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A computer system for the leukocytes classification in medical images

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Abstract. The paper is about the development of a computer system for the white blood cells images classification. Solving the leukocytes classification task makes it possible to diagnose not only the blood diseases, but also a wide range of other diseases, as well as to evaluate the overall state of a person's health. Modern leukocytes classification methods have a fairly large number of shortcomings, which make a problem of finding the most effective method as a tool to solve this task. In our computer system we use the method based on using a trained convolutional neural network as a binary classifier for the leukocytes classification. This study shows the advantages of using this architecture and a deep learning technology to solve the objects classification task in medical digital images. The developed system allows one, in most cases, correctly and with a high speed to determine whether the white blood cell belongs to one of the two classes, which indicates to the possibility of using this system as an auxiliary tool for the blood hematological analysis.

1. Introduction

Currently one of the most dangerous common diseases is leukemia, which is also known as "blood cancer" [13]. This disease leads to the disruption of the health blood cells production, resulting in the accumulation of abnormal immature blood cells in various parts of a body, thereby causing illness and infection. Without timely diagnosis and treatment, leukemia leads to a patient's death in less than six months [8]. For this reason, along with a general clinical blood test, a doctor prescribes the calculation and study of the leukocyte formula, which reflects the total concentration of leukocytes in the human blood and the percentage of their various types.

Leukocytes, also known as "white blood cells", are agents of the immune system. They perform a protective function against infections, bacteria and other foreign bodies can harm the body. Even a small deviation in the percentage of these cells from the norm can provide that important information about the human health state. In the clinical practice, the five main types of leukocytes are studied: lymphocytes, monocytes, neutrophils, basophils and eosinophils [2]. Now the main leukocytes classification methods are the flow cytometry and the visual method [2, 3].

The flow cytometry method makes it possible to register the total set of results of the analysis of the scattering pattern and electrodynamic signs for single passing cells in the flow, which are used for



the single white blood cell classification. This method allows one to quickly obtain a quantitative assessment of many white blood cells and the concentration of each class of the white blood cells. The main disadvantage of this method is a very high cost of equipment, so not any laboratory can afford the flow cytometer. Another disadvantage is that this classification method does not allow one to assess the morphological features of a cell, which may cause problems with the identification of cells which have pathology [2].

One more method is the visual method consisting in the manual analysis of a blood smear under a microscope, which is performed by a hematologist. The result of the classification in this case always depends on the doctor's experience, as he makes conclusions after the visual examination and highlighting those signs of the cells that he knows. The visual method is bad in that it is a complicated and lengthy process, which also depends on the qualification of a laboratory assistant [4].

Along with the two methods described above, automated systems are now widely used for the leukocytes classification in digital blood cells images [3]. Most of these systems are an expensive software and apply high demands on the source data. For example, the poor quality of medical images can significantly affect the correctness of a result to be obtained. Thus, to create a computer system for the classification of leukocytes, it is necessary to use a method that would solve this problem, regardless of the quality of the samples of images and the hardware of the equipment to obtain them.

The main aim of this research is to create a computer system that would solve the leukocytes classification task in blood cell images, which is based on using such an automated method that would take into account the shortcomings of other currently existing methods. To achieve this aim it is necessary to complete the following tasks: to carry out a research into existing automated methods and to choose the most effective one; to determine the functionality of the future software and chose the tools for its implementation; to implement the computer system and to carry out a computational experiment.

2. Analysis of existing methods for the leukocytes classification

Methods for creating the automated leukocytes classification have been for a long time actively used as a tool for medical diagnostics [20], however, since they offer a complete or partial absence of the participation of a laboratory assistant in the process of obtaining results, one cannot completely rely on the results obtained. The main common feature of these methods is using a computer vision technology, which would allow one to automate the analysis of blood smears.

In this paper, [21] the authors describe the proposed architecture called W-net which is based on the CNN and used for the five main types of leukocytes classification. This model contains three convolutional layers for the features extraction from the white blood cells images, followed by the two fully connected layers for the classification. Before passing the images to the model input it needs to be preprocessed: cropping, resizing, and normalizing. The last stage is necessary to convert the pixel values into the float format in range from 0 to 1. The results of the experiments using the dataset of 6562 real leukocytes images have shown the accuracy level 95-97%.

So, the method proposed in the paper [12] by Zh.V. Stadelmann and I.N. Spiridonov uses the AdaBoost algorithm along with deep training to isolate the white blood cells, which implies strengthening weak classifiers by combining them into one. The algorithm presented by the authors consists in sequential scanning of the entire image with a window, whose size was obtained based on the size of the largest type of white blood cells. To avoid re-detection of the same cell as a result of overlapping the position of the window, post-processing was performed by analyzing the distances between the positions of the window where the leukocyte was isolated. This method provides a high speed and relatively a low probability of false detection of cells in the image, is about 15%.

Another way of an artificial neural network using to solve the leukocytes classification task was described by V.K. Belyakov et al. [7]. The authors used an advanced combined image segmentation method, as well as an object feature vector. The following morphological parameters were selected to evaluate the signs of cells: the relative size of the segments and nuclei, as well as the minimum and

maximum sizes of a segment; the ratio of the area of the core to the area of the described rectangle; the moment of the boundary of the maximum nucleus and the coefficient of its shape; color characteristics of the cell, etc. With using a multilayer artificial neural network as a classifier and chosen features, the authors of the method were able to reduce the number of errors on the test data set to 0.1%.

Hamed Talebi et al. in their work [22] introduced the WBC classification method that uses Naïve Bayes clustering for the cells segmentation and the TSLDA classifier, which is supplied by features acquired from a covariance descriptor. The authors used 260 images dataset from the Research Center of Oncology, Hematology, and Bone Marrow Transplantation of Imam Khomeini in Tehran. The used classifier at the training phase calculates within a class means using the training dataset then, at the test phase calculates the Riemannian distance between each one test sample and each calculated within the class means. Hence, each sample belongs to the group with a minimum distance. The proposed method has allowed one to reach the accuracy of 98.02% which is a high value for this task.

Ensaf H. Mohamed, Wessam H. El-Behaidy et al. in their study [23] tried to combine the advantages of deep models in their hybrid architecture, which consists of ten different pretrained models with six types of classifiers. The authors used the image segmentation via the threshold methods, which divide the image pixels with respect to their intensity level because it is the simplest and one of the fastest techniques. Then segmented images split for training and testing batches. The next stage is the features extraction: the proposed hybrid architecture uses ten different pre-trained models to get segmented cells images features: VGG, ResNet, DenseNet, Inception, Xception et al. Their evaluation process has shown a high accuracy level, is 97.03%, that also shows the advantages of using even ready pretrained models to solve the leukocytes segmentation and classification tasks.

I.A. Belyaev and S.V. Kucheryavsky used the classification model based on the feature vector, which was obtained by the method of medium-angle spectra [1]. This vector acts as a generalized to approach the analysis of one-dimensional and two-dimensional signals. The method proposed in the paper made it possible to determine the class of leukocytes with an accuracy of 97%.

It is easy to notice that those existing methods for the leukocytes classification, based on the blood cells images that have shown the greatest efficiency in practice are often based on using artificial neural networks and machine learning methods, in particular, deep learning [3, 11]. This eliminates the need to determine the features of the object under study for its analysis and classification by replacing complex calculations with simple, automatically trained models. As part of the solution of the leukocytes classification task, the main advantage of using deep learning is that in case of variability of the source images, the method allows additional training with the model on the new source data, which only increases the accuracy of results. Another important advantage is the scalability feature, which allows one to use the deep learning technology to process both a small amount of data and a significant amount of information [15].

3. Determination of system functionality and choice of implementation tools

The future computer system as a part of this study must solve the leukocytes classification task in the blood cell images and consider the main shortcomings of existing methods: it is possible to do with using an artificial neural network and deep learning at the algorithm of the program. To train a neural network model, one will need a set of input data [17], i.e. many classified images of blood cells that can be used as a training sample. Due to the fact that the training data directly affects the accuracy of results, a training set must be large enough to detect as many possible variations of the morphological characteristics of cells as possible, also the features of the set of obtained images: color reproduction, illumination of objects, image resolution, etc. The final program must have a simple and user-friendly interface by which it would be possible to upload a specific image (a picture of blood cells) into the program and get the final result of the leukocyte classification with relatively a high accuracy.

As a toolkit for the software implementation of the computer systems, the Python programming language was chosen. Python is currently one of the most common programming languages and it is widely used in solving many problems associated with machine learning algorithms [10]. Also, it was

decided to use additional libraries, which are: Tensorflow, Keras, OpenCV and Tkinter. These libraries are the most widely used in solving problems of machine learning and images processing. A combination of Tensorflow and Keras allows one to create, to train and to put into practice different neural network models [5, 6], and the OpenCV and Tkinter libraries allow to use a wide range of additional packages and tools for working with images and creating GUI [9].

4. Program implementation

To work with digital images and video in the field of machine learning, the convolutional neural network architecture is used [15, 16], which was proposed in the early 80s to solve the problem of the optical character recognition on bank checks, but its use was considered impossible due to high requirements for the computing equipment [19]. This architecture has got its name from the convolution operation on which it is based: the input image is scanned for features with using small windows (3x3, 5x5 pixels); the features highlighted in each window are presented as a separate matrix — a feature map. Thus, convolution is the operation of calculating the new value of a given pixel, considering the value of the neighboring pixels surrounding it. In 2012, this architecture saw a new light, and using the model learning acceleration with graphic processors made it possible to use convolutional neural networks as a universal tool for solving problems associated with digital image processing [14, 20].

The number of neural network layers and their characteristics can be different depending on the complexity of a task [18]. The model used in this study is shown in Figure 1, from which it can be noted that it consists of three repeating cascades: a convolutional layer and a subsample layer, which is responsible for compiling the characteristics cards obtained on the previous layer in order to “generalize” the signs; after three cascade layers there is a fully connected neural network consisting of two layers. Thus, there are 9 layers in the model. In the framework of this study, leukocytes were classified according to two the classes; therefore, the last component (Fig. 1) is a binary classifier indicating that the cell image belongs to one of the two possible classes.

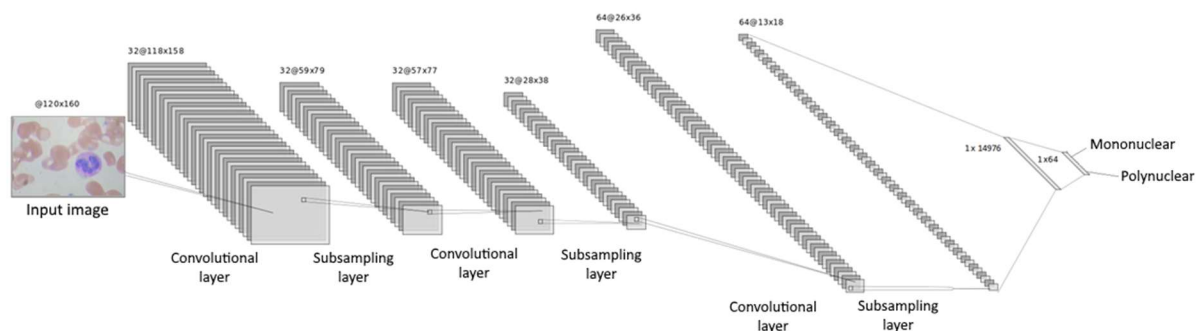


Figure 1. Visual representation of the used neural network model

Before using this model to classify the white blood cell images, one must first train it on a large data set. For training, we used the Blood Cell Images dataset (dataset) from the Kaggle service, which is a popular community for an exchange of knowledge related to machine learning, as well as for various competitions. Inside this dataset there are several thousand samples of the white blood cell images. 80% of all images will be used as a training set, and the remaining 20% as a test set, on which testing and assessment of the accuracy of the trained model will be performed. In Figure 2, one can see examples of images of blood cells from this dataset

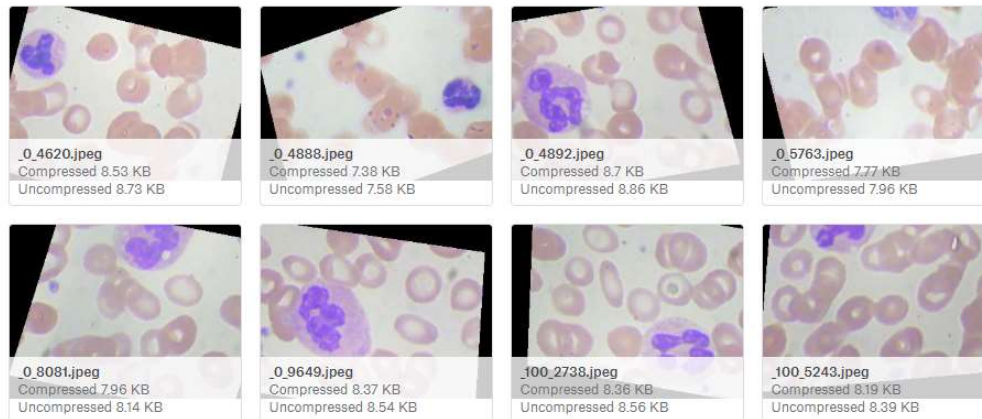


Figure 2. Blood image samples from the dataset

The training process consists in feeding many sample images to the input of a model compiled, as well as information on the correct classification of each of them – the names of one of the two classes of white blood cells. As a result of the automatic analysis of images and finding features in them, the network will configure its parameters in such a way as to consolidate the accumulated "knowledge" and use them in further research. There is the preprocessing for each input image, consisting of the three main stages:

- Vectorization of the input image that is necessary to represent the input data in a form suitable for input, as a vector [10].
- Adding a label with a correct answer – for training, each input sample image from the training set must be supported by a text label characterizing the belonging of this image to one of two classes.
- Normalization of input values – translation of the value of each pixel from a range from 0 to 255 to a range from 0 to 1.

The training data consists of pairs of an input vector and the corresponding output vector, where the answer key as a label. The current model is run with a training dataset and produces a result, which is then compared with the target, for each input vector in the training dataset. Based on the result of the comparison and a specific of used learning algorithm, the parameters of the model are adjusted. So, after preprocessing step, two vectors of data which are normalized and vectorized arrays of the images supported by a text label of the correct class are send to the model input layer.

Model training in this study was carried out over 20 epochs. Epoch is the one training pass on the entire data array. After the model training, it was saved to a file to use in the future without repeated training. As it was described earlier, a good user interface will reduce the number of problems with using the program by ordinary users.

The Tkinter library for the Python language allows one to create a fully customizable window application. Using this tool, one can quickly create a graphical program window, at whose launch the saved trained model will be loaded from a file. Pre-compilation for the model is not needed, thus it will be sufficiently to initialize the trained convolutional neural network. The developed GUI of the computer system is shown in Figure 3, where one can also see the result of the classification of uploaded images into the program.

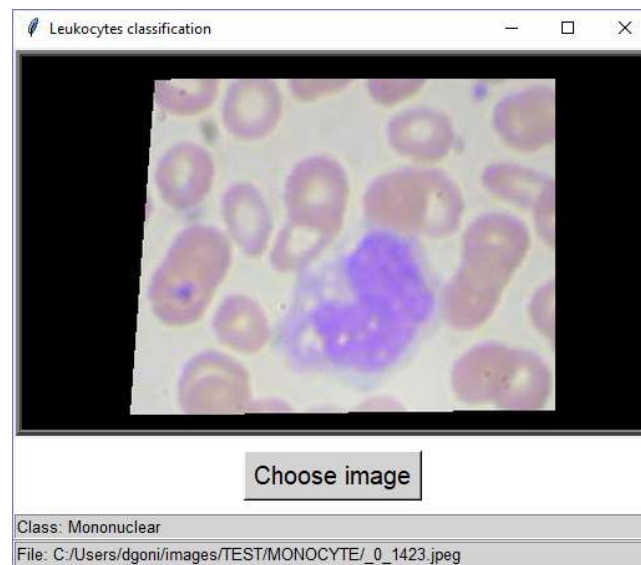


Figure 3. An example of the developed program

5. Computational experiment

At the stage of the training sample formation, an array with data to test the accuracy of the model after its training was created. The data from this sample were not a part of the training set, therefore it makes it possible to evaluate the network ability to generalize the characteristics of an object by classifying a new image for it. The result of the assessment of the accuracy of the trained model on the test sample is 97%.

For a visual assessment of the quality of the implemented model the graphs that show the dependence of the error value on the number of training epochs, as well as the value of the accuracy of determination, based on the proportion of correctly classified images from the sample, on the number of epochs were implemented. Both graphs are presented below in Figure 4.

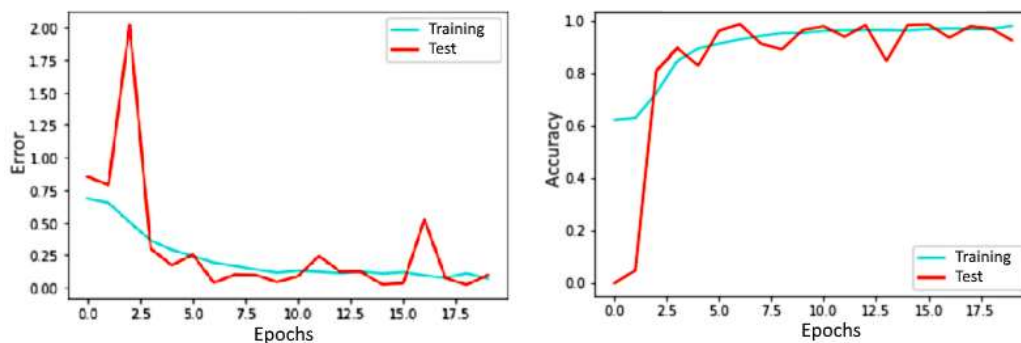


Figure 4. Dependencies of error and classification accuracy on the number of eras, respectively

Based on the figure above, it can be noted that both graphs have a legend describing the designation of the colors of the curves connecting the values marked in the graph. The blue curve characterizes the changes in the error value or in the accuracy of the network for a training sample, and the red curve indicates, to the same metrics, but to the test data set. One may notice that for the training sample, the graph in both cases has a smoother curve than for the test sample. This is since at the training stage, the distance between the answers received and the correct ones is systematically evaluated, which allows a regular adjustment of the weights to minimize errors. This determines the smoothness of the

blue curve. Via the graphs obtained it can be concluded that in the course of twenty epochs of training, the value of the accuracy significantly increases, and the magnitude of the error decreases.

6. Conclusion

As a result of the research done, all the tasks were completed: the existing automated methods for classifying leukocytes were studied, and the most effective one was chosen; the functionality of the future software was determined and the tools for its implementation were chosen; The software implementation of the computer system was also performed, and a computational experiment was carried out. All the tasks implementation has allowed one to achieve the main aim of this study – a computer system that solves the leukocytes classification task was developed, which is based on using a convolutional neural network and the deep learning.

A relatively high accuracy of the developed software provides the possibility of using artificial neural networks as an auxiliary tool for leukocytes classification as part of a hematological blood test.

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