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ARTIFICIAL INTELLIGENCE IN HEMATOLOGY

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Abstract. Given the current trend, artificial intelligence technologies are likely to be increasingly integrated into research and practical medicine, including hematology. Thus, artificial intelligence and machine learning deserve attention and understanding from researchers and clinicians. This review describes important terminological concepts and basic concepts of the designated technologies, as well as provides examples of their practical use in the scientific and practical work of a hematologist.

Keywords: artificial intelligence, machine learning, neural network.

INTRODUCTION

Software products created with the help of ML are based on the use of various types of data separately or in combination with each other, the degree of pre-processing of which depends on the mathematical model used. The selection of data for analysis usually needs to be done before developing an ML model, which entails tasks such as searching and structuring potentially useful information and removing unnecessary information. These tasks can be performed manually based on knowledge of the subject area (for example, a researcher deliberately selects the parameters of a general blood test and myelogram to diagnose hematological diseases), algorithmically (auxiliary algorithms help remove unnecessary parameters from the sample or reduce their number by combining - reduction dimensionality) or empirically, when data is selected and changed based on the results obtained already in the course of MR.

MATERIALS AND METHODS

Advances in the field of machine learning have allowed such technologies to establish themselves in various fields of medicine, including hematology. Today's progress in the development of AI technologies promises to optimize existing diagnostic and treatment care, facilitating new discoveries of effective and personalized therapies. Although many of the solutions are still in the early stages of development and testing, they have undoubted prospects for use in clinical practice. In hematology, ML can be used to solve a wider range of problems than standard statistics, the number of which is growing from year to year [1]. First of all, ML technologies are used in radiology, where, using deep learning algorithms, automatic analysis of tomogram images is carried out to search for visual signs of various diseases, such as lung cancer, tuberculosis, COVID-19, etc.

RESULTS AND DISCUSSION

In hematology, the computer vision method can be especially useful in the morphological analysis of digitized (from photos) blood smears, bone marrow and histological preparations. Thus, for example, accurate classification of leukocytes in peripheral blood smears, a task that usually requires considerable time and knowledge, can

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be performed by CNN-based models with an accuracy of more than 95% for most cell lines. Misclassification errors persist between cells that look similar, such as lymphocytes and reactive lymphocytes [2]. This can significantly speed up the diagnostic process and save human resources. Thus, one of the commercial research companies has developed and offers AI technologies for automated classification and counting of cells on digitized bone marrow smears [4]. A digital photo of a bone marrow smear is analyzed using an AI algorithm, after which a conclusion is generated, which is validated by a doctor (Fig. 1).

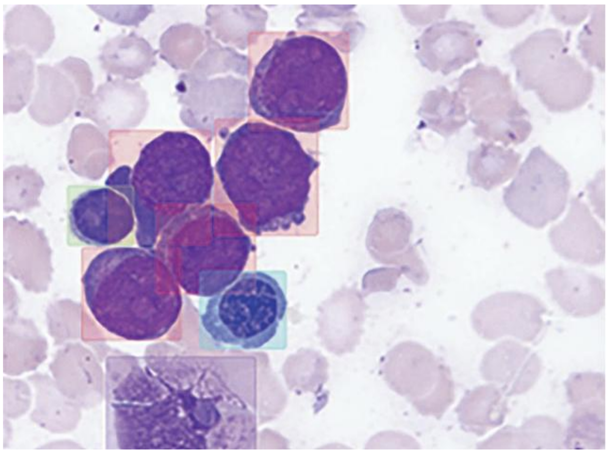

Fig.1 Recognition of cell images and their counting in bone marrow smears using computer vision

An urgent problem is the histopathological diagnosis of cancer, which requires highly qualified morphologist and largely depends on the quality of production of histological materials. This problem in oncology already has a number of solutions in the form of automated diagnostic systems based on deep learning [3]. In a study published in 2019, the authors classified 2,560 images of histological slides of lymph nodes to train a computer model to make four types of diagnosis: normal lymph node, diffuse large B-cell lymphoma, Burkitt's lymphoma, and small lymphocyte lymphoma [2]. Deep learning was used as a ML method. The diagnostic accuracy of the CNN-based model based on testing results was 95%. In another study, scientists were able to achieve 96% sensitivity and at least 87% specificity in identifying lymphoma tumor cells using digital images of peripheral blood smears [4]. In the diagnosis of multiple myeloma, computer vision technologies can be used to screen for lytic lesions using combined CT and skeletal positron emission computed tomography (PET-CT) data [20, 21].

ML technologies have also proven effective in predicting relapses of acute lymphoblastic leukemia (ALL) in children. The small study included 50 patients. Each case was characterized by 15 different attributes. Four supervised ML algorithms, including Classification and Regression Trees (CART), Random Forests, Gradient Boosting, and the C5.0 Decision Tree algorithm, were used to determine the most useful distinguishing features. The CART method showed the best results with an error-free prediction accuracy of 99.8%. The accuracy of the C5.0 method was 98.6%, the random forests method was 94.4%, and the gradient boosting method was 95.6%. Significant prognostic factors were the levels of platelets, hemoglobin, leukocytes and the sex of the child. At the same time, deviation from the norm in the platelet count was considered as the most important factor influencing the prognosis of relapse of ALL in children. The final accuracy of the classifier as a result of ten-fold cross-validation was 87.4% [2].

CONCLUSION

Despite marked improvements in treatment outcomes for patients with some hematologic malignancies, leukemia and lymphoma often remain incurable. A new ML approach that can help solve this problem is reinforcement learning. Research in this area is based on a large amount of retrospective and prospective data, and algorithms are built on the selection of various combinations of sequential strategies and tactics for treating patients.

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