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## METHODOLOGY FOR ASSESSING THE IMPACT OF EMERGENCIES ON THE SPREAD OF INFECTIOUS DISEASES

The spread of infectious diseases is significantly influenced by emergencies, particularly military conflicts, which disrupt healthcare systems and increase the risks of epidemics. The full-scale Russian invasion of Ukraine has exacerbated these challenges, causing environmental damage, mass displacement, and the breakdown of healthcare services, all of which contribute to the spread of infectious diseases. This study aims to develop a comprehensive methodology for assessing the impact of emergencies on the spread of infectious diseases, focusing on the full-scale invasion of Ukraine. The object of this study is to address epidemic threats posed by emergencies, particularly the increased spread of infectious diseases due to war-related disruptions. The subject of this study is methods and models of infectious disease transmission under conditions of emergencies, emphasizing the Russian full-scale invasion of Ukraine. The tasks of this study are to provide an analysis of the current state of research and develop a methodology for assessing the impact of emergencies on the spread of infectious diseases. The proposed methodology includes several key components. Comprehensive data from public health organizations includes infectious disease statistics, demographic shifts, healthcare disruptions, and environmental factors exacerbated by emergencies. Data preprocessing removes inconsistencies, standardization of formats, and normalization for population size differences. Machine learning models, including convolutional neural networks and recurrent neural networks, have been developed to simulate the spread of diseases based on demographic, environmental, and healthcare-related variables. Deep learning models analyze spatial and temporal patterns, whereas compartmental models such as SIR estimate changes in reproductive numbers ( $R_0$  and  $R_e$ ). Additionally, models of excess mortality incorporate mixed effects to account for regional and time-based variations. The methodology incorporates real-time monitoring of epidemic threats using real-time data from multiple sources, enabling dynamic assessments of disease spread and facilitating predictive modeling. The models were trained on historical data and validated using cross-validation techniques to ensure robustness and reliability, with a specific focus on the pre- and post-invasion phases in Ukraine. **Results:** The study provides a comprehensive framework for collecting and processing data on infectious diseases and epidemic threats in emergencies. The proposed model introduces advanced machine learning and epidemiological models trained on pre- and post-invasion data to analyze disease transmission patterns and forecast future epidemic dynamics. **Conclusion:** The proposed methodology addresses current gaps in infectious disease during emergencies by integrating real-time data and machine learning techniques. This research improves decision-making in public health management and biosafety during crises, particularly in war-affected regions like Ukraine.

**Keywords:** epidemic model; emergency; war; epidemic process; simulation; infectious disease.

### 1. Introduction

The spread of infectious diseases is heavily influenced by various factors, including environmental disruptions and social upheavals caused by emergencies [1]. Among the most impactful emergencies are wars and military conflicts, which not only disrupt healthcare systems but also create conditions that foster the rapid spread of infectious diseases [2]. Historically, wars have demonstrated a significant correlation between conflict

and infection outbreaks, with diseases often resulting in higher mortality rates than combat-related injuries.

The ongoing war in Ukraine, resulting from Russia's full-scale invasion, has triggered a complex emergency that affects not only public health but also the environment [3]. This emergency has given rise to additional crises, including the risk of chemical contamination, wildfires, and damage to critical infrastructure, all of which contribute to deteriorating public health. Under such conditions, the risk of infectious disease outbreaks



dramatically increases, compounded by mass displacement, shelter overcrowding, and the collapse of essential services like water supply and sanitation [4]. The health risks are further exacerbated by environmental degradation, such as pollution and biodiversity loss, which can facilitate the spread of zoonotic diseases.

Epidemiological diagnostics, which include retrospective and real-time epidemiological analyses and field investigations, play a leading role in assessing the risks of deteriorating epidemic conditions and the spread of infectious diseases.

Advances in epidemiology and healthcare have enhanced the ability to respond to infectious diseases; however, the complexities of large-scale emergencies require more dynamic and flexible analysis methods. Traditional epidemic models, such as compartmental models, are insufficient for addressing heterogeneous populations and rapidly changing conditions typical of emergencies [5]. In particular, there is a need for real-time data integration and adaptive models that can account for the unpredictable factors that arise during such crises.

The scientific application of mathematical models and simulation techniques in healthcare has been well established [6]. The COVID-19 pandemic has spurred the development of methods for modeling epidemic processes. However, compartmental modeling remains the most popular method. Existing methods for modeling epidemic processes have several drawbacks, including low flexibility, difficulty accounting for heterogeneous populations, high computational complexity, and the inability to adapt models to new epidemic processes [7-8]. These shortcomings make it impossible to use existing approaches during emergencies and analyze dynamic processes caused by emergencies. This is due to the need for rapid analysis of influencing factors and environmental changes and an adequate assessment of the situation. The multidisciplinary approach proposed in this project overcomes these limitations and achieves results that could lead to global leadership.

In recent years, the “Big Safety” concept has emerged as a framework for addressing multidimensional risks that extend across various critical domains, including infection control and disaster response [9]. This research explores how infection safety and disaster-related health risks can be integrated into public health policies, particularly in conflict zones. By recognizing the interconnectedness of these safety dimensions, a holistic approach can be developed to safeguard vulnerable populations during times of crisis.

This paper aims to develop a comprehensive methodology for assessing the impact of emergencies on the spread of infectious diseases, focusing on modern conflicts like the full-scale Russian invasion of Ukraine. Using a multidisciplinary approach that integrates epidemiological analysis, machine learning, and real-time data

analytics, this study sought to overcome the limitations of existing models. This paper is the study protocol of the project “Multidisciplinary study of the impact of emergency situations on infectious diseases spreading to support management decision-making in the field of population biosafety”. It proposes a preliminary study for that project. Through this work, we contribute to the growing field of predictive epidemiology and provide essential tools for mitigating the public health impacts of large-scale emergencies.

In this paper, section 2, namely, Background, discusses the impact of emergencies, particularly military conflicts, on epidemic process dynamics. Section 3, titled Current Research Analysis, discusses the current state of research in emergent disease simulation, estimation of excess morbidity and mortality, and basic and effective reproductive number evaluation. Section 4, Methodology, presents the methodology for assessing the impact of emergencies on the spread of infectious diseases. Section 5, namely Discussion, discusses the proposed methodology and highlights its novelty, applicability, and limitations. Conclusions describe the outcomes of the research.

## 2. Background

Wars and military conflicts have a particularly negative impact on human health during emergencies. Wars are always accompanied by outbreaks of infectious diseases, increased morbidity, and mortality [10]. The history of wars has revealed that deaths from infections often exceed those from combat injuries [11]. Despite advancements in modern medicine, infections continue to accompany wars in the 21st century. For instance, in Syria, after no measles cases were recorded since 1999, outbreaks occurred in 2017-2018 due to the civil war caused by disruptions in immunization programs [12]. The civil war in Yemen led to a cholera outbreak in 2017, resulting in 2.5 million suspected cases and 3,868 deaths, despite no cases having been recorded in the country before the war [13]. Research indicates that living conditions during wartime (stress, limited access to safe water and food, lack of environmental and personal hygiene, etc.) contribute to the spread of numerous infections. Examples of diseases spreading during military conflicts include COVID-19, tuberculosis, viral hepatitis A, diarrheal diseases, respiratory infections, HIV, leishmaniasis, and dengue fever, among others, in Turkey [14], Libya, Yemen [15], and Syria [16]. In the scientific literature, many examples exist of how conditions for spreading infections are created during war [17, 18].

Russia’s full-scale aggression in Ukraine has caused a large-scale emergency that has affected all aspects of people’s lives and is creating additional emer-

gencies, such as floods and droughts (caused by the destruction of the Kakhovka Hydroelectric Power Plant) [19], the risk of radionuclide contamination (events at the Chornobyl and Zaporizhzhia nuclear power plants) [20], wildfires (fires on the Kinburn Spit that destroyed over 1,500 hectares of forest) [21], chemical leaks (chlorine, ammonia, etc.) [22], and more.

The full-scale Russian invasion of Ukraine has had a profound impact on public health, worsening the spread of infectious diseases and further challenging the country's healthcare system. The war has caused widespread displacement, with millions of Ukrainians becoming internally displaced persons or fleeing to neighboring countries, increasing the risk of disease outbreaks in overcrowded and unsanitary conditions [23]. The disruption of vaccination programs, particularly in regions like Transcarpathia, has led to decreased immunization rates, increasing the likelihood of outbreaks of diseases such as polio and measles [24]. The war has also intensified the spread of antimicrobial-resistant bacteria, a growing global health threat. The overuse of antibiotics, especially for treating war-related injuries, combined with inadequate healthcare infrastructure has contributed to the rise of resistant pathogens, posing significant challenges for medical treatment [25]. Environmental degradation, including contamination of water sources and damaged sanitation systems, has also created further public health risks, particularly the spread of waterborne diseases [26]. The ongoing war highlights the need for coordinated international efforts to address both immediate health challenges and the long-term impacts on Ukraine's healthcare system.

During emergencies, the dynamics and manifestations of epidemic processes may differ from the natural course of events. Key risk factors influencing epidemic conditions in cascading emergencies triggered by war include intense population migration, overcrowding in bomb shelters and migration routes, stress and increased susceptibility to infections, disruption of water and energy supplies, mass rodent proliferation and outbreaks of diseases among them, food contamination, chemical runoff into water bodies, flooding of natural biocenoses, activation of infection transmission mechanisms, an increase in stray animals and their contact with wild animals, and environmental pollution caused by missile and artillery strikes, as well as landmines. Consuming large amounts of fuel during wars leads to significant carbon dioxide (CO<sub>2</sub>) emissions, contributing to climate change and the expansion of animal habitats that are sources of infections and vectors of pathogens [27]. At the same time, the environmental consequences of military actions reduce biodiversity, which increases the risk of spreading infectious diseases [28].

The destruction of healthcare infrastructure, medical facilities, and equipment and the loss of healthcare

workers lead to a significant mismatch between healthcare services' needs and their ability to assist victims [29]. This results in disruptions to the operations of healthcare institutions and the Disease Control and Prevention, as well as an inability to conduct timely sanitary, hygienic, epidemiological, and preventive measures.

The Russian full-scale invasion of Ukraine fundamentally differs from other wars, making it essential to study the conditions and risks of infectious disease spread and the unique characteristics of epidemic processes. This can form the basis for developing effective tools for making informed and rational management decisions to ensure population epidemiological welfare and biosecurity.

### 3. Current Research Analysis

The analysis of current infectious disease research focuses on key methodologies developed to understand, predict, and mitigate the spread of emerging pathogens. Simulation models play a crucial role in forecasting outbreaks and informing public health strategies. These models, ranging from compartmental frameworks like SIR to more advanced agent-based and network-based models, allow for detailed examination of disease transmission dynamics. Additionally, methods for estimating excess mortality provide a clearer understanding of the broader impact of outbreaks by comparing observed deaths with expected baselines. Evaluation of the basic reproductive number ( $R_0$ ), a critical parameter in infectious disease modeling, is essential for determining the potential spread of a pathogen. This section reviews the methodologies employed in these areas and highlights their importance in modern epidemiological research and public health decision-making.

#### 3.1. Modern Approaches to Emerging Diseases Simulation

The study [30] explores a novel approach for detecting emerging infectious diseases using a two-layer model. Based on the TextCNN-Attention model, the first layer classifies cases as infectious or non-infectious, and the second layer, using LightGBM, identifies whether infectious cases represent emerging diseases. The study utilised medical records from five institutions in Beijing, providing a robust real-world dataset for analysis. A key strength of this study is the high accuracy and low false-positive rate achieved by the model, which makes it suitable for real-time monitoring in clinical settings. However, the study's limitation lies in its inability to fully account for the complexity of real-world scenarios in which emerging infectious diseases may evolve in unpredictable ways, and the model's reliance on retrospective data may not fully capture these dynamics.

The study [31] evaluated the performance of 16 forecasting models during the 2015-2016 Zika epidemic in Colombia. This study explores how varying assumptions about human mobility, transmission potential, and virus introduction affect model accuracy. The authors found that individual models sometimes outperform ensemble forecasts early in the epidemic, but ensemble models provide more robust forecasts overall. A limitation of this study is its retrospective nature, which may not fully account for real-time uncertainties or delays in data reporting.

The paper [32] presents a compartmental SEIR (Susceptible-Exposed-Infectious-Recovered) model that investigates the role of asymptomatic infections in emerging infectious disease dynamics. The model explores the possibility that some pathogens maintain stable and endemic circulation in populations through asymptomatic carriers, potentially affecting future outbreaks. A notable study strength is its flexibility, as the model can be applied to a range of diseases in which asymptomatic carriers play a critical role. However, the model's assumptions, such as the absence of pathogen mutations and the focus on viral infections, may not fully capture the complexity of disease dynamics across different pathogens.

The study [33] used an SEIR compartmental model to examine how vaccine hesitancy influences the spread of infectious diseases. The model includes differential morbidity with separate compartments for mild, moderate, and severe symptoms and incorporates vaccine efficacy and hesitancy as key variables. This study found that vaccine hesitancy significantly reduced the effectiveness of vaccination programs, requiring highly effective vaccines to control outbreaks, especially when hesitancy levels were high. A notable limitation of this study is its reliance on a hypothetical population, which limits the practical applicability of its findings.

The study [34] explores the dynamics of emerging infectious diseases using an age-structured SEIR model, focusing on the effectiveness of vaccination and physical distancing interventions across different age groups. This study uses mathematical modeling to calculate the basic reproductive number and evaluate the cost-effectiveness of control strategies. A notable strength of this paper is its comprehensive approach, which combines optimal control theory with age-heterogeneous transmission dynamics to identify the most efficient interventions. However, the study's limitation lies in its reliance on idealized conditions, such as homogeneous population behavior within age groups and fixed intervention parameters, which may not fully reflect the complexities of real-world disease transmission and response variability.

The study [35] investigated how variations in host community structure, particularly the presence of intermediate hosts, influence the spread of zoonotic diseases.

Using a stochastic Susceptible-Infectious-Recovered (SIR) model, the authors compare three community structures with increasing complexity, analyzing how they affect the incidence and prevalence of infections in target populations. The results show that intermediate hosts can either amplify or dilute epidemic outcomes, depending on their role as a bridge or secondary source of infection. One limitation of this study is the assumption of fixed community structures and uniform host behaviors, which may not fully capture the dynamic nature of real-world ecosystems and host interactions.

The study [36] presented a mathematical model that incorporates travel between two regions (patches) and the influence of disease surveillance on the infection force. This study analyzes how changes in human movement and delayed behavior changes due to past disease surveillance data impact the dynamics of an emerging infectious disease. A significant contribution of this work is the incorporation of surveillance-mediated infection forces, which provide a more realistic view of how public health data influence the spread of diseases. However, one limitation of this study is its assumption of homogeneous populations within each patch, which may not accurately represent the diverse social and behavioral factors affecting disease transmission in real-world scenarios.

In the study [37] a differential equation model was employed to examine the impact of quarantining close contacts on infectious disease transmission dynamics. The study found that the timing of quarantine measures is crucial, with early interventions significantly reducing the cumulative number of cases and deaths. The model reveals a phase-transition structure, indicating that implementing quarantine measures before a critical moment can stabilize the epidemic at lower levels. However, one limitation of this study is its reliance on idealized population structures and assumptions about uniform quarantine compliance, which may not accurately reflect the complexities of real-world epidemics.

Research [38] presented a novel outbreak prediction approach using the Mamdani fuzzy inference system. The study integrates five input variables—change in landscape, gateway of travel, hygiene, sanitation, housing, regularity of surveillance – Change in Landscape, Gateway of Travel, Hygiene, Sanitation, and Housing, Regularity of Surveillance, and Health Infrastructure – to assess the probability of disease outbreaks. This model emphasizes how complex environmental and human factors contribute to the emergence of infectious diseases and how fuzzy logic can be used to simulate such dynamics. A notable strength of this method is the flexibility of the fuzzy inference system, which effectively models uncertainties in epidemiological predictions. However, one limitation of this study is its reliance on theoretical inputs and lack of real-world data validation, which may limit its immediate applicability to public health planning.

The paper [39] explores the role of environmental pollution and time delays due to disease incubation periods in the spread of infectious diseases. By developing a delayed SIS model, the authors demonstrated that pollution increases the susceptibility of populations and amplifies disease transmission, particularly when combined with incubation periods that obscure early detection and control efforts. The model identifies the basic reproduction number and investigates its stability through Hopf

bifurcation analysis, revealing that pollution intensifies disease dynamics by extending the time during which infections remain undetected. A limitation of this study is its focus on theoretical simulations, which lack real-world data validation, making it harder to directly apply the results to specific disease outbreaks.

Table 1 presents an overview of emerging disease simulation methods.

Table 1

The overview of the emerging diseases simulation methods

| Paper  | Task  | Method              | Findings   |
|--|---|---------------------|--|
| Wang M. et al. [30]                            | Early detection of emerging disease.  | Deep learning (CNN) | The proposed hierarchical diagnosis model, which combines TextCNN-Attention and LightGBM, demonstrated high accuracy and efficiency in real-time detection of emerging infectious diseases with significant potential for clinical application.  |
| Oidtman R.J. et al. [31]                       | To assess the potential for uncertainty regarding emerging pathogens forecasting by example of Zika epidemic.   | Stochastic models   | Ensemble forecasting models, which incorporate multiple assumptions, consistently outperformed individual models in predicting the course of the Zika epidemic, especially as the outbreak progressed.   |
| Siewe N., Greening B., Fefferman N.H. [32]     | To explore the impact of asymptomatic infections on the spread and persistence of emerging infectious diseases  | Compartmental model | Asymptomatic infections can play a significant role in the sustained, endemic circulation of certain pathogens, potentially influencing the dynamics of future outbreaks.  |
| Hewage I.M., Church K.E.M., Schwartz E.J. [33] | To explore the effects of vaccine hesitancy and efficacy on the spread of an emerging infectious disease.   | Compartmental model | Vaccine hesitancy drastically reduces the effectiveness of vaccination for controlling infectious disease outbreaks, requiring vaccines with extremely high efficacy to mitigate the impact, especially in populations with high levels of hesitancy.                                  |
| Jia P., Yang J., Li X. [34]                    | To evaluate the effectiveness and cost-efficiency of vaccination and social distancing interventions in reducing the spread of emerging infectious diseases.                                    | Compartmental model | A combined strategy of vaccination and physical distancing is the most cost effective approach for controlling emerging infectious diseases, particularly among the age groups most vulnerable to severe outcomes.   |
| Voinson M., Smadi C., Billiard S. [35]         | To investigate how different host community structures, including reservoirs and intermediate hosts, impact the epidemiological dynamics of emerging infectious diseases in target populations. | Compartmental model | The structure of the host community, particularly the presence of intermediate hosts, can either amplify or dilute the spread of zoonotic diseases in the target population, depending on the complexity of the transmission route.  |
| Sun G., Jin Z., Mai A. [36]                    | To investigate the impact of travel between regions and disease surveillance-mediated infection forces on the transmission dynamics of emerging infectious diseases.                            | Compartmental model | Inter-patch travel and surveillance-mediated infection forces significantly affect the spread of infectious diseases, with disease persistence and equilibrium states being influenced by travel patterns and the responsiveness of susceptible individuals to past surveillance data. |

Continuation of Table 1

| Paper                               | Task   | Method                 | Findings   |
|-------------------------------------|--|------------------------|--|
| Pan Q., Song S., He M. [37]         | To study the effect of quarantine measures on the transmission dynamics of infectious diseases with infectivity during the incubation period.  | Compartmental model    | Early implementation of quarantine measures for close contacts reduces the spread of infectious diseases and minimizes the cumulative number of cases and deaths.  |
| Adak S., Kar T.K., Jana S. [38]     | To predict the probability of disease outbreaks based on key factors such as landscape changes, travel patterns, hygiene, surveillance, and health infrastructure.                   | Fuzzy inference system | The fuzzy inference system effectively predicts the likelihood of infectious disease outbreaks by incorporating environmental and health-related factors, thus offering a flexible approach to outbreak modelling. |
| Gupta S., Bhatia S.K., Arya N. [39] | To analyze the combined effects of pollution and disease incubation periods on the transmission dynamics of infectious diseases, with a focus on stability and bifurcation behavior. | Compartmental model    | Environmental pollution and incubation significantly delay the transmission and persistence of infectious diseases, making early detection and control more challenging.   |

The studies reviewed in this subsection collectively highlight various innovative approaches to modeling and predicting emerging infectious diseases, each with unique strengths and limitations. These approaches, ranging from machine learning techniques to compartmental and stochastic models, emphasize the importance of real-time data integration, population dynamics, and environmental factors in understanding disease spread, particularly in emergent contexts. The ongoing Russian full-scale invasion of Ukraine serves as a crucial example of how emergencies such as wars significantly alter disease dynamics by disrupting healthcare systems, causing population displacement, and degrading environmental conditions. In such settings, existing models face challenges in capturing the full complexity of disease transmission because they often rely on assumptions like homogeneous populations or idealized conditions, which do not reflect the chaotic and rapidly evolving nature of real-world epidemics in conflict zones. Furthermore, although several models have excelled in theoretical simulation, the lack of real-world data validation, particularly in conflict-affected regions, limits their immediate applicability to public health planning. These limitations underscore the need for further research to refine these models, better account for unpredictable factors in emergencies, and improve their effectiveness in crises like the Russian invasion of Ukraine.

### 3.2. Methods of Excess Morbidity and Mortality Estimation

The paper [40] proposed a linear mixed model for estimating excess mortality caused by the COVID-19 pandemic in Belgium and the Netherlands. This model

improves upon the traditional 5-year weekly average approach by incorporating year-specific predictions and down-weighting the influence of historical excess mortality events such as heatwaves and influenza outbreaks. The proposed method enhances forecasting accuracy and provides more reliable estimates of excess mortality. However, one limitation of the study is its focus on high-mortality events, which may not generalize well to settings with more moderate fluctuations in mortality, and the reliance on retrospective data limits its real-time applicability.

The study [41] introduced a novel approach for estimating excess mortality during the COVID-19 pandemic using principal component analysis combined with a Lee-Carter mortality model. This method addresses the limitations of the previous model by considering long-term mortality trends and correlations among demographic groups and countries. This study provides insights into excess mortality patterns across 19 countries, emphasizing the heterogeneous impact of the pandemic on different age and sex groups. A key strength of this study is its use of a comprehensive dataset and stochastic modeling techniques to account for variability and uncertainty in mortality trends. However, one limitation is the lack of real-time applicability because the model relies heavily on historical data, which may not fully reflect immediate or rapidly changing conditions during a pandemic.

Sirag and Gissler [42] presented a methodology for estimating excess mortality in Canada during the COVID-19 pandemic. To estimate baseline mortality, the authors used an overdispersed Poisson generalized linear model with seasonal adjustments based on a rolling reference period from 2016 to 2020. The model was further

enhanced to adjust for provisional death counts and to account for reporting delays due to the pandemic. Although the study provides timely and reliable estimates of excess mortality, a significant limitation is its reliance on provisional death data, which are subject to delays and underreporting, particularly in the early stages of the pandemic. This limitation may affect the accuracy of real-time mortality estimates and hinder the ability to capture the full impact of the pandemic on mortality.

Research [43] investigated the spatial heterogeneity of excess mortality in Mexico during the COVID-19 pandemic. Using Serfling regression models, the authors estimated all-cause excess mortality across 32 states, finding significant variations influenced by sociodemographic factors, such as aging, household size, and marginalization. Central states had higher mortality rates, whereas southern states, with higher indigenous populations, exhibited lower mortality rates. A notable strength of this study is its use of a comprehensive set of demographic and environmental variables to explain these variations. However, this approach is limited by reliance on aggregated state-level data, which may obscure individual-level risk factors and lead to potential ecological fallacy.

The study [44] compared five approaches to estimating excess mortality during the pandemic, including quasi-Poisson models, the European Monitoring of Excess Mortality algorithm, and a 5-year average model. Each method captures varying aspects of mortality trends, such as seasonal fluctuations and registration delays, and adjusts for factors like the reduced circulation of other infections during lockdowns. A key strength of this paper is its comprehensive comparison of different methodologies, which enhances our understanding of excess mortality estimation during health crises. However, one limitation is the inconsistency in adjusting for factors like mortality displacement and differences between models using date of occurrence versus registration, which can affect the comparability of results.

The paper [45] introduced a method for assessing hospital performance by calculating the excess cumulative incidence of cause-specific outcomes, such as cerebrovascular deaths, in stroke patients. This approach contrasts a hospital's observed outcomes with the expected outcomes if the same patients were treated at another hospital. The proposed method offers a practical interpretation that can guide improvements in healthcare delivery. However, one limitation of this study is its reliance on the assumption of proportional cause-specific hazards, which may not hold in all real-world settings.

Delbrouck and Alonso-García [46] integrated epidemiological and actuarial models to estimate the excess mortality caused by COVID-19 in Belgium in 2020. These findings are applied to assess the financial impact on life insurance products. By combining a SIRD

(Susceptible-Infectious-Recovered-Death) epidemiological model with an actuarial mortality model, the authors provide detailed insights into how the pandemic has affected mortality rates across different age groups and its implications for the insurance industry. A key strength of this study is its ability to provide a comprehensive framework that bridges epidemiological forecasting with actuarial risk assessments. However, this study has a limitation in that it focuses on short-term excess mortality during the first year of the pandemic, which may not capture the long-term effects on mortality trends or fully account for potential waves of future infections.

Research [47] has examined the impact of COVID-19 on excess mortality among different age groups in Malaysia. Using various parametric models, such as the Heligman-Pollard model for men and the Rogers-Planck model for women, the study forecasts mortality rates under both normal and COVID-19 conditions. The analysis highlights that excess mortality was observed primarily among individuals aged 60 years, with men's mortality rates showing a delayed but prolonged increase compared with women's. A limitation of this study is its reliance on historical data up to 2020, which may not fully capture the long-term effects of the pandemic or account for future variants and waves of infection.

The study [48] applies generalized linear mixed models to estimate excess all-cause and pneumonia mortality during the COVID-19 outbreak in Thailand from April to October 2021. The study found that cumulative excess deaths were significantly higher during this period, with most increases observed in older age groups and in males. Approximately 75% of the excess deaths were directly attributed to COVID-19, while the remaining 25% were likely due to indirect effects, such as healthcare disruptions. A notable strength of this study is its incorporation of detailed age- and sex-specific mortality data, which provides a clearer understanding of the pandemic's demographic impact. However, one limitation is the lack of data on other contributing factors, such as influenza and pollution, which could influence the accuracy of mortality estimates.

The study [49] estimates excess mortality across Italian regions during the initial stages of the Omicron variant wave in early 2022. Using a generalized linear mixed model trained on pre-pandemic mortality data from 2011 to 2019, this study captures excess deaths by adjusting for seasonal patterns and regional variations. The findings reveal that 14 of 20 Italian regions experienced significant excess mortality during January, with a marked decline in February. A key study strength is its ability to model regional-specific mortality patterns during the Omicron wave. However, one limitation of this study is its reliance on aggregated regional data, which might obscure localized factors, such as hospital capacity or vaccination coverage, influencing mortality outcomes.

Table 2 presents an overview of excess morbidity and mortality methods.

The analysis of these studies collectively highlights the diversity of methodologies used to estimate the excess mortality and morbidity of different infectious diseases, each offering unique insights and contributing to a more nuanced understanding of the pandemic's impact. While some approaches, such as generalized linear mixed models and principal component analysis, provide robust frameworks for estimating mortality by incorporating demographic, seasonal, and geographic variables, their re-

liance on historical data and assumptions about population behaviour can limit their applicability in rapidly evolving real-world conditions. This challenge is especially evident in emergent contexts, such as the full-scale Russian invasion of Ukraine, where war-induced disruptions to healthcare, infrastructure, and population stability likely have exacerbated public health crises, including infectious disease outbreaks and increased mortality. The impact of conflict on public health introduces unique complexities that many existing models may not fully account for, such as mass displacement, interruptions in healthcare services, and environmental degradation.

Table 2

The overview of the excess morbidity and mortality methods

| Paper  | Task  | Method                              | Findings  |
|--|---|-------------------------------------|---|
| Verbeeck J. et al. [40]                          | To estimate excess mortality during the COVID-19 pandemic, improve existing methods by addressing limitations such as historical mortality biases and forecasting precision.  | Linear mixed model                  | The proposed linear mixed model provides more accurate and reliable estimates of excess COVID-19 mortality than the traditional 5-year weekly average method by accounting for year-specific trends and reducing the impact of past mortality spikes.           |
| Vanella P., Basellini U., Lange B. [41]          | To estimate excess mortality during pandemics, focusing on capturing long-term mortality trends and cross-country correlations.   | Principal component analysis        | Principal component analysis combined with the Lee-Carter mortality model provides a more accurate estimation of excess mortality during the COVID-19 pandemic by accounting for long-term trends and demographic correlations across countries.                |
| Sirag E., Gissler G. [42]                        | To estimate excess mortality during the COVID-19 pandemic, adjusting for undercoverage and reporting delays.  | Poisson generalized linear model    | The adapted statistical model effectively estimates excess mortality during the COVID-19 pandemic in Canada despite challenges in reporting data and provisional death counts.  |
| Dahal S. et al. [43]                             | To estimate the spatial distribution of excess mortality in Mexico during the COVID-19 pandemic and analyze how socio-demographic, climate, and population health characteristics contribute to this geospatial variability.                        | Serfling regression model           | Excess mortality during the COVID-19 pandemic in Mexico showed significant spatial variation, with higher mortality rates in central states and lower rates in southern regions, influenced by socio-demographic and environmental factors.                     |
| Barnard S. et al. [44]                           | To evaluate and compare multiple statistical approaches for modeling excess mortality across England during the COVID-19 pandemic, aiming to identify the most reliable method for estimating mortality under fluctuating public health conditions. | Poisson model, 5-year average model | Different models for estimating excess mortality during the COVID-19 pandemic in England yielded varying results, with methods like quasi-Poisson models providing more accurate adjustments for seasonal effects and reporting delays than simpler approaches. |
| Van Rompaye B., Eriksson M., Goetghebeur E. [45] | To assess hospital performance by comparing observed cause-specific outcomes with expected outcomes, aiming to identify areas where hospitals can improve their care quality.   | Statistical model                   | The proposed method for evaluating hospital performance based on excess cause-specific incidence provides a detailed assessment of hospital outcomes and highlights performance gaps in specific disease treatment areas.                                       |



Continuation of Table 2

| Paper  | Task   | Method                                      | Findings   |
|--|--|---|--|
| Delbrouck C., Alonso-Garcia J. [46]            | To estimate excess mortality due to COVID-19 in Belgium and assess its implications for life insurance liabilities and risk management.  | Actuarial mortality model                   | Integrating epidemiological and actuarial models provides a more accurate estimation of excess COVID-19 mortality and its financial impact on life insurance products.                                     |
| Erdus R.A. et al. [47]                         | To compare forecasted mortality rates under normal conditions with the excess mortality caused by the COVID-19 pandemic in Malaysia, using parametric models to assess the pandemic's age-specific impacts.        | Heligman-Pollard model, Rogers Planck model | COVID-19 has led to significant excess mortality in Malaysia, particularly among individuals aged 60 and over, with men experiencing a delayed but more prolonged increase in mortality compared to women. |
| Wilasang C et al. [48]                         | To estimate excess all-cause and pneumonia mortality in Thailand during the COVID-19 outbreak, using generalized linear mixed models to assess the direct and indirect impacts of the pandemic on mortality rates. | Linear mixed model                          | The COVID-19 pandemic has significantly increased all-cause mortality in Thailand, with most excess deaths occurring among older males and 75% directly attributable to COVID-19.                          |
| Maruotti A., Ciccozzi M., Jona-Lasinio G. [49] | To estimate COVID-19-induced excess mortality during the Omicron wave in Italy using a generalized linear mixed model that accounts for regional variations and seasonal mortality patterns.                       | Linear mixed model                          | The Omicron variant caused significant excess mortality in several Italian regions during early 2022 although the impact was notably less severe than in previous COVID-19 waves.                          |

### 3.3. Methods of Basic and Effective Reproductive Number Evaluation

Sisk and Fefferman [50] introduced a novel approach for calculating the basic reproductive number ( $R_0$ ) using network theory, specifically, the Max-Flow Min-Cut (MFMC) theorem. The proposed method simplifies the traditionally complex next-generation matrix approach, making it more accessible to a broader scientific community by reducing the mathematical burden. The results demonstrate that the MFMC method is equivalent to the next-generation matrix method and can be applied to simple and complex epidemiological models. A key strength of this approach is its accessibility and intuitive nature, particularly for non-mathematicians, which can accelerate real-time responses during outbreaks. However, a limitation is that the MFMC method may require additional adjustments for models with non-closed systems or more complex dynamics, potentially reintroducing some of the computational difficulties it was designed to avoid.

The study [51] presented a comprehensive framework for comparing and combining different early estimates of the basic reproductive number during the initial phase of COVID-19. By decomposing  $R_0$  into three key components – exponential growth rate, mean generation interval, and generation – interval dispersion – the study

enables a more consistent evaluation of disparate estimates. This paper highlights that many early  $R_0$  estimates were overly confident because uncertainties in these components. A key limitation of this study is its reliance on early outbreak data from a narrow window in January 2020, which may not have captured the full scope of uncertainties as the pandemic progressed.

Research [52] employs the Next Generation Method approach to estimate the basic number of women who have contracted COVID-19 in Ghana. The authors used a SEIAHR (Susceptible, Exposed, Infectious, Asymptomatic, Symptomatic, and Recovered) compartmental model and parameter estimates from real-world data to determine that the  $R_0$  for Ghana was approximately 2.52. This study provides valuable insights into the transmission dynamics of COVID-19 in Ghana, emphasizing how a small increase in transmission rates significantly affects  $R_0$ . However, one limitation of this study is its reliance on data up to July 2020, which may not reflect the impact of subsequent pandemic waves or the introduction of vaccines, potentially limiting the long-term applicability of the results.

The study [53] outlined a framework for estimating  $R_0$  during infectious disease outbreaks using case notification data. This study explores various statistical methods, including the sequential Bayesian approach and maximum likelihood estimation, and highlights the

importance of the generation or serial interval in calculating  $R_0$ . This work's practical application is a key strength because it allows real-time monitoring and assessment of intervention effectiveness during outbreaks. However, one limitation of this study is its reliance on complete and accurate case notification data, which may be unavailable or incomplete in real-world situations, potentially affecting the accuracy of  $R_0$  estimates.

Al-Raei M. [54] applies the SIRD (Susceptible, Infected, Recovered, Deceased) model to estimate  $R_0$  for COVID-19 in multiple countries using real-world data up to July 2020. The study finds that the  $R_0$  values across these countries range between 1.0011 and 2.7936, with the Syrian Arab Republic having the highest  $R_0$ , indicating a higher transmission rate. A strength of this study is its application of a consistent model across diverse geographical contexts, offering comparative insights into the pandemic's spread. However, one limitation is the use of early pandemic data, which may not fully account for later waves of infection or the effects of interventions such as vaccination campaigns.

The paper [55] investigated the discrepancies in the estimated effective reproductive number ( $R_e$ ) for COVID-19 across various research groups in Germany during 2020 and 2021. The authors assessed within- and between-method variations by comparing the results of the eight methods. They identified that differences in the analytical choices, such as the data source, preprocessing, generation time distribution, and delay assumptions, play a significant role in shaping the results, sometimes more than the statistical method. This paper's systematic approach to standardizing these analytical choices is a strength that helps understand the sources of disagreement between  $R_e$  estimates. However, one limitation of the study is that it focuses on retrospective analysis, which may not fully capture the real-time challenges of updating estimates during an evolving outbreak.

The study [56] presented a detailed analysis of the transmission dynamics and reproductive numbers ( $R_0$  and  $R_e$ ) of hypervirulent *Neisseria meningitidis* strains circulating in Italy between 2012 and 2017, including a major outbreak in Tuscany. Using a Bayesian method and whole-genome sequencing, the study estimates  $R_0$  to be between 1.22 and 1.4 for different subsets of the data, with a peak  $R_e$  of 3.22 during the 2015 outbreak. A significant strength of this study is its use of molecular epidemiology to track population changes and transmission dynamics. However, this approach is limited by reliance on historical data, which may not fully account for emerging strains or new public health interventions that could influence transmission.

The paper [57] analyzes the effectiveness of lockdown strategies in controlling the spread of COVID-19 by calculating  $R_0$  across different phases of lockdown

implementation. Using data from the Saudi Ministry of Health and Google Mobility Reports, the study divided the outbreak timeline into three intervals: pre-lockdown, partial lockdown, and full lockdown. The results indicate that  $R_0$  values slightly increased during the full lockdown period, which the authors attribute to enhanced active surveillance and improved healthcare accessibility, including free medical care for all residents regardless of their legal status. A limitation of this study is its reliance on short time intervals for analysis, which may not fully capture the long-term effectiveness of lockdown measures. In addition, using mobility data from Google does not represent the entire population because it is limited to individuals with GPS-enabled devices.

The study [58] estimated  $R_0$  of monkeypox during the initial outbreak phase in three countries: England, Portugal, and Spain. Using a branching process with Poisson likelihood and gamma-distributed serial intervals, the study found that  $R_0$  ranges from 1.4 in Portugal to 1.8 in Spain, indicating sustained transmission in these populations. A key strength of this study is its early estimation of transmissibility, which provides valuable data for informing public health responses. However, a limitation of this research is its focus on a homogeneous mixing assumption and its reliance on early outbreak data, which may not fully represent ongoing transmission dynamics, particularly in more diverse populations or as the outbreak evolves.

The study [59] presented a novel approach using network theory to estimate  $R_0$  for infectious diseases. By applying graph-based models, this study demonstrates how  $R_0$  can be accurately determined based on the structure of contact networks rather than relying solely on compartmental models. This method accounts for heterogeneous contact patterns within populations, which can significantly impact disease spread. A key strength of this approach is its flexibility in capturing complex transmission dynamics, especially when traditional models are insufficient. However, this method has the limitation that it requires detailed contact pattern data, which may not always be available in real-world settings.

Table 3 presents the overview of the  $R_0$  and  $R_e$ .

The reviewed papers illustrate a diverse range of approaches to estimating and analyzing  $R_0$  across various infectious diseases, each of which contributes valuable insights into the complexities of disease transmission and the effectiveness of public health interventions. From network-based models that account for heterogeneous contact patterns to traditional compartmental models and molecular epidemiology, these methods offer robust tools for understanding disease spread. However, many of these studies reveal limitations associated with early outbreak data, population homogeneity assumptions, and the availability of real-world contact patterns.

Table 3

The overview of the basic and effective reproductive number evaluation methods

| Paper                                  | Task   | Method   | Findings  |
|--|--|--|---|
| Sisk A., Fefferman N.H. [50]           | To calculate the basic reproductive number that simplifies the complex mathematical processes of traditional approaches, making it more accessible for real-time application in infectious disease modeling.         | Max-Flow Min-Cut method                                  | The Max-Flow Min-Cut (MFMC) theorem is an accessible and computationally efficient alternative to the traditional next-generation matrix method for calculating the basic reproductive number in epidemiological models.  |
| Park S.W. et al. [51]                  | To reconcile and combine early outbreak estimates of $R_0$ while accounting for uncertainties in growth rates and generation intervals, focusing on the initial phase of the COVID-19 pandemic.                      | Deterministic and stochastic branching process model     | Early estimates of the basic reproductive number for COVID-19 were often overly confident due to underestimating uncertainties in key components like the exponential growth rate and generation interval.  |
| Otoo D., Donkoh E.K., Kessie J.A. [52] | To estimate $R_0$ of COVID-19 in Ghana using the Next Generation Method and a SEIAHR compartmental model based on real-world data from March to July 2020.   | Next Generation Method                                   | $R_0$ for COVID-19 in Ghana was 2.52, indicating that each infected person was likely to spread the virus to more than two other individuals during the early stages of the pandemic.   |
| White L.F. et al. [53]                 | To estimate $R_0$ from the case notification data to enable real-time monitoring during infectious disease outbreaks.  | Sequential Bayes estimator and maximum likelihood method | Real-time estimation of $R_0$ using case notification data can provide timely insights into outbreak dynamics, but its accuracy depends on the completeness and reliability of the data.  |
| Al-Raei M. [54]                        | To estimate $R_0$ for COVID-19 in eight countries using the SIRD model, analyzing differences in transmission rates and providing insights into the pandemic's progression up to July 2020.                          | Runge-Kutta method                                       | $R_0$ for COVID-19 across eight countries ranged from 1.0011 to 2.7936, with the highest $R_0$ observed in the Syrian Arab Republic, indicating widespread transmission in that region.   |
| Brockhaus E.K. et al. [55]             | To estimate the effective reproductive number ( $R_e$ ) for COVID-19, identify the sources of variation, and propose ways to standardize analytical choices to improve consistency in real-time outbreak monitoring. | Cori method  | Discrepancies in estimates of the effective reproductive number ( $R_e$ ) for COVID-19 in Germany are largely due to differences in data sources, preprocessing methods, and assumptions about generation time and delays rather than the statistical methods themselves. |
| Lo Presti A. et al. [56]               | To estimate the reproductive numbers and analyze the demographic dynamics of <i>Neisseria meningitidis</i> strains in Italy, using Bayesian methods and genomic data to track transmission during outbreaks.         | Bayesian method  | $R_0$ for hypervirulent <i>Neisseria meningitidis</i> strains circulating in Italy ranged from 1.22 to 1.4, with a peak $R_t$ of 3.22 during the 2015 outbreak, indicating significant transmission potential.  |
| Ahmad Alajlan S. et al. [57]           | To evaluate the effectiveness of various lockdown phases in Saudi Arabia by calculating $R_0$ for COVID-19 during different stages of the outbreak using mobility data and government-reported infection rates.      | Compartmental model                                      | While the early implementation of lockdown strategies in Saudi Arabia helped contain the COVID-19 outbreak, $R_0$ slightly increased during the full lockdown period due to enhanced active surveillance and broader healthcare access.                                   |

Continuation of Table 3

| Paper                    | Task   | Method                    | Findings  |
|--------------------------|--|---------------------------|---|
| Kwok K.O. et al. [58]    | To estimate $R_0$ for monkeypox in the early phase of the 2022 outbreak using daily case data from three high-incidence populations to inform public health strategies for outbreak control. | Poisson likelihood method | $R_0$ values for monkeypox during the early 2022 outbreak ranged from 1.4 to 1.8 across England, Portugal, and Spain, indicating sustained transmission in immunologically naive populations.             |
| Huisman J.S. et al. [59] | To calculate $R_0$ in infectious diseases, and demonstrate its advantages over traditional compartmental models in capturing complex transmission patterns.                                  | Cori method               | A network-theoretic approach offers a more precise estimation of $R_0$ by accounting for heterogeneous contact patterns within populations, improving the understanding of disease transmission dynamics. |

The research on effective reproductive numbers further underscores the impact of methodological choices on the variability of estimates and highlights the need for standardized approaches to ensure consistency.

These limitations become more pronounced in the context of emergent crises, particularly the full-scale Russian invasion of Ukraine. The war has created conditions where infectious disease outbreaks are more likely due to overcrowding, limited medical access, and deteriorating sanitary conditions, further complicating the calculation of  $R_0$  and the design of effective interventions. These emergent contexts underscore the need for flexible, real-time models that incorporate rapidly changing conditions and provide actionable insights for public health responses in conflict zones and other crises.

#### 4. Methodology

The proposed methodology is illustrated in Figure 1.

The first step of the proposed methodology is data preparation aimed at classifying and analyzing epidemic threats caused by emergencies. This research also involves conducting a retrospective and real-time epidemiological analysis of infectious disease morbidity in the context of changes in the dynamics and manifestations of epidemic processes due to Russia's full-scale invasion of Ukraine.

The methodology involves comprehensive data collection, which focuses on gathering information on emergencies-related epidemic threats through collaboration with public health organizations. Specifically, for the analysis related to Russia's full-scale invasion of Ukraine, data on infectious diseases, demographic shifts, and other factors that may influence disease spread will be collected. The next step is data preprocessing, which includes cleaning to remove inconsistencies, duplicates, and missing values and standardizing important variable formats, such as dates, geographic identifiers, and disease

classifications, to ensure smooth integration and compatibility of various datasets. Data normalization to facilitate comparative analysis by adjusting for differences in population size, reporting standards, and diagnostic criteria over time is also part of this stage.

Epidemiological analysis forms the methodology's core, encompassing both retrospective and real-time aspects. The retrospective analysis focuses on identifying trends in infectious disease dynamics before and after emergencies, with particular emphasis on Russia's invasion of Ukraine, and assesses changes in morbidity rates, transmission patterns, and population vulnerability. Real-time analysis focuses on monitoring the epidemiological situation using near real-time data from various sources to assess the current spread of infectious diseases and the factors driving their dynamics. It also uses predictive modeling to forecast the Russian war's short- and long-term impacts on infectious disease dynamics.

The results of this comprehensive methodology include a detailed database of epidemic threats and infectious disease data related to emergencies, with a specific focus on the effects of Russia's invasion of Ukraine. The methodology also includes a set of classification schemes for epidemic threats and epidemiological analyses designed to support informed decision-making in public health and biosecurity.

The development of machine learning models to assess the impact of emergencies on infectious diseases begins with feature selection and design to identify key variables affecting disease transmission, such as changes in population density, healthcare availability, and environmental factors. Statistical machine learning methods process nonlinear relationships and interactions between these variables. To ensure reliability and generalizability, these models will be trained and validated on historical datasets using cross-validation techniques. To assess the impact of Russia's full-scale war on Ukraine, the models will be trained on data before the military invasion of February 24, 2022, and applied to subsequent data.

For deep learning, convolutional neural networks (CNN) will be designed to analyze spatial patterns of disease spread based on incidence data. In contrast, recurrent neural networks (RNN), particularly long short-term memory (LSTM) networks, will be deployed to analyze temporal dependencies and predict future epidemic dynamics based on past trends. Deep learning models will

be trained using backpropagation to minimize prediction errors and using dropout and batch normalization to prevent overfitting.

The framework for estimating the changes in epidemic process dynamics caused by emergencies through simulation is presented in Figure 2.

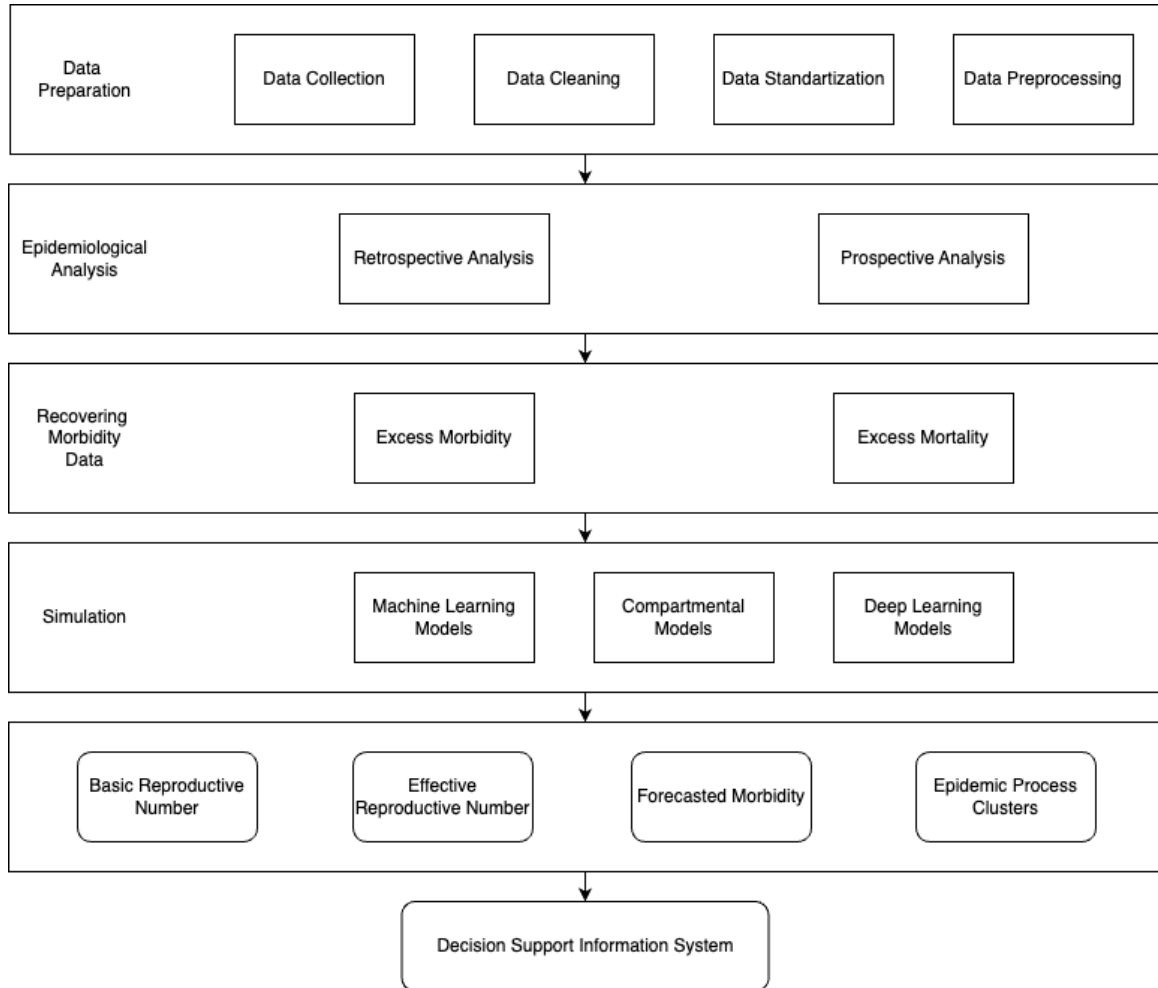


Fig. 1. Methodology of assessing the impact of emergencies on the spread of infectious diseases

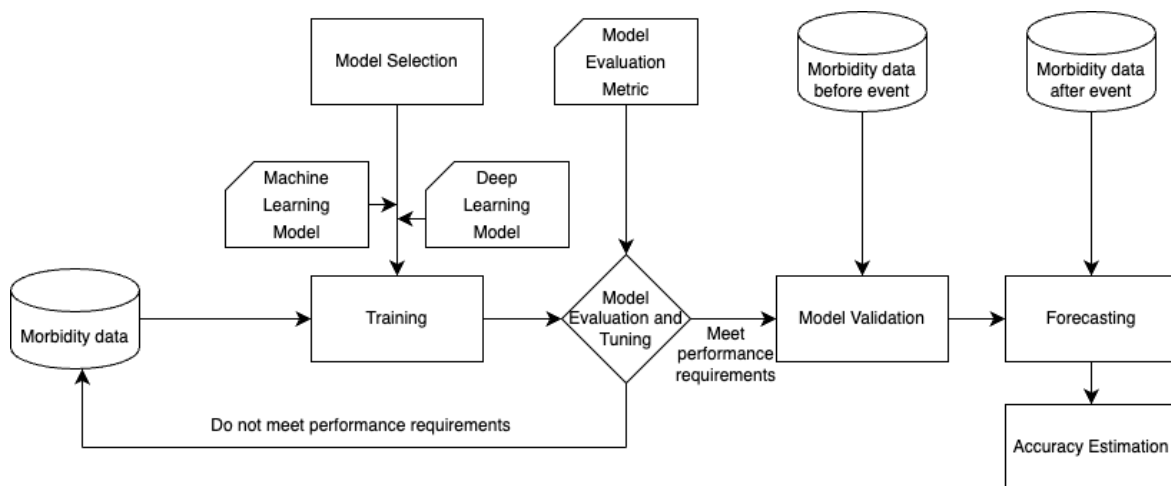


Fig. 2. Framework for assessing the impact of emergency situations on infectious diseases dynamics

Mixed-effects models will be developed to assess excess mortality from infectious diseases caused by emergencies. These models incorporate random effects that account for differences across regions and periods. The proposed model compares observed mortality levels during emergencies with those predicted by the model under normal conditions, adjusting for factors such as age, gender, and underlying health conditions.

To assess changes in the reproductive number ( $R_0$  and  $R_e$ ) of infectious diseases, this methodology proposes developing compartmental epidemiological models, such as the SIR model, enhanced with additional states, interaction rules between states, and Bayesian inference methods for parameter estimation under uncertainty. These models will be adapted to incorporate mobility data, vaccination rates, and non-pharmaceutical interventions to dynamically assess how  $R_0$  and  $R_e$  evolve in response to emergencies.

Experimental studies and the implementation of technologies to support biosecurity decision-making during emergencies include the creation of an information system prototype based on the developed architecture and specifications. A series of experimental studies is planned during which the prototype will be tested under simulated conditions mimicking real emergency scenarios. The developed models, methods, and information technologies will be implemented in Ukraine's healthcare system.

## 5. Discussion

This study introduces an innovative methodology designed to assess the impact of emergencies on the spread of infectious diseases, with a particular focus on the complexities of large-scale conflicts like the full-scale Russian invasion of Ukraine. The urgency of developing such a methodology is underscored by the profound disruptions that emergencies impose on social structures, healthcare systems, and environmental conditions, significantly altering the dynamics of epidemic processes.

The scientific novelty of our approach lies in its integrated use of advanced data analytics, machine learning, deep learning, and systems modeling to address complex biosecurity and epidemiological challenges in the context of emergencies. Unlike traditional models, our methodology accounts for many factors that are often overlooked but crucial during emergencies. These include biobehavioral changes, social disruptions, and environmental alterations that emerge as risk factors and drivers of infectious disease spread during conflicts.

Technically, the methodology begins with a comprehensive data preparation phase that involves classifying and analyzing epidemic threats specific to emergencies. This includes collecting extensive data on infectious diseases, demographic changes, environmental

conditions, and healthcare disruptions. The data were subjected to rigorous preprocessing to ensure accuracy and consistency, involving cleaning to remove inconsistencies and standardization of variables to facilitate integration from diverse sources.

A core component of the proposed methodology is the integration of machine learning and deep learning models to consider how emergencies affect infectious disease dynamics. By identifying key variables influencing disease transmission, such as population displacement, healthcare accessibility, and environmental degradation, we employ statistical machine learning methods to process complex, nonlinear relationships between these factors. For example, CNNs are used to analyze spatial patterns of disease spread. At the same time, RNNs, particularly LSTM networks, capture temporal dependencies and forecast future epidemic trends based on historical data.

A significant innovation is the development of an information system architecture specifically designed for analyzing epidemic threats in real-time. The proposed system leverages the latest advances in data processing and artificial intelligence to handle and analyze large volumes of heterogeneous data. The ability to dynamically adapt analytical models in response to the evolving nature of emergencies ensures that decision-makers receive relevant and up-to-date information. This dynamic adaptability is achieved through the system's capacity to incorporate new data streams and adjust model parameters as conditions change, providing a more accurate and timely assessment of epidemic threats.

Our methodology includes developing sophisticated models for assessing excess mortality and evaluating changes in key epidemiological parameters, such as the basic reproductive number ( $R_0$ ) and effective reproductive number ( $R_e$ ), during emergencies. By incorporating complex variables affected by emergencies, such as healthcare system disruptions and behavioral changes in the population, we can offer a more precise and dynamic evaluation of the impact on public health. For example, mixed-effects models are employed to assess excess mortality, accounting for variations across regions and periods, while enhanced compartmental models are adapted to reflect altered transmission dynamics during emergencies.

The practical implications of this methodology are substantial. Providing a comprehensive and nuanced analysis of the factors influencing disease spread during emergencies enables policymakers and public health officials to make informed decisions regarding resource allocation, intervention strategies, and preventive measures. The ability to predict disease spread and identify high-risk areas facilitates targeted actions that are crucial for mitigating the impact of infectious diseases during crises.

One of the key advantages of this methodology over existing models is its holistic risk assessment approach. Integrating biobehavioral, social, and environmental factors generated by emergencies captures the multifaceted nature of epidemic threats in a way that traditional models, which often assume homogeneous populations and static conditions, cannot. The methodology's flexibility and adaptability are also significant strengths. It is designed to adjust dynamically as new data become available and conditions evolve, ensuring that it remains relevant and effective during an emergency.

The urgency of implementing such a methodology in the modern world is evident. The increasing frequency and complexity of emergencies demand advanced tools capable of handling their multifaceted challenges. Societies' interconnectedness means that local emergencies can have global repercussions, making it imperative to enhance our capacity to assess and respond to epidemic threats swiftly and effectively.

Despite the strengths and innovations of the proposed methodology, several limitations must be acknowledged. The primary limitation is the dependency on data quality and availability during emergencies. Emergencies, particularly large-scale conflicts, often disrupt data collection processes, leading to incomplete, inconsistent, or delayed datasets. This can adversely affect the accuracy and reliability of machine learning models and simulations, potentially limiting their predictive ability. To address these challenges, future research could explore integrating alternative data sources, such as satellite imagery, remote sensing, and mobile data. These methods can provide valuable insights in environments where traditional data collection is hindered or incomplete.

Additionally, integrating diverse data sources, including epidemiological, demographic, environmental, and social data, poses challenges in harmonization and standardization. The computational demands of advanced machine learning and deep learning models are also limited because they require substantial computational resources and technical expertise that may not be readily available in all settings, especially in low-resource environments or during acute phases of emergencies. To mitigate the computational demands, future efforts could involve partnerships with international organizations or leverage cloud-based platforms to ensure access to scalable computational resources in low-resource or conflict-affected environments.

This study significantly contributes to biosecurity, public health preparedness, and emergency response by presenting a methodology that advances our ability to control epidemic threats during emergencies. Integrating advanced analytics, machine learning, deep learning, and system modeling provides a more accurate, dynamic, and comprehensive assessment of the impact on public health. This methodology not only fills current research

and application gaps but also sets the stage for more effective epidemic threat management in an increasingly uncertain world.

These findings align with the principles of Big Safety, which emphasize the integration of diverse safety concerns, such as infection control and disaster mitigation. This multidimensional approach is essential for formulating effective responses to public health emergencies, particularly in conflict zones where disaster effects and infectious disease outbreaks are often intertwined. Addressing these interconnected risks through a Big Safety lens enhances the resilience and preparedness of healthcare systems in such environments.

## Conclusions

This study presents a comprehensive methodology for assessing the impact of emergencies on the spread of infectious diseases, using the full-scale Russian invasion of Ukraine as a case study. This research has introduced significant advancements in biosecurity and epidemiology by integrating advanced data analytics, machine learning, deep learning, and system modeling.

The novelty of our approach lies in its integrated methodology, which combines cutting-edge data analytics with machine learning and deep learning models to tackle complex biosecurity and epidemiological challenges in the context of emergencies. For the first time, we have identified the driving forces, developmental characteristics, and manifestations of the epidemic processes of current infectious diseases during a large-scale war in a European country. This includes accounting for the complex interplay between social and natural factors. Unlike existing models, our methodology incorporates biobehavioral, social, and environmental components generated by the conflict, recognizing their roles as risk factors and drivers of epidemic processes. This comprehensive perspective enables the development of strategies to mitigate or eliminate the negative impact of infectious disease morbidity.

A key contribution of this study is the development of an information system architecture specifically designed for analyzing epidemic threats. This new structure integrates real-time data collection, advanced analytics, and ergonomic information visualization. The proposed system can handle and analyze large volumes of heterogeneous data by leveraging the latest advances in data processing and artificial intelligence. Its ability to dynamically adapt analytical models in response to the evolving nature of emergencies provides decision-makers with relevant and timely information, enhancing their capacity to implement effective interventions.

Integrating machine learning and deep learning models allows to explore more deeply how emergencies influence the dynamics of infectious diseases. We have

developed new models and methods capable of rapidly adapting to emergencies by considering new factors that affect epidemic processes. This represents a significant advancement in predictive epidemiology, providing detailed and comprehensive insights into disease dynamics in crisis contexts.

The study contributes to the field by developing sophisticated models for assessing excess mortality and evaluating changes in key epidemiological parameters, such as the basic reproductive number ( $R_0$ ) and effective reproductive number ( $R_e$ ), during emergencies. By incorporating complex variables affected by emergencies, such as healthcare system disruptions and changes in human behavior, our approach provides a more accurate and dynamic assessment of their impact on public health.

In future research, it will be essential to validate and refine the proposed methodology across different types of emergencies and regions to enhance its generalizability and effectiveness. Improving data collection methods during emergencies is crucial, potentially through remote sensing technologies, mobile data collection platforms, or international collaborations to ensure reliable and timely data. Optimizing the computational efficiency of models will also make advanced modeling techniques more accessible in various settings, including low-resource environments.

**Contributions of authors:** conceptualization – **Dmytro Chumachenko**; methodology – **Dmytro Chumachenko, K. Bazilevych, Mykola Butkevych, Ievgen Meniailov, Yurii Parfeniuk, Ievgen Sidenko, Tetyana Chumachenko**; formulation of tasks – **Dmytro Chumachenko, K. Bazilevych, Mykola Butkevych, Ievgen Meniailov, Yurii Parfeniuk, Ievgen Sidenko, Tetyana Chumachenko**; analysis – **Dmytro Chumachenko, K. Bazilevych, Mykola Butkevych, Ievgen Meniailov, Yurii Parfeniuk, Ievgen Sidenko, Tetyana Chumachenko**; development of model – **Dmytro Chumachenko, K. Bazilevych, Mykola Butkevych, Ievgen Meniailov, Yurii Parfeniuk, Ievgen Sidenko, Tetyana Chumachenko**; verification – **Dmytro Chumachenko, Tetyana Chumachenko**; visualization – **Dmytro Chumachenko**; epidemiological analysis – **Tetyana Chumachenko**; design and architecture – **Kseniia Bazilevych, Ievgen Meniailov, Yurii Parfeniuk**; machine learning models development – **Dmytro Chumachenko, Mykola Butkevych, Ievgen Meniailov**; deep learning models development – **Dmytro Chumachenko, Mykola Butkevych, Ievgen Sidenko**; excess mortality methods development – **Dmytro Chumachenko, Mykola Butkevych, Ievgen Meniailov**; compartmental models development – **Dmytro Chumachenko, Kseniia Bazilevych, Ievgen Meniailov**; writing – original draft preparation – **Dmytro Chumachenko**; writing – review and editing – **Kseniia Bazilevych, Mykola Butkevych,**

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### Conflict of interest

The authors declare that they have no conflict of interest concerning this research, whether financial, personal, authorship, or otherwise, that could affect the research and its results presented in this paper.

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### Project information

The 2023.03/0197 project “Multidisciplinary study of the impact of emergency situations on the infectious diseases spreading to support management decision-making in the field of population biosafety” aimed to enhance the effectiveness of decision-making for ensuring the biosecurity of the population during emergencies through the development of intelligent information technologies for assessing changes in epidemic situations caused by emergencies.

The project represents an interdisciplinary study that combines scientific results obtained by specialists in artificial intelligence systems and tools, mathematical modeling, epidemiology, information technology, and public health. The project involves retrospective and operational epidemiological analyses of infectious disease incidence in the context of changing dynamics and manifestations of epidemic processes caused by Russia’s full-scale invasion of Ukraine; the development of machine learning and deep learning models to assess the impact of emergencies on the dynamics of infectious disease incidence; the development of methods for assessing excess mortality due to infectious diseases; and the development of an intelligent information system for decision support during emergencies. The implementation of research results will enhance the effectiveness of management decisions regarding the biosecurity of the population and the development of strategies for preventive measures.

The scientific novelty of this project lies in its integrated approach to combining advanced data analytics, machine learning, deep learning, and system modeling methods to address the complex issues of biosecurity and epidemiology in the context of emergencies. This project features several innovative elements that address current gaps in research and application aimed at improving the understanding and management of epidemic threats during emergencies.



The scientific and scientific-technical production created by this project is a comprehensive intellectual decision-support system for biosecurity in emergencies, which, unlike existing ones, will identify factors affecting the epidemic process and quickly adapt to emergent diseases and the spread of new dangerous pathogens. Unlike existing models, new epidemic process models and epidemiological diagnostic methods will allow the development of effective scientifically-based strategies for disease prevention and epidemic dynamics mitigation.

The practical value of the project results consists not only of the social and medical components, dictated by the reduction of epidemic morbidity but also of an important economic component, dictated by the scientific justification of anti-epidemic measures, including restrictive and isolation measures, which will significantly reduce the economic losses caused by infectious diseases during wartime conditions.

The implementation of the project's scientific and applied results in the Public Health Centers of Ukraine and preventive medicine facilities will ensure the making of effective preventive decisions and reduce the negative economic, medical, and social impact of epidemics on society and the state conditions of Russia's full-scale invasion of Ukraine.

#### Data availability

The manuscript contains no associated data

#### Use of Artificial Intelligence

The authors confirm that they did not use generative artificial intelligence methods in their work.

All the authors have read and agreed to the publication of the final version of this manuscript.

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## МЕТОДОЛОГІЯ ОЦІНКИ ВПЛИВУ НАДЗВИЧАЙНИХ СИТУАЦІЙ НА ПОШИРЕННЯ ІНФЕКЦІЙНИХ ХВОРОБ

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На поширення інфекційних захворювань значно впливають надзвичайні ситуації, зокрема військові конфлікти, які порушують функціонування систем охорони здоров'я та підвищують ризики епідемій. Повномасштабне російське вторгнення в Україну ще більше загострило ці проблеми, спричинивши екологічні пошкодження, масові переміщення населення та руйнування системи охорони здоров'я, що сприяє поширенню інфекційних захворювань. **Метою** дослідження є розробка комплексної методології для оцінки впливу надзвичайних ситуацій на поширення інфекційних захворювань, зосереджуючись на повномасштабному вторгненні Росії в Україну. **Об'єктом** дослідження є епідемічні загрози, що виникають у зв'язку з надзвичайними ситуаціями, зокрема збільшене поширення інфекційних захворювань через фактори, викликані війною. **Предметом** дослідження є методи і моделі передачі інфекційних захворювань в умовах надзвичайних ситуацій, з акцентом на повномасштабне російське вторгнення в Україну. **Задачі** дослідження полягають в аналізі поточного стану досліджень і розробці методології оцінки впливу надзвичайних ситуацій на поширення інфекційних захворювань. Запропонована **методологія** включає кілька ключових компонентів. Комплексні дані від установ охорони здоров'я містять статистику інфекційних захворювань, демографічні зміни, порушення в охороні здоров'я та екологічні фактори, загострені надзвичайними ситуаціями. Попередня обробка даних забезпечує усунення невідповідностей, стандартизацію форматів і нормалізацію для врахування різниці в розмірах населення. Моделі машинного навчання, включаючи згорткові нейронні мережі та рекурентні нейронні мережі, розробляються для моделювання поширення захворювань на основі демографічних, екологічних і медичних змінних. Моделі глибокого навчання аналізують просторові та часові закономірності, тоді як компартментні моделі, такі як SIR, оцінюють зміни в репродуктивних числах ( $R_0$  і  $R_e$ ). Крім того, моделі надлишкової смертності включають змішані ефекти для врахування регіональних та часових варіацій. Методологія включає моніторинг епідемічних загроз у режимі реального часу з використанням даних з різних джерел, що дає змогу динамічно оцінювати поширення захворювань і сприяє прогнозуванню моделюванню. Моделі тренуються на історичних даних і верифікуються за допомогою методів перехресної перевірки, щоб забезпечити надійність і можливість узагальнення, з особливим акцентом на періоди до і після вторгнення в Україну. **Результати:** Дослідження пропонує комплексний фреймворк для збору та обробки даних про інфекційні захворювання та епідемічні загрози в умовах надзвичайних ситуацій. Розроблені моделі машинного навчання та епідеміологічні моделі, які тренувалися на даних до та після вторгнення, дозволять аналізувати закономірності передачі захворювань та прогнозувати динаміку майбутніх епідемій. **Висновок:** Запропонована методологія усуває поточні прогалини в моделюванні інфекційних захворювань в умовах надзвичайних ситуацій, інтегруючи дані в реальному часі та техніки машинного навчання. Це дослідження покращує процес прийняття рішень у сфері

управління охороною здоров'я та біобезпеки під час криз, особливо в регіонах, постраждалих від війни, таких як Україна.

**Ключові слова:** епідемічна модель; надзвичайна ситуація; війна; епідемічний процес; моделювання; інфекційні хвороби.

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