Development of a Genetic Method for Image Recognition in the Form of Radiographs

Ievgen Fedorchenko*a*, Andrii Oliinyk^a, Alexander Stepanenko^a, Tetiana Fedoronchak^a, Yuliia Fedorchenko^a, Anastasiia Kharchenko^a and Dmytro Goncharenko^a

^a Department of Software Tools, National University "Zaporizhzhia Polytechnic", 64 Zhukovskoho str., Zaporizhzhia, Ukraine, 69063

Abstract

Modern medicine depends on technical advances in the field of medical instrumentation and the development of medical software. One of the most important tasks facing doctors is to determine the exact boundaries of tumors and other abnormal formations in the tissues of the human body. The paper considers the problems and methods of machine classification and image recognition in the form of radiographs, as well as the improvement of artificial neural networks, which are used to improve the quality and accuracy of detection of abnormal structures on chest radiographs. A modified genetic method for optimizing the model parameters on the basis of a convolutional neural network has been developed to solve the problem of recognizing diagnostically significant signs of pneumonia on an X-ray of the lungs. Practical use of the developed method will allow to reduce complexity, to increase reliability of search, to accelerate process of diagnosis of diseases and to reduce a part of errors and repeated inspections of patients.

Keywords 1

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1. Introduction

To date, there are a huge number of diseases that pose a serious threat to public health, including respiratory diseases. In 2016, the World Health Organization (WHO) included them among the top 10 causes of death in the world [1].

Thus, respiratory diseases require careful and timely diagnosis, on which the patient's life can often depend.

Among all methods of instrumental diagnosis of respiratory diseases, the most frequently used and reliable is the X-ray method of diagnosis, the main task of which is the analysis of X-rays in order to identify signs of pathology [2].

The traditional expert method of diagnosing pathology by X-ray of the lungs is based on the search and evaluation by a specialist in the field of analysis of X-rays of the lungs characteristic of a particular pathology of radiological signs. The expert follows a certain sequence of actions. First of all, the shadow picture is described, ie it is determined whether the selected area of the image (object) is obscuration or enlightenment. Then the localization of the object is determined by the lobes and segments of the lungs. Next, the size, shape, contours, intensity and structure of the object are evaluated [3].

That is why the method of visual search and evaluation of small low-contrast diagnostically significant objects on the X-ray is labor-intensive, requires highly qualified radiologist and in a limited time to describe the image does not exclude diagnostic errors.

In the last few years, significant progress has been made in the development and use of neural networks and methods of so-called deep learning. These methods have shown high efficiency in solving a wide range of problems of analysis, classification and recognition of X-ray digital images [4].

Thus, the development of methods and algorithms for image recognition in the form of radiographs, in particular methods based on the use of neural networks that speed up the diagnosis of diseases and reduce the proportion of re-examinations, is an urgent task [4].

This paper proposes a modified genetic method for recognizing diagnostically significant signs of pneumonia on an X-ray of the lungs, which reduces the complexity, increases the reliability of the search, speeds up the process of diagnosing diseases and reduces some errors and re-examinations of patients.

2. Analysis of published data and problem definition

The article [5] considers the method of image recognition in the form of radiographs, based on the method of the decision tree. The authors showed that the proposed method saves computing resources, allows to optimize the procedures for selecting classification features and significantly limit the number of features used in the recognition of specific objects. The disadvantage of this method is that in the process of building a decision tree can be created too complex structures that do not fully represent the data.

In [7] the method of computer diagnostics of respiratory diseases by means of the textural analysis of X-rays is offered and investigated. An approximate search algorithm for the nearest neighbor is proposed, in which the standard to be tested next is selected so as to maximize the conditional probability density of the distances to the reference images tested in the previous steps. The results of experiments showed increased computational efficiency of the developed algorithm in comparison with known methods. The disadvantage of this method is that finding the nearest neighbor in a reasonable time is not easy. You must have enough memory to store the entire sample, as well as a search procedure that allows you to quickly find the nearest neighbor to the item that has been retrieved.

In [8] the solution of the problem of classification of chest X-rays by means of the convolutional neural network trained on small data sets is presented. The training binary classifier is used to detect the presence or absence of pathology of the lower respiratory tract. This paper presents the results of a computational experiment and shows that the use of convolutional neural networks to isolate quantitative features of images is a much more effective approach compared to traditional methods. Also, the use of emergencies provides such advantages as: adaptation to environmental changes, resistance to noise in the input data and potential speed.

Along with the above advantages, modern deep learning methods have one significant drawback: effective learning of a convolutional neural network requires a very large number (tens and hundreds of thousands) of annotated images, which is especially difficult to provide in the case of biomedical images.

After analyzing the work [5-8], it was found that in the process of image recognition in images when making decisions, medical professionals face a number of problems: incomplete and inaccurate source information, high variability of attributes and small sample size, limited decision time for conclusions.

These factors often lead to errors in diagnosis. In order to improve the efficiency and quality of medical image processing, such as chest radiography, it is necessary to improve and modify the methods of analysis of visual data to improve the accuracy and quality of disease diagnosis [8].

3. The purpose and objectives of the study

The object of the research is the process of recognizing patterns of pneumonia disease.

The subject of research is methods of image recognition in the form of radiographs.

The aim of the work is to develop a modified genetic method for optimizing model parameters based on convolutional neural networks to solve the problem of recognizing diagnostically significant signs of pneumonia on an X-ray image of the lungs.

Research method - traditional models (decision trees, nearest neighbor method, ant colony method), neural networks, combined methods (neural networks and genetic algorithms, neural networks and multi-agent systems).

4. Development of a modified genetic method for optimizing model parameters based on a convolutional neural network

To solve this problem, it was decided to develop a modification of the GA, which will increase the accuracy of the neural network. The task of learning neural networks is to adjust the weights, and here the most acceptable way can be considered genetic methods. This assumption follows from the fact that in the initial stages of the network there is no information about the input parameters for adjusting the weight parameters of the neural network. Under conditions of uncertainty, evolutionary algorithms show the greatest efficiency [9]. The developed modification offers specialized crossing, selection and mutation operators that provide maximum adaptation to the specifics of the problem.

Initially, the proposed genetic method carries out the formation of the initial population, namely, a randomly generated final set of test solutions according to formula (1):

$$g^1 = \left\{ g_1^1 ... g_n^1 \right\}, g_n^1 \in X. \tag{1}$$

where g is the generation; n is the size of the population; X is a gene [9].

In the developed genetic method, a vector consisting of columns of the weight matrix W acts as a chromosome, and the following formula (2) is used to encode possible solutions in chromosomes:

$$d_i = q_i \frac{(v_i - w_i)}{2^M - 1} + w_i, \tag{2}$$

where M is the length (bit) of one gene; q_i is an integer value of the i-th gene of chromosome from the set $\{0, \ .., 2^M\}$; d_i is a real number from the range of admissible solutions $[v_i, w_i]$ of the optimized parameter.

After the formation of the initial population, the fitness function is estimated for the matrix W. Since the weight matrix is part of a neural network that recognizes pathologies, it must be reduced to such a value that the suitability function value is maximal. To do this, compare the obtained source vector Y with the reference sample Y′ using the Euclidean distance. Consequently, the suitability function is determined on the basis of the calculated distance and is calculated by formulas (3) and (4):

$$f = \frac{1}{R}, \tag{3}$$

$$R = \left| Y - Y^{'} \right| = \sqrt{\sum_{j=1}^{M} \left(y_i - y_i' \right)^2}, \tag{4}$$

where R is the Euclidean distance, y is the value of the original vector Y′, y′ is the value of the vector Y', which is a reference pattern.

The assessment of the suitability of the current generation is calculated by formula (5):

$$F^k = \left\{ f_1^k ... f_n^k \right\} \quad f_n^k = \left(p_n^k \right). \tag{5}$$

where f is the suitability function; k is the generation number [10].

Then the method selects those individuals whose genetic material will participate in the formation of the next population of decisions, ie in the creation of the next generation. The developed genetic method uses the method of selection, called the roulette method. The idea behind this method is that individuals are selected using n roulette wheel runs, where n is the number of individuals in the population. The roulette wheel contains one sector for each member of the population. The size of the i-th sector is proportional to the probability of an individual entering a new population P (i) and is calculated by the formula (6):

$$P(i) = \frac{f(i)}{\sum\limits_{i=1}^{n} f(i)}, \tag{6}$$

where f(i) is the value of the fitness function of i - individual. The expected number of copies of the i-th chromosome after the roulette operator is determined by formula (7):

$$n_i = P(i)n. \tag{7}$$

In this selection, members of the population with a higher value of the suitability function will be selected more often than individuals with low values [11].

The application of genetic operators to chromosomes selected by selection leads to the formation of a new population of offspring from the parent population created in the previous step. In the proposed genetic method, two main genetic operators are used: the crossing operator and the mutation operator.

The generation of a new generation occurs using the operators of selection S, crossing C and mutations M by formula (8) [12]:

$$p^{k+1} = M * C * S\left(g^k, F^k\right). \tag{8}$$

where p^k is the generation; g^k – an individuals selected by roulette selection in the previous step.

Uneven arithmetic crossing is chosen as the crossing operator. When using this crossing, based on the values of the genes of the parent chromosomes P_1 and P_2, two descendants p_1 and p_2 are created the values of the i-th genes of which are calculated by formulas (9) and (10):

$$p_1 = s \cdot P_1 + (1-s) P_2, \tag{9}$$

$$p_2 = s \cdot P_2 + (1-s) P_1, \tag{10}$$

where $s \in [0; 1]$ is a real coefficient that is generated randomly on each iteration [13-14].

The mutation is performed with a certain probability P_m, in which the allele is replaced by a random value. It is selected with equal probability in the field of gene determination. Note that it is due to mutation that the field of genetic search is expanding.

When performing a mutation, the mutation coefficient Rm is set and a random number N_m is generated, evenly distributed on the segment [0, 1]. If $R_m > N_m$, then the mutation point z is randomly selected [15].

The method then evaluates the suitability of the offspring obtained as a result of the crossover operation, as well as evaluates the individuals that were obtained as a result of the mutation operator. Based on the obtained values of the suitability function for each individual of the new population, the removal of those individuals in which the values of the suitability function are the smallest. The method implements this task by sequentially removing an individual with a minimum value of the suitability function until the population size returns to its original value. The number of "dead" individuals is calculated by the formula (11):

$$C_d = C_k - C_m, \tag{11}$$

where C_d is the number of "dead" individuals, C_k is the number of offspring obtained, Cm is the number of individuals obtained using the mutation operator [16-17].

In the developed method as a stop criterion the mechanism which is based on absence of changes of function of suitability of the best individual for a certain number of iterations is used. It is also advisable to stop the method after reaching a certain number of iterations. If the stop condition is fulfilled, the algorithm gives the optimal solution, represented by the best individual, which will be transferred to the neural network as the initial matrix of weights W [17-19].

Thus, as a result of the work of the genetic method, a set of weight coefficients is obtained that ensure the correct operation of the neural network. The paper develops a modified genetic algorithm that uses real, not binary, numbers as gene values. This is because genes serve as the number of neurons that will be fed to the neural network.

5. Experiments of initialization methods for initial population in evolutionary algorithm

A dataset with pictures of pneumonia called "Chest X-Ray Images (Pneumonia)" was used to develop and test the models [20]. This data set was divided into three other datasets: one for training, the second for re-checking the accuracy of neural networks at the end of each era, and the third for final verification after training neural networks. Each dataset contains two folders, pictures with pneumonia and without pneumonia. In the work, 5875 images of fluorography were used, of which 1583 images without signs of pneumonia, and 4274 images with a diagnosis of pneumonia. Pictures are presented in shades of gray. 70% of the dataset (4313 images) was used for training, 20% (1175 images) for algorithm tuning (validation set), and 10% (587 images) for testing.

An important requirement for modeling data is their quantity and quality. If the data contain excessive noise, unclear sequence and incorrect format - this negatively affects the accuracy of forecasts, performance and quality of models [21-22].

Also, data intended for use as training datasets for classical and evolutionary methods should be normalized and reduced to one type, to reduce error and improve training quality.

Processing of the initial data before the presentation of the model was done in the following sequence.

- Provided labels, class numbers for all photographs for division into two classes, pictures with pneumonia and without pneumonia;
- Reduction of data to the types that will be used in the calculations [22].

Testing was performed on a computer with the following parameters: Windows: 10 CPU: Intel Core i5, HDD 100 GB, RAM: 8 GB, Ethernet: 10/100 Mb. The NVIDIA GeForce GTX 1050 TI GPU with CUDA architecture support is used to speed up the calculations. The Keras library [23] and the Theano library [24] were used to build a model of the neural network and work with it. For convenient work with data arrays and formation of a dataset the NumPy library - Python package for scientific calculations is used.

To begin work on this topic, it was decided to test the quality of the work of classical methods of pattern recognition. A number of experiments were performed with such classical methods of pattern recognition as.

- Decision trees;
- Method of the nearest neighbor;
- Ant colony method.

The results of the comparison of classical methods in terms of accuracy and execution time are given in Table. 1. Comparison of the accuracy of classical methods is shown in Figure 1.

Table 1
Comparison of classical methods

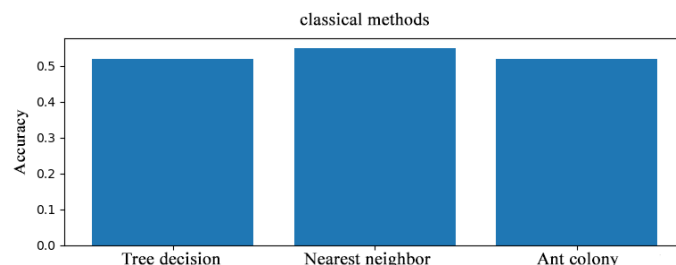| Method name	Accuracy, %	Time, sec
Decision trees	52%	280
The method of the nearest neighbor	55%	435
Ant colony method	52%	194

Figure 1: Comparison of the accuracy of classical methods

From the Table. 1 and Figure 1 you can see that the best result is obtained using the method of the nearest neighbor, the accuracy of which is 55%. He showed a high percentage of correct answers in 435 seconds. Solution trees and the ant colony method show 52% accuracy in solving 280 problems in 194

seconds, respectively. But the ant colony method is more optimal, it spent the least time, 194 seconds, and gave 3% less accuracy than the nearest neighbor method. We will not dwell on the classical methods, we will move on to testing neural boundaries.

Next, we consider and compare the results of classical and modern neural networks, from a single-layer perceptron to convolutional neural networks. Convolutional neural networks are theoretically well suited for this task, but this should be tested in practice. The inspection will take place under the same conditions.

- Number of epochs;
- Sub-sample size;
- The size of datasets for training, testing, verification;
- Metrics;
- Optimizer.

The following neural networks were chosen for experiments [25-28].

- NN single-layer perceptron;
- MLP two-layer perceptron;
- RBNS - radially basic neural network;
- CNN - convolutional neural network;
- Inception v3– Inception v3 convolutional neurometer;
- LSTM network of long short-term memory.

In Figure 2 and Figure 3 shows the training of the RBF neural network.
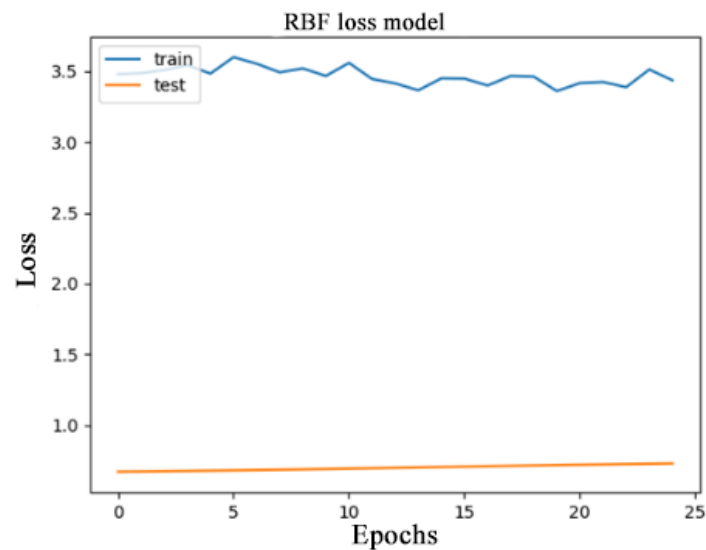

Figure 2: Graph of the dependence of the error of the loss network on the number of training cycles of epochs for the RBNS model
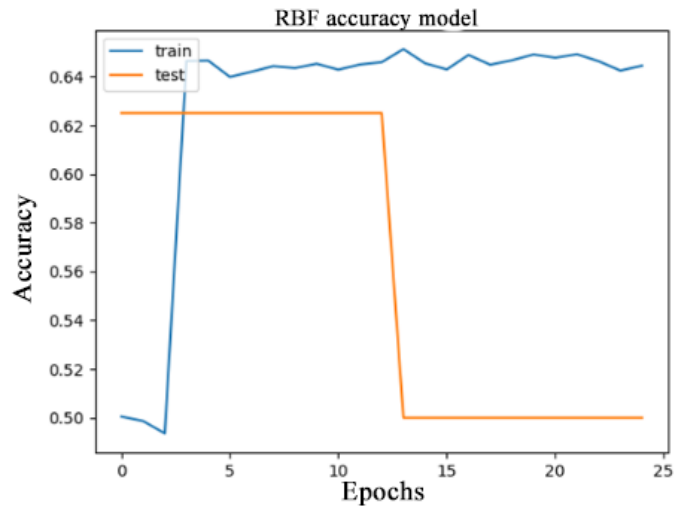
Figure 3: Graph of the dependence of the accuracy network error on the number of learning cycles of epochs for the RBNS model

From Figure 2 and Figure 3 it can be seen that the RBNS model will differ from the previous ones, but is also not suitable for solving this problem. In Figure 3 it is observed that in the 13th epoch of neural network learning it falls sharply, but the check on the validation dataset gives 62% accuracy.

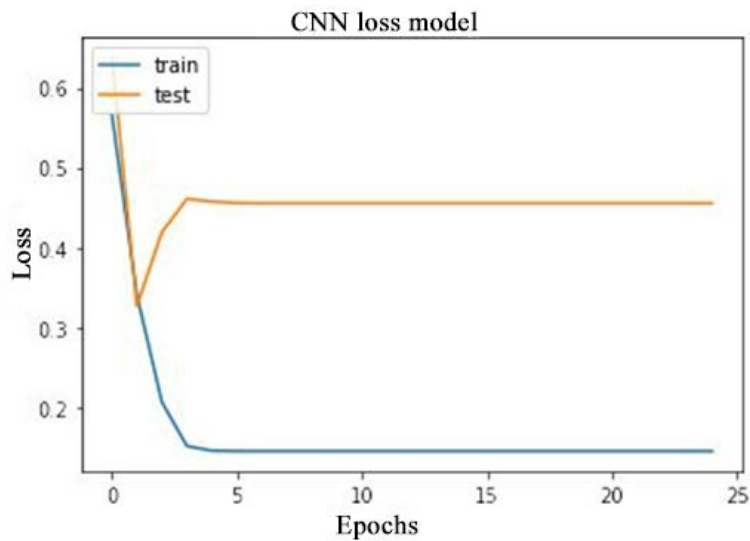In Figure 4 and Figure 5 shows the learning of the CNN neural network.

Figure 4: Graph of the dependence of the network loss error on the number of learning cycles of epochs for the CNN model
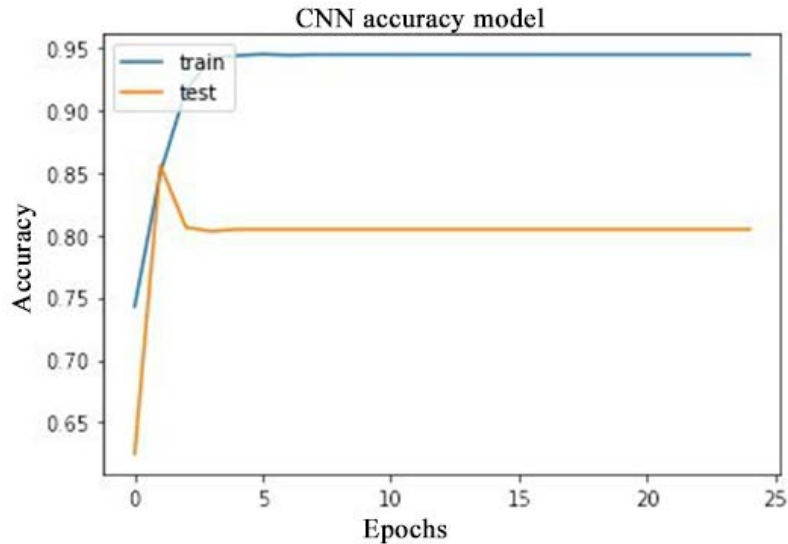
Figure 5: Graph of the dependence of the accuracy network error on the number of echo learning cycles for the CNN model

From Figure 4 and Figure 5 you can see that the CNN neural network gives a fairly high accuracy. Visually, the graph of the accuracy of the network accuracy for the CNN model (Figure 5) is similar to the graph of the error of the network accuracy for the model NN and MLP, but the difference is that the validation dataset was much higher. So in the process of learning this network there was a "retraining", it can be corrected by changing the hyper - and macro - parameters of the neural network.

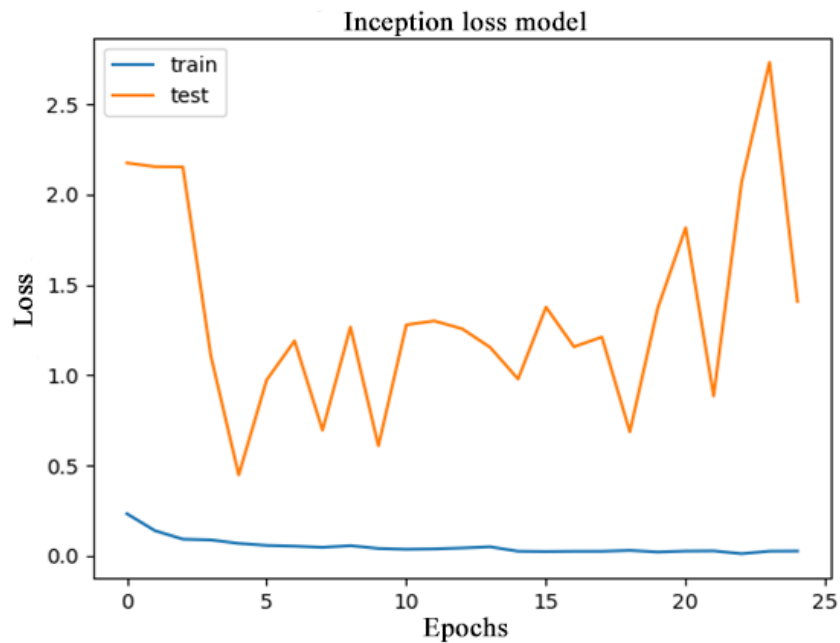In Figure 6 and Figure 7 shows the training of the Inception neural network.

Figure 6: Graph of the dependence of the network loss error on the number of learning cycles of epochs for the Inception model
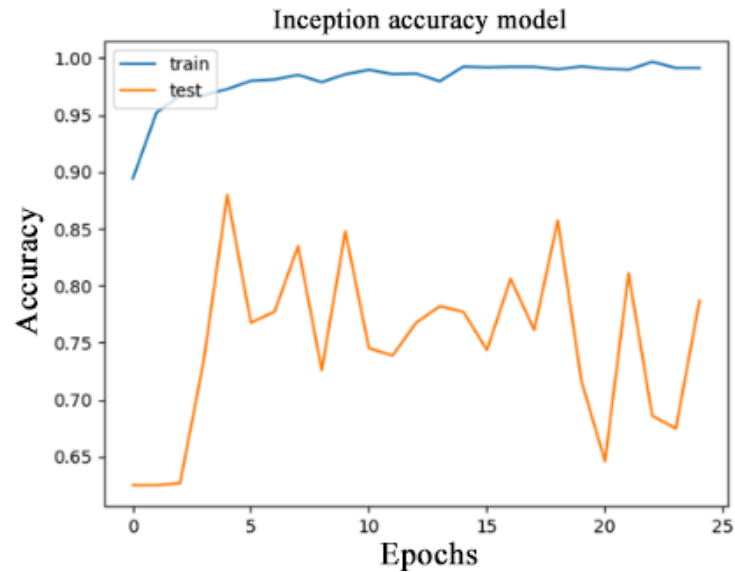
Figure 7: Graph of the dependence of the accuracy network error on the number of echo learning cycles for the Inception model

From Figure 6 and Figure 7 you can see that the Inception neural network gives 85% accuracy for about 3 learning epochs, and then gives less successful results. This suggests that further training is unlikely to yield better results.

In Figure 8 shows the training of the LSTM neural network.
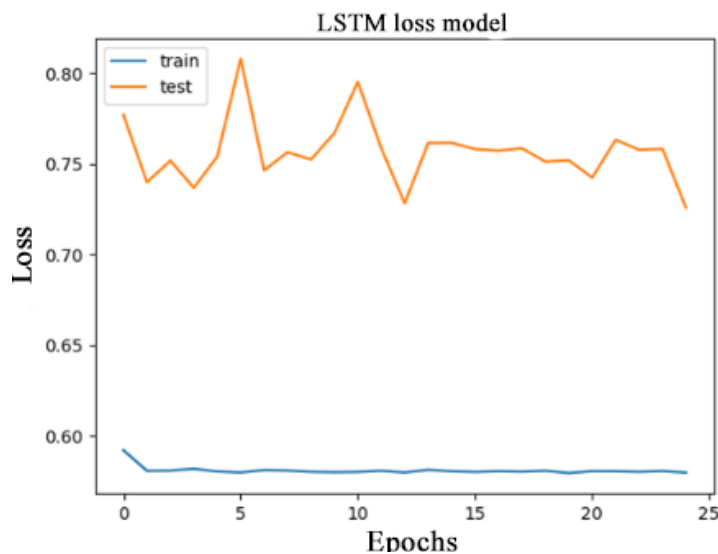
Figure 8: Graph of the dependence of the loss network error on the number of training cycles of epochs for the LSTM model

From Figure 8 it can be seen that learning takes place during the first epochs. Thus, the neural network is not suitable for solving the problem of pattern recognition of pneumonia. High accuracy on the test dataset is not the final criterion for checking the performance of the neural network. The end result can be obtained by checking the neural network on the validation set.

Let's compare neural networks on the following grounds (Table 2): accuracy on the validation set, working time and number of epochs.

Table 2

Comparison of learning outcomes of neural networks

Network name	Accuracy on te validation set, %	Time, sec	Number of epochs
NN	76%	390	25
MLP	78%	410	25
RBF	82%	910	25
CNN	89%	3334	25
Inception	83%	4158	25
LSTM	84%	2154	25

From Table 2 you can see the three basis columns that have the most value for testing and comparing neural networks. Accuracy on the validation set means how the neural network works with images that it has not seen in the learning process. The neural network on the test dataset may show a high percentage of correct answers (for example, 80-90 ~ percent), and on the validation low percentage (for example, 60-70 ~ percent). Training time is also an important criterion, because if the training lasts long enough, it will be impossible to predict systemic, but other failures. The last criterion, the number of epochs, in the presence of a large number of epochs, the neural network will be "relearned" and will give a large error on the validation dataset, and on the test, the accuracy will be quite high, about 90%. From Table 2 you can see that the best result shows CNN (89%). Next is Inception (83%), followed by NN (76%) and MLP (78%), followed by LSTM (84%). Optimal choice would be CNN neural networks, based on accuracy (89%) \ training time (3334).

Let's compare the work of classical methods with neural networks. In the Table 3 shows the results of methods and neural networks on those parameters that can be compared.

Table 3

Comparison of neural networks and classical methods

Name	Accuracy, %	Time, sec
Decision trees	52%	280
The method of the nearest neighbor	55%	435
Ant colony method	52%	194
NN	76%	390
MLP	78%	410
RBF	82%	910
CNN	89%	3334
Inception	83%	4158
LSTM	84%	2154

In Table 3 can be seen that in the first place remained CNN (89%), Inception (83%) and RBF (82%). They are followed by perceptrons and methods that have approximately the same result.

In the Table 4 presents the parameters that were used to upgrade CNN and their selected values.

Table 4

Setting ON (modified) to upgrade CNN

Parameter name	Value
Number of people	10
Number of populations	10
The number of neurons in the first layer	0 – 128(at 0 the layer is not created)
The number of neurons in the second layer	0 – 128(at 0 the layer is not created)
The number of neurons in the third layer	0 – 128(at 0 the layer is not created)
The number of neurons in the fourth layer	0 – 128(at 0 the layer is not created)

The number of neurons in the fifth layer	0 – 128(at 0 the layer is not created)
Dropout chance	0.2 – 0.6

In Figure 9 and Figure 10 you can see graphs of training of the best model of the neural network, which was obtained after the modernization with the help of a modified GA.
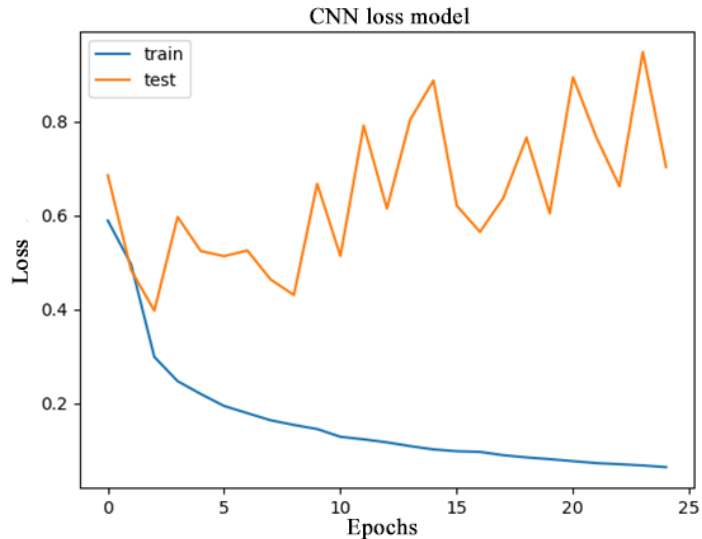

Figure 9: Graph of the dependence of the network loss error on the number of learning cycles of epochs for the CNN model

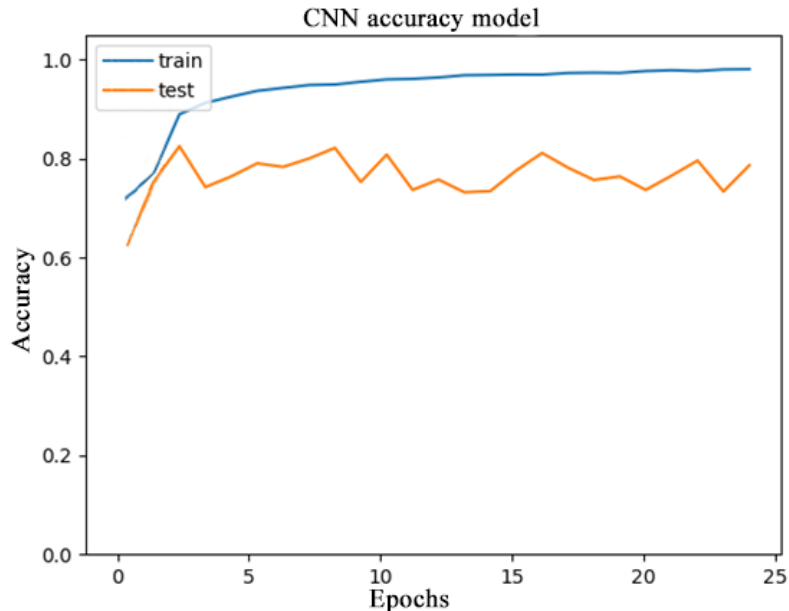**Figure 10:** Graph of the dependence of the accuracy network error on the number of echo learning cycles for the CNN model

From Figure 10 it can be seen that the modernization of the CNN neural network gives a significantly better increase in working time, as well as an increase in forecasting accuracy.

We will perform a comparative analysis of the CNN neural network and the CNN neural network modernized with GA (Table 5).

Table 5
Neural network CNN upgraded from GA

Name	Accuracy, %	Time, sec
CNN	89%	3334
CNN– GA (modified)	95%	2563

Thus, a modified genetic method has been developed to solve the problem of image recognition in the form of radiographs, which will develop an effective NM architecture and increase the accuracy of recognition of pathological structures on radiographs.

6. Conclusions

The problems of machine classification and recognition of images in the form of radiographs, as well as the improvement of artificial neural networks, which are used to improve the quality and accuracy of detection of abnormal structures on chest radiographs, were considered. An overview of existing methods of deep learning and methods of X-ray recognition is made. A comparative analysis of classical methods and modern neural networks, from a single-layer perceptron to convolutional neural networks in terms of accuracy and execution time. It was found that the best results of recognition of pathological structures on radiographs were obtained using a convolutional neural network. The recognition accuracy of this model was 89% (for comparison, the accuracy of the ant colony method is 52%), but it is lower than the execution time, which is equal to 3334s (the execution time of the ant colony method is equal to 194s). To overcome this problem, a modified genetic method for optimizing the model parameters based on a convolutional neural network was developed. The presented method allows to solve the problem of recognizing diagnostically significant signs of pneumonia on an X-ray of the lungs. Testing of the developed method showed that its recognition accuracy increased to 95%, and time decreased to 2563s, which is an acceptable indicator. Practical use of the developed method will allow to reduce labor intensity, to increase reliability of search, to accelerate process of diagnosis of diseases and to reduce a part of errors and repeated inspections of patients.

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