

Modified Convolutional Neural Network for Pattern Recognition of Malaria Cells

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Abstract

A review and analysis of known solutions to the problem of detecting malaria from blood pictures of patients using machine learning algorithms was carried out. After developing a machine learning model to solve the given problem based on convolutional neural networks, the accuracy of the model was tested and compared with the analogs discussed above. Based on the results of the testing, it was established that the model is at the level of the best considered models in terms of classification accuracy, with a classification accuracy of 98.08%.

Keywords ¹

Convolutional neural network, machine learning, malaria, pattern recognition

1. Introduction

Nowadays pattern recognition methods are widely used in medical diagnostics. Malaria is a dangerous disease caused by parasites of the genus *Plasmodium*. Despite the development of medicine, including antimalarial drugs, this disease remains the most dangerous problem in the field of health care in tropical and subtropical regions, as well as a global problem for all mankind. [1] As of 2020, the estimated number of deaths from malaria worldwide was 627,000 [2].

The most important part of the malaria control strategy is correct and rapid diagnosis. Diagnosis of malaria involves the detection of antigens in the patient's blood. In this paper, attention will be paid to the process of detecting parasites in blood, which is usually performed by visual observation of plasmodia in a stained patient's blood sample using a light microscope. This method is very cheap and popular, it is usually used in real medical practice. [1]

Although the accuracy of this method is quite high, but it's not guaranteed. Thus, the study [3], which was conducted in Tanzania, i.e. in the country with the most vulnerable region to malaria, shows the accuracy of microscopy at the level of 93.5%. Development of an automated method for processing patient blood samples to detect malaria infection could improve accuracy by eliminating the human factor, i.e. inattention or fatigue of the laboratory staff performing the visual analysis.

In recent years, machine learning technologies have found more and more applications in medicine. Using large patient data sets collected over years of follow-up, it is possible to develop models that help doctors with diagnosis, that form a prognosis of the patient's condition, that automatically develop the best treatment.

In areas related to image processing (histology, radiology, oncology), the so-called deep convolutional neural networks have gained popularity.

Deep learning is a method of building artificial neural networks characterized by several hidden layers of nodes that process data representations, abstracting them in various ways. Having a large number of internal layers in the network allows for a more accurate representation of the complex

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relationships between the input data. One of the applications of deep learning technology is convolutional neural networks.

Convolutional neural networks are characterized by image transformation into "feature maps" by applying the image "folding" operation. Feature maps contain higher order data such as contrast, lines, color, shapes. The feature maps are then combined or "pooled" in various ways to form deeper metadata about the input image. Parameters of convolutional neural networks are optimized using previously annotated, i.e., training data. In this way, learning with a teacher (supervised learning) takes place [4].

Further, the article considers the method of automating the determination of malaria infection based on microphotographs of blood samples based on a convolutional neural network. A publicly available dataset was used as training and test data for the model. The dataset includes Giemsa-stained thin blood smear slides from 150 malaria-infected and 50 healthy patients. A total of 27,558 images [5].

2. Related Works

Recognition is the assignment of presented objects to certain classes using known classification rules. More formally, the classification process can be defined as follows. Each instance in the training set belongs to a certain set of predefined labels in a multi-class classification. The goal of classification methods is to build a learning model based on a given set of training data in such a way as to be able to classify new objects with unknown labels. Suppose that the training data set is given in the form $(x_i; y_i)$, where $x_i \in \mathbb{R}^N$ is the attribute vector of the i -th object, and y_i is the i -th class label. We aim to find a training model H such that $H(x_i) = y_i$ for new unlabeled objects. In the following, we will assume that binary classification is sufficient for the case of the current problem, that is, there are only two classes of objects: infected and healthy. [6]

Recent advances in the field of data collection and storage related to medicine have made it possible to develop automated systems capable of assisting physicians in making clinical decisions. In particular, machine learning methods that perform the task of pattern recognition have been widely used. Over the past decade, various pattern recognition techniques have been applied to biomedical data for machine-based clinical diagnosis and therapeutic support. The development of new pattern recognition methods and algorithms with high efficiency in terms of accuracy or speed improves treatment outcomes, allowing doctors to make more informed decisions in a timely manner. This is extremely important, especially when a quick clinical decision needs to be made in a stressful environment, such as in intensive care units. [7].

The starting point of this study is the document [8] published in 2018. In it, the authors consider the possibility of creating software that will assist in the detection of malaria in the field, using classification algorithms with the help of machine learning. The dataset created by the authors of the document on the basis of 150 images obtained using a smartphone attached to a conventional light microscope is also used in this work. The authors of the document selected from the images only the parts necessary for the recognition of malarial plasmodia, so in the future in this work we focused on the recognition of malaria at the cellular level. In general, the authors [8] managed to achieve a recognition accuracy of 98.6% on their original dataset. To achieve such results, the authors used a convolutional neural network with a complex architecture.

The task of determining malaria damage is solved in [9]. The authors proposed a model that detects malaria from images of blood samples of patients obtained using a light microscope. Their model is based on a simple feedforward neural network. It shows a rather low accuracy of 73.3%, and only 15 samples are used for testing, which is insufficient for an objective assessment of the accuracy of the algorithm.

A similar problem was solved in [10]. Using a dataset of 4,100 patient blood images, the authors classified the images into two classes: malaria infected and uninfected. A model based on a deep belief network (deep belief network) was used for classification, which was the first application of this algorithm to recognize malaria infection. According to the results of the research, the authors managed to achieve a classification accuracy of 96.3%.

Very significant results in the recognition of malaria were achieved in [11]. The authors compared the capabilities of models based on the support vector method with models based on convolutional neural networks. And if with the help of the method of support vectors it was possible to achieve a

classification accuracy of approximately 92%, then with the help of the well-known GoogLeNet neural network architecture, the authors achieved an accuracy of 98.1%.

Another document that considers the use of convolutional neural networks for the detection of malaria is [12]. The neural network proposed by the authors achieves the accuracy of binary classification (infected or not) of blood samples in 97.37%.

The support vector method used in [11] is a widespread machine learning algorithm with a teacher used in classification problems. Its advantages include its simplicity. However, in terms of the task, it has many disadvantages. Among them is the need for data preprocessing, as this algorithm cannot efficiently process raw image data. Its most important drawback is the rather low ability of the algorithm to recognize complex relationships in the input data, which leads to relatively low classification accuracy, as shown in [11].

Artificial neural networks, including simple ones considered in [9], a deep belief network [10], as well as convolutional neural networks [8,11,12] are distinguished by a high ability to detect complex relationships in input data, although for this and the complexity of the network architecture has to be increased, which leads to a large expenditure of computing power to train and operate the networks. All neural networks also share one drawback: they are opaque models, i.e. they do not reveal the principles of decision-making during classification. At the same time, neural networks, especially convolutional neural networks, can accept raw data as input, achieving high values of image classification accuracy.

In general, the literature data indicate the prospects of using convolutional neural networks both in similar tasks from the field of medicine and in the task of recognizing malaria infection from blood samples of patients. Studies comparing convolutional neural networks with other models show the superiority of convolutional neural networks. In the following, a modified model based on convolutional neural networks will be shown and tested.

3. The purpose and objectives of the research

The object of the study is the process of detecting malaria infection using images of microscopic images of blood samples from patients. Blood samples should be Giemsa stained.

The subject of the research is pattern recognition methods that can be used to solve the given problems.

The purpose of the work is to develop a modified machine learning algorithm for effective detection of malaria lesions based on relevant images of blood sample images.

The research method is machine learning models, in particular convolutional neural networks.

4. Development of a machine learning model

The dataset [5] includes 27,558 images of various sizes. However, as indicated in the study [13], where the same dataset is used, some of the images are annotated incorrectly. An example of such an image is shown in fig. 1. And although in [3] this image is annotated as a cell not affected by malaria, in [13] it is indicated that the cell is infected. In the future, the corrected data set with corrections from [13] will be used in the study.

The input data format from the dataset is not suitable for most machine learning models. The entire dataset was transformed to obtain two datasets: a set of 50 by 50 images and a 100 by 100 set. The OpenCV on Wheels Python library was used for the transformation.

To solve the problem of image classification, a modification of the convolutional neural network was built, the architecture of which is given in the table. 1. Graphically, the structure is shown in fig. 2. The TensorFlow library for the Python language was used for the software implementation of the network.

To create graphs that visualize the accuracy and loss functions during training of neural networks (fig. 3,4,5,6), the Matplotlib library for Python was used.

The network consists of 5 pairs of convolution and pooling layers, one dropout layer, and 5 fully connected layers.

The convolutional layers, which are located at the beginning of the network together with the pooling layers, are used to build so-called feature maps, i.e. matrices that store the results of searching for two-dimensional patterns in the results of the previous layers of the network. A special feature of convolutional layers and their difference from fully connected ones is the fact that convolutional layers

find patterns in the input data that are transfer invariant. This leads to an efficient search for relationships in two-dimensional images. Convolutional layers use activation functions that are applied to the output of the layer. In the proposed model, ReLu is used as the activation function for convolutional layers given in formula 1. Convolutional layers contain weight matrices applied to input data. Each of the weights is a parameter for training.

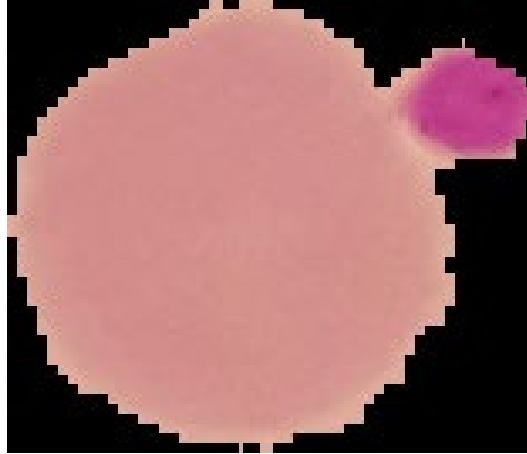


Figure 1: Image from the dataset that was incorrectly annotated in [5]

Pooling layers are used to reduce the dimensionality of feature maps. Unlike convolutional and fully connected layers, pooling layers do not contain parameters for training, but apply a rigidly specified operation to the input data. Usually, the selection of the average or maximum value on each of the given sections in the input feature map is used as an operation. In the case of the proposed model, the operation of selecting the maximum value is used, which is given in formula 4, where X is the matrix of values from some part of the input feature map.

The dropout layer randomly sets the output of some neurons in the previous layer to zero while training the network, which helps prevent overtraining. The values of other outputs that are not set to zero are scaled by $1/(1 - \text{the dropout value})$ so that the sum of all output values of the layer does not change. In the current network, the dropout value is set to 10%, which was chosen empirically.

Fully connected layers, which are usually located after convolutional, pooling layers or dropout layers, in the case of the proposed model are located between the dropout layer and the output layer of the network. The mathematical representation of a fully connected layer is given in formula 3, where f_{act} is the activation function used, in this case ReLu, given in formula 1; kernel and bias – parameters for training; input - matrix of input data from the previous layer [11 - 15].

In the last fully connected layer, the Softmax function is used, which is given in formula 2. Softmax is used to convert the output values of the neural network into the probability of matching the input data for one of the classes. Thus, the sum of the values of all neurons of the last layer of the network is always equal to 1.

The Adam algorithm is used to train the network with the “learning rate” parameter set to 0.0005.

$$f(x) = \max(0, x), \quad (1)$$

$$\sigma(z)_i = \frac{e^{z_i}}{\sum_{k=1}^K e^{z_k}}, \quad (2)$$

$$f(\text{output}) = f_{act}(\text{input} \cdot \text{kernel} + \text{bias}), \quad (3)$$

$$f(X) = \max(x_i), x_i \in X, \quad (4)$$

The output data of the network is whether the input image belongs to one of two classes, i.e. binary classification is performed.

80% of the input data from the dataset is used for training the neural network, and the other 20% is used for validation.

Table 1

Modified convolutional neural network structure

Layer type	Output Shape	Number of parameters for training
Rescaling	(None, 100, 100, 3)	0
Conv2D (6x6x3@4)	(None, 100, 100, 4)	436
MaxPooling2D (f=2;s=2)	(None, 50, 50, 4)	0
Conv2D (4x4x4@8)	(None, 50, 50, 8)	520
MaxPooling2D (f=2;s=2)	(None, 25, 25, 8)	0
Conv2D (4x4x8@16)	(None, 25, 25, 16)	2064
MaxPooling2D (f=2;s=2)	(None, 12, 12, 16)	0
Conv2D (4x4x16@32)	(None, 12, 12, 32)	8224
MaxPooling2D (f=2;s=2)	(None, 6, 6, 32)	0
Conv2D (4x4x32@64)	(None, 6, 6, 64)	32832
MaxPooling2D (f=2;s=2)	(None, 3, 3, 64)	0
Dropout (10%)	(None, 3, 3, 64)	0
Flatten	(None, 576)	0
Dense (1024)	(None, 1024)	11214976
Dense (1024)	(None, 1024)	1049600
Dense (1024)	(None, 1024)	1049600
Dense (1024)	(None, 1024)	1049600
Softmax (2)	(None, 2)	2050

5. Results and Discussions

A neural network was trained on two sets of data: with the size of images 50 by 50 and with the size of 100 by 100.

The results of training networks during 30 epochs are shown in accordance with fig. 3, fig. 4, fig. 5 and fig. 6.

According to the results of the tests, the neural network achieved the following maximum classification accuracy values: 96.68% for the dataset with 50 by 50 images, 98.08% for the dataset with 100 by 100 images.

As you can see in fig. 4 and fig. 6, starting from the 15th epoch, the value of the loss function no longer became smaller, but also increased.

At the same time, the value of the classification accuracy remained in a certain range, showing no further growth.

Clearly an overfitting phenomenon has occurred. Considering these indicators, we can say that this result is the best for the developed neural network architecture in combination with the given dataset.

A comparison of the obtained results of the accuracy of the neural network with the results of other works is given in the table. 2.

The support vector method is a surface method, that is, unlike deep methods, which include neural networks, it cannot handle many layers of data representation. Thus, this method cannot detect deep relationships in the raw data. This determines the fact that according to the data [11] given in table. 2, the SVM-based model did not achieve high classification accuracy values.

Models based on neural networks demonstrate greater efficiency. In particular, all models based on Deep belief network and convolutional neural networks show a classification accuracy greater than 95%, which can be seen in table. 2.

This is explained by the use of so-called deep methods, that is, the construction of multi-layer models capable of revealing more complex relationships in the input data.

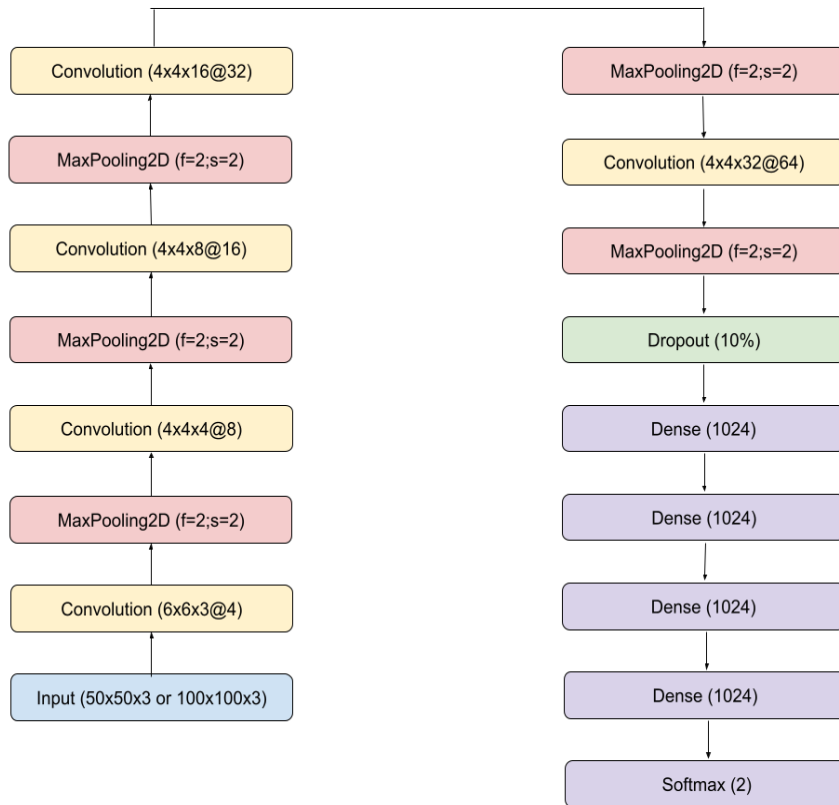


Figure 2: Network structure, shown graphically. Cyan color - input layer, yellow color - convolutional layers, red color - pooling layers, green color - dropout layer, blue color - fully connected layers

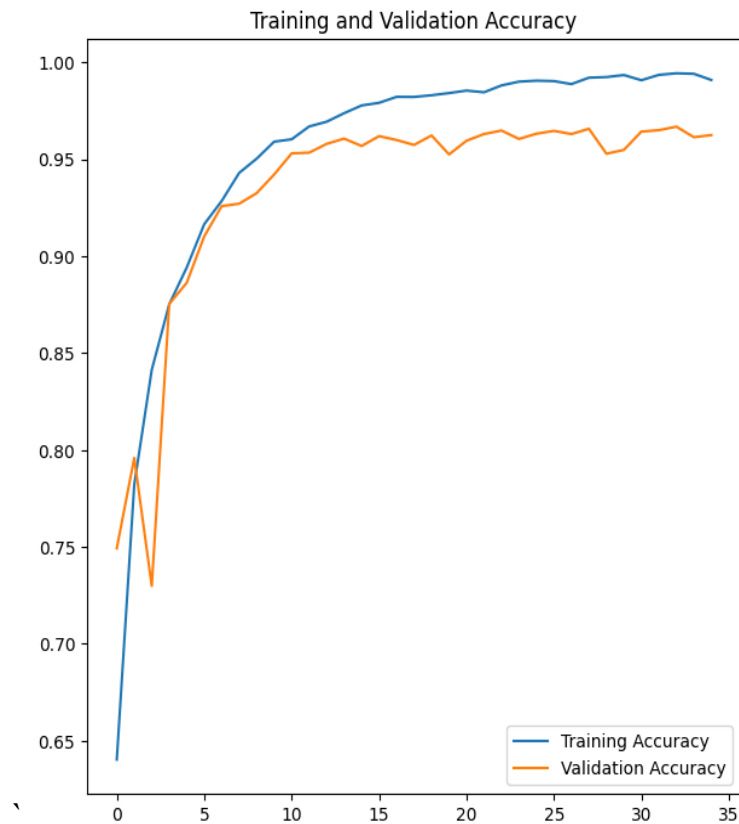


Figure 3: Training accuracy results of a modified convolutional neural network on a 50 by 50 image dataset

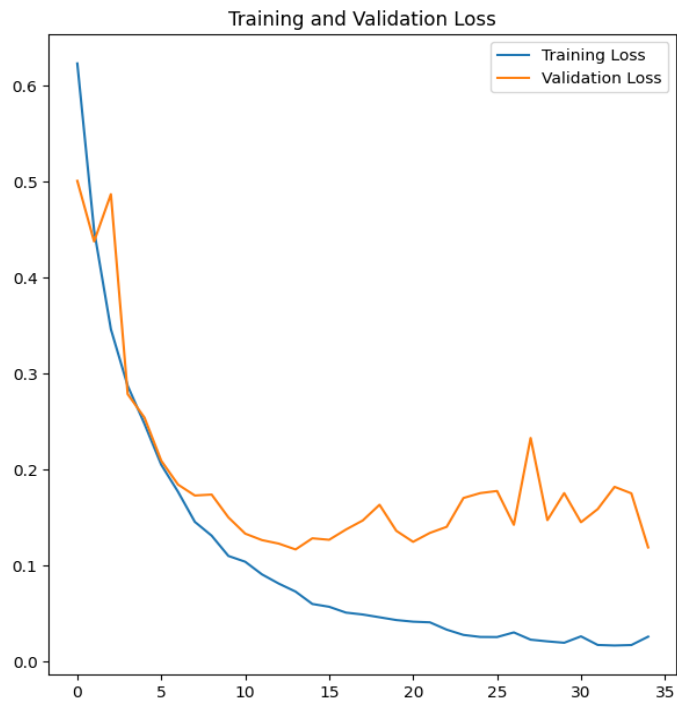


Figure 4: Training loss results of a modified convolutional neural network on a 50 by 50 image dataset

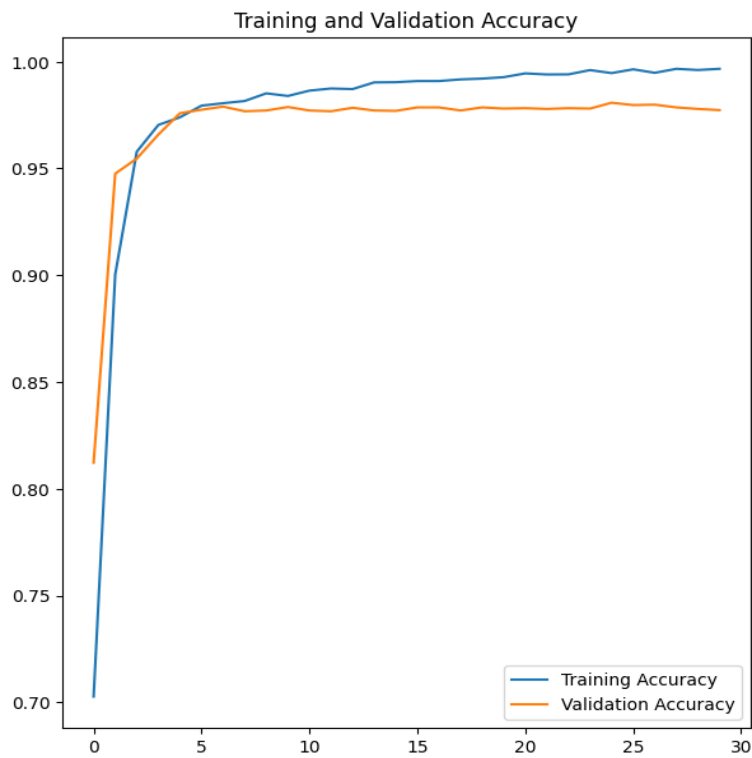


Figure 5: Training accuracy results of a modified convolutional neural network on a 100 by 100 image dataset

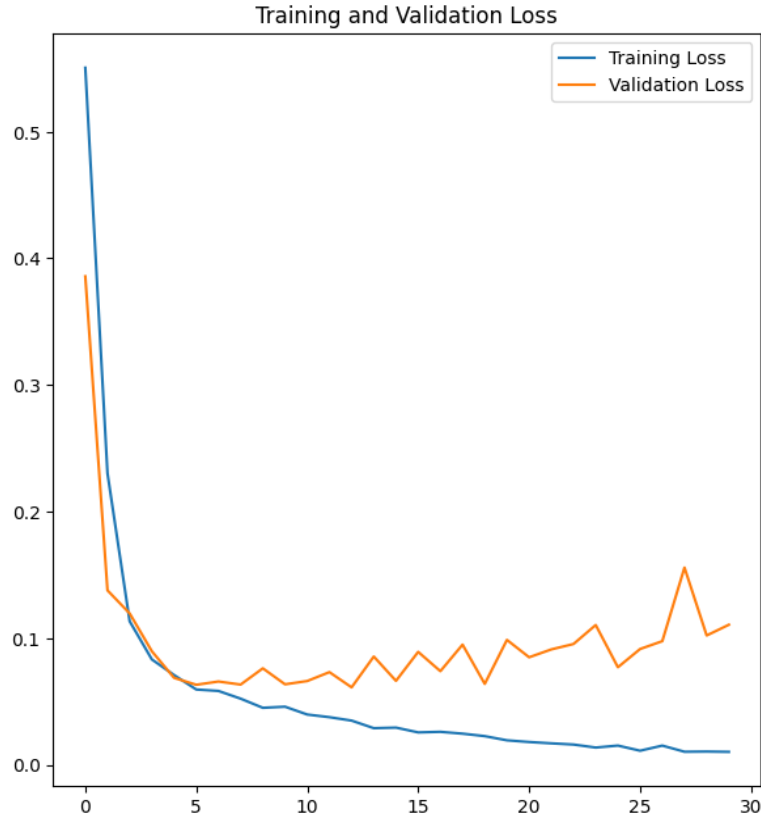


Figure 6: Training loss results of a modified convolutional neural network on a 100 by 100 image dataset

However, the model based on the Deep belief network from work [10] is inferior in accuracy to all models based on convolutional neural networks. This is explained by the fact that convolutional neural networks are one of the most effective machine learning algorithms in the field of image processing.

The model proposed in this paper shows one of the best classification accuracy results (98.08%) on the dataset, the images of which are reduced to the size of 100 by 100 pixels. According to table. 2 shows that the proposed model shows classification accuracy at the level of the best models from the literature data reviewed above.

Table 2

Comparison of the accuracy results of the neural network with the results of other works

Machine learning model	Result, classification accuracy	Algorithm used
[9]	73.3%	Feedforward neural network
[8] (cell level)	98.6%	CNN
[10]	96.3%	Deep belief network
[11]	91.66%	SVM
[11]	98.13%	CNN
[12]	97.37%	CNN
Proposed model (50 by 50 images)	96.68%	CNN
Proposed model (100 by 100 images)	98.08%	CNN

6. Conclusion

As part of the work, the task of building a machine learning model for recognizing malaria lesions based on photographs of blood samples of patients was set. As a result of the analysis of literary data,

it was established that a similar problem can be solved using models based on various well-known algorithms: the method of support vectors, a deep belief network, and a convolutional neural network. However, the considered data indicate that convolutional neural networks, on the basis of which it was decided to develop the model, have the greatest potential in this and similar areas.

A machine learning model based on a modified convolutional neural network was developed. It is tested on two datasets obtained from a simple preprocessing of a publicly available dataset [5]: a set with images of size 50 by 50 and a set with images of size 100 by 100. A corrected version of the dataset was used, since errors were made in the original dataset in the data abstract [11-27].

As a result of network testing, it was possible to achieve a classification accuracy of 96.68% for a dataset with 50 by 50 images, 98.08% for a dataset with 100 by 100 images, which is a relatively high indicator for a similar task at the cellular level. A comparison with the results of similar studies is given in table. 2.

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