**Serhii KRIVTSOV[1], Ievgen MENIAILOV[2],**
**Kseniia BAZILEVYCH[1], Dmytro CHUMACHENKO[1]**

[1] *National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine*
[2] *V. N. Karazin Kharkiv National University, Kharkiv, Ukraine*

## PREDICTIVE MODEL OF COVID-19 EPIDEMIC PROCESS BASED ON NEURAL NETWORK

*The COVID-19 pandemic, which has been going on for almost three years, has shown that public health systems are not ready for such a challenge. Measures taken by governments in the healthcare sector in the context of a sharp increase in the pressure on it include containment of the transmission and spread of the virus, providing sufficient space for medical care, ensuring the availability of testing facilities and medical care, and mobilizing and retraining medical personnel. The pandemic has changed government and business processes, digitalizing the economy and healthcare. Global challenges have stimulated data-driven medicine research. Forecasting the epidemic process of infectious processes would make it possible to assess the scale of the impending pandemic to plan the necessary control measures. The study **builds** a model of the COVID-19 epidemic process to predict its dynamics based on neural networks. The **target** of the research is the infectious diseases epidemic process in the example of COVID-19. The research **subjects** are the methods and models of epidemic process simulation based on neural networks. As a **result** of this research, a simulation model of COVID-19 epidemic process based on a neural network was built. The model showed high accuracy: from 93.11% to 93.96% for Germany, from 95.53% to 95.54% for Japan, from 97.49% to 98.43% for South Korea, from 93.34% up to 94.18% for Ukraine, depending on the forecasting period. The assessment of absolute errors confirms that the model can be used in healthcare practice to develop control measures to contain the COVID-19 pandemic. The respective contribution of this research is two-fold. Firstly, the development of models based on the neural network approach will allow estimate the accuracy of such methods applied to the simulation of the COVID-19 epidemic process. Secondly, an investigation of the experimental study with a developed model applied to data from four countries will contribute to empirical evaluation of the effectiveness of its application not only to COVID-19 but also to other infectious diseases simulations. **Conclusions.** The research's significance lies in the fact that automated decision support systems for epidemiologists and other public health workers can improve the efficiency of making anti-epidemic decisions. This study is especially relevant in the context of the escalation of the Russian war in Ukraine when the healthcare system's resources are limited.*

*Keywords: epidemic model; epidemic process; epidemic simulation; simulation; COVID-19; neural network.*

## Introduction

The COVID-19 pandemic, which has been going on for almost three years, has shown that public health systems are not ready for such a challenge [1]. As of September 2022, more than 630 million people fell ill worldwide, more than 6.5 million of whom died [2].

In the context of the spread of COVID-19, national health systems have experienced an excessive load, which included a lack of medical personnel, a shortage of necessary equipment, overburdened hospitals, a lack of diagnostics and specific treatment, etc. In some countries, such as the UK and Italy, a higher proportion of severe and extremely severe forms of novel coronavirus infection has been observed, which has led to a rapid depletion of human resources for providing medical care, the stock of biomedical materials, and beds to accommodate patients [3, 4]. South Korea has experienced a shortage of hospital beds, resulting in patients dying at home while waiting to be admitted to the hospital [5]. With the onset of the pandemic in the United States, there was a shortage of personal protective equipment and medical personnel in the country [6].

Measures taken by governments in the healthcare sector in the context of a sharp increase in the pressure on it include containment of the transmission and spread of the virus, providing sufficient space for medical care, ensuring the availability of testing facilities and medical care, and mobilizing and retraining medical personnel [7]. Some countries have timely introduced innovative approaches to contain the pandemic. For example, thanks to mass screening of morbidity and technologies for contact tracing of infected patients, Singapore made it possible to introduce 14-day isolation of people who had contact with patients [8]. In countries with high healthcare funding, such as Sweden, the capacity of the national healthcare system made it possible to provide patients with specialized beds, which

made it possible not to implement a complete lockdown [9]. However, no country has been able to properly implement the full range of measures necessary to contain the spread of new coronavirus infection.

The pandemic has changed government and business processes, digitalizing the economy and healthcare. Global challenges have stimulated data-driven medicine research aimed at the analysis of medical data [10], automated medical diagnostics [11], analysis of medical images [12], the study of molecular structures [13], identification of factors affecting the development of the disease [14] and spread of the epidemic process [15], etc.

Forecasting the epidemic process of infectious processes would make it possible to assess the scale of the impending pandemic to plan the necessary control measures.

Therefore, this study aims to build a model of the COVID-19 epidemic process to predict its dynamics based on neural networks. The research is targeted at the infectious diseases epidemic process by the example of COVID-19. The research subjects are meth-ods and models of epidemic process simulation based on neural networks.

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

1. Methods and models of COVID-19 forecasting should be analyzed.

2. A simulation model of the COVID-19 epidemic process based on neural networks should be developed.

3. The selection of hyperparameters of the developed model should be optimized using the grid search method.

4. Verification of the developed model should be provided.

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

The respective contribution of this research is two-fold. Firstly, the development of models based on the neural network approach will allow estimating the accuracy of such methods applied to the simulation of the COVID-19 epidemic process. Secondly, an investigation of the experimental study with a developed model applied to data from four countries will contribute to empirical evaluation of the effectiveness of its application not only to COVID-19 but also to other infectious diseases simulations.

In this paper, section 1, namely the current research analysis, provides the current state of COVID-19 epidemic process simulation methods and models. Section 2, namely Materials and Methods, provides methods of neural network models development, methods of software implementation, and model of COVID-19 based on neural network. Section 4 provides the results of forecasting of COVID-19 morbidity for Germany, Japan, South

Korea and Ukraine. Conclusions describe the outcomes of the investigation.

Given research is part of a project on development of complex intelligent information system for epidemiological diagnostics, the concept of which is discussed in [16].

## 1. Current Research Analysis

Methods for predicting the dynamics of infectious morbidity have been known for more than a century, and research in this direction begins with the work of Kermack and McKendrick. They formulated the classical SIR model [17]. Models of the epidemic process have significantly developed with the spread of the COVID-19 pandemic. At the same time, most of the research is still based on the compartmental approach, i.e., the development of the classic SIR model developed almost 100 years ago.

Thus, in [18], two compartmental models of the dynamics of the incidence of COVID-19 were considered to study individual behavior during the spread and containment of the epidemic. The results show that the best investment strategy in social distancing reduces the epidemic peak for infected cases. By increasing the vaccine coverage, the epidemic peak for infected cases decreases. The authors of [19] use the SEIR model to model the dynamics of COVID-19 in Slovenia. The standard model has been extended to distinguish between age groups, symptomatic versus asymptomatic disease progression, and vaccinated and unvaccinated populations.

The study [20] is devoted to developing a compartmental model of COVID-19, which includes the effect of unconnected infectious links of the transmission. The discontinuous ties model proposed by the authors quantitatively describes the mechanism of suppression of secondary transmission of COVID-19. The study results show that the shape of epicurves of confirmed cases is determined by the probability of unrelated infectious associations, and the magnitude of cases is proportional to the exponent of the base reproduction number in each infectious burst generated by the virus, the base reproduction number.

The authors of [21] extend the SEIRD model of the COVID-19 epidemic process by adding a vaccinated population and forming a global model. The study results show that 30-day forecasts reproduce the spread of the infection well, better for regional than national data. The study [22] adapts the SIR epidemiological model to study the evolution of the spread of COVID-19 in Germany and Brazil. The authors propose a simple probabilistic method for the evolution of active cases, which is helpful for automatically estimating the parameters of an epidemiological model.

However, the compartmental approach to modeling the epidemic process has some disadvantages, including insufficient accuracy, low adaptability of the model to external factors, the high computational complexity of the model, etc.

Models based on machine learning show higher accuracy in predicting the dynamics of COVID-19. The study [23] considers ARIMA, SARIMA, and Prophet models to predict daily new cases and cumulative confirmed cases of COVID-19 in the US, Brazil, and India over 30 days. The authors of [24] explore standard statistical machine learning models for COVID-19 modeling: linear regression, least total shrinkage and determination administrator, and support vector machine. To improve accuracy, the authors apply exponential smoothing to each model. The resulting ensembles effectively predict the dynamics of COVID-19 over the next 30 days and the impact of proactive assessments, such as social exclusion and isolation, on the spread of COVID-19.

The authors of [25] use a random forest model to predict the number of COVID-19 cases at the US county level. At the same time, the authors propose a new function for training input data. The training uses case projections created by matching the estimated effective reproductive number against real-time test data until they are maximally correlated, helping the model better fit the epidemic trajectory set by traditional models.

The study [26] proposes to apply Bayesian optimization to tune Gaussian process regression hyperparameters to develop an efficient model for predicting recovered and confirmed cases of COVID-19 in India and Brazil. The authors of [27] propose a comprehensive forecasting ensemble framework based on six single prediction models, including time-varying Jackknife model averaging, time-varying parameters, time-varying parameter SIR, logistic regression, polynomial regression, autoregressive moving average.

All considered models based on statistical machine learning methods show accuracy sufficient for use in public health practice. However, only some models can use a large set of heterogeneous input data.

On the other hand, some works devoted to applying the neural network approach to modeling COVID-19 show even more relevant results in the healthcare system.

Thus, the study [28] is devoted to building a model based on artificial neural networks to predict the effective reproductive number $R_t$ trend. At the same time, the authors use various architectures of neural networks, such as Feed Forward, Mono-Dimensional Convolutional, and Lon Short-Term Memory. As a result, the authors obtained an $R_t$ forecast with daily time resolution instead of the weekly resolution provided by official sources.

The authors of [29] compared the prediction performance of linear and non-linear prediction models using daily COVID-19 incidence data. In particular, Nonlinear Autoregressive Neural Network-work, Autoregressive Integrated Moving Average, TBATS, and Exponential Smoothing are considered. The results showed that the model based on neural networks shows the highest accuracy.

The study [30] proposed an approach based on multi-source deep transfer learning to effectively predict the dynamics of COVID-19 in conditions of a small amount of data. This approach overcomes the problems of low variance and high bias in the model. The authors show that in addition to the dynamics of morbidity, the population density and economic conditions of the selected territory are also critical. Long Short-Term Memory architecture is used for modeling.

Paper [31] proposes a Convolutional Neural Network with Long Short-Term Memory architecture using a spatio-temporal approach to predict the dynamics of COVID-19 for 7 days. Spatiotemporal representation allows you to borrow data from neighbors for cell-level prediction. This allows accurate forecasts at the county level, which is essential for optimizing the allocation of healthcare resources in real-time.

Taking into account recent advances in the development of neural network models for the analysis of epidemic data, in this study, we propose a model of the COVID-19 epidemic process based on a neural network.

## 2. Materials and Methods

### 2.1. Development of Neural Network Model

Training the developed network configuration is carried out iteratively following the error backpropagation method. At the first stage of each iteration, the data of the following training example is fed to the neurons of the input layer and propagated from the first layer to the last. In contrast, the initial value of each neuron is calculated by the formula (1):

$$OUT_q = f_a\left(\sum_{p=1}^{N} OUT_p w_{pq}\right), \qquad (1)$$

where $OUT_q$, and $OUT_p$ are output values of q and p neurons;

$f_a$ is activation function;

$w_{pq}$ is connection between p and q neurons weight coefficient.

At the second stage of the training iteration, the weight coefficients of neural connections are recalculated according to formula (2). Recalculation is performed starting from the last layer and ending with the first:

$$w_{pq} = (i + 1) = w_{pq}(i) + n\delta_q OUT_p, \qquad (2)$$

where $w_{pq}(i+1)$ is new value of connection between p and q neurons weight coefficient;

$w_{pq}$ is old value of pq-connection weight coefficient;

n is speed of training;

$\delta_q$ is delta coefficient of neuron q;

$OUT_p$ is output value of neuron p.

The delta coefficient involved in the calculation of weight values for the original layer is calculated by the formula (3) and for hidden layers by formula (4):

$$\delta_q = OUT_q(q - OUT_q)(v_q - OUT_q), \qquad (3)$$

$$\delta_q = OUT_q(1 - OUT_q)\sum_{p=1}^{N} OUT_p w_{pq}, \quad (4)$$

where $OUT_q$, $OUT_p$ are input values of neurons q and p;

$w_{pq}$ is connection between p and q neurons weight coefficient;

v is valid value.

### 2.2. Features of Neural Network Model Software Implementation

The Dense layer implements the operation:

output = activation (dot (input, kernel) + bias),

where activation is the element-by-element activation function passed as the activation argument, Kernel is the weight matrix created by the layer, and Bias is the bias vector created by the layer (only applies if use_bias is True). If the input to the layer has a rank greater than 2, it is smoothed before the output from the Kernel. The arguments are:

− units are natural numbers, the dimension of the source space;

− activation is the activation function to use. If nothing is specified, no activation is applied (i.e. "linear" activation: a(x) = x);

− use_bias is a boolean whether the layer uses a bias vector;

− kernel_initializer is the initializer for the Kernel weight matrix;

− bias_initializer is the initializer for the bias vector;

− kernel_regularizer is a regulator function applied to the Kernel weight matrix;

− bias_regularizer is the regularizer function applied to the bias vector;

− activity_regularized is the regulator function applied to the layer's output (its "activation");

− kernel_constraint is a constraint function applied to the Kernel weight matrix;

− bias_constraint is the constraint function applied to the bias vector.

The Dropout layer randomly sets the fraction of input units to 0 each time it is updated during training, which helps prevent overfitting. The arguments are:

− rate which floats between 0 and 1 and is a percentage of input blocks to turn off;

− noise_shape is a 1D integer tensor representing the shape of the binary dropout mask that will be multiplied by the input;

− seed is a Python integer to use as a random seed.

Flatten layer, Keras.Layers.Flatten (data_format = None) flattens the input. The argument is data_format, a string, one of channels_last (default) or channels_first, the order in which the sizes are passed on the inputs. The purpose of this argument is to preserve weight ordering when switching the model from one data format to another. channels_last corresponds to form inputs (batch, …, channels), and channels_first corresponds to form inputs (batch, channels, …).

The Input layer, Keras.engine.input_layer.Input() is used to initialize the Keras tensor. A Keras tensor is an underlay tensor object (Theano, TensorFlow, or CNTK) that we augment with specific attributes to allow us to build a Keras model simply by knowing the model's inputs and outputs. Its arguments:

− shape is a tuple of shape (integer), regardless of batch size. For example, shape=(32,) indicates that the expected input will be batches of 32-dimensional vectors;

− batch_shape is a shape tuple (integer), including batch size. For example, batch_shape=(10, 32) indicates that the expected input will be batched with ten 32-dimensional vectors. batch_shape=(None, 32) specifies that batches with any number of 32-dimensional vectors;

− name is an optional name string for the layer. It must be unique in the model. It will be automatically generated if it is not provided;

− dtype is the data type expected in the input as a string (float32, float64, int32, ...);

− sparse is a Boolean function indicating whether the created holder is sparse;

− tensor is an additional existing tensor to wrap in the input layer.

The Reshape layer, Keras.layers.Reshape(target_shape) reformats the output into a specific shape. The argument is target_shape, the target shape which is a tuple of integers. The input form is arbitrary, although all sizes in the input form must be fixed. The keyword argument input_shape (a tuple of integers that does not include a reference axis) is used when using this layer as the first layer in the model.

The Permute layer, keras.layers.Permute(dims) keeps the size of the input according to the given pattern. It is useful, for example, for connecting RNNs and convolutions. The argument is dims, a tuple of integers, which does not include sample dimensions. Indexing starts from 1. For example, (2, 1) takes on the first and second dimensions of the input parameter. The input form is arbitrary. The keyword argument input_shape (a tuple of integers that does not include a reference axis) is used when using this layer as the first layer in the model.

ActivityRegularization layer, keras.layers.ActivityRegularization (l1 = 0.0, l2 = 0.0) is a layer that applies an update to input data based on a cost function. The keyword argument input_shape (a tuple of integers that does not include a reference axis) is used when using this layer as the first layer in the model.

Activations can be used either through the activations layer or the activations argument supported by all previous layers. The following activation functions are available:

− Elu is an exponential linear block that returns an exponential linear activation function: x if x>0 and alpha*(exp(x)-1) if x<0;

− Softmax activation function that returns a tensor as the output of a softmax transformation;

− Selu is scaling exponential linear unit (SELU). SELU is: scale*elu(x, alpha), where alpha and scale are predefined constants. The values of alpha and scale are chosen such that the mean and variance of the inputs are maintained between two successive layers as long as the weights are properly initialized (see Lecun_normal initialization). The number of inputs is "large enough" (see links for more information). Returns a resized exponential activation function: scale*elu(x, alpha);

− Softplus activation function, which returns the Softplus activation function: log(exp(x)+1);

− Softsign activation function, which returns the softsign activation function: x/(abs(x)+1);

− Relu is a rectification, linear block with default values that returns element by element. max(x,0). Otherwise: f(x)=max_value for x>=max_value, f(x)=x for threshold<=x<max_value, f(x)=alpha*(x - threshold);

− Tanh is the activation function in the form of a hyperbolic tangent, that returns the hyperbolic function: tanh(x) = (exp(x) − exp(-x))/(exp(x) + exp(-x));

− Sigmoid is an activation function in the form of a sigmoid, that returns the sigmoidal activation function: 1/(1+exp(-x));

− Hard_sigmoid is the "hard" sigmoid activation function, which is faster to compute than the sigmoid activation function. It returns: 0 if x<-2.5, 1 if x>2.5, 0.2*x+0.5 if -2.5<=x<=2.5;

− Exponential (basic) activation function, that returns the exponential activation function: exp(x);

− Linear (that is, identification) activation function returns the incoming tensor, unchanged.

A metric is a function used to evaluate the performance of the model. Metric functions are provided in the metrics parameter when the model is compiled. The metric function is similar to the loss function, except that the results of the metric evaluation are not used when training the model. Any of the loss functions can be used as a metric function. Available metrics: accuracy, binary_accuracy, categorical_accuracy, sparse_categorical_accuracy, top_k_categorical_accuracy, sparse_top_k_categorical_accuracy, cosine_proximity, clone_metric.

The optimizer is one of the two arguments required to compile Keras. It is possible to either instantiate the optimizer before passing it to model.compile() or call it by name. In the latter case, the default optimizer settings will be used. The following optimizers are available:

− SGD, Stochastic Gradient Descent Optimizer includes momentum support, learning rate decay, and Nesterov momentum;

− RMSprop optimizer is recommended to leave the parameters of this optimizer at their default values (except for the learning rate, which can be freely configured);

− Adagrad is an optimizer where the learning rate depends on specific parameters adapted to how often the parameter is updated during training. The more updates a parameter receives, the slower the learning rate. It is recommended to leave the optimizer parameters at their default values;

− Adadelta is a more robust extension of Adagrad that adapts the learning rate based on a sliding gradient update window instead of accumulating all the gradients from previous years. Thus, Adadelta continues to learn even when many updates have been made. Compared to Adagrad, there is no need to set the initial learning rate in the original version of Adadelta. Like most Keras optimizers in this version, the user can set the initial learning rate and decay factor. Leaving the parameters of this optimizer at their default values is recommended;

− Adam optimizer is the default parameter corresponding to the parameters specified in the original work;

− Adamax is a variant of Adam based on the infinity norm;

− Nadam is a Nesterov Adam optimizer. Just as Adam is essentially RMSprop with momentum, Nadam is RMSprop with Nesterov momentum.

### 2.3. Neural Network Model of COVID-19 Epidemic Process

Building a neural network system includes processing input data, developing an architecture, and training the network. There is no general implementation algorithm for each listed stage; the system configuration depends on many factors covered by a particular task. So, to obtain a forecast, when developing a neural network, the nature of the predicted time series, the desired form of obtaining the forecast, the forecasting horizon, the requirement for the time of obtaining the forecast, and the volume of input data are taken into account. Flexibility and lack of strict formalization in the development of the system provide a wide range of opportunities for research, improvement, and adaptation of existing models

of neural networks in order to improve the accuracy of the forecast.

When solving the forecasting problem, the neural network system is built in the following way: the input layer contains several neurons, to which the values of the time series under study are supplied, and the last layer consists of one neuron, the output of which is a forecast.

The disadvantage of implementing this algorithm is relatively fast error accumulation.

As a result of the research, a solution was developed and tested to eliminate the drawback described above to increase the forecast's accuracy. According to the results obtained, it is proposed to make the following changes to the architecture of the predictive neural network:

– increase the number of neurons in the initial layer, determined by the number of prediction steps;

– introduce connections between neurons of the initial layer.

An increase in the accuracy of the forecast occurs due to the connection of the output neurons with each other so that the value obtained on the first output neuron is fed to the input of the second output neuron, and the value obtained on the first and second is taken into account on the third, etc. In other words, for each next neuron of the initial layer, in addition to the signals from the neurons of the penultimate layer, the signals received already at the previous outputs of the network should be fed.

To predict the dynamics of COVID-19, the following neural network was built with the structure: 6 pairs of layers Dense (relu activation, 64 neurons) and Dropout, the last layer is Dense (relu activation), one output, optimizer is rmsprop, error function is mse.

## 3. Results

Developed neural network model was implemented in the Python programming language. An experimental study was carried out to forecast new cumulative cases of COVID-19 in specified territory for 3, 7, 10, 14, 21 and 30 days.

### 3.1. COVID-19 Dynamics Forecasting

Data from the John Hopkins Coronavirus Resource Center [32] on new cases of COVID-19 was used for the pilot study. A neural network model has been applied to predict new cumulative COVID-19 cases in Germany, Japan, South Korea, and Ukraine. These countries were selected because The dynamics of the spread of COVID-19 and the control measures implemented in these territories differed. The forecast was built for the dynamics of the epidemic process until February 24, 2022, because The escalation of the Russian war in Ukraine has signifi-

cantly affected the dynamics of COVID-19 and the registration of new cases on the territory of Ukraine. The dashboard does not provide data on the spread of COVID-19 in Ukraine after February 24, 2022.

Figure 1 presents the results of predicting new cumulative cases of COVID-19 in Germany. Figure 2 presents the prediction results for new cumulative cases of COVID-19 in Japan.
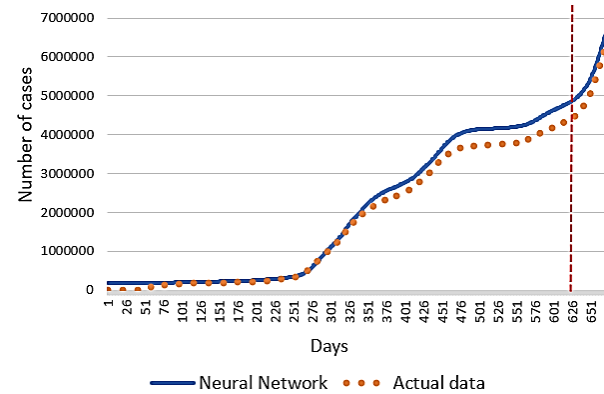


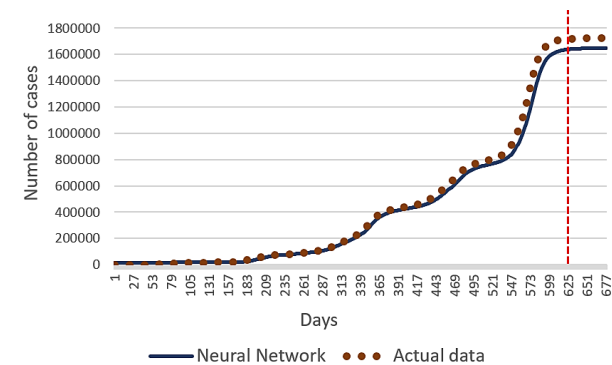Fig. 1. Forecasting of COVID-19 new cases
in Germany



Fig. 2. Forecasting of COVID-19 new cases
in Japan

Figure 3 presents the results of predicting new cumulative cases of COVID-19 in South Korea.
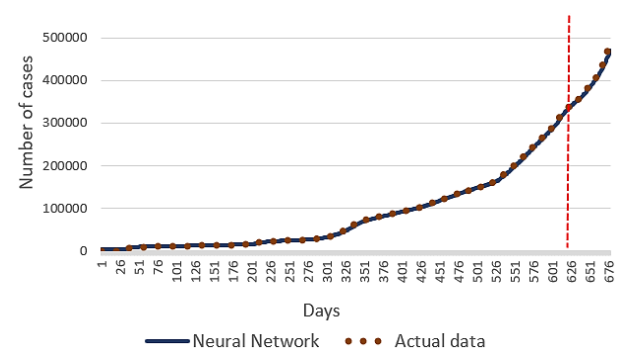


Fig. 3. Forecasting of COVID-19 new cases
in South Korea

Figure 4 presents the results of predicting new cumulative cases of COVID-19 in Ukraine.
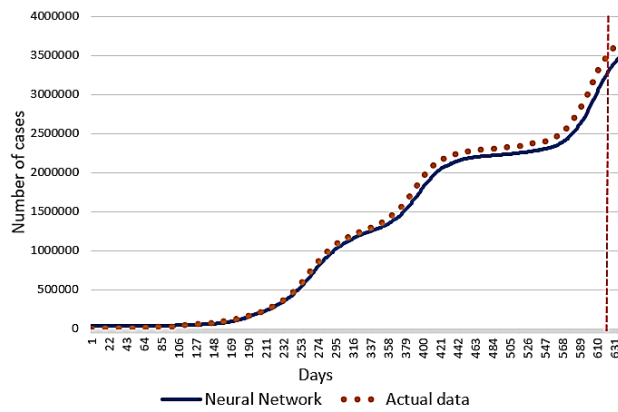


Fig. 4. Forecasting of COVID-19 new cases in Ukraine

### 3.2. Forecast Accuracy Estimation

Using the relative error of the training data, one can assess the adequacy of the constructed model. Relative errors were calculated for retrospective cumulative new cases forecast for 3, 7, 10, 14, 21, and 30 days to assess the accuracy of the constructed forecasts. The relative error of the forecasted data shows the accuracy of the constructed forecast of cumulative new cases of COVID-19.

Table 1 presents the values of relative error for 3, 7, 10, 14, 21, and 30 day forecasts of cumulative new COVID-19 cases in Germany, Japan, South Korea, and Ukraine. Relative error values show the accuracy of the model obtained but are not informative for use in public health practice. Therefore, indicators of the average absolute error were also calculated, shown in Table 2.

The results of building test models showed that it takes 50 to 55 days of information on the incidence to train the model, so 55 days were used to train the model. That is, such a model cannot be used at the pandemic's beginning.

Table 1

Relative error of forecast (%)

| Duration of forecast (days) | Germany | Japan | South Korea | Ukraine |
|---|---|---|---|---|
| Training 3 | 12,2841 | 22,3998 | 1,9539 | 13,7484 |
| Forecast 3 | 6,8896 | 4,4620 | 2,5084 | 5,8373 |
| Training 7 | 12,3262 | 22,5172 | 1,9517 | 13,8039 |
| Forecast 7 | 6,2943 | 4,4612 | 2,3792 | 5,8247 |
| Training 10 | 12,3562 | 22,6063 | 1,9507 | 13,8439 |
| Forecast 10 | 6,2792 | 4,4614 | 2,3142 | 5,9379 |
| Training 14 | 12,4020 | 22,7264 | 1,9523 | 13,8974 |
| Forecast 14 | 6,0395 | 4,4636 | 2,1418 | 6,0404 |
| Training 21 | 12,4740 | 22,9403 | 1,9609 | 13,9856 |
| Forecast 21 | 6,1131 | 4,4683 | 1,8332 | 6,3146 |
| Training 30 | 12,5513 | 23,2229 | 1,9761 | 14,0927 |
| Forecast 30 | 6,5074 | 4,4734 | 1,5740 | 6,6558 |

Table 2

Mean absolute error of forecast (number of cases)

| Duration of forecast (days) | Germany | Japan | South Korea | Ukraine |
|---|---|---|---|---|
| Training 3 | 197468 | 32652 | 1473 | 74829 |
| Forecast 3 | 430169 | 77053 | 11583 | 213606 |
| Training 7 | 196427 | 32361 | 1416 | 73883 |
| Forecast 7 | 388059 | 77030 | 10783 | 211625 |
| Training 10 | 195590 | 32141 | 1377 | 73102 |
| Forecast 10 | 381425 | 77027 | 10358 | 214719 |
| Training 14 | 194834 | 31843 | 1338 | 75994 |
| Forecast 14 | 45122 | 9633 | 1182 | 27097 |
| Training 21 | 193181 | 31310 | 1296 | 69992 |
| Forecast 21 | 352587 | 77120 | 7940 | 223187 |
| Training 30 | 190476 | 30606 | 1259 | 67131 |
| Forecast 30 | 357787 | 77180 | 6674 | 229591 |

### 3.3. Optimizing Model Hyperparameters with Mesh Search

Almost every machine learning method has hyperparameters - characteristics, the value of which determines the model's training process. The process of finding the best hyperparameters is called hyperparameterization.

In order to automate the selection of hyperparameters, the GridSearchCV class was used. The method using this class is straightforward:

– a grid is supplied with different values for each hyperparameter;

– for each sample from the Cartesian product of sets, the model is trained;

– with the help of different metrics, the models are compared with each other;

– based on the comparison results, the best model is selected.

Let us assume that our model has three hyperparameters - alpha, gamma, and n_iter. Let the following possible values be given to them:

– alpha = [0.1, 0.2, 0.3, 0.4, 0.5];

– gamma = [1, 2, 3, 4, 5, 6, 7, 8, 9, 10];

– n_iter = [100, 200, 300, 400, 500].

According to the laws of combinatorics, the total number of trained models is 5*10*5=250. All these models are compared using the evaluation metric, and the best one is selected.

To evaluate the model on more than just the training data passed to the fit() method, use the PredefinedSplit class and create a pipeline like this:

```
X, y = data
X_train, X_test, y_train, y_test = train_test_split (X, y)
cv = PredefinedSplit ([- 1 if x in X_train else 0 for x in X])
# Create Pipeline
...
pipeline = Pipeline (...)
# Create GridSearch
...
grid_search = GridSearchCV (estimator = pipeline, cv = cv, ...)
# Fit model
grid_search.fit (X, y)
# Get best model for current task
model = grid_search.best_estimator_
```

### Conclusions

The article is devoted to developing a neural network model for predicting the dynamics of the incidence of COVID-19 in a selected area. The adequacy of the model was tested on data on the incidence of COVID-19 in Germany, Japan, South Korea, and Ukraine, taken from the John Hopkins Coronavirus Resource Center.

The model showed high accuracy: from 93.11% to 93.96% for Germany, from 95.53% to 95.54% for Japan, from 97.49% to 98.43% for South Korea, from 93.34% up to 94.18% for Ukraine, depending on the forecasting period. The assessment of absolute errors confirms that the model can be used in healthcare practice to develop control measures to contain the COVID-19 pandemic.

The scientific novelty of the study lies in a new approach to solving the problem of predicting epidemic processes. As part of the approach, several neural networks are created, tested by mistake, and the best configuration of the neural network parameters is automatically selected. The final forecast is built based on the best model. Thus, the proposed model does not require manual tuning, which allows its use in automated decision support systems for epidemiological diagnostics.

The study's practical significance lies in the fact that automated decision support systems for epidemiologists and other public health workers can improve the efficiency of making anti-epidemic decisions. This study is especially relevant in the context of the escalation of the Russian war in Ukraine when the healthcare system's resources are limited.

**Future research development.** The simulation model of the COVID-19 epidemic process developed as part of this study is highly accurate. The adequacy of the model is sufficient to assess the further development of the pandemic in a specific area. However, the disadvantage of all models based on neural networks is their low interpretability. So, specialists making decisions regarding preventive measures cannot identify factors influencing the development of infectious morbidity. Therefore, further research aims to combine neural networks, statistical machine learning, and agent-based models to obtain a hybrid information support decision-making system about epidemic well-being. The concept of the proposed system is described in [16], some of the models which are parts of the system were published in [33]. Using agent-based models will make it possible to conduct experiments to evaluate the information content of external factors that affect the dynamics of the epidemic process. Furthermore, neural network models of epidemic processes will improve the accuracy of forecasts by calibrating the agent-based model on the results obtained using machine learning models.

**Contributions of authors:** conceptualization – **Ievgen Meniailov, Dmytro Chumachenko**; methodology – **Serhii Krivtsov, Ievgen Meniailov, Dmytro Chumachenko**; formulation of tasks – **Ievgen Meniailov, Kseniia Bazilevych, Dmytro**

**Chumachenko**; analysis – **Serhii Krivtsov, Dmytro Chumachenko**; development of model – **Serhii Krivtsov, Ievgen Meniailov, Kseniia Bazilevych, Dmytro Chumachenko**; software – **Serhii Krivtsov**; verification – **Ievgen Meniailov, Dmytro Chumachenko**; analysis of results – **Ievgen Meniailov, Dmytro Chumachenko**; visualization – **Serhii Krivtsov, Ievgen Meniailov**; writing – original draft preparation – **Ievgen Meniailov, Dmytro Chumachenko**; writing – review and editing – **Serhii Krivtsov, Kseniia Bazilevych**.

All the authors have read and agreed to the published version of the manuscript.

## References (GOST 7.1:2006)

1. *COVID-19: a multidisciplinary review* [Text] / N. Chams, S. Chams, R. Badran et al. // Frontiers in Public Health. – 2020. – Vol. 8. – Article No. 383. DOI: 10.3389/fpubh.2020.00383.

2. *Worldometer: COVID-19 Coronavirus Pandemic* [Electronic resource]. – 2022. Available at: https://www.worldometers.info/coronavirus/ – 31.08.2022.

3. *Comparing public perceptions and preventive behaviors during the early phase of the COVID-19 pandemic in Hong Kong and the United Kingdom: cross-sectional survey study* [Text] / L. Bowman, K. O. Kwok et al. // Journal of medical Internet research. – 2021. – Vol. 23, iss. 3. – Article No. e23231. DOI: 10.2196/23231.

4. *Santeramo, F. G. On the management of COVID-19 pandemic in Italy* [Text] / F. G. Santeramo, M. Tappi, E. Lamonaca // Health Policy. – 2021. – Vol. 125, iss. 8. – P. 995-1001. DOI: 10.1016/j.healthpol.2021.05.014.

5. *Flattering the curve on COVID-19: South Korea's measures in tackling initial outbreak of Coronavirus* [Text] / D. Lee, K. Heo et al. // American Journal of Epidemiology. – 2021. – Vol. 190, iss. 4. – P. 496-505. DOI: 10.1093/aje/kwaa217.

6. *Diagnostics for COVID-19: moving from pandemic response to control* [Text] / R. W. Peeling, D. L. Heymann, Y. Y. Teo, P. J. Garcia // Lancet. – 2022. – Vol. 399, iss. 10326. – P. 757-768. DOI: 10.1016/S0140-6736(21)02346-1.

7. *Comparative study of government response measures and epidemic trends for COVID-19 global pandemic* [Text] / C. Wang, H. Zhang, Y. Gao, Q. Deng // Risk Analysis: an official publication of the Society for Risk Analysis. – 2022. – Vol. 42, iss. 1. – P. 40-55. DOI: 10.1111/risa.13817.

8. *Abdou, A. M. Good governance and COVID-19: the digital bureaucracy to response the pandemic (Singapore as a model)* [Text] / A. M. Abdou // Journal of Public Affairs. – 2021. – Vol. 21, iss. 4. – Article No. e2656. DOI: 10.1002/pa.2656.

9. *Open schools, COVID-19, and child and teacher morbidity in Sweden* [Text] / J. F. Ludvigsson, L. Engerstrom, C. Nordenhall, E. Larsson // The New England Journal of Medicine. – 2021. – Vol. 384, iss. 7. – P. 669-671. DOI: 10.1056/NEJMc2026670.

10. *Predictive modeling based on small data in clinical medicine: RBF-based additive input-doubling method* [Text] / I. Izonin, R. Tkachenko et al. // Mathematical Biosciences and Engineering. – 2021. – Vol. 18, iss. 3. – P. 2599-2613. DOI: 10.3934/mbe.2021132.

11. *Agent-oriented data clustering for medical monitoring* [Text] / V. Strilets, V. Donets, M. Ugryumov, S. Artiuch, R. Zelenskyi, T. Goncharova // Radioelectronic and Computer Systems. – 2022. – No. 1 (101). – P. 103-114. DOI: 10.32620/reks.2022.1.08.

12. *Solutions to the 3rd model problem of pressure measurement in the area of maxillary sinus anastomosis* [Text] / A. Nechyporenko, V. Reshetnik, D. Shyian, V. Alekseeva, R. Radutny, V. Gargin // CEUR Workshop Proceedings. – 2020. – Vol. 2753. – P. 275-284.

13. *Semi-refined carrageenan promotes generation of reactive oxygen species in leukocytes of rats upon oral exposure but not in vitro* [Text] / A. Tkachenko, Y. Kot, V. Kapustnik et al. // Wiener Medizinische Wochenschrift. – 2021. – Vol. 171, iss. 3-4. – P. 68-78. DOI: 10.1007/s10354-020-00786-7.

14. *Evaluation of the informative features of cardiac studies diagnostic data using the Kullback method* [Text] / O. Skitsan, I. Meniailov, K. Bazilevych, H. Padalko // CEUR Workshop Proceedings. – 2021. – Vol. 2917. – P. 186-195.

15. *Monitoring of urban freight flows distribution considering the human factor* [Text] / N. Davidich, A. Galkin, S. Iwan, K. Kijewska, I. Chumachenko, Y. Davidich // Sustainable Cities and Society. – 2021. – vol. 75. – Article ID 103168. DOI: 10.1016/j.scs.2021.103168.

16. *The concept of developing a decision support system for the epidemic morbidity control* [Text] / S. Yakovlev, K. Bazilevych, D. Chumachenko, T. Chumachenko et al. // CEUR Workshop Proceedings. – 2020. – Vol. 2753. – P. 265–274.

17. *Kermack, W. O. A contribution to the mathematical theory of epidemics* [Text] / W. O. Kermack, A. G. McKendrick // Proceedings of the Royal Society London. – 1927. – Vol. 115, iss. 772. – P. 700-721. DOI: 10.1098/rspa.1927.0118.

18. *Dashtbali, M. A compartmental model that predicts the effect of social distancing and vaccination on controlling COVID-19* [Text] / M. Dashtbali, M. Mirzaie // Scientific Reports. – 2021. – Vol. 11. – Article No. 8191. DOI: 10.1038/s41598-021-86873-0.

19. *Extended compartmental model for modeling COVID-19 epidemic in Slovenia* [Text] / M. Fosnaric, T. Kamensek, J. Z. Gros, J. Zibert // Scientific Reports. –

2022. – Vol. 12. – Article No. 16916. DOI: 10.1038/s41598-022-21612-7.

20. Ikeda, Y. A new compartment model of COVID-19 transmission: the broken-link model [Text] / Y. Ikeda, K. Sasaki, T. Nakano // International Journal of Environmental Research and Public Health. – 2022. – Vol. 19, iss. 11. – Article No. 6864. DOI: 10.3390/ijerph19116864.

21. Antonelli, E. Switched forced SEIRDV compartmental models to monitor COVID-19 spread and immunization in Italy [Text] / E. Antonelli, E. L. Piccolomini, F. Zama // Infectious Disease Modelling. – 2022. – Vol. 7, iss. 1. – P. 1-15. DOI: 10.1016/j.idm.2021.11.001.

22. Batista, A. A. An epidemiological compartmental model with automated parameter estimation and forecasting of the spread of COVID-19 with analysis of data from Germany and Brazil [Text] / A. A. Batista, S. H. da Silva // Frontiers in Applied Mathematics and Statistics. – 2022. – Vol. 8. – Article No. 645614. DOI: 10.3389/fams.2022.645614.

23. Prediction and analysis of COVID-19 daily new cases and cumulative cases: times series forecasting and machine learning models [Text] / Y. Wang, Z. Yan et al. // BMC Infectious Diseases. – 2022. – Vol. 22. – Article No. 495. DOI: 10.1186/s12879-022-07472-6.

24. Administered machine learning models for COVID-19 future forecasting [Text] / K. Atchaya, M. Darshinii, R. Harini, T. Suganya // Journal of Physics: Conference Series. – 2021. – Vol. 1916. – Article No. 012157. DOI: 10.1088/1742-6596/1916/1/012157.

25. Galasso, J. A random forest model for forecasting regional COVID-19 cases utilizing reproduction number estimates and demographic data [Text] / J. Galasso, D. M. Cao, R. Hochberg // Chaos, Solitons, Fractals. – 2022. – Vol. 156. – Article No. 111779. DOI: 10.1016/j.chaos.2021.111779.

26. Alali, Y. A proficient approach to forecast COVID-19 spread via optimized dynamic machine learning model [Text] / Y. Alali, F. Harrou, Y. Sun // Scientific Reports. – 2022. – Vol. 12. – Article No. 2467. DOI: 10.1038/s41598-022-06218-3.

27. COVID-19 epidemic forecasting based on a comprehensive ensemble method [Text] / Y. Bai, Z. Qian, Y. Sun, S. Wang // System Engineering Theory and Practice. – 2022. – Vol. 42, iss. 6. – P. 1678-1693. DOI: 10.12011/SETP2021-3005.

28. An artificial neural network-based approach for predicting the COVID-19 daily effective reproduction number Rt in Italy [Text] / A. Gatto, V. Aloisi et al. // AI. – 2022. – Vol. 3, iss. 1. – P. 146-163. DOI: 10.3390/ai3010009.

29. Saliaj, L. An application of neural network to predict COVID-19 cases in Italy [Text] / L. Saliaj, E. Nissi // Engineering Proceedings. – 2022. – Vol. 18, iss. 1. – Article No. 11. DOI: 10.3390/engproc2022018011.

30. Garg, S. A novel approach for COVID-19 infection forecasting based on multi-source deep transfer learning [Text] / S. Garg, S. Kumar, P. K. Muhuri // Computers in Biology and Medicine. – 2022. – Vol. 149.

– Article No. 105915. DOI: 10.1016/j.compbiomed.2022.105915.

31. A deep learning approach for spatio-temporal forecasting of new cases and new hospital admissions of COVID-19 spread in Reggio Emilia, Northern Italy [Text] / V. Sciannameo, A. Goffi et al. // Journal of Biomedical Informatics. – 2022. – Vol. 132. – Article No. 104132. DOI: 10.1016/j.jbi.2022.104132.

32. Coronavirus Resource Center. Johns Hopkins University & Medicine. 2022 [Electronic resource]. – Available at: https://coronavirus.jhu.edu/map.html – 31.08.2022.

33. On COVID-19 epidemic process simulation: three regression approaches investigations [Text] / D. Chumachenko, I. Meniailov, K. Bazilevych, O. Chub // Radioelectronic and Computer Systems. – 2022. – № 1 (101). – P. 6-22. DOI: 10.32620/reks.2022.1.01.

## References (BSI)

1. Chams, N., Chams, S. et al. COVID-19: a multidisciplinary review. *Frontiers in Public Health*, 2020, vol. 8, article no. 383. DOI: 10.3389/fpubh.2020.00383.

2. *Worldometer: COVID-19 Coronavirus Pandemic*, 2022. Available at: https://www.worldometers.info/coronavirus/ (accessed 31.08.2022).

3. Bowman, L., Kwok, K.O. et al. Comparing public perceptions and preventive behaviors during the early phase of the COVID-19 pandemic in Hong Kong and the United Kingdom: cross-sectional survey study. *Journal of medical Internet research*, 2021, vol. 23, iss. 3, article no. e23231. DOI: 10.2196/23231.

4. Santeramo, F. G., Tappi, M., Lamonaca, E. On the management of COVID-19 pandemic in Italy. *Health Policy*, 2021, vol. 125, iss. 8, pp. 995-1001. DOI: 10.1016/j.healthpol.2021.05.014.

5. Lee, D., Heo, K. et al. Flattering the curve on COVID-19: South Korea's measures in tackling initial outbreak of Coronavirus. *American Journal of Epidemiology*, 2021, vol. 190, iss. 4, pp. 496-505. DOI: 10.1093/aje/kwaa217.

6. Peeling, R.W., Heymann, D. L., Teo, Y.Y., Garcia, P.J. Diagnostics for COVID-19: moving from pandemic response to control. *Lancet*, 2022, vol. 399, iss. 10326, pp. 757-768. DOI: 10.1016/S0140-6736(21)02346-1.

7. Wang, C., Zhang, H., Gao, Y., Deng, Q. Comparative study of government response measures and epidemic trends for COVID-19 global pandemic. *Risk Analysis: an official publication of the Society for Risk Analysis*, 2022, vol. 42, iss. 1, pp. 40-55. DOI: 10.1111/risa.13817.

8. Abdou, A. M. Good governance and COVID-19: the digital bureaucracy to response the pandemic (Singapore as a model). *Journal of Public Affairs*, 2021, vol. 21, iss. 4, article no. e2656. DOI: 10.1002/pa.2656.

9. Ludvigsson, J. F., Engerstrom, L., Nordenhall, C., Larsson, E. Open schools, COVID-19, and child and teacher morbidity in Sweden. *The New England*

*Journal of Medicine*, 2021, vol. 384, iss. 7, pp. 669-671. DOI: 10.1056/NEJMc2026670.

10. Izonin, I., Tkachenko, R. et al. Predictive modeling based on small data in clinical medicine: RBF-based additive input-doubling method. *Mathematical Biosciences and Engineering*, 2021, vol. 18, iss. 3, pp. 2599-2613. DOI: 10.3934/mbe.2021132.

11. Strilets, V., Donets, V., Ugryumov, M., Artiuch, S., Zelenskyi, R., Goncharova, T. Agent-oriented data clustering for medical monitoring. *Radioelectronic and Computer Systems*, 2022, no. 1 (101), pp. 103-114. DOI: 10.32620/reks.2022.1.08.

12. Nechyporenko, A., Reshetnik, V., Shyian, D., Alekseeva, V., Radutny, R., Gargin, V. Solutions to the 3rd model problem of pressure measurement in the area of maxillary sinus anastomosis. *CEUR Workshop Proceedings*, 2020, vol. 2753, pp. 275-284.

13. Tkachenko, A., Kot, Y. et al. Semi-refined carrageenan promotes generation of reactive oxygen species in leukocytes of rats upon oral exposure but not in vitro. *Wiener Medizinische Wochenschrift*, 2021, vol. 171, iss. 3-4, pp. 68-78. DOI: 10.1007/s10354-020-00786-7.

14. Skitsan, O., Meniailov, I., Bazilevych, K., Padalko, H. Evaluation of the informative features of cardiac studies diagnostic data using the Kullback method. *CEUR Workshop Proceedings*, 2021, vol. 2917, pp. 186-195.

15. Davidich, N., Galkin, A., Iwan, S., Kijewska, K., Chumachenko, I., Davidich, Y. Monitoring of urban freight flows distribution considering the human factor. *Sustainable Cities and Society*, 2021, vol. 75, article id 103168. DOI: 10.1016/j.scs.2021.103168.

16. Yakovlev, S., Bazilevych, K., Chumachenko, D., Chumachenko, T. et al. The concept of developing a decision support system for the epidemic morbidity control. *CEUR Workshop Proceedings*, 2020, vol. 2753, pp. 265–274.

17. Kermack, W. O., McKendrick, A. G. A contribution to the mathematical theory of epidemics. *Proceedings of the Royal Society London*, 1927, vol. 115, iss. 772, pp. 700-721. DOI: 10.1098/rspa.1927.0118.

18. Dashtbali, M., Mirzaie, M. A compartmental model that predicts the effect of social distancing and vaccination on controlling COVID-19. *Scientific Reports*, 2021, vol. 11, article no. 8191. DOI: 10.1038/s41598-021-86873-0.

19. Fosnaric, M., Kamensek, T., Gros, J.Z., Zibert, J. Extended compartmental model for modeling COVID-19 epidemic in Slovenia. *Scientific Reports*, 2022, vol. 12, article no. 16916. DOI: 10.1038/s41598-022-21612-7.

20. Ikeda, Y., Sasaki, K., Nakano, T. A new compartment model of COVID-19 transmission: the broken-link model. *International Journal of Environmental Research and Public Health*, 2022, vol. 19, iss. 11, article no. 6864. DOI: 10.3390/ijerph19116864.

21. Antonelli, E., Piccolomini, E. L., Zama, F. Switched forced SEIRDV compartmental models to monitor COVID-19 spread and immunization in Italy. *Infectious Disease Modelling*, 2022, vol. 7, iss. 1, pp. 1-15.

DOI: 10.1016/j.idm.2021.11.001.

22. Batista, A. A., da Silva, S. H. An epidemiological compartmental model with automated parameter estimation and forecasting of the spread of COVID-19 with analysis of data from Germany and Brazil. *Frontiers in Applied Mathematics and Statistics*, 2022, vol. 8, article no. 645614. DOI: 10.3389/fams.2022.645614.

23. Wang, Y., Yan, Z. et al. Prediction and analysis of COVID-19 daily new cases and cumulative cases: times series forecasting and machine learning models. *BMC Infectious Diseases*, 2022, vol. 22, article no. 495. DOI: 10.1186/s12879-022-07472-6.

24. Atchaya, K., Darshinii, M., Harini, R., Suganya, T. Administered machine learning models for COVID-19 future forecasting. *Journal of Physics: Conference Series*, 2021, vol. 1916, article no. 012157. DOI: 10.1088/1742-6596/1916/1/012157.

25. Galasso, J., Cao, D. M., Hochberg, R. A random forest model for forecasting regional COVID-19 cases utilizing reproduction number estimates and demographic data. *Chaos, Solitons, Fractals*, 2022, vol. 156, article no. 111779. DOI: 10.1016/j.chaos.2021.111779.

26. Alali, Y., Harrou, F., Sun, Y. A proficient approach to forecast COVID-19 spread via optimized dynamic machine learning model. *Scientific Reports*, 2022, vol. 12, article no. 2467. DOI: 10.1038/s41598-022-06218-3.

27. Bai, Y., Qian, Z., Sun, Y., Wang, S. COVID-19 epidemic forecasting based on a comprehensive ensemble method. *System Engineering Theory and Practice*, 2022, vol. 42, iss. 6, pp. 1678-1693. DOI: 10.12011/SETP2021-3005.

28. Gatto, A., Aloisi, V. et al. An artificial neural network-based approach for predicting the COVID-19 daily effective reproduction number Rt in Italy. *AI*, 2022, vol. 3, iss. 1, pp. 146-163. DOI: 10.3390/ai3010009.

29. Saliaj, L., Nissi, E. An application of neural network to predict COVID-19 cases in Italy. *Engineering Proceedings*, 2022, vol. 18, iss. 1, article no. 11. DOI: 10.3390/engproc2022018011.

30. Garg, S., Kumar, S., Muhuri, P. K. A novel approach for COVID-19 infection forecasting based on multi-source deep transfer learning. *Computers in Biology and Medicine*, 2022, vol. 149, article no. 105915. DOI: 10.1016/j.compbiomed.2022.105915.

31. Sciannameo, V., Goffi, A. et al. A deep learning approach for spatio-temporal forecasting of new cases and new hospital admissions of COVID-19 spread in Reggio Emilia, Northern Italy. *Journal of Biomedical Informatics*, 2022, vol. 132, article no. 104132. DOI: 10.1016/j.jbi.2022.104132.

32. *Coronavirus Resource Center. Johns Hopkins University & Medicine*, 2022. Available at: https://coronavirus.jhu.edu/map.html (accessed 31.08.2022).

33. Chumachenko, D., Meniailov, I., Bazilevych, K., Chub, O. On COVID-19 epidemic process simulation: three regression approaches investigations. *Radioelectronic and Computer Systems*, 2022, no. 1 (101), pp. 6-22. DOI: 10.32620/reks.2022.1.01.

# ПРОГНОЗНА МОДЕЛЬ ЕПІДЕМІЧНОГО ПРОЦЕСУ COVID-19 НА ОСНОВІ НЕЙРОННОЇ МЕРЕЖІ

*Сергій Кривцов, Євген Меняйлов, Ксенія Базілевич, Дмитро Чумаченко*

Пандемія COVID-19, що триває майже три роки, показала, що системи охорони здоров'я не готові до такого виклику. Заходи, які вживаються урядами у сфері охорони здоров'я в умовах різкого посилення навантаження на неї, включають стримування передачі та поширення вірусу, надання достатнього простору для надання медичної допомоги, забезпечення доступності лабораторій для тестування та медичної допомоги, а також мобілізацію перепідготовки медичних кадрів. Пандемія змінила державні та бізнес-процеси, оцифрувавши економіку та охорону здоров'я. Глобальні виклики стимулювали дослідження в галузі медицини на основі даних. Прогнозування епідемічного перебігу інфекційних процесів дозволило б оцінити масштаби пандемії, що насувається, для планування необхідних заходів боротьби. **Метою дослідження** є побудова моделі епідемічного процесу COVID-19 для прогнозування його динаміки на основі нейронних мереж. **Об'єкт дослідження** – епідемічний процес інфекційних захворювань на прикладі COVID-19. **Предмет дослідження** – моделі та методи моделювання епідемічного процесу на основі нейронних мереж. В **результаті** дослідження побудовано імітаційну модель епідемічного процесу COVID-19 на основі нейронної мережі. Модель показала високу точність: від 93,11% до 93,96% для Німеччини, від 95,53% до 95,54% для Японії, від 97,49% до 98,43% для Південної Кореї, від 93,34% до 94,18% для України, залежно від періоду прогнозування. Оцінка абсолютних похибок підтверджує, що модель може бути використана в практиці охорони здоров'я для розробки заходів контролю за стримуванням пандемії COVID-19. Внесок цього дослідження у галузь подвійний. По-перше, розробка моделей на основі нейромережевого підходу дозволить оцінити точність таких методів стосовно моделювання епідемічного процесу COVID-19. По-друге, вивчення експериментального дослідження із застосуванням розробленої моделі до даних із чотирьох країн сприятиме емпіричній оцінці ефективності її застосування не лише до COVID-19, а й до інших симуляцій інфекційних захворювань. **Висновки.** Значимість дослідження полягає в тому, що автоматизовані системи підтримки прийняття рішень епідеміологами та іншими працівниками охорони здоров'я дають змогу підвищити ефективність прийняття протиепідемічних рішень. Це дослідження особливо актуальне в умовах ескалації російської війни в Україні, коли ресурси системи охорони здоров'я обмежені.

**Ключові слова:** епідемічна модель; епідемічний процес; моделювання епідемії; імітаційне моделювання; COVID-19; нейронна мережа.

**Кривцов Сергій Олегович** – здобувач каф. математичного моделювання та штучного інтелекту, Національний аерокосмічний університет ім. М. Є. Жуковського «Харківський авіаційний інститут», Харків, Україна.

**Меняйлов Євген Сергійович** – канд. техн. наук, в.о. зав. каф. теоретичної та прикладної інформатики, Харківський національний університет ім. В. Н. Каразіна, Харків, Україна.

**Базілевич Ксенія Олексіївна** – канд. техн. наук, доц. каф. математичного моделювання та штучного інтелекту, Національний аерокосмічний університет ім. М. Є. Жуковського «Харківський авіаційний інститут», Харків, Україна.

**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.

**Serhii Krivtsov** – Applicant of Mathematical Modelling and Artificial Intelligence Department, National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine,
e-mail: krivtsovpro@gmail.com, ORCID: 0000-0001-5214-0927.

**Ievgen Meniailov** – PhD in Mathematical Modelling and Optimization Methods, Acting Head of Theoretical and Applied Informatics Department, V. N. Karazin Kharkiv National University, Kharkiv, Ukraine,
e-mail: evgenii.menyailov@gmail.com, ORCID: 0000-0002-9440-8378.

**Kseniia Bazilevych** – PhD in Information Technologies, Associate Professor of Mathematical Modelling and Artificial Intelligence Department, National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine,
e-mail: ksenia.bazilevich@gmail.com, ORCID: 0000-0001-5332-9545.

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