

Simulation of Influenza Dynamics in Kharkiv Oblast (Ukraine) using ARIMA Model

Mykola Butkevych and Dmytro Chumachenko

National Aerospace University "Kharkiv Aviation Institute", Vadym Manko str., 17, Kharkiv, 61070, Ukraine

Abstract

Influenza remains a significant public health concern globally, with its seasonal outbreaks leading to high morbidity and mortality. This is especially relevant in conflict-affected regions like Kharkiv Oblast, Ukraine, where the ongoing Russian war has severely disrupted the healthcare system. This study aimed to develop an ARIMA-based model to simulate and forecast influenza incidence in Kharkiv Oblast, aiding public health decision-making in a challenging environment. The study utilized monthly influenza incidence data from January 2013 to April 2024, sourced from the Kharkiv Oblast Centre for Disease Control and Prevention. The data were normalized using Min-Max scaling, and 90% of the dataset was used for training, with the remaining 10% reserved for testing. The ARIMA model was selected for its ability to handle non-stationary data and suitability for time-series forecasting. Model performance was evaluated using Mean Absolute Percentage Error (MAPE) and Mean Absolute Error (MAE). The results showed that the ARIMA (10,1,11) model achieved a MAPE of 9.5879% and an MAE of 37.5099, indicating strong predictive accuracy. This suggests that ARIMA modelling can effectively forecast influenza trends, even in regions with strained healthcare systems and unreliable real-time data collection. This study demonstrates ARIMA models' practical and scientific potential for disease forecasting in conflict-affected regions. These findings contribute to using data-driven models to enhance public health interventions in unstable environments.

Keywords

Epidemic model, machine learning, influenza, Ukraine, infectious disease simulation

1. Introduction

Influenza, commonly known as the flu, is a highly contagious respiratory illness. These viruses primarily infect the upper and lower respiratory tracts, leading to symptoms such as sudden onset of high fever, cough, sore throat, muscle and joint pain, headache, and severe fatigue [1]. Influenza viruses are categorized into three main types affecting humans: A, B, and C. Types A and B are responsible for the seasonal epidemics observed annually [2]. In contrast, type C infections cause mild respiratory illnesses and are not associated with epidemics. Influenza viruses' rapid mutation rate is a defining characteristic, particularly through mechanisms like antigenic drift and antigenic shift [3]. Antigenic drift involves small genetic changes over time, leading to new virus strains that the immune system may not recognize. Antigenic shift, which occurs only in type A viruses, involves abrupt, major changes resulting in new hemagglutinin or neuraminidase proteins, potentially leading to pandemics due to a lack of population immunity.

Globally, influenza represents a significant public health concern, contributing to yearly morbidity and mortality [4]. The World Health Organization estimates that annual influenza epidemics result in about 1 billion infections worldwide, including 3 to 5 million cases of severe illness and 290,000 to 650,000 respiratory deaths [5]. The impact of influenza extends beyond health, imposing considerable economic burdens due to increased healthcare costs, hospitalizations, and loss of productivity from work and school absenteeism [6]. Influenza pandemics, such as the 2009 H1N1 pandemic, have demonstrated the virus's potential for widespread devastation, emphasizing vigilant surveillance and prompt response strategies. Vaccination remains the most effective preventive measure against influenza [7]. Yet, the virus's antigenic variability can compromise vaccine efficacy,

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✉ m.v.butkevych@khai.edu (M. Butkevych); dichumachenko@gmail.com (D. Chumachenko)

ORCID 0000-0001-8189-631X (M. Butkevych); 0000-0003-2623-3294 (D. Chumachenko)

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and global vaccination coverage often falls short of targets due to factors like vaccine hesitancy and accessibility issues.

Influenza continues to pose a critical health challenge in Ukraine, particularly in regions such as Kharkiv Oblast [8]. The full-scale Russian invasion that began in 2022 has exacerbated existing public health issues by severely disrupting healthcare infrastructure and disease surveillance systems [9]. The war has led to significant population displacement, with many individuals residing in overcrowded shelters or temporary accommodations lacking adequate sanitation and healthcare services. These conditions facilitate the transmission of infectious diseases, including influenza, by increasing close contact among individuals and reducing access to preventive measures like vaccination and antiviral medications [10]. Additionally, the strain on healthcare resources hinders effective diagnosis, treatment, and reporting of influenza cases, complicating efforts to monitor and control outbreaks. Understanding influenza dynamics in this context is crucial for developing targeted interventions to protect vulnerable populations and prevent further strain on the already challenged healthcare system.

Data-driven healthcare approaches have become increasingly vital in controlling and managing epidemic processes, especially when traditional surveillance methods are compromised [11]. Statistical models, such as the Autoregressive Integrated Moving Average (ARIMA) model, offer powerful tools for analyzing time-series data to understand past trends and forecast future disease incidence [12]. By leveraging historical influenza data, ARIMA models can provide accurate short-term predictions of influenza activity, enabling health authorities to allocate resources efficiently, plan vaccination campaigns, and implement timely public health interventions [13]. In conflict-affected regions like Kharkiv Oblast, where data collection may be fragmented, predictive modelling can compensate for gaps in surveillance by identifying patterns and potential outbreaks based on available information. Incorporating data-driven methodologies into public health strategies enhances the capacity to respond proactively to influenza epidemics, ultimately reducing the disease burden and improving health outcomes for the affected populations.

The research aims to develop an ARIMA-based forecasting model of influenza in Kharkiv oblast of Ukraine.

Current research is a part of the comprehensive information system for assessing the impact of emergencies on the spread of infectious diseases described in [14].

2. Current research analysis

The application of the ARIMA model in simulating and forecasting influenza dynamics has gained significant attention in epidemiological research. ARIMA models have been utilized to analyze time-series data of influenza cases, enabling researchers to predict future trends and understand the temporal patterns of outbreaks. These models effectively capture the seasonality and fluctuations in influenza incidence, providing valuable insights for public health planning and intervention strategies. The flexibility of ARIMA in handling non-stationary data and its capacity to incorporate both autoregressive and moving average components make it a suitable tool for modelling the complex behaviour of influenza transmission. Researchers have applied ARIMA models across various geographical regions and contexts, demonstrating their adaptability and effectiveness in different epidemiological settings.

The study [16] focuses on the epidemiology of influenza viruses among children in Wuhan, China, using data from a nine-year surveillance period and forecasting future trends with ARIMA models. The primary objective was to analyze the positive rates of influenza virus types and apply time series models for short-term predictions. One strength of this research is its comprehensive data collection over a substantial period, which enables more reliable statistical modelling. However, the study has limitations. First, the consistency of throat swab quality across different hospitals could not be ensured, potentially affecting the accuracy of influenza detection. Additionally, the limited number of swabs taken per week from a high-volume hospital might not fully represent the broader

population, limiting the generalizability of the findings. Improving the homogeneity of sample collection and expanding surveillance coverage could enhance future studies.

Paper [16] compares the effectiveness of ARIMA and LSTM models in predicting influenza trends using air quality data from central Taiwan between 2014 and 2018. Both models were applied to datasets from three regions: Changhua County, Taichung City, and Nantou County. LSTM models, particularly the variant incorporating the Extra Trees Classifier feature selection, demonstrated superior accuracy over ARIMA. This was especially notable in Taichung City, where LSTM ETC improved prediction accuracy by 73%. However, the study has limitations. The scope of the prediction relies heavily on air quality and meteorological data, which may not account for other factors influencing influenza trends, such as population behaviour or healthcare interventions. Additionally, using a limited geographical area and timeframe may restrict the generalizability of the findings to other regions or longer periods.

The study [17] investigates using ARIMA and LSTM models to predict influenza-like illness and respiratory diseases based on air quality data from Taiwan. By comparing both models across five- and ten-year datasets, the results demonstrate that LSTM models outperform ARIMA regarding prediction accuracy, particularly when extended to longer periods. LSTM models also benefit from feature selection techniques, such as matrix correlation and extra trees classifier, which enhance the prediction results. However, a key limitation of the study is its reliance on data from a single geographical region, which may limit the generalizability of the results to other locations. Additionally, while LSTM models show higher accuracy, they require significantly more computational resources than ARIMA, which could be challenging in large-scale applications. Moreover, future work may explore real-time data integration and further feature selection improvements to enhance prediction reliability.

The paper [18] compares the predictive capabilities of ARIMA, GLARMA, and Random Forest (RF) models in forecasting the frequency of influenza A virus in Ontario swine populations. The RF model consistently outperformed the ARIMA and GLARMA models in predicting increases in diagnostic and positive virological submissions, particularly at weekly and monthly intervals. The RF model demonstrated greater sensitivity and lower error rates, making it a more reliable tool for surveillance purposes. However, the study has limitations. The data used were based on voluntary diagnostic submissions, which may not fully represent the swine population, leading to potential biases in the results. Furthermore, the analysis did not include environmental factors that could influence IAV trends, limiting the comprehensiveness of the predictive models.

The study [19] examines the relationship between influenza incidence and various climate indicators in Guangxi, China, using ARIMA and ARIMAX models for predictive analysis. The findings indicate that air pollution variables, such as NO₂ and SO₂, and meteorological factors, like temperature and humidity, significantly influence influenza incidence, with NO₂ showing the strongest positive correlation. The ARIMAX model, which incorporates these exogenous variables, performed better than the standard ARIMA model, offering improved prediction accuracy. However, the study is limited by its reliance on data from a single region, which may limit the generalizability of the results to other geographic areas or climates. Additionally, the influence of other potential factors, such as healthcare interventions or population movement, was not considered, which could affect the accuracy of the predictions.

The paper [20] compares the ARIMA and Holt-Winters Exponential Smoothing (HWES) models for predicting influenza outbreaks based on Twitter data from Australia collected between 2015 and 2017. Both models were tested for their ability to predict influenza cases by analyzing tweets related to flu symptoms and comparing them to confirmed cases from the Centers for Disease Control. The ARIMA model showed superior predictive accuracy with a mean relative error of 7.25%, compared to 11.29% for the HWES model. A major strength of this study lies in utilizing social media data, which allows for earlier detection of influenza trends compared to traditional CDC reports. However, the study has limitations, including the inherent noise in social media data, as flu-related tweets do not always correspond to confirmed cases.

The paper [21] evaluates the effectiveness of different time series models, ARIMA, SARIMA, and XGBoost, in predicting monthly seasonal influenza cases in Saudi Arabia. The analysis demonstrates that the XGBoost model significantly outperforms both ARIMA and SARIMA models in accuracy, as indicated by lower mean absolute error, mean squared error, and root mean squared error. The XGBoost model's ability to capture complex, nonlinear relationships is well-suited for influenza prediction. However, one limitation of the study is its reliance on a relatively short dataset covering just five years, which may not fully capture long-term trends and seasonal variations. Additionally, the study does not account for other potential influencing factors, such as public health interventions or demographic variables, which could further improve the predictive power of the models.

Despite the extensive application of ARIMA models in forecasting influenza dynamics across various regions and contexts, there remains a gap in research focusing on emergent settings like Kharkiv Oblast. The unique challenges posed by the full-scale Russian invasion necessitate a tailored approach to influenza modelling. Our study aims to address this gap by applying the ARIMA model to simulate and predict influenza trends in Kharkiv oblast under these atypical conditions. By focusing on this emergent setting, we contribute to the existing body of knowledge by demonstrating the adaptability and effectiveness of ARIMA modelling in environments with limited data and heightened public health challenges. This research enhances the understanding of influenza dynamics in conflict-affected regions and underscores the critical role of data-driven methodologies in informing public health interventions amidst crises.

3. Materials and methods

For this study, we obtained monthly influenza incidence data from the Kharkiv Oblast Centre for Disease Control and Prevention. The dataset spans from January 2013 to April 2024 and consists of 136 observations representing the number of reported influenza cases in Kharkiv Oblast during this period. Figure 1 presents the distribution of influenza cases in Kharkiv oblast of Ukraine.

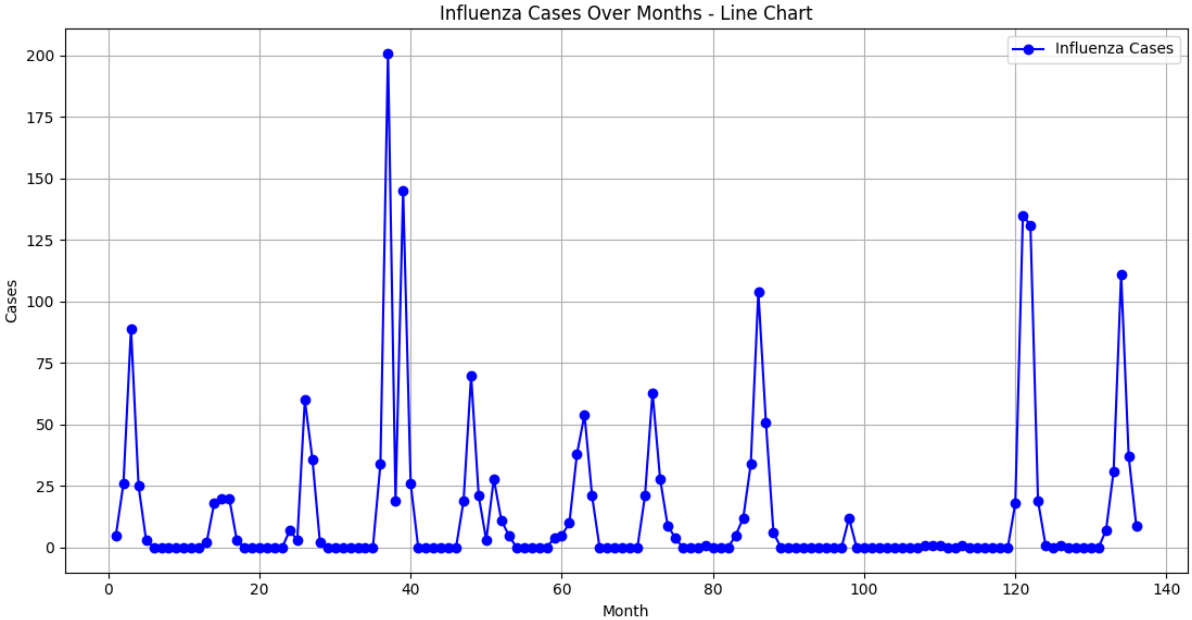


Figure 1: The distribution of influenza morbidity in Kharkiv oblast of Ukraine

We applied Min-Max normalization to the influenza incidence values to prepare the data for analysis. This scaling technique transforms the data to a fixed range, specifically from 1 to 2. Normalization is essential for standardizing the data, reducing the impact of varying scales, and enhancing the performance of the ARIMA model.

The Min-Max normalization is defined as:

$$X_{scaled} = X_{min} + \frac{(X - X_{orig\ min})(X_{max} - X_{min})}{X_{orig\ max} - X_{orig\ min}}, \quad (1)$$

where X is the original data point, X_{scaled} is the normalized data point, X_{min} and X_{max} are the desired scaling range, $X_{orig\ min}$ and $X_{orig\ max}$ are the minimum and maximum values of the original dataset.

The normalized dataset was then divided into training and testing sets to evaluate the forecasting capability of the model. The training set included 90% of the data (122 observations from January 2013 to October 2023), while the testing set comprised the remaining 10% (14 observations from November 2023 to April 2024). This split allows the model to be trained on historical data and tested on future, unseen data, providing a robust assessment of its predictive accuracy.

The ARIMA model is a widely used statistical approach for time series forecasting [22]. It combines three components:

1. Autoregressive (AR) Component models the relationship between an observation and a number of lagged observations.
2. Integrated (I) Component involves differencing the time series to achieve stationarity.
3. Moving Average (MA) Component models the relationship between an observation and a residual error from a moving average model applied to lagged observations.

An ARIMA model is denoted as ARIMA (p, d, q), where p is the order of the autoregressive part, d is the degree of differencing, q is the order of the moving average part.

The general form of the ARIMA (p, d, q) model is:

$$\Phi(B)(1 - B)^d y_t = \Theta(B)\epsilon_t, \quad (2)$$

where y_t is the time series at time t , B is the backshift operator ($By_t = y_{t-1}$), $\Phi(B) = 1 - \phi_1 B - \phi_2 B^2 - \dots - \phi_p B^p$ is the autoregressive operator, $\Theta(B) = 1 - \theta_1 B - \theta_2 B^2 - \dots - \theta_q B^q$ is the moving average operator, ϵ_t is the error term at time t .

4. Results

To identify the appropriate ARIMA model for our data, we followed these steps:

1. Stationarity Testing: We conducted the Augmented Dickey-Fuller test to assess whether the time series is stationary. If the series was non-stationary, we applied differencing until stationarity was achieved, determining the value of d.
2. Autocorrelation Analysis: We analyzed the Autocorrelation Function (ACF) and Partial Autocorrelation Function (PACF) plots of the stationary series to identify potential values for p and q.
 - a. ACF measures the correlation between the time series and its lagged values.
 - b. PACF measures the correlation between the time series and its lagged values after removing the effects of shorter lags.
3. Model Selection: Based on the ACF and PACF analyses, we tested multiple ARIMA models with different combinations of p, d, and q. We evaluated these models using the Akaike Information Criterion and the Bayesian Information Criterion, selecting the model with the lowest AIC and BIC values as the optimal one.
4. Parameter Estimation: The parameters of the selected ARIMA model were estimated using the Maximum Likelihood Estimation (MLE) method. MLE finds the parameter values that maximize the likelihood function, which measures how well the model explains the observed data.

With a validated ARIMA model, we proceeded to forecast influenza incidence for the testing period (November 2023 to April 2024). To evaluate the forecasting performance, we calculated the following error metrics.

Mean Absolute Percentage Error (MAPE):

$$\text{MAPE} = \frac{100\%}{n} \sum_{t=1}^n \left| \frac{A_t - F_t}{A_t} \right|, \quad (3)$$

where A_t is the actual value at time t , F_t is the forecasted value at time t , n is the number of forecasts.

Mean Absolute Error (MAE):

$$\text{MAE} = \frac{1}{n} \sum_{t=1}^n |A_t - F_t|. \quad (4)$$

The best ARIMA order is (10, 1, 11).

Figure 2 presents the forecasted influenza morbidity in Kharkiv oblast of Ukraine.

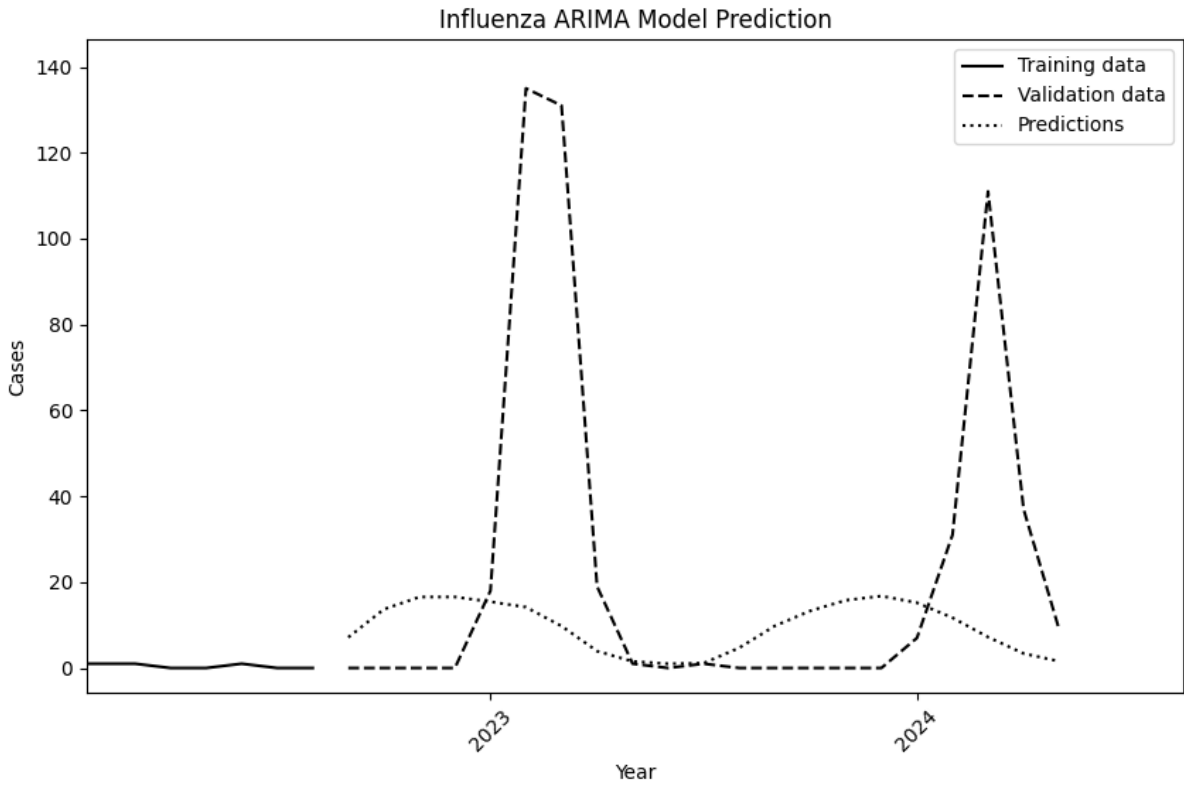


Figure 2: The forecasted influenza morbidity in Kharkiv oblast of Ukraine

MAPE of the model is 9.5879.

MAE of the model is 37.5099.

5. Discussion

The paper applied the ARIMA model to simulate and predict influenza trends in the Kharkiv Oblast of Ukraine, demonstrating the model's adaptability to conflict-affected regions where healthcare and surveillance systems are under stress. Applying time-series models like ARIMA provides valuable insights for public health planning, particularly in areas where real-time data collection may be

compromised. The results of this study underscore the potential of data-driven models to aid decision-making processes in regions facing complex socio-political challenges.

The ARIMA (10,1,11) model was selected as the optimal model, ensuring minimal forecast error. This choice reflects ARIMA's robustness in capturing the seasonality and fluctuations in influenza dynamics, which are influenced by environmental and behavioural factors.

The model's performance was evaluated using standard metrics like MAPE and MAE. The model demonstrated strong predictive accuracy with a MAPE of 9.5879% and an MAE of 37.5099. These results suggest the model is well-suited for forecasting influenza trends in regions where data quality and availability may vary. However, while the error margins are within an acceptable range, there is room for improvement. The performance might be further optimized by integrating additional variables such as climate data, healthcare access, or vaccination rates, which have been shown in other studies to influence influenza transmission.

This study's findings highlight the ARIMA models' significant role in informing public health interventions, especially in conflict-affected regions like Kharkiv oblast. The ability to forecast influenza incidence with reasonable accuracy enables health authorities to allocate resources effectively, plan vaccination campaigns, and implement early interventions to curb outbreaks.

The situation in Kharkiv Oblast, exacerbated by the Russian invasion, presents a unique case where healthcare infrastructure is strained, and access to basic services, including vaccinations and antiviral medications, is limited. In this context, predictive models like ARIMA become essential tools for disease surveillance, compensating for gaps in real-time data collection. By identifying trends in influenza transmission, authorities can take preemptive measures to protect vulnerable populations, particularly those displaced by the conflict and living in overcrowded conditions.

While the study demonstrates the effectiveness of the ARIMA model, it is important to acknowledge its limitations. While capable of capturing time-series patterns, the ARIMA model is inherently limited by its linear nature. Influenza dynamics, influenced by non-linear factors such as sudden changes in weather, migration patterns, or population immunity, may not be fully accounted for by the ARIMA model alone. To address these limitations, future studies could explore the integration of machine learning approaches, such as Long Short-Term Memory (LSTM) models, which have been shown to outperform ARIMA in certain contexts due to their ability to capture non-linear relationships in the data.

In conflict-affected regions, interruptions in surveillance systems can result in incomplete or fragmented data, potentially affecting the accuracy of the forecasts. Future studies could improve model robustness by incorporating real-time data sources, such as social media signals or environmental data, to enhance the model's predictive capabilities.

6. Conclusions

This study developed and applied an ARIMA (10,1,11) model to forecast influenza dynamics in Kharkiv Oblast, Ukraine, a region facing significant public health challenges due to the ongoing full-scale Russian invasion. The model demonstrated strong predictive accuracy, as indicated by the low error margins, providing essential insights for influenza forecasting in regions with disrupted healthcare systems.

The primary contribution of this study lies in its application of ARIMA modelling to a conflict-affected region, emphasizing the adaptability of time-series models in non-ideal conditions. Focusing on Kharkiv oblast, the study highlights the capacity of data-driven models to fill gaps left by compromised traditional surveillance systems. This research offers a data-centric approach to support public health efforts where direct interventions and accurate data collection may be difficult.

This scientific novelty stems from applying ARIMA in a complex, conflict-affected setting. While ARIMA has been widely used for influenza forecasting in stable environments, this study shows that the model can be adapted for effective forecasting even in regions with unreliable or incomplete data. This research also lays the foundation for further exploration into how predictive models can be tailored to dynamic, high-risk environments with limited surveillance infrastructure.

The study's practical novelty is demonstrated through its immediate applicability in real-world scenarios where public health authorities face resource constraints. The ARIMA model provides health agencies in Kharkiv and similar regions with a practical tool to effectively forecast influenza outbreaks and allocate resources. As the region's healthcare infrastructure continues to be under strain due to conflict, such models could help prioritize vaccination campaigns and emergency responses to mitigate the spread of influenza.

While this study focused on the ARIMA model, future research could expand the scope by incorporating other predictive models, such as LSTM or hybrid approaches, to improve forecasting accuracy in highly dynamic environments. Additionally, integrating real-time data sources, including climate, migration, and social media indicators, would enhance the model's robustness and predictive power. Expanding this research to other conflict-affected regions or including other infectious diseases would also provide a broader understanding of how predictive models can aid public health decision-making in volatile situations.

In conclusion, this research underscores the importance of predictive modelling in public health, particularly in conflict-affected regions. It offers a roadmap for future studies to build upon its findings by incorporating more advanced methodologies and diverse data sources.

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