

D. CHUMACHENKO¹, I. MENIAILOV¹, A. HRIMOV¹,
V. LOPATKA¹, O. MOROZ², O. TOLSTOLUZKA²

¹ National Aerospace University “Kharkiv Aviation Institute”, Ukraine

² V. N. Karazin Kharkiv National University, Ukraine

SIMULATION AND FORECASTING OF THE INFLUENZA EPIDEMIC PROCESS USING SEASONAL AUTOREGRESSIVE INTEGRATED MOVING AVERAGE MODEL

Today's global COVID-19 pandemic has affected the spread of influenza. COVID-19 and influenza are respiratory infections and have several similar symptoms. They are, however, caused by various viruses; there are also some differences in the categories of people most at risk of severe forms of these diseases. The strategies for their treatment are also different. Mathematical modeling is an effective tool for controlling the epidemic process of influenza in specified territories. The results of modeling and forecasts obtained with the help of simulation models make it possible to develop timely justified anti-epidemic measures to reduce the dynamics of the incidence of influenza. The study aims to develop a seasonal autoregressive integrated moving average (SARIMA) model for influenza epidemic process simulation and to investigate the experimental results of the simulation. The work is targeted at the influenza epidemic process and its dynamic in the territory of Ukraine. The **subjects** of the research are methods and models of epidemic process simulation, which include machine learning methods, in particular the SARIMA model. To achieve the aim of the research, we have used **methods** of forecasting and have built the influenza epidemic process SARIMA model. Because of experiments with the developed model, the predictive dynamics of the epidemic process of influenza for 10 weeks were obtained. Such a forecast can be used by persons making decisions on the implementation of anti-epidemic and deterrent measures if the forecast exceeds the epidemic thresholds of morbidity. **Conclusions.** The paper describes experimental research on the application of the SARIMA model to the epidemic process of influenza simulation. Models have been verified by influenza morbidity in the Kharkiv region (Ukraine) in epidemic seasons for the time ranges as follows: 2017-18, 2018-19, 2019-20, and 2020-21. Data were provided by the Kharkiv Regional Centers for Disease Control and Prevention of the Ministry of Health of Ukraine. The forecasting results show a downward trend in the dynamics of the epidemic process of influenza in the Kharkiv region. It is due to the introduction of anti-epidemic measures aimed at combating COVID-19. Activities such as wearing masks, social distancing, and lockdown also contribute to reducing seasonal influenza epidemics.

Keywords: epidemic model; epidemic process; epidemic simulation; simulation; SARIMA model; influenza.

Introduction

Influenza is an acute viral infection that spreads easily from person to person. The flu circulates around the world, causing epidemics and affecting people of all ages. In addition to seasonal epidemics, the emergence of a new subtype of influenza virus can provoke influenza pandemics. Influenza affects primarily the upper respiratory tract, including the nose and throat, as well as the bronchi, less often the lungs. The disease occurs all over the world and spreads very quickly among the population, especially in crowded places. Influenza epidemics occur annually in the Northern Hemisphere in autumn and winter, during which the infection affects approximately 5...15 % of the population [1].

Influenza is characterized by the acute development of symptoms such as a sharp increase in body temperature, cough, headache, muscle and joint pain, malaise,

runny nose, and lasts from 2 to 7 days. Influenza usually manifests itself in mild, uncomplicated form, and in most cases, infected people recover without any specific treatment. However, influenza infection can sometimes cause serious illness and death, especially among the elderly, pregnant women, young children, and people with certain health conditions (including chronic diseases of the heart, lungs, kidneys, liver, blood, with metabolic disorders, with a weakened immune system) [2].

Influenza epidemics, be they mild, moderate, or severe, affect a large portion of the population, placing significant strain on the health care system and other essential services, and can lead to significant economic losses. Because an influenza epidemic can last for months or even years, the health sector, as well as other sectors providing basic services such as energy and food production, must respond systematically [3]. For this reason, countries create multi-sectoral preparedness plans that

describe the strategy and operational plans for responding to an epidemic.

Today's global COVID-19 pandemic has affected the spread of influenza [4]. COVID-19 and influenza are respiratory infections and have many similar symptoms. They are, however, caused by various viruses; there are also some differences in the categories of people most at risk of severe forms of these diseases. The strategies for their treatment are also different.

Both infections, COVID-19 and influenza, are transmitted by droplets or aerosols released by an infected person when they cough, sneeze, speak, sing, or breathe. Drops and aerosols can get into the eyes, nasopharynx, or mouth of people around, usually, if they are less than 1 m from the infected person, but sometimes even further. You can also get COVID-19 and influenza by touching contaminated surfaces and then touching your eyes, nose, or mouth with unwashed hands. This means that the measures to counter the increase in the incidence are similar for influenza and COVID-19. The active fight against the COVID-19 pandemic has led to a decrease in the incidence of illness and influenza [5], however, on the other hand, all forces today are concentrated on the fight against the coronavirus, and the fight against the spread of influenza has receded into the background [6].

Also, the importance of introducing measures against the incidence of influenza is dictated by the increased likelihood of death with the simultaneous illness of influenza and COVID-19 [7].

In Ukraine, the incidence of influenza and acute respiratory viral infections is seasonal. The epidemic season is counted from 41 to 13 weeks [8]. Morbidity data are recorded only during epidemic seasons. Even though 1.25 million doses of influenza vaccines are planned for the epidemic season 2021-22, the level of immunization of the population is low and insufficient to prevent an epidemic from emerging [9]. During the epidemic season 2020-2021, 13.1 % of the country's population fell ill with influenza and acute respiratory viral infections, 147,232 people were hospitalized, of which 24.1 % were children under 17 years old, no deaths due to influenza were recorded [10].

The paper aims to develop a seasonal autoregressive integrated moving average (SARIMA) model for influenza epidemic process simulation and to investigate the experimental results of the simulation. The research is targeted at the influenza epidemic process. The subjects of research are methods and models of epidemic process simulation, which includes machine learning methods, in particular the SARIMA model.

To achieve the aim of the research following tasks have been formulated:

1. Methods and models of the influenza epidemic process should be analyzed.

2. SARIMA model of influenza epidemic process based on linear regression method should be developed.

3. Data on influenza morbidity in Ukraine should be prepared for model application.

4. Experimental evaluation of the SARIMA model of the influenza epidemic process should be provided.

5. Results obtained during the experimental studies should be analyzed.

The respective contribution of this study is two-fold. Firstly, the development of models based on the SARIMA approach will allow estimating the accuracy of simple machine learning methods applied to the simulation of the epidemic process. Secondly, the application of the SARIMA model to the influenza epidemic process in Ukraine will allow estimating its dynamics.

In this paper, section 1, namely the current research analysis provides the current state of influenza simulation methods and models. Section 2, namely materials and methods, provides a brief overview of moving average, autoregressive, autoregressive integrated moving average, seasonal autoregressive integrated moving average approaches, and developed methods of data preprocessing and preparation. Section 3 provides the results of data preparation, preprocessing, and stationing. Also, the forecasting of influenza morbidity dynamics in the Kharkiv region (Ukraine) is done. Conclusions describe the outcomes of the proposed methodology.

Given research is part of a complex intelligent information system for epidemiological diagnostics, the concept of which is discussed in [11].

1. Current Research Analysis

Methods of mathematical modeling have been developed for over 100 years. Among the models of influenza and acute respiratory viral diseases, one can single out the study of Rvachev [12], who, using classical compartment models, simulated the spread of influenza in the USSR in the middle of the XX century.

Other scientists have also used the apparatus of systems of differential equations to model the incidence of influenza. In paper [13] classical Susceptible–Infected–Recovered (SIR) model has been extended with assumptions that the magnitude of transmission does not vary between influenza A and B. The model has been applied to Israel dataset regarding influenza morbidity. Authors of [14] proposed to extend the SIR model to higher dimensions, allowing the modeling of a population infected by multiple viruses. The proposed model was applied to a five-year seasonal influenza-like illness rate, estimated from Twitter data. Paper [15] proposes a multi-strain SIR epidemic model with selective immunity by vaccination. Authors assume that the newer strain does not exhibit cross-immunity with the original strain, hence those who

are vaccinated and recovered from the original strain become susceptible to the newer strain. Paper [16] proposes an extended SIR model for analysis of the transmission dynamics of influenza A virus having incorporated the aspect of drug resistance. Numerical simulations reveal that despite vaccination reducing the reproduction number below unity, influenza persists in the population. Paper [17] describes a parametric bootstrap approach to generate simulated data from dynamical systems to quantify parameter uncertainty and identifiability with application to low-complexity SEIR model of influenza, Ebola, and Zika pandemics.

The main disadvantage of classical compartment models based on systems of differential equations is the complexity of making changes to the model. When the virulence of the virus changes, the infectivity index increases, and the population groups most susceptible to infection change. Also, the introduction of preventive measures to reduce the dynamics of morbidity affects the rules for the spread of the virus. To take into account the dynamically changing parameters of the system of differential equations, it is necessary to build anew, which leads to untimely decision-making regarding control anti-epidemic measures. These drawbacks can be eliminated by using statistical and machine learning methods of epidemic process simulation.

The authors of [18] applied a 3-weeks moving average model to investigate the seasonal dynamics of influenza in the WHO European Region. The authors of the paper [19] applied an exponentially weighted moving average method to detect the start of influenza outbreak in Viktoria, Australia. Paper [20] investigates the effectiveness of the application of the exponentially weighted moving average method to timely detection of influenza outbreaks in Iran. Paper [21] describes the regressive integrated moving average model based on surveillance data from Google Trends on influenza morbidity to forecast type-specific seasonal influenza. In [22, 23] the autoregressive moving average model has been proposed to investigate the dynamics of influenza.

The disadvantage of the proposed methods is that they do not take into account the seasonal dynamics of the epidemic process. The application of artificial intelligence-based methods and models are popular approaches to analysis the dynamical systems, in particular in healthcare: for prediction tasks [24], small data analysis [25], data openness estimation [26], simulation modeling [27], healthcare information systems integration [28], medical diagnostics [29], development of intelligent systems [30], etc. But due to the representation of morbidity data in Ukraine as a time-series that methods are hard to implement in the current task. This study proposes the development of a SARIMA model for predicting the dynamics of influenza in Ukraine.

2. Models and Methods

2.1. Simple Moving Average

Moving average belongs to the class of trend-following indicators, it helps to determine the beginning of a new trend and its end, its slope angle can be used to determine the strength (speed of movement), it is also used as a basis (or a smoothing factor) in a large number of other technical indicators [31]. Sometimes a moving average is called a trend line.

$$SMA = \frac{\sum_{i=1}^n P_i}{n}, \quad (1)$$

where P_i is the value of time series, n is the smoothing length or moving average period.

Moving averages will not predict changes in the trend, but will only signal an already emerging trend. Since moving averages are trend-following indicators, it is better to use them during trend periods, and when the trend is not present in the process under study, they become completely ineffective. Therefore, before using these indicators, it is necessary to conduct a separate analysis of the trend properties of specific values of the time series.

2.2. Autoregressive Model

An autoregressive model is a time series model in which its current value linearly depends on the previous values of the same series [32]. Linear relationship means that the current value is equal to the weighted sum of several previous values in the series

$$Y(t) = C + \sum_{i=1}^n b_i Y_{t-n} + \varepsilon_t, \quad (2)$$

where C is a constant, which for simplicity is often assumed to be 0; n is the number of retrospective values of the series taken into account in the model (the order of the model); b_i are coefficients (parameters) of the model that need to be estimated when building it; ε_t is a random component reflecting the probabilistic nature of the model.

Thus, knowing the parameters of the model and the corresponding retrospective values of the time series, we can predict its future values.

2.3. Autoregressive Integrated Moving Average Model

The Autoregressive Integrated Moving Average Model (ARIMA) is a time series forecasting method created by regressing the dependent variable only on its lag

value and the current value and lag value of the random error term in the process of converting non-stationary time series to stationary time series [33].

The model treats the sequence of data generated by the predicted object over time as a random sequence and uses a mathematical model to describe this sequence. Once the model is identified, the future values of the time series can be predicted from the past and current values of the time series.

The autoregressive model with integration and moving average of orders (p, d, q) is the sum of the autoregressive model from the past values of p periods and the moving average model of the previous q periods, and can be represented as

$$\Delta^d X_t = C + \sum_{i=1}^p a_i \Delta^d X_{t-i} + \sum_{j=1}^q b_j \varepsilon_{t-j} + \varepsilon_t, \quad (3)$$

where ε_t is stationary time series; c, a_i , b_j are parameters of the model; Δ^d is the operator of the difference of the time series of order d (sequential taking of d times of the differences of the first order - first from the time series, then from the obtained differences of the first order, then from the second order, etc.)

ARIMA's approach to time series is that the stationarity of the series is assessed first. Various tests reveal the presence of unit roots and the order of integration of the time series. Further, if necessary, the series is transformed by taking the difference of the corresponding order, and already for the transformed model, a certain ARIMA model is constructed, since it is assumed that the resulting process is stationary, in contrast to the original non-stationary process.

The problem with ARIMA is that it doesn't support seasonal data. This is a time series with a repeating cycle.

2.4. Seasonal Autoregressive Integrated Moving Average Model

Seasonal Autoregressive Integrated Moving Average (SARIMA) method for forecasting time series with univariate data containing trends and seasonality is an ARIMA extension that supports direct modeling of the seasonal component of the series [34].

It adds three new hyperparameters for specifying autoregressive (AR), integrated (I), and moving average (MA) for the seasonal component of the series, as well as an additional parameter for the seasonality period. The SARIMA model is generated by including additional seasonal parameters in ARIMA. The seasonal part of the model consists of parameters that include reverse shifts of the seasonal period.

SARIMA model can be represented as:

$$\varphi_p(L^m)\varphi(L)\nabla_m^D\nabla^d y_t = \theta_Q(L^m)\theta(L)\varepsilon_t, \quad (4)$$

where the autoregression and moving average parameters are represented by polynomials $\varphi(L)$ and $\theta(L)$ of orders p and q, and the seasonal autoregressive and moving average parameters $\varphi_p(L^m)$ and $\theta_Q(L^m)$ are of orders P and Q. ∇_m^D and ∇^d are the parameters of differentiation of regular and seasonal data; L is the lag operator; m is seasonality.

$$\varphi_p(L^m) = 1 - \varphi_1 L^m - \varphi_2 L^{2m} - \dots - \varphi_p L^{pm}, \quad (5)$$

$$\varphi(L) = 1 - \varphi_1(L) - \varphi_2 L^2 - \dots - \varphi_p L^p, \quad (6)$$

$$\theta_Q(L^m) = 1 + \theta_1(L^m) + \theta_2(L^{2m}) + \dots + \theta_Q(L^{Qm}), \quad (7)$$

$$\nabla_m^D = (1 - L^m)^D, \quad (8)$$

$$\nabla^d = (1 - L)^d, \quad (9)$$

$$L^k y_t = y_{t-k}. \quad (10)$$

Thus, in addition to the three parameters of the ARIMA model: p (trend autoregressive order), d (trend change order), and q (moving average trend), there are four seasonal elements in the SARIMA model: P (seasonal autoregressive order), D (order of seasonal differences), Q (seasonal moving average order) and m (number of time steps in one seasonal period).

2.5. Methods of Data Preprocessing and Preparation

Methods of formal verification and means of software implementation of their main stages have been developed, including the following main parts: compilation semantic-numerical verification, decompilation semantic-numerical verification, and verification of satisfaction of requirements/constraints.

Compilation semantic-numerical verification provides a check of the syntactic and temporal correctness of the formal synthesis of the structures of the semantic-digital specification of verification objects in the dynamics of the design of these objects.

Decompilation semantic-numerical verification verifies the logical equivalence of synthesized multi-parallel programs and/or digital hardware and source codes of C-program tasks after all stages of synthesis are completed (by decompilation of the synthesis result and comparison with the source text). Semantic verification consists in checking (in dynamics or after the completion of all stages of synthesis) the coincidence of units of measurement of physical quantities obtained in the formal synthesis of multi-parallel programs and/or digital hardware, as well as units of measurement of input and input data

of tasks set by users.

Verification of the fulfillment of requirements/restrictions consists in checking the degree of compliance of the requirements/restrictions and is provided by a synthesized software and/or hardware verification object and requirements/restrictions that were specified by the user. The initial data for all types of verification and the basis for maintaining the automatic nature of verification is that at all stages of synthesis, structures of the semantic-numerical specification are formed (including C-programs of tasks; temporal parallel task models; time-parameterized parallel programs; functional, logical and gate circuits parallel hardware, communication topologies of computer networks, etc.). Methods of semantic-numerical formal verification and means of software implementation of the main stages have been developed, which provide an explicit reflection in the designs of parallel programs and digital devices of the units of measurement (semantics) of the processed data, which has a significant impact on the efficiency of software and hardware of parallel computing systems.

Specific examples of formal verification of clock-parameterized semantic-numerical specifications of C-programs of tasks, multi-parallel process models, time-parameterized multi-parallel programs, and digital devices, and software implementations of the main stages

confirm the operability and efficiency of the methods developed and implementing these methods. It should be noted that the authors did not find similar results in the available scientific and technical literature.

3. Results

3.1. Data Preparation

For the study, data on influenza morbidity in the Kharkiv region (Ukraine) for 2017-18, 2018-19,

2019-20, and 2020-21 epidemic seasons were used. Data was provided by the Kharkiv Regional Center for Disease Control and Prevention of the Ministry of Health of Ukraine.

The view of the initial data frame after data import is shown in Figure 1.

After preprocessing and data preparation, it is presented in a form that is convenient for understanding and building a model (Fig. 2).

The next step involves a visual analysis of the data concerning epidemic thresholds (Fig. 3) and an analysis of the distribution of the incidence rate by age group and the general population (Fig. 4).

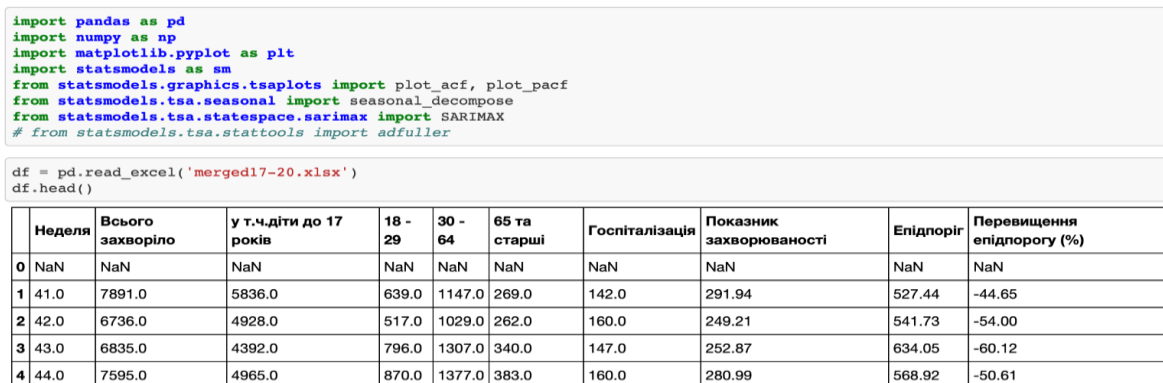


Fig. 1. Initial dataframe

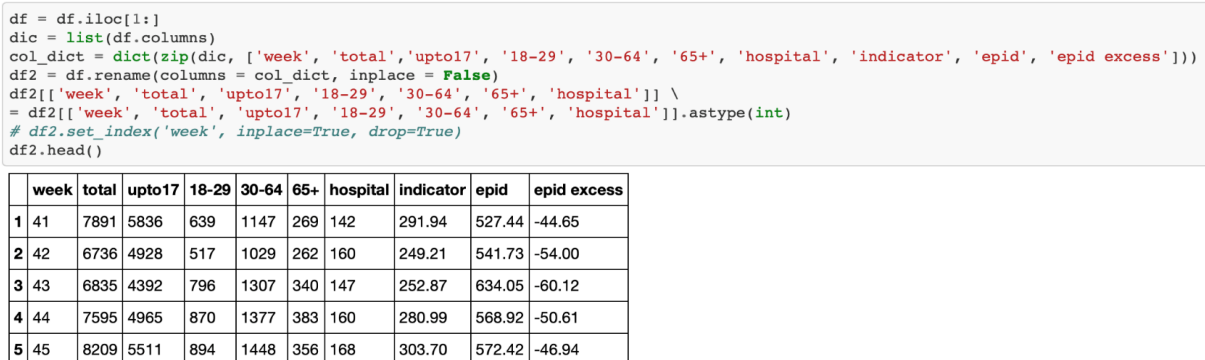


Fig. 2. Modified dataframe

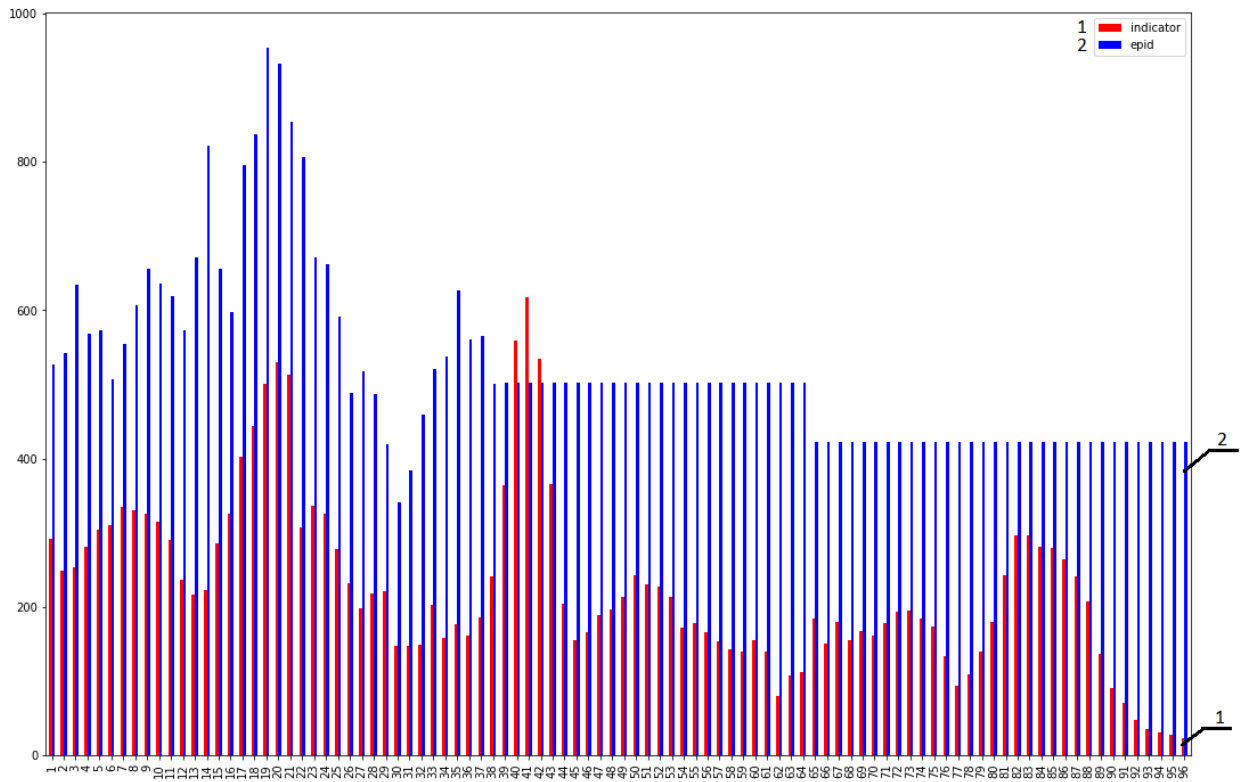


Fig. 3. Incidence rate with epidemic thresholds

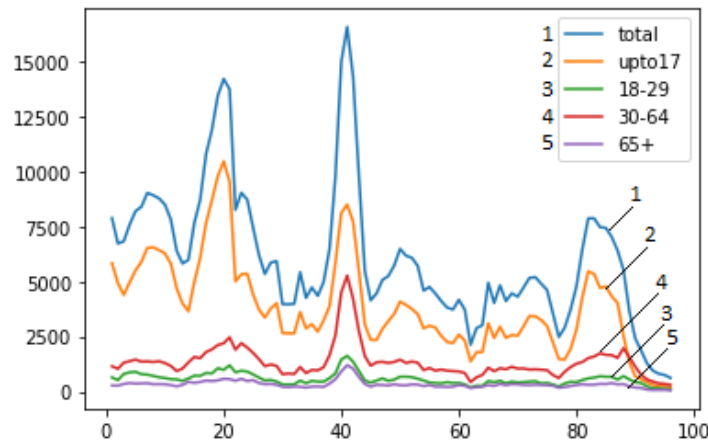


Fig. 4. distribution of the incidence rate by age group and the general population

3.2. Data Preprocessing

To view the seasonality of the data, we have used a seasonal decomposition to better see the trend of the sample (Fig. 5).

Plots before decomposition into seasonal, trend, seasonality, and residuals are shown in Figures 6-9.

```
decomposition = seasonal_decompose(df2.total, period=7)
fig = plt.figure()
fig = decomposition.plot()
fig.set_size_inches(10, 20)
```

Fig. 5. Seasonal decomposition

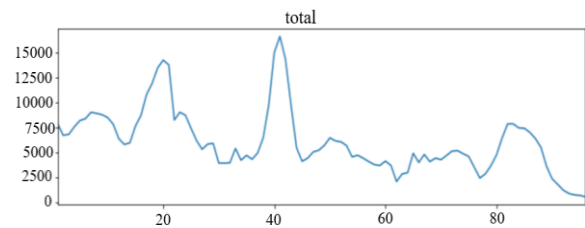


Fig. 6. Data before the decomposition into seasonality

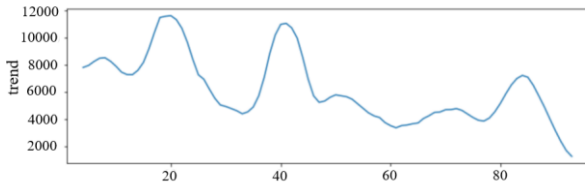


Fig. 7. Trend plot

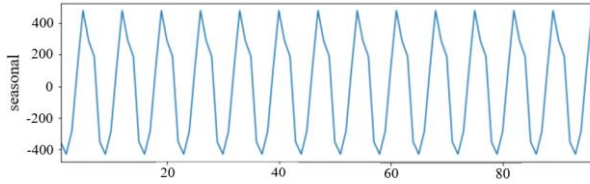


Fig. 8. Seasonality plot

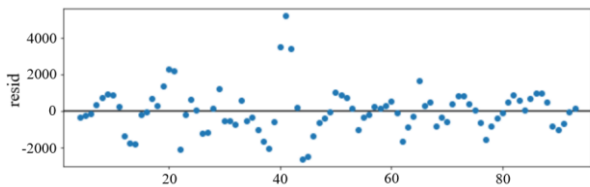


Fig. 9. Residuals plot

3.3. Data Stationing

When using linear regression, it is assumed that all cases are independent of each other. However, in time series, we know that observations are time-dependent. It turns out that many good results that are the result of independent random variables (the law of large numbers and the central limit theorem, for example) adhere to stationary random variables. Thus, by making the data stationary, we can apply regression methods to this time-dependent variable.

The easiest way to check data for stationarity is visual. But for a more accurate assessment, there is the Dickey-Fuller test [35]. If the test statistic is greater than the Critical Value, then the time series are stationary. The result of checking the data for stationarity is shown in Figure 10.

Our task is to make the Test Statistic parameter less than the Critical Value (1 %). Even though we have already achieved this, it is better to achieve a larger finite difference, so we will also find the first difference for our data.

The first time series difference is a series of changes from one period to the next. If Y_t denotes the value of time series Y over period t , then the first difference Y over period t is equal to $Y_t - Y_{t-1}$. If the first difference Y is stationary and also completely random (not autocorrelated), then Y is described by a random walk model: each value is a random step from the previous value. If the first difference Y is stationary but not completely random –

that is, if its value in period t is automatically correlated with its value in previous periods - then a more complex forecasting model such as exponential smoothing or ARIMA, as in our case, may be appropriate (Fig. 11).

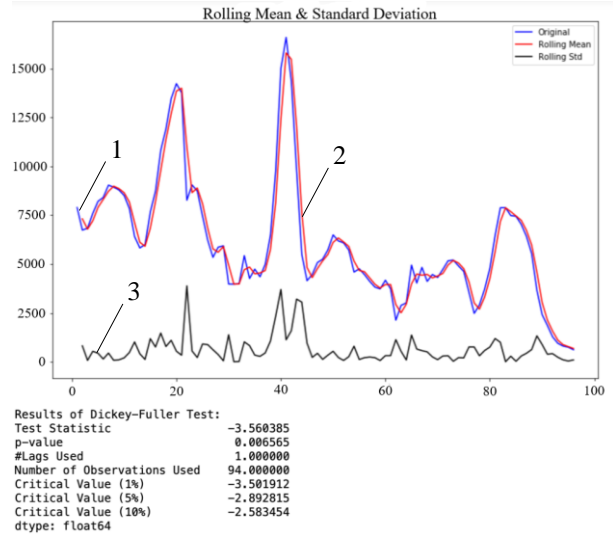


Fig. 10. Results of Dickey-Fuller Test:
1 – Original, 2 – Rolling Mean, 3 – Rolling Std

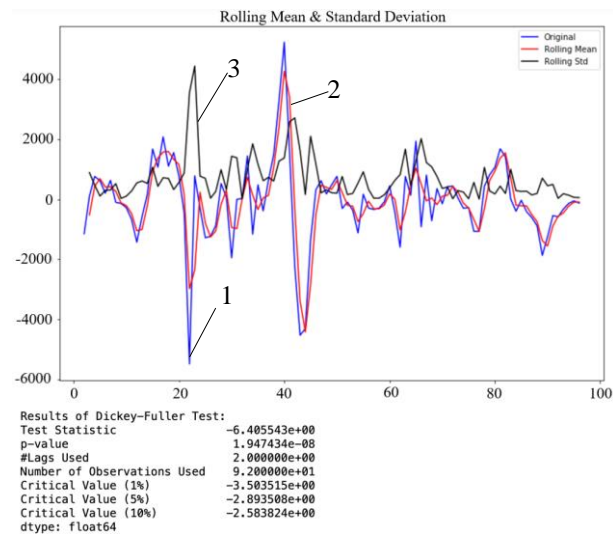


Fig. 11. Data stationarity plot for the first difference:
1 – Original, 2 – Rolling Mean, 3 – Rolling Std

The next step is to find the optimal model parameters using the computational capabilities of the Python language. All parameters of the constructed model are shown in Figure 12.

3.4. Forecasting

On the basis of statistics on the incidence of influenza in the Kharkiv region, a short-term forecast of the dynamics of the incidence for 10 weeks was built (Fig. 13). Such a forecast can be used by persons making

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Dep. Variable:                total      No. Observations:      96
Model:                        SARIMAX(2, 1, 2)x(2, 1, 2, 32)  Log Likelihood         -521.940
Date:                          Sat, 03 Jul 2021      AIC                    1061.879
Time:                          17:32:10          BIC                    1081.167
Sample:                          0              HQIC                   1069.465
                                - 96
Covariance Type:                opg
=====

```

	coef	std err	z	P> z	[0.025	0.975]
ar.L1	1.1559	0.303	3.816	0.000	0.562	1.750
ar.L2	-0.4266	0.264	-1.613	0.107	-0.945	0.092
ma.L1	-0.9006	0.401	-2.247	0.025	-1.686	-0.115
ma.L2	-0.0872	0.393	-0.222	0.824	-0.858	0.684
ar.S.L32	-0.7589	3.700	-0.205	0.837	-8.010	6.493
ar.S.L64	-0.7793	0.436	-1.787	0.074	-1.634	0.075
ma.S.L32	-1.7092	17.578	-0.097	0.923	-36.161	32.742
ma.S.L64	0.9264	47.716	0.019	0.985	-92.596	94.449
sigma2	6.853e+04	0.000	1.78e+08	0.000	6.85e+04	6.85e+04

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Ljung-Box (L1) (Q):                2.82      Jarque-Bera (JB):                27.86
Prob(Q):                          0.09      Prob(JB):                       0.00
Heteroskedasticity (H):            0.47      Skew:                           0.99
Prob(H) (two-sided):              0.09      Kurtosis:                       5.59
=====

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Fig. 12. Parameters of the model

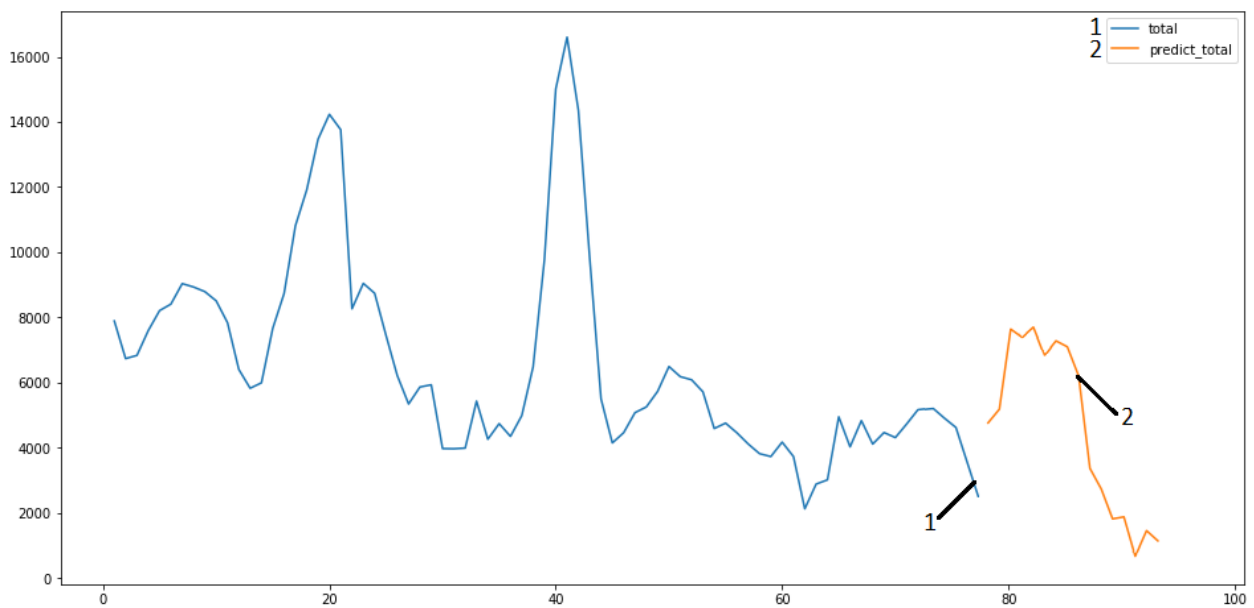


Fig. 13. Forecast of influenza epidemic process

decisions on the implementation of anti-epidemic and deterrent measures in the event that the forecast exceeds the epidemic thresholds of morbidity.

Conclusions

The paper describes experimental research on the implementation of the SARIMA model to the epidemic process of influenza simulation. Models were verified by influenza morbidity in the Kharkiv region (Ukraine) for the 2017-18, 2018-19, 2019-20, and 2020-21 epidemic

seasons. Data was provided by the Kharkiv Regional Center for Disease Control and Prevention of the Ministry of Health of Ukraine.

The novelty of the research is the development of an epidemic process model based on state-of-art methods and approaches applied to the influenza epidemic process in a certain territory. The distinctive point about the proposed study is that the model includes the seasonality of the influenza epidemic process. It allows increasing the accuracy of the developed forecast.

The obtained forecasting result has sufficient accuracy for planning prophylactic and control measures for the next epidemic season of influenza and influenza-like diseases in Ukraine. These activities include planning the provision of hospitals and health facilities with influenza drugs, planning the provision of beds and redesigning hospitals, and strengthening the information campaign on the need for annual influenza vaccination. In the context of the current COVID-19 pandemic, it is extremely important to plan material resources that can be reallocated from the influenza campaign to activities related to the provision and support of patients with the new version of coronavirus.

The forecasting results show a downward trend in the dynamics of the epidemic process of influenza in the Kharkiv region. This is due to the introduction of anti-epidemic measures aimed at combating COVID-19. Activities such as wearing masks, social distancing, and lockdowns also contribute to reducing seasonal influenza epidemics. The main carriers of the influenza virus are children and young people who have the most active lifestyle, characterized by a high chance to contact. Therefore, distance learning in schools, and higher education institutions, the closure of public places, restrictions on public transport, and the prohibition of mass events are affecting the reduction of the spread of the virus. The decrease in the diagnosis of influenza due to the high incidence of COVID-19 also has an impact on reducing the incidence of influenza and influenza-like infections in Ukraine. According to the low level of annual vaccination against influenza in Ukraine, it is not a decisive factor in reducing the intensification of the epidemic process. Nevertheless, vaccination is an effective tool to reduce the dynamics of the incidence of influenza and influenza-like infections in Ukraine.

Future research development. The constructed model showed sufficient forecast accuracy for adjusting anti-epidemic measures planned to reduce the incidence of influenza and influenza-like infections in Ukraine. However, statistical methods prohibit identifying factors influencing the dynamics of the epidemic process. Thus, it is planned to build an intelligent multiagent model that takes into account the peculiarities of the behavior of the population and the circulation of the virus in it. The multiagent model will make it possible to conduct an experimental study of the informativeness and significance of the model parameters, which will make it possible to evaluate the effectiveness of specific measures aimed at reducing the epidemic incidence. At the same time, to improve the accuracy of the multiagent model, it is supposed to be calibrated on the SARIMA model proposed in this paper, which will improve the accuracy of the obtained forecast

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МОДЕЛЮВАННЯ І ПРОГНОЗУВАННЯ ЕПІДЕМІЧНОГО ПРОЦЕСУ ГРИПУ ЗА ДОПОМОГОЮ МОДЕЛІ СЕЗОННОЇ АВТОРЕГРЕСІЙНОЇ ІНТЕГРОВАНОЇ КОВЗНОЇ СЕРЕДНЬОЇ

Д. І. Чумаченко, Є. С. Меньялов, А. А. Грімов, В. В. Лопатка,
О. Ю. Мороз, О. Г. Толстолузька

Сьогоднішня глобальна пандемія COVID-19 вплинула на поширення грипу. COVID-19 та грип є респіраторними інфекціями та мають ряд схожих симптомів. Але вони викликаються різними вірусами. Є також деякі відмінності в категоріях людей, найбільш схильних до ризику важких форм цих захворювань. Стратегії їхнього лікування також різні. Математичне моделювання – ефективний інструмент контролю епідемічного

процесу грипу на визначених територіях. Результати моделювання та прогнози, отримані за допомогою імітаційних моделей, дозволяють своєчасно розробити обґрунтовані протиепідемічні заходи щодо зниження динаміки захворюваності на грип. **Метою статті** є розробка моделі сезонного авторегресійного інтегрованого ковзного середнього (SARIMA) для моделювання епідемічного процесу грипу та дослідження експериментальних результатів моделювання. **Об'єкт дослідження** – епідемічний процес грипу та його динаміка на території України. **Предметом дослідження** є моделі та методи імітаційного моделювання епідемічних процесів, у тому числі методи машинного навчання, зокрема модель SARIMA. Для досягнення мети дослідження ми використовували **методи** прогнозування та побудували модель SARIMA епідемічного процесу грипу. У **результаті** експериментів з розробленою моделлю було отримано прогнозну динаміку епідемічного процесу грипу на 10 тижнів. Такий прогноз може бути використаний особами, що приймають рішення про реалізацію протиепідемічних і стримуючих заходів у разі перевищення прогнозом епідемічних порогів захворюваності. **Висновки.** У статті описані експериментальні дослідження щодо застосування моделі SARIMA для моделювання епідемічного процесу грипу. Моделі верифіковані на захворюваності на грип у Харківській області (Україна) за епідемічні сезони 2017-18, 2018-19, 2019-20 та 2020-21 рр. Дані надані Харківським обласним центром з контролю та профілактики захворювань Міністерства охорони здоров'я України. Результати прогнозування показують тенденцію до зниження динаміки епідемічного процесу грипу у Харківській області. Це пов'язано з введенням протиепідемічних заходів, вкладених у боротьбу з COVID-19. Такі дії, як носіння масок, соціальне дистанціювання та ізоляція також сприяють зниженню епідемічної захворюваності на сезонний грип.

Ключові слова: модель епідемії; епідемічний процес; моделювання епідемії; імітаційне моделювання; модель SARIMA; грип.

МОДЕЛИРОВАНИЕ И ПРОГНОЗИРОВАНИЕ ЭПИДЕМИЧЕСКОГО ПРОЦЕССА ГРИППА С ПОМОЩЬЮ МОДЕЛИ СЕЗОННОГО АВТОРЕГРЕССИОННОГО ИНТЕГРИРОВАННОГО СКОЛЬЗЯЩЕГО СРЕДНЕГО

*Д. И. Чумаченко, Е. С. Меньялов, А. А. Гримов, В. В. Лопатка,
О. Ю. Мороз, Е. Г. Толстолужская*

Сегодняшняя глобальная пандемия COVID-19 повлияла на распространение гриппа. COVID-19 и грипп являются респираторными инфекциями и имеют ряд схожих симптомов. Однако они вызываются различными вирусами. Есть также некоторые различия в категориях людей, наиболее подверженных риску тяжелых форм этих заболеваний. Стратегии их лечения также разные. Математическое моделирование – эффективный инструмент контроля эпидемического процесса гриппа на определенных территориях. Результаты моделирования и прогнозы, полученные с помощью имитационных моделей, позволяют своевременно разработать обоснованные противоэпидемические меры по снижению динамики заболеваемости гриппом. **Целью статьи** является разработка модели сезонного авторегрессионного интегрированного скользящего среднего (SARIMA) для моделирования эпидемического процесса гриппа и исследование экспериментальных результатов моделирования. **Объект исследования** – эпидемический процесс гриппа и его динамика на территории Украины. **Предметом исследования** являются модели и методы имитационного моделирования эпидемических процессов, в том числе методы машинного обучения, в частности модель SARIMA. Для достижения цели исследования мы использовали **методы** прогнозирования и построили модель SARIMA эпидемического процесса гриппа. В **результате** экспериментов с разработанной моделью была получена прогнозная динамика эпидемического процесса гриппа на 10 недель. Такой прогноз может быть использован лицами, принимающими решения о реализации противоэпидемических и сдерживающих мер в случае превышения прогнозом эпидемических порогов заболеваемости. **Выводы.** В статье описаны экспериментальные исследования по применению модели SARIMA к моделированию эпидемического процесса гриппа. Модели верифицированы на заболеваемости гриппом в Харьковской области (Украина) за эпидемические сезоны 2017-18, 2018-19, 2019-20 и 2020-21 гг. Данные предоставлены Харьковским областным центром по контролю и профилактике заболеваний Министерства здравоохранения Украины. Результаты прогнозирования показывают тенденцию к снижению динамики эпидемического процесса гриппа в Харьковской области. Это связано с введением противоэпидемических мероприятий, направленных на борьбу с COVID-19. Такие действия, как ношение масок, социальное дистанцирование и изоляция также способствуют снижению эпидемической заболеваемости сезонного гриппа.

Ключевые слова: модель эпидемии; эпидемический процесс; моделирование эпидемии; имитационное моделирование; модель SARIMA; грип.

Чумаченко Дмитро Ігорович – канд. техн. наук, доц., доц. каф. математичного моделювання та штучного інтелекту, Національний аерокосмічний університет ім. М. Є. Жуковського «Харківський авіаційний інститут», Харків, Україна.

Меняйлов Євген Сергійович – канд. техн. наук, старш. викл. каф. математичного моделювання та штучного інтелекту, Національний аерокосмічний університет ім. М. С. Жуковського «Харківський авіаційний інститут», Харків, Україна.

Грімів Андрій Артемович – здобувач каф. математичного моделювання та штучного інтелекту, Національний аерокосмічний університет ім. М. С. Жуковського «Харківський авіаційний інститут», Харків, Україна.

Лопатка Владислав Вадимович – здобувач каф. математичного моделювання та штучного інтелекту, Національний аерокосмічний університет ім. М. С. Жуковського «Харківський авіаційний інститут», Харків, Україна.

Мороз Ольга Юрїївна – ст. викл. каф. теоретичної та прикладної системотехніки, Харківський національний університет імені В.Н. Каразіна, Харків, Україна

Толстолузька Олена Геннадіївна – д-р техн. наук, старш. наук. співроб., проф. каф. теоретичної та прикладної системотехніки, Харківський національний університет імені В. Н. Каразіна, Харків, Україна.

Dmytro Chumachenko – PhD in Artificial Intelligence, Associate Professor of Department of Mathematical Modelling and Artificial Intelligence, National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine, e-mail: dichumachenko@gmail.com, ORCID: 0000-0003-2623-3294.

Ievgen Meniailov – PhD in Mathematical Modelling and Optimization Methods, Senior Lecturer of Department of Mathematical Modelling and Artificial Intelligence, National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine, e-mail: evgenii.menyailov@gmail.com, ORCID: 0000-0002-9440-8378.

Andrii Hrimov – Applicant of Department of Mathematical Modelling and Artificial Intelligence, National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine e-mail: andrew.hrimov@gmail.com, ORCID: 0000-0001-5696-3779.

Vladislav Lopatka – Applicant of Department of Mathematical Modelling and Artificial Intelligence, National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine, e-mail: v.lopatka.v@gmail.com, ORCID: 0000-0002-1339-3849.

Olha Moroz – Senior lecturer of the Department of Theoretical and Applied Systems Engineering, V. N. Karazin Kharkiv National University, Kharkiv, Ukraine, e-mail: o.moroz@karazin.ua, ORCID: 0000-0002-4920-4093.

Olena Tolstoluzka – Dr.Sc. (Technical), Senior Research Fellow, Professor of the Department of Theoretical and Applied Systems Engineering, V. N. Karazin Kharkiv National University, Kharkiv, Ukraine, e-mail: elena.tolstoluzka@karazin.ua, ORCID: 0000-0003-1241-7906.