Use of Neural Network-based Models to Predict theSeverity of Bronchial Asthma in Children

Oleh Pihnastyi[1], Olha Kozhyna[2] and Iuliia Karpushenko[2]

[1] National Technical University "KhPI", 2 Kyrpychova, Kharkiv, 61002, Ukraine
[2] Kharkiv National Medical University, 4 Nauky Avenue, Kharkiv, 61022, Ukraine

Abstract

Problem of early diagnosis of bronchial asthma in children is due to the heterogeneity of the disease. The time of onset of the first symptoms of the disease, their severity, and the possibility of controlling exacerbations are determined by the interrelation of a factors numerous. The aim of the study is to develop a method for predicting the severity of bronchial asthma based on the factors numerous for prediction. A clinical and paraclinical examination of 70 children with a diagnosis of bronchial asthma at the age from 6 to 18 years was carried out. 142 factors were analysed and the degree of interrelationship between them was determined. A model for predicting the degree of severity of bronchial asthma in children, the foundation of which is a neural network, is presented. A multilayer perceptron with an architecture containing one and two hidden layers was used to build the model. A comparative analysis of prediction results for models using neural network architecture with different number of nodes in hidden layers was performed. MSE (Mean Squared Error) values were calculated for training and test data set for architecture variants with different number of nodes in hidden layers. Comparative characteristics for models used for prediction of linear regression equation and models based on neural networks are presented. Quantitative results for predicting the severity class of the course of bronchial asthma are given. The results indicate the effectiveness of using neural network based models to predict outcomes that depend on a large number of factors.

Keywords

Correlation, perceptron, neural network, bronchial asthma, child

1. Introduction

Bronchial asthma is a noncommunicable disease that affects children. In 2019, the number of asthma patients was 262 million and 455,000 deaths due to this disease were reported [1]. The pathophysiological aspects of bronchial asthma are complex and diverse. Multifactoriality, the lack of reliable monopredictors of development and the peculiarities of the course of bronchial asthma cause the difficulty of diagnosing the disease in children [2]. The study of asthma pathogenesis mechanisms and the development of new effective medical drugs are aimed at determining their prognostic value in achieving control of disease symptoms. The problem of early diagnosis and timely prediction of the course of the disease remains acute.

To predict the bronchial asthma development, linear regression models are frequently utilized [3]. The work of Yan Zhao et al identified factors (age, parental asthma, early frequent wheezing, allergic rhinitis, eczema, allergic conjunctivitis, obesity and dust mite aeroallergen), and used a logistic regression model to predict asthma in school-age children [4]. Author Amani F. Hamad et al developed a model for predicting the risk of asthma in children using data on comorbid conditions among children and parents [5]. The use of a binary logistic regression model has improved the accuracy of diagnosing asthma in children and adults under 25 years of age in primary care by identifying the most valuable combination of predictors based on clinical assessment [6]. Studying the association between birth weight and asthma in children using univariate and multivariate logistic models identified factors (premature birth, age, sex, race, family poverty, health insurance, smoking, maternal age) that play an important role in the formation of diseases [7].

CMIS-2024: Seventh International Workshop on Computer Modeling and Intelligent Systems, May 3, 2024, Zaporizhzhia, Ukraine

pihnastyi@gmail.com (O. Pihnastyi); olga.kozhyna.s@gmail.com (O. Kozhyna); yv.karpushenko@knmu.edu.ua (I. Karpushenko)

0000-0002-5424-9843 (O. Pihnastyi); 0000-0002-4549-6105 (O. Kozhyna); 0000-0002-2196-8817 (I. Karpushenko)

Regression model relies on a non-invasive forecasting method and an expanded factors number. The identification of predictors for model development consists of analysing the observed value dependence on other factors. Because of the heterogeneity of childhood asthma, many predictors are considered: wheezing after exercise; wheezing causing dyspnoea; cough during exercise; atopic dermatitis and allergic sensitisation [8]. The use of CHART screening allows symptom-based identification of children at high risk of developing asthma as early as 3 years of age, developed using predictive models [9, 10]. The difference between models is the absence in the model of quantitative factors characterising the results of laboratory examinations. Linear regression four factors mode (hospitalisation, eczema, parental atopy, the positive and negative predictive value of specific Ig E to inhalant allergens) was studied in [11], which made it possible to increase the predictive value of the model. In [12], a simplified methodology allowing to construct the observed value dependence on quantitative factors was considered. When using a one-dimensional and three-dimensional model together instead of a four-dimensional one, the computational complexity of the process of constructing regression models is reduced. Another way to reduce the computational complexity is related to the use of approximate methods for building regression models [13]. The works used the technique of constructing approximate one- and two-parameter models (TSLP, severe, pillow feather, bronchial asthma in relatives of second generation, allergic rhinitis, atopic dermatitis, domestic dust) and using their combinations to analyse the degree of prognosis of the bronchial asthma course in children as a way of replacing multifactorial linear regression models was proposed.

To improve the accuracy of prognosis of the bronchial asthma course, models based on neural networks have been proposed.

To understand the heterogeneity of the disease and to identify asthma subtypes, cluster analysis was used based on the definition of four distinguishing features: age of onset, allergic sensitisation, severity and exacerbations in the previous year [14]. The authors M. Lovrić, I. Banić et al. applied neural network based models to predict treatment outcomes in children with mild to severe asthma by changes in asthma control, lung function (SPF1 and MEF50) and FENO values after 6 months of control medication [15]. A research paper [16] presents machine learning algorithms for asthma phenotype detection and prediction of clinical outcomes to find heterogeneous relationships between clinical features and outcomes [16]. In [17] a review of algorithms of machine learning methods for predicting asthma exacerbation was conducted to identify characteristic features of the disease course. Asthma prediction on conventional blood biomarkers using an improved classifier (AGEC) with affinity graph improves the accuracy of asthma prediction compared to five state-of-the-art prediction models [18]. An automatic machine learning model is used to develop a prediction model for severe asthma exacerbation [19]. The presented model demonstrates the ability to identify children who are not at risk of exacerbation. Data from retrospective electronic medical records (EMR) of patients were used to identify asthma signs in children in paediatric hospitals in China. To improve the quality of asthma diagnosis, models based on machine learning CatBoost, Naive Bayes, support vector machines (SVM) have been developed and are constantly being improved [20].

The aim of the study is to develop a method for predicting the severity of the bronchial asthma course, based on the factors numerous for prediction. The vast majority of studies devoted to prognosis of bronchial asthma in children are based on linear regression models that contain a small number of regressors (no more than ten) and one observed parameter. The feature of the study of the bronchial asthma severity is the dependence of the observed parameter on the factors numerous of regressors, which have a small correlation coefficient between the observed value and the regressor. The use of linear models based on a small number of regressors, as well as the lack of regression models for classifying the severity of bronchial asthma, does not allow obtaining the required accuracy of prediction results for clinical studies. In this regard, an urgent problem in conducting clinical research is the construction of nonlinear prediction models containing several dozen regressors in the presence of the required number of observable factors. The scientific novelty of this work is the construction of a classification nonlinear model based on a neural network to predict the severity of bronchial asthma, containing several dozen regressors.

2. Problem statement

90 children aged from 6 to 18 years were involved in the study of the course of bronchial asthma: the main group is 70 children diagnosed with bronchial asthma; the control group is 20 children. The

average age of children with bronchial asthma was 11 years. For each patient, information on 142 factors that could be the cause of bronchial asthma was collected, processed and analysed. The study is carried out in compliance with scientific ethics and biomedical standards [21]. Parents were interviewed about the patients' symptoms characteristic of bronchial asthma, as well as the patients' medical history. The survey data were added to the patient's materials. Clinical features of the disease and the results of laboratory methods of investigation were studied.

In this study, a prediction model based on a neural network was developed to predict the severity of the disease course. Selection criteria were introduced to select the m-factors of the model

$$r_{y_\alpha x_m} \to \max, \quad r_{x_m x_v} \to \min, \tag{1}$$

где $r_{y x_m}$ is correlation coefficients between model factors model factor X_m and the observed parameter Y_α; $r_{x_m x_v}$ are correlation coefficients between factors X_m and X_ϑ:

$$r_{x_k x_v} = \frac{\frac{1}{n}\sum_{i=1}^{n}\left(X_{ki} - m_{x_k}\right)\left(X_{vi} - m_{x_v}\right)}{\sigma_{x_k}\sigma_{x_v}}, \ \sigma_{x_k} = \sqrt{\frac{1}{n}\sum_{i=1}^{n}\left(X_{k\,i} - m_{x_k}\right)^2}, \ m_{x_k} = \frac{1}{n}\sum_{i=1}^{n} X_{ki}, \ k = 1..K. \tag{2}$$

$$r_{y_\alpha x_k} = \frac{\frac{1}{n}\sum_{i=1}^{n}\left(X_{ki} - m_{x_k}\right)\left(Y_{\alpha i} - m_{y_\alpha}\right)}{\sigma_{x_k}\sigma_{y_\alpha}}, \quad \sigma_{y_\alpha} = \sqrt{\frac{1}{n}\sum_{i=1}^{n}\left(Y_{\alpha i} - m_{y_\alpha}\right)^2}, \ m_{y_\alpha} = \frac{1}{n}\sum_{i=1}^{n} Y_{\alpha i}, \ \alpha = 1..Z. \tag{3}$$

Experimental data of laboratory clinical changes, which were used to calculate correlation coefficients $r_{y x_m}$, $r_{x_m x_v}$ are presented in [22]. The numerical characteristics of the selected set of factors in accordance with the criteria (1) are given in Table 1.

Table 1
Numerical the factors characteristics

Code	Regressor name	m_x, m_y	σ_x, σ_y
X_1	Atopic dermatitis	0.0562	0.2303
X_2	Bronchial asthma in relatives of second generation	0.0658	0.2479
X_3	Allergic rhinitis	0.4494	0.4974
X_4	Sheep wool	0.5217	0.6507
X_5	Domestic dust	2.2319	1.1312
X_6	Pillow feather	0.7536	0.8059
X_7	Dog hair	0.5362	0,8090
X_8	Bronchial asthma in father	0.0864	0.2810
X_9	Age	11.0674	3,6220
X_{10}	CD25 10*3 cells	0.6937	0.3087
Y_1	SEVERE PERSISTENT	0.0444	0.2082
Y_2	MODERATE PERSISTENT	0.3111	0.4657
Y_3	MILD PERSISTENT	0.3111	0.4562
Y_4	INTERMITTENT	0.3333	0.4740

The calculated correlation coefficients values between the model factors $r_{x_m x_v}$, as well as between the model factors and the observed value are also $r_{y_\alpha x_m}$ presented in Table 2.

Table 2

Correlation coefficients values $r_{x_m x_v}$, $r_{y_\alpha x_m}$

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}
X_1	-	0.08	0.08	0.03	0.26	0.6	0.11	0.08	0.03	0.17
X_2	-0.08	-	0.10	0.21	0.25	0.29	0.00	-0.09	0.16	-0.22
X_3	0.08	0.10	-	-0.01	0.27	0.09	-0.19	0.24	0.16	-0.03
X_4	-0.03	0.21	-0.01	-	0.16	0.34	0.20	0.02	0.00	-0.17
X_5	0.26	0.25	0.27	0.16	-	0.19	0.12	-0.05	0.17	-0.07
X_6	0.06	0.29	0.09	0.34	0.19	-	0.11	-0.05	0.04	0.08
X_7	0.11	0.00	-0.19	0.20	0.12	0.11	-	-0.17	-0.02	-0.07
X_8	0.08	0.09	0.24	0.02	-0.05	-0.05	-0.17	-	0.12	-0.05
X_9	-0.03	0.16	0.16	0.00	0.17	0.04	-0.02	-0.12	-	-0.22
X_{10}	-0.17	-0.22	-0.03	-0.17	0.07	0.08	-0.07	-0.05	-0.22	-
Y_1	0.23	0.44	0.31	0.31	0.32	0.38	0.20	-0.10	0.18	-0.20
Y_2	-0.12	-0.22	0.23	-0.29	0.01	-0.28	-0.14	0.32	-0.17	-0.28
Y_3	0.02	-0.22	-0.08	-0.05	-0.14	-0.11	0.16	-0.05	-0.01	0.11
Y_4	-0.12	0.44	0.12	0.08	-0,11	-0,18	0,20	-0,05	-0,22	-0,18

To build a model for predicting the severity of bronchial asthma in children, a multilayer perceptron consisting of several layers of neurons, each of which is connected with the previous layer (from which it receives input data) and the subsequent layer (which it, in turn, affects), was used in this study. The task of classifying the severity of the course of bronchial asthma Y_α depending on the values of input factors X_m. Softmax activation function was used to form the output parameters. This approach guarantees that the output nodes take values from 0 to 1, and the sum of all values of the output nodes is equal to one, which can be associated with the probability of the degree of the bronchial asthma course Y_α.

3. Bronchial asthma severity prediction model

Linear models is studied in [23, 24] to predict of the disease course of bronchial asthma:

$$Y_{\alpha i} = w_{\alpha 0} + \sum_{m=1}^{M} w_{\alpha m} X_{mi},\ \alpha = 1..Z. \quad (4)$$

Overcoming the limitation of a linear model of type (4) is achieved by including a nonlinear transformation mechanism in the presented model [25]:

$$Y_{\alpha i} = f\left(w_{\alpha 0} + \sum_{m=1}^{M} w_{\alpha m} X_{mi} \right), \quad (5)$$

where $f(x)$ - nonlinear transformation function. When using analytical methods to calculate the coefficients $w_{\alpha 0}$, $w_{\alpha m}$ in the linear regression model (4) and transformed linear regression model (5), as a rule, for each observed factor is performed independently [26]. On the other hand, the model coefficients are functions dependent on the values of the regressors X_m and the observed parameter Y_α :

$$w_{\alpha 0} = w_{\alpha 0}(Y_\alpha, X_1,...,X_M), \quad w_{\alpha m} = w_{\alpha m}(Y_\alpha, X_1,...,X_M). \quad (6)$$

Increasing the accuracy of predicting the values of the observed parameters is achieved by switching to numerical methods to calculate the coefficients $w_{\alpha 0}, w_{\alpha m}$ which depend on all the observed parameters Y_α:

$$w_{\alpha 0} = w_{\alpha 0}(Y_1,...,Y_Z, X_1,...,X_M), \quad w_{\alpha m} = w_{\alpha m}(Y_1,...,Y_Z, X_1,...,X_M). \quad (7)$$

Thus, the transition from the model consisting of -equations with independent coefficients (5) to the model represented by the system of -equations is made:

$$\begin{cases} Y_{1i} = f\left(w_{10} + \sum_{m=1}^{M} w_{1m} X_{mi} \right), \\ \ldots\ldots\ldots \\ Y_{\alpha i} = f\left(w_{\alpha 0} + \sum_{m=1}^{M} w_{\alpha m} X_{mi} \right), \\ \ldots\ldots\ldots \\ Y_{Zi} = f\left(w_{Z0} + \sum_{m=1}^{M} w_{Zm} X_{mi} \right). \end{cases} \quad (8)$$

In common, a unique transformation function $Y_{\alpha i} = f_{\alpha}(x_{\alpha})$ can be chosen for each observed quantity Y_{α}. Although the last system of equations contains nonlinear transformation functions for the output parameter, by introducing the inverse function of the $f^{-1}(y) = x$ for the reciprocal-ambiguous function $y = f(x)$ system of equations (8) is transformed into a linear system of equations for the transformed observables $Y_{T\alpha}$ relative to input factors X_m:

$$\begin{cases} Y_{T1i} = w_{10} + \sum_{m=1}^{M} w_{1m} X_{mi}, \\ \ldots\ldots\ldots \\ Y_{T\alpha i} = w_{\alpha 0} + \sum_{m=1}^{M} w_{\alpha m} X_{mi}, \qquad Y_{T\alpha i} = f^{-1}(Y_{\alpha i}). \\ \ldots\ldots\ldots \\ Y_{TZi} = w_{Z0} + \sum_{m=1}^{M} w_{Zm} X_{mi}, \end{cases} \quad (9)$$

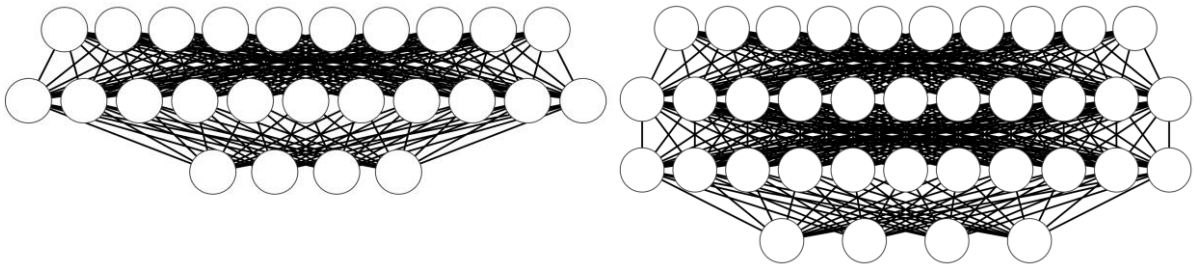
As the next step to build non-linear models for calculating the observed parameters Y_{α} uses a multi-layer architecture in which each k level (layer, $k = 1..L$) is represented by a separate system of equations:

$$\begin{cases} H_{11i} = f_1\left(w_{110} + \sum_{m=1}^{M} w_{11m} X_{mi} \right), \\ H_{12i} = f_1\left(w_{120} + \sum_{m=1}^{M} w_{12m} X_{mi} \right), \\ \ldots\ldots\ldots \\ H_{1M_1 i} = f_1\left(w_{1M_1 0} + \sum_{m=1}^{M} w_{1M_1 m} X_{mi} \right), \end{cases} \begin{cases} H_{k1i} = f_k\left(w_{k10} + \sum_{m=1}^{M_{k-1}} w_{k1m} H_{(k-1)mi} \right), \\ H_{k2i} = f_k\left(w_{k20} + \sum_{m=1}^{M_{k-1}} w_{k2m} H_{(k-1)mi} \right), \\ \ldots\ldots\ldots \\ H_{kM_k i} = f_k\left(w_{kM_k 0} + \sum_{m=1}^{M_{k-1}} w_{kM_k m} H_{(k-1)mi} \right), \end{cases} \begin{cases} Y_{1i} = f_Y\left(w_{Y10} + \sum_{m=1}^{M_L} w_{Y1m} H_{Lmi} \right), \\ \ldots\ldots\ldots \\ Y_{\alpha i} = f_Y\left(w_{Y\alpha 0} + \sum_{m=1}^{M_L} w_{Y\alpha m} H_{Lmi} \right), \\ \ldots\ldots\ldots \\ Y_{Zi} = f_Y\left(w_{YZ0} + \sum_{m=1}^{M_L} w_{YZm} H_{Lmi} \right). \end{cases} \quad (10)$$

Procedure for calculating the coefficients $w_{kM_k 0}$, $w_{kM_k m}$, w_{YZ0}, w_{YZm} requires a prepared dataset for training the neural network, in which each row of values of input factors X_m corresponds to the string of values of the observed parameters Y_{α}. One way to calculate the coefficients $w_{kM_k 0}$, $w_{kM_k m}$, w_{YZ0}, w_{YZm} is the method of error back propagation. The coefficients are calculated by the method of successive approximation. Stopping of calculations occurs when the accuracy of calculation of the values of the observed parameters Y_{α} reaches the specified accuracy or the number of approximations has exceeded the maximum permissible specified value. In direct propagation, intermediate values of variables are sequentially calculated and stored in the computational graph defined by the computational procedure. The calculation is performed sequentially from the input layer to the output layer. In back propagation, the gradients of intermediate variables and parameters are sequentially computed and stored. The computation is performed in reverse order sequentially from output layer to output layer.

A multilayer perceptron with an architecture containing a single M-M_1-Z (L=1) and two M-M_1-M_2-Z hidden layers (L=2), where M- number of input factors in the prediction model; M_k – the nodes

number in k hidden layer; Z- the nodes number in the output layer. The architecture of the neural network is shown in Fig. 1. The values of the neural network nodes are calculated in accordance with the system of equations (10).



a) 10-M_1-4 (L=1) b) 10- M_1-M_2-4 (L=2)

Figure 1: Neural network architecture in a model for predicting the severity of the course of bronchial asthma: (a) one M-M1-Z hidden layer (L=1); (b) two M-M1-M2-Z hidden layers (L=2).

For the hidden layer nodes, let us represent the activation function as a Sigmoid-function

$$f_1(x) = \frac{1}{1+\exp(-x)}. \tag{11}$$

As the activation function for the last (output) layer, choose Softmax function:

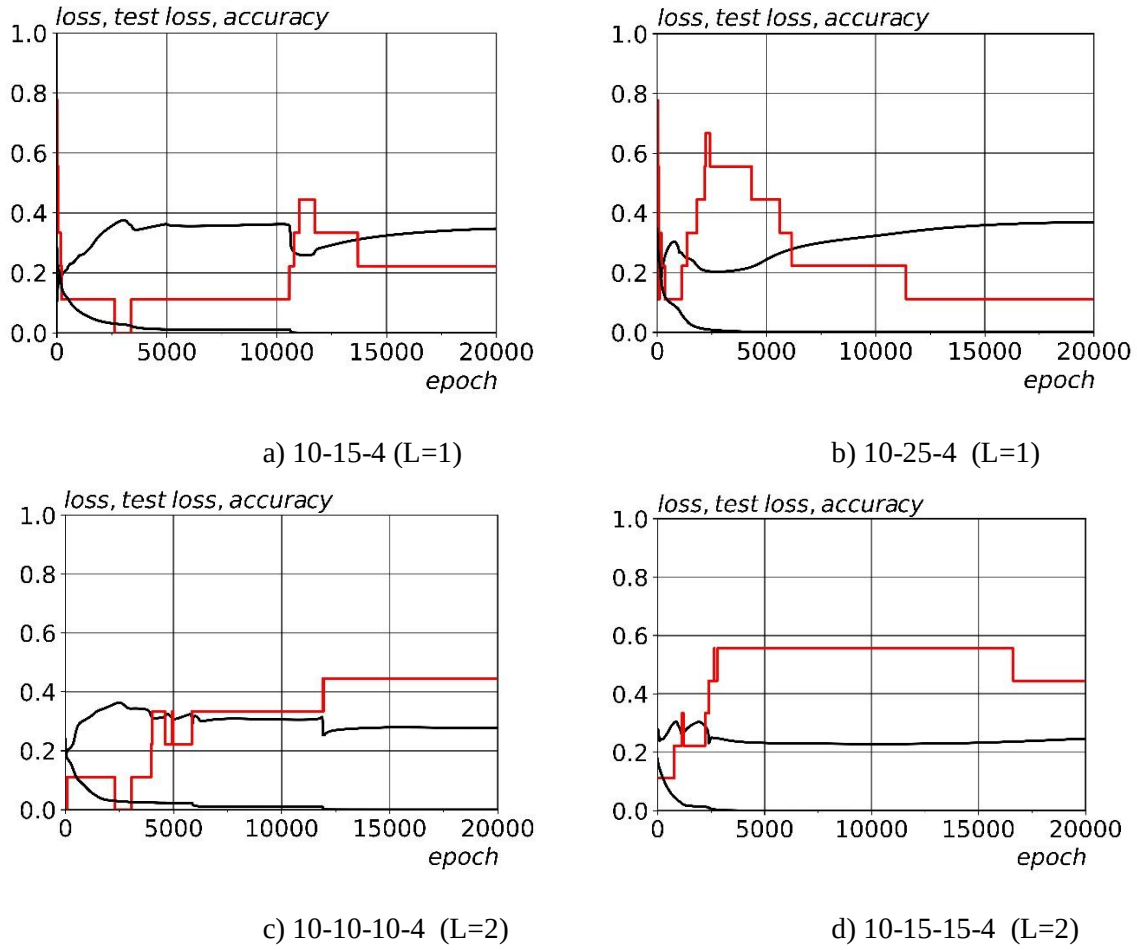
$$f_{Y\alpha}(x_\alpha) = \frac{\exp(-x_\alpha)}{\sum_{\alpha=1}^{Z}\exp(-x_\alpha)}. \tag{12}$$

This approach normalises the values of the output parameters of the bronchial asthma severity prediction model, optimises the discrete output spaces and treats these values as the probability of a patient having a disease corresponding to the bronchial asthma severity classification. The key point is the application of a probabilistic approach that allows discrete categories to be treated as examples of samples from a probability distribution. Thus, the use of softmax activation function for the output layer allowed us to transform the values of the output layer of the neural network into actual discrete probability distributions of bronchial asthma severity.

As the method of initialisation of model weights and bias, the normal law distribution of values with distribution parameters $N(0,1)$. As shown by numerical experiments, the method of initialisation of weights plays an important role in the construction of the prediction model, allows to accelerate the convergence of training and improve the quality of the model. When training the neural network in the prediction model, the following model hyperparameters are set: learning rate is $lr = 0.001$, maximum number of epochs is $epoch_{\max} = 20000$, the size of the packet used in training is $batch = 1$.

4. Analysing the results

When building the prediction model, the sample for training the neural network is divided into two sets of data. The first dataset directly serves for training the neural network and makes up 80%, the second dataset (test dataset), which makes up 20%, is used to verify the prediction accuracy. The training process of the neural network with different architectures is shown in Fig. 2. Quantitative indicators characterising the quality of the neural network training process are presented in Table 3.



a) 10-15-4 (L=1)

b) 10-25-4 (L=1)

c) 10-10-10-4 (L=2)

d) 10-15-15-4 (L=2)

Figure 2: Neural network training results for different architectures with one hidden layer M-M_1-Z (L=1) and two hidden layers M-M_1-M_2-Z (L=2); the loss function for the lerning dataset (loss) and the loss function for the test dataset (test loss) is black line; the prediction accuracy is red line.

Table 3
Learning rates of neural network for different architectures

	regression model	10-15-4 (L=1)	10-25-4 (L=1)	10-10-10-4 (L=2)	10-15-15-4 (L=2)
loss value, MSE	0.0713	5.77e-07	1.06e-07	3.94e-07	0.16e-07
best test loss value, MSE	0.5051	0.2607	0,2061	0.2674	0.2473
best test accuracy		0.4444	0.6677	0.4556	0.5556
best test epoch value		11027	2214	11905	2635

A test dataset was used to determine the prediction accuracy. The severity of the disease corresponded to the value of the predicted class having the maximum probability value. Table 3 shows the comparative analysis of the training results of the neural network with one and two hidden layers and different number of nodes in the hidden layer. When carrying out the comparative analysis, the random sequence of numbers used in the initialisation of the neural network weights was a fixed sequence of numbers. As would be expected, increasing the number of nodes for a neural network with both one and two hidden layers results in a significant decrease in MSE. Similar behaviour is observed for the MSE values corresponding to the test dataset. The decrease in MSE values leads to an increase in the prediction accuracy determined with the test dataset. As a comparison of the prediction quality, Table 3 presents the MSE value for the prediction model based on the linear regression model [27].

The coefficients of the linear regression equation for the above model are given in Table 4, for the calculation of which the same data set was used as for training the neural network. The MSE value for the test dataset in the neural network based prediction models is half that for the prediction model using the linear regression equation. Particular attention should be paid to the strong difference in the MSE

values obtained for the training dataset. The latter fact clearly demonstrates the property of the neural network to approximate the values for the test dataset. It is expected that as the sample size for training the neural network increases, a similar trend will be observed for the MSE values obtained for the test dataset of the dataset.

Table 4
Linear regression mode coefficients for the value Severe Persisten [27].

№		$\sqrt{MSE}$	X_0	X_1	X_2	X_3	X_4	X_5	X_7	X_8	X_9	X_{10}	X_{12}
17	56	0.267	0.1617	0.1493	0.4965	-0.1139	0.3788	0.0314	0.0259	0.0775	0.0791	-0.0029	0.0004

To quantify the quality of prediction of the bronchial asthma course, Table 5 and Table 6 present the prediction values obtained for a model based on a neural network with a 10-15-4 architecture consisting of an input layer with ten nodes (model input factors X_m , Table 2), output layer with four nodes (observed model parameters Y_α , Table 2) and one hidden layer with fifteen nodes.

Table 5
Model prediction results for the training dataset

	initial				predict			
N#	SEVERE PERSISTENT	MODERATE PERSISTENT	MILD PERSISTENT	INTER MITTENT	SEVERE PERSISTENT	MODERATE PERSISTENT	MILD PERSISTENT	INTER MITTENT
1	0	0	**1**	0	0.0	0.0289	**0.9415**	0.0294
2	0	**1**	0	0	0.0024	**0.8718**	0.0604	0.0653
3	0	0	0	**1**	0.0011	0.0471	0.1133	**0.8385**
4	0	0	0	**1**	0.0002	0.0113	0.1042	**0.8843**
5	0	0	**1**	0	0.0068	0.1163	**0.8384**	0.0387
6	0	0	**1**	0	0.0008	0.0004	**0.9615**	0.0373
7	0	0	**1**	0	0.0	0.0147	**0.9170**	0.0683
8	0	0	**1**	0	0.0015	0.0340	**0.9496**	0.0149
9	0	0	**1**	0	0.0	0.0778	**0.9032**	0.0189
10	0	0	**1**	0	0.0	0.0035	**0.9513**	0.0452
11	0	0	**1**	0	0.0031	0.0023	**0.9743**	0.0203
12	0	**1**	0	0	0.0003	**0.8380**	0.1061	0.0556
13	0	**1**	0	0	0.0006	**0.9466**	0.0042	0.0486
14	0	**1**	0	0	0.0004	**0.8859**	0.0223	0.0915
15	0	0	0	**1**	0.0137	0.1030	0.0455	**0.8378**
16	**1**	0	0	0	**0.8815**	0.0375	0.0329	0.0480
17	0	0	**1**	0	0.0	0.1084	**0.8901**	0.0015
...	...	...	...	...	...	...	**...**	...

Table 6
Model prediction results for the test dataset

	initial				predict			
N#	SEVERE PERSISTENT	MODERATE PERSISTENT	MILD PERSISTENT	INTERMITTENT	SEVERE PERSISTENT	MODERATE PERSISTENT	MILD PERSISTENT	INTERMITTENT
1	0	0	0	1	0.0040	0.0012	0.8675	0.1273
2	0	0	0	1	0.0001	0.0030	0.9824	0.0145
3	0	**1**	0	0	0.0	**0.7886**	0.2009	0.0105
4	0	0	1	0	0.0002	0.9660	0.0131	0.0208
5	0	0	0	**1**	0.0200	0.3471	0.2856	**0.3474**
6	0	0	0	**1**	0.0473	0.1614	0.3864	**0.4049**
7	0	0	0	**1**	0.0089	0.3165	0.0480	**0.6265**
8	0	0	0	**1**	0.2180	0.0613	0.3427	**0.3781**
9	0	0	0	**1**	0.0016	0.0445	0.0721	**0.8818**

The accuracy of predicting the severity class of bronchial asthma using the developed model was determined as follows: for each class corresponding to the severity class, the prediction probability is calculated based on the Softmax function; the column with the maximum probability value for the training dataset is determined; the severity class for the resulting column is considered as the prediction result. The severity class of the disease course for each patient is determined according to the given value provided in the training dataset. This result is expected, which is explained by the low value of MSE corresponding to the training dataset. Table 6 gives the quantitative values of predicting of the bronchial asthma course for the test dataset. The bronchial asthma course severity was correctly predicted for 70% of the patients from the test dataset. This is an encouraging result compared to studies based on a linear regression model. To conduct the study, software libraries in Python were used for data processing and analysis: Pandas (version 2.0.0), Pytorch (version 2.0.0).

5. Conclusion

In this paper, a neural network based model for predicting the severity of the course of bronchial asthma in children has been reviewed. 142 factors that could be responsible for the occurrence of bronchial asthma disease were analysed. The training sample is divided into two parts, for training the neural network and testing the training results, in the proportion of 80/20. The model architecture is represented by a multilayer perceptron. The dependence of MSE value for training and test data set at different values of nodes in hidden layers has been analysed. A comparative analysis of MSE values for the model using linear regression equation for prediction and neural network based models is presented.

The developed model for predicting the severity of bronchial asthma, the foundation of which is a neural network, allowed to correctly determine the severity class of the disease for 70% of patients from the test dataset. For the remaining 30%, the model predicted the result as a neighbouring severity class. The result of further research is to investigate the dependence of the number of regressors of the model on the accuracy of the results of predicting the severity class of bronchial asthma. A critical issue for future research is to identify factors that can identify disease severity based on the results of clinical blood and urine tests. This will reduce the cost of conducting examinations, which require significant financial costs and conducting research in clinics with access to specialized and expensive equipment.

References

[1] Global burden of 369 diseases and injuries in 204 countries and territories, 1990–2019: a systematic analysis for the Global Burden of Disease Study 2019, Lancet, 2020; 396(10258), pp. 1204-1222, https://doi.org/10.1016/S0140-6736(20)30925-9.

[2] WHO. Asthma/ WHO, 2023, https://www.who.int/ru/news-room/fact-sheets/detail/asthma
[3] A. Fitzpatrick, L. Bacharier, D. Jackson et al. Heterogeneity of mild to moderate persistent asthma in children: confirmation by latent class analysis and association with 1-year outcomes, J Allergy Clin Immunol Pract, vol. 8(8), 2020, pp.2617-2627.e4, doi: 10.1016/j.jaip.2020.02.032.
[4] Y. Zhao, J. Patel, X. Xu et al. Development and validation of a prediction model to predict school-age asthma in preschool children, Pediatr Pulmonol, vol. 58(5), 2023, pp. 1391-1400, doi: 10.1002/ppul.26331.
[5] A. F. Hamad, L. Yan, M. J. Jozani et al. Developing a prediction model of children asthma risk using population-based family history health records, Pediatr Allergy Immunol, vol. 34(10), 2023, https://doi.org/10.1111/pai.14032.
[6] L. Daines, L. J Bonnett, H. Tibble, A. Boyd, R. Thomas et al. Deriving and validating an asthma diagnosis prediction model for children and young people in primary care, Wellcome Open Research, vol. 8, 2023, https://doi.org/10.12688/wellcomeopenres.19078.1.
[7] M. Ni, B. Li, Q. Zhang, J. Zhao, W. Li et al. Relationship between birth weight and asthma diagnosis: a cross-sectional survey study based on the National Survey of Children's Health in the U.S, BMJ Open, vol. 13, 2023, doi:10.1136/bmjopen-2023-076884.
[8] R. Wang, A. Simpson, A. Custovic, P. Foden, D. Belgrave, C. Murray, Individual risk assessment tool for school-age asthma prediction in UK birth cohort, Clin Exp Allergy, , vol. 49(3), 2019, pp. 292-298, doi: 10.1111/cea.13319.
[9] M. Reyna, R. Dai, M. Tran et al, Development of a symptom-based tool for screening of children at high risk of preschool asthma, JAMA Network Open, vol.5(10), 2022, doi:10.1001/jamanetworkopen.2022.34714.
[10] D. Leisman, M. Harhay, D. Lederer, M. Abramson, A. A Adjei et al. Development and reporting of prediction models: guidance for authors from editors of respiratory, sleep, and critical care journals, Crit CareMed, vol. 48(5), 2020, pp. 623-633,doi:10.1097/CCM.0000000000004246.
[11] N. A Boersma, R. WH Meijneke, J. C Kelder, C. K van der Ent, W. A F Balemans, Sensitization predicts asthma development among wheezing toddlers in secondary healthcare, Pediatr Pulmonol, vol. 52(6), 2017, pp. 729-736, doi: 10.1002/ppul.23668.
[12] R. J Kurukulaaratchy, S. Matthews, S. T Holgate, S. H Arshad, Predicting persistent disease among children who wheeze during early life, Eur Respir J, vol. 22(5), 2003, pp. 767-771, doi: 10.1183/09031936.03.00005903.
[13] O. Pihnastyi, O. Kozhyna, Methods for constructing estimated two-factor linear regression models for diagnosing the severity of bronchial asthma in children, Innovare Journal of Medical Sciences, vol. 9(1), 2021; pp. 23-30, doi:10.22159/ijms.2021.v9i1.40408.
[14] M. Deliu, TS. Yavuz, M. Sperrin M et al. Features of asthma which provide meaningful insights for understanding the disease heterogeneity, Clin Exp Allergy, vol. 48(1), 2018, pp. 39-47, doi: 10.1111/cea.13014.
[15] M. Lovrić, I. Banić, E. Lacić, K. Pavlović, R. Kern et al, Predicting treatment outcomes using explainable machine learning in children with asthma, Children (Basel), vol. 8(5), 2021, p. 376, doi: 10.3390/children8050376.
[16] M. K Ross, J. Yoon, A. van der Schaar, M. van der Schaar, Discovering pediatric asthma phenotypes on the basis of response to controller medication using machine learning, Ann Am Thorac Soc, vol. 15(1), 2018, pp. 49-58, doi: 10.1513/AnnalsATS.201702-101OC.
[17] N. A Molfino, G. Turcatel, D. Riskin, Machine learning approaches to predict asthma exacerbations: A narrative review, Adv Ther, vol. 41(2), 2024, pp. 534-552, doi: 10.1007/s12325-023-02743-3.
[18] D. Li, S. Ebhohimhen Abhadiomhen, D. Zhou, Xiang-Jun Shen, L. Shi et al, Asthma prediction via affinity graph enhanced classifier: a machine learning approach based on routine blood biomarkers, Journal of Translational Medicine, vol. 22(1), 2024, doi:10.1186/s12967-024-04866-9.
[19] G. Luo, S. He, B. L Stone, F. L Nkoy, M. D Johnson, Developing a model to predict hospital encounters for asthma in asthmatic patients: secondary analysis, JMIR Med Inform vol. 8(1), 2020, e16080, doi: 10.2196/16080.
[20] G. Yu, Z. Li, S. Li, J. Liu, M. Sun et al, The role of artificial intelligence in identifying asthma in pediatric inpatient setting, Ann Transl Med, vol. 8(21), 2020, p.1367, doi: 10.21037/atm-20- 2.
[21] UNESCO.ORG, Universal Declaration on Bioethics and Human Rights, 2005, http://portal.unesco.org/en/ev.php. 2005.

[22] O. Kozhyna, O. Pihnastyi, Data structure of clinical research, Human Health & Disease, vol. 3(9), 2019, pp. 71-79.
[23] A. J Farhan, D. M Kothalawala, R. J Kurukulaaratchy, R. Granell, A. Simpson et al, Prediction of adult asthma risk in early childhood using novel adult asthma predictive risk scores, Allergy, vol. 78(11), 2023, pp. 2969-2979. doi: 10.1111/all.15876.
[24] A. F. Hamad, L. Yan, M. J Jozani, P. Hu, J. A. Delaney et al, Developing a prediction model of children asthma risk using population-based family history health records, Pediatr Allergy Immunol, vol. 34(10), 2023, doi: 10.1111/pai.14032.
[25] C. Domínguez-Martína, A. Canoa, N. Díez-Mongea et al, Clinical performance of spirometry and respiratory oscillometry for prediction of severe exacerbations in schoolchildren with asthma, Anales de Pediatría, vol. 98(6), 2023, pp. 427-435, doi: 10.1016/j.anpede.2023.05.003
[26] O. Pihnastyi, O. Kozhyna, T. Kulik, Linear Regression Approximate models for predicting severe course of bronchial asthma, CEUR Workshop Proceedings, vol. 3309, 2022, pp. 55-65.
[27] O. Pihnastyi, O. Kozhyna, K. Voloshyn, Linear regression models for bronchial asthma severity prediction based on TSLP, Proceedings of the 11-th International Conference "Information Control Systems & Technologies", vol. 3513, 2023, pp. 276-290.