine to Italy on 24 February 2022, 80% of the population was fully vaccinated, and 86% received at least one vaccination. In addition, within 48 h after entering Italy, at the Sanitary Service Department (ASL) at the place of residence, arrivals had to do a test for SARS-CoV-2, which made it possible to identify and isolate arriving sources of infection. Within five days after the test, it was necessary to adhere to the regime of self-observation with the obligatory wearing of an FFP2-type mask. It was obligatory to wear an FFP2-type mask and present a certificate with a negative result of a molecular test made no earlier than 72 h before or an antigen test 48 h before. The implemented disease prevention and control measures, primarily high vaccination coverage of the population, helped to limit the spread of the SARS-CoV-2 virus, despite the influx of many refugees from Ukraine.

Many published works confirm our point of view. One study [56] analyzes the measures taken by the Italian government and their impact on the spread of the virus during the first and second waves of the pandemic from 2 April 2020 to 7 February 2021, when vaccination was just being introduced in Italy. Vaccination coverage was low, without significant effect on morbidity. The authors conclude that the policy of soft restrictions had only a minor impact on the spread of the virus and was ineffective in combating newer, more contagious variants.

One study [57], devoted to modeling the impact of interventions to contain transmission of the pathogen on the consequences of an unfolding epidemic, assesses the potential spread of infection in the absence of interventions to contain foci and various scenarios of containment measures and their impact on the spread of the epidemic. The results show that a sequence of restrictions placed on mobility and interaction between people reduced the transmission of the virus by 45% (from 42 to 49%). The authors conclude that planning emergency measures based on mathematical modeling can be effective.

The mathematical model presented in [58] was also used to study various alternative scenarios for Italy's exit strategy after the quarantine imposed in connection with the COVID-19 epidemic. The authors conclude that two critical conditions are necessary to prevent the epidemic situation from worsening: low reproduction number and low incidence. However, even with a significant decrease in the transmission rate, the resumption of social contacts at pre-pandemic levels rapidly increases the burden of COVID-19. Low incidence, in our opinion, is an indicator of a small number of sources of COVID-19 infection. The arrival of a large number of refugees from Ukraine due to Russian aggression, including non-isolated patients with COVID-19, should have affected the epidemic situation, causing an increase in the number of cases of COVID-19. However, by the end of February 2022, another deterrent appeared in Italy—the majority of the Italian population was vaccinated or partially vaccinated against COVID-19, which created a significant layer of immunity in the population and limited the circulation of the pathogen.

One paper [32] presented a deterministic compartmental model to describe the evolution of COVID-19 in Italy as a combined effect of a vaccination campaign, the spread of new variants, and restrictions on mobility. The authors emphasize the importance of vaccination to contain the spread of infection. They argue that in the absence of vaccines, with a changing dominant strain of the virus, the emerging scenario of the COVID-19 epidemic process would be dramatic: the difference in the percentage of total infections and total deaths in both cases would exceed fifty percent.

Our results demonstrated that the mild increase in COVID-19 cases observed in Italy during February–March 2022 was not directly linked to the influx of migrants from Ukraine. It is crucial to highlight that, by March 2022, the Omicron strain had become ubiquitous, accounting for 100% of coronavirus infections and effectively supplanting the Delta variant. The presence of at least three distinct subvariants of Omicron further complicated the epidemiological landscape.

The prevalence of the Omicron strain significantly influenced the dynamics of the COVID-19 epidemic in Italy, as evidenced by its rapid dissemination and displacement of the previous Delta strain. This shift in the etiological structure of the virus necessitates reevaluating the strategies employed to mitigate the spread of COVID-19, considering the unique characteristics and transmission dynamics of the Omicron variant.

Moreover, the widespread distribution of Omicron subvariants underscores the necessity for continuous genomic surveillance and research to monitor the emergence of new variants and assess their potential impact on public health. This knowledge is vital for developing targeted interventions and policies to manage and eventually curb the COVID-19 pandemic effectively.

In light of these findings, future research should focus on investigating the specific factors contributing to the spread of Omicron and its subvariants in Italy and other countries, as well as exploring the efficacy of existing vaccines and treatments against these new strains. Additionally, further studies are needed to assess the long-term consequences of the COVID-19 pandemic, particularly regarding the social, economic, and psychological impacts on affected populations.

Thus, to develop public policy plans for the regional elimination of COVID-19, it is necessary to use epidemic modeling data to consider new risks of spreading infections and determine the most effective and rational preventive and control measures.

The main advantage of the proposed methodology is its flexibility and simplicity. The proposed approach can be applied not only to the territory of Italy but also to other territories that have received many refugees from Ukraine. In this article, the XGBoost method is considered the primary method for the methodology. However, in practice, any machine learning or deep learning method can be used. This allows the proposed approach to be implemented in the healthcare system at any level, including ministries of health and medical and preventive institutions.

In numerous research endeavors to understand the dynamics of the COVID-19 pandemic, employing varied forecasting scenarios has been a frequent methodological choice. These scenarios, often grounded in hypothetical assumptions, serve as tools to envision potential future trajectories of the epidemic. Such projections, while essential in shaping preemptive policy decisions, often contend with uncertainties inherent to the factors influencing the pandemic's evolution.

However, our study adopts a distinct methodological stance, primarily anchored in a retrospective analysis of the epidemic's past dynamics. The rationale for this approach is grounded in the belief that the past holds valuable empirical evidence that can be leveraged to understand the key determinants and patterns of the epidemic. By eschewing speculative scenarios and centering our focus on actual historical data, we ensure a rigorous empirical foundation for our analysis.

Furthermore, to ensure the robustness and validity of our model, its performance was not gauged through hypothetical scenarios but by juxtaposing its retrospective forecasts against actual, observed data from the past. This comparative evaluation not only strengthens the credibility of our model but also accentuates its relevance. By drawing insights directly from historical data, we minimize potential biases or inaccuracies that could arise from speculative scenarios, thereby ensuring that our findings are empirically grounded and indicative of the epidemic's actual dynamics.

While multiple scenarios serve as valuable tools in many research contexts, our emphasis on analyzing past epidemic dynamics via a retrospective lens offers a reliable and data-driven methodology that stands firm against the litmus test of empirical validation.

The main limitation of the proposed approach is the difficulty of interpreting the machine learning methods on which the methodology is based. Therefore, for a deeper analysis of the impact of the Russian war in Ukraine on the dynamics of the epidemic, the cooperation of data scientists and epidemiologists is necessary.

6. Conclusions

This study assesses the impact of Russia's full-scale military invasion of Ukraine on Italy's COVID-19 epidemic trajectory through a novel methodology that utilizes predictive machine learning techniques, primarily the XGBoost model. The model was validated with COVID-19 morbidity and mortality data in Italy from 25 January to 23 February 2022, before applying it to analyze the epidemic dynamics from 24 February to 25 March 2022, the initial 30 days following the Russian invasion.

Effective COVID-19 vaccines have been pivotal in mitigating the disease's spread globally, with significant progress observed in countries like Italy, where high vaccination rates provided a buffer against potential outbreaks from the Ukrainian refugee influx. Concurrently, non-drug preventive measures, including face masks, social distancing, and sanitization, have reduced transmission. These measures were exemplified by Italy's stringent guidelines for incoming refugees. Despite the complexities introduced by external events such as the Russian invasion of Ukraine and the emergence of new strains like Omicron, our data indicate that the minor surge in Italy's COVID-19 cases during early 2022 cannot be primarily attributed to Ukrainian refugees.

A salient feature of this paper is the multidisciplinary collaboration between data scientists and epidemiologists. This collective expertise has facilitated a richer understanding of the epidemic dynamics, especially in the context of the geopolitical events of the Russian invasion. Epidemic modeling data become indispensable for framing public policy plans, and when combined with a cross-disciplinary approach, the outcome is more insightful and comprehensive.

The methodology presented in this paper is adaptable and straightforward, primarily using the XGBoost method but also allowing for the integration of various machine learning and deep learning techniques. This flexibility makes it applicable across diverse healthcare settings. Nevertheless, interpreting machine learning outcomes can be challenging, highlighting the need for ongoing collaboration between data scientists and epidemiologists to achieve precise and insightful results. This research demonstrates the complex relationship between vaccination efforts, preventive strategies, external influences, and the importance of a collaborative, multidisciplinary approach to addressing the pandemic.

The model's limitations lie in the difficulty of interpreting machine learning models. Therefore, epidemiologists were involved in the analysis of the obtained results. As a result of the analysis of the results, it was revealed that the natural increase in the incidence of COVID-19 in Italy was not associated with migrants from Ukraine. As of March 2022, the Omicron strain was detected in 100% of cases of coronavirus infection, completely replacing the Delta strain. At least three varieties of Omicron have been distributed. The changes in the etiological structure of COVID-19 determined the picture of the epidemic situation in Italy.

The scientific novelty of our research is centered around crafting a universal methodology that evaluates the repercussions of unforeseen events on the dynamics of infectious diseases within specific locales. What further enhances the versatility of this methodology is its compatibility with various machine learning and deep learning algorithms. Such flexibility ensures that the technique is not solely reliant on high-end computational resources, making it feasible for implementation even in medical and preventive institutions that lack specialized computing infrastructure.

The practical novelty of the study lies in the assessment of Russia's full-scale invasion of Ukraine on the dynamics of COVID-19 in Italy. At the same time, it should be noted that this methodology can be applied to other territories that have received many refugees from Ukraine.

Data Availability Statement: The data used in the research were provided by World Health Organization Dashboard and available by the link https://covid19.who.int/ (accessed on 20 May 2023). The source code is available upon request from the corresponding author.

Conflicts of Interest: The authors declare no conflict of interest.

Appendix A

Table A1. The overview of the COVID-19 epidemic process models in Italy.

Paper	Task	Method	Findings
G. Giordano, et al. [19]	To predict the course of the epidemic to help plan an effective control strategy.	Compartmental model	A combination of stringent social distancing protocols, extensive testing, and thorough contact tracing is imperative to terminate the COVID-19 pandemic.
H. Sjödin, et al. [20]	In order to calculate the burden of the disease and determine the duration necessary before quarantine measures can be lifted, it is essential to consider the duration individuals spend in public spaces and the size of their households.	Compartmental model	Unless the most rigorous community quarantine measures are implemented in a lockdown situation, entailing a near-total curtailment of all communal activities, transmission of the disease will persist.
J.M. Carcione, et al. [21]	To compute the infected population and the number of casualties of this epidemic	Compartmental model	A reduction in contacts leads to a diminished peak intensity, albeit with a broader temporal distribution and a delayed occurrence. Conversely, a higher count of exposed individuals does not influence the peak's intensity but accelerates the onset of the epidemic.
M. D'Arienzo, A. Coniglio [22]	To evaluate the basic reproduction number (R_0) of SARS-CoV-2, data from the initial stages of the outbreak in Italy were analyzed.	Compartmental model	Interventions such as social distancing, quarantine measures, and travel restrictions are crucial to mitigate the further dissemination of the epidemic, particularly in nations witnessing a delay compared to the outbreak in Italy.
N. Chintalapudi, et al. [23]	To forecast the COVID-19 evaluation of Italy condition and the possible effects, if this lockdown could continue for another 60 days.	ARIMA model	The country lockdown and self isolation to control the disease transmissibility among the Italian population through data driven model analysis is important.

Table A1. *Cont.*

Paper	Task	Method	Findings
A. Atangana [24]	To predict the future behavior of the COVID-19 spread.	Compartmental model	The fundamental statistical metrics were provided to illustrate the spread profile, and numerical simulations underscored the efficacy of the lockdown measures.
F.D. Rossa, et al. [25]	To identify if and when measures taken by the Italian government had an effect at both the national, but most importantly, at the regional level.	Compartmental model	The study validates the efficacy of the national lockdown strategy at the regional level and advocates for synchronized regional interventions. These interventions aim to avert the necessity of future nationwide lockdowns, prevent overburdening regional health systems, and minimize economic repercussions.
Y. Hao, et al. [26]	To investigate the link between regional spreading patterns of COVID-19 development in Italy and regional factors	Poisson regression model	Geographical patterns play a crucial role and can confound variables in epidemiological research.
N. Bartolomeo, et al. [27]	To make short-term forecast by defining and evaluating the daily growth rate and applying the cumulative and weighted average of the crude daily growth rate to an epidemic curve.	Exponential decay model	Applying an exponential decay model to the accumulated and weighted average daily growth rate proves valuable in approximating the number of cases and the peak of the COVID-19 outbreak in Italy, demonstrating heightened reliability during the exponential growth phase.
G. Perone [28]	To calculate short-term and medium-term projections for the number of patients admitted to hospitals due to COVID-19 during the pandemic's second infection wave.	ARIMA, Exponential smoothing, Neural network autoregression, trigonometric exponential smoothing state space models	While the hybrid models demonstrated adequate precision, it is imperative to emphasize that statistical techniques can introduce inevitable uncertainty and bias. These discrepancies can expand over time due to the gradual enactment of non-pharmaceutical interventions (NPIs) by public authorities, including the shutdown of communal areas and the imposition of national or regional lockdowns, which may not be fully accounted for in the projections.
P. Di Giamberardino, et al. [29]	To examine the implications of the reinstated inter-regional mobility following the conclusion of the initial stringent lockdown in Italy.	Compartmental model	Unregulated mobility seems inadequate to precipitate the second wave; however, human movements played a pivotal role in homogenizing the spatial distribution of the infection nationwide. This, in conjunction with the resumption of production, commerce, and educational operations, expedited the escalation of contagion from September 2020 onwards.

Table A1. *Cont.*

Paper	Task	Method	Findings
A.J. Zeleke, et al. [30]	To identify and explore the hospital admission risk factors associated with the length of stay by applying a relatively novel statistical method for count data using predictors among COVID-19 patients in Bologna, Italy.	Poisson, negative binomial, and Hurdle models	The variables about the intensive care unit setting, hospitals with prolonged hospitalization durations, the initial wave, and the subsequent waves were statistically significant across all modeled quantiles.
N. Parolini, et al. [31]	To account for the effect of the vaccination campaign, from one side, and the possible coexistence of different virus variants, from the other side.	Compartmental model	The findings underscore the efficacy of the suggested model in providing dependable short-term predictions of cases (up to a two-week horizon). Moreover, for long-term horizon scenarios (up to four weeks), successful projections can be achieved by incorporating forecasts of fatalities.
A. Fierro, et al. [32]	The objective is to construct a mean-field model that closely aligns with empirical data over an extensive time frame. Subsequently, individual mechanisms will be sequentially deactivated to assess their respective contributions to the trajectory of the epidemiological curve.	Compartmental model	The analysis substantiates the significant seasonal pattern of the epidemic. It underscores the importance of awareness mechanisms in curbing the spread of the virus through proactive protective behaviors adopted in response to heightened risk perception. Conversely, the emergence of the Delta variant and increased summer contacts had a negligible impact, only slightly elevating the summer peak, with the mitigating influence of summer temperatures prevailing.
S. Paul, et al. [33]	To examine the dynamics of COVID-19 transmission within Italy.	Compartmental model	Consistent and appropriate utilization of face masks can mitigate the spread of COVID-19. Health ministries and public health experts should formulate strategic approaches to bridge vaccination disparities and prevent future outbreaks.

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