The use of neural networks for the classification of anomaly blood cells

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Abstract — This paper presents an approach to the classification of digital images of lymphoblasts and lymphocytes using convolutional neural network. A comparative analysis of various architectures of convolutional networks was also carried out with respect to specific data domain. Experiments were conducted using Python programming language and tensorflow library.

I. INTRODUCTION

Acute lymphoblastic leukemia (ALL) is a malignant disease of the hematopoietic system, which is caused by extensively proliferating lymphoblasts (immature lymphocytes). It is included in a large group of leukemias. Unlike other leukemias, it is a rapidly progressive disease, in the absence of appropriate and timely treatment, it can lead to death in a few months. About 85% of all cases are among children and adolescents under 15 years of age.

A distinctive feature of ALL is a strong morphological similarity between normal lymphoid cells and abnormalities. Early diagnostic methods were based on morphological examination of peripheral blood smears, but now, cytogenetic examination, bone marrow biopsy and lumbar puncture have become the main diagnostic tools. Such approaches require highly qualified doctors and pathologists, special conditions and equipment. Therefore, such studies are usually not available to everyone.

The purpose of this study is to analyze blood cell data with respect to its specifics and to conduct a comparative study of various neural network architectures.

II. FEATURES OF MICROSCOPIC IMAGES

The first stage of classification pipeline is data study, including the calculation of numerical characteristics and revealing distinctive features that can be used in the future. When working with cellular images, it is worth paying attention to several features:

1) Small amount of available data.
2) Dataset imbalance.
3) Specific errors and noise.
4) Pre-segmentation.
5) Requires deep domain knowledge to manually construct features.
6) High intra-class variability.
7) Variation among subjects.

TABLE I. EVALUATION RESULTS ON THE TRAIN SET

		Metrics				
		Time, ***ms***	Precision	Recall	F1	ΔF1, %
Models	***Xception***	410	0.97	0.97	0.97	3.4
	VGG16	564	0.98	0.97	0.98	4.3
	ResNet152V2	549	0.99	0.99	0.99	5.4
	EfficientNetB5	790	0.97	0.97	0.97	3.4
	EfficientNetV2M	654	0.99	0.99	0.99	5.4

TABLE II. EVALUATION RESULTS ON THE TEST SET

		Metrics				
		Time, ***ms***	Precision	Recall	F1	ΔF1, %
Models	***Xception***	410	0.81	0.88	0.79	1.2
	VGG16	564	0.84	0.86	0.80	2.5
	ResNet152V2	549	0.84	0.88	081	3.8
	EfficientNetB5	790	0.84	0.92	0.83	5.1
	EfficientNetV2M	654	0.86	0.91	0.85	9

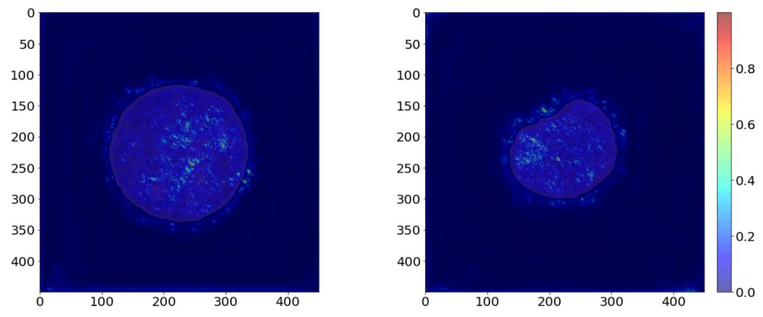

Fig. 1. Saliency maps for EfficientNetV2M

III. EXPERIMENTS

The data set consists of 10,581 digital photographs of lymphoid blood cells, among which two classes are represented: a normal cell and an abnormal one (lymphoblast). The files have a .bmp extension and a resolution of 600x600.

As all of selected models were pretrained, suitable the strategy for changing the learning rate parameter was chosen.

The original dataset was split in a ratio of 90:5:5 (training, validation and test sets). The partitioning was performed with respect to the fact that cell properties, in particular morphological properties, can vary greatly among subjects. Thus, when partitioning, the sets do not intersect in terms of subjects.

IV. RESULTS

During experiments several neural network architectures were used. All of them were pre-trained on the ImageNet dataset. Also, a small SimpleNet architecture (simple sequence of several convolutional layers) was trained from scratch. During the experiment, the models were trained for 200 epochs. The results of the trained models on train and test sets are presented in tables 1-2.

The EfficientNetV2M showed the best results, while its operation time differs little from other models (86.5 ms more than the average). The SimpleNet showed worst results and demonstrated the impossibility of applying small and primitive architectures on the given dataset.

Exploring saliency maps (fig. 1) for the best model (EfficientNetB5) also gives some insight. All important regions bounded are located within a cell or its vicinity, therefore we can conclude, that model has learned patterns possessed by a cell itself. Important regions are located both inside and on the border of a cell indicating that learned patterns influenced by some morphological cell features such as its shape.

V. CONCLUSION

In the course of the work, the features of the analysis of cellular images were identified, the data were augmented and divided into training and test sets, taking into account the distribution of subjects, experiments were carried out and model's outputs were interpreted. It was found that the best results on the given dataset were shown by the EfficientNetV2M architecture (the value of the target metric F1 is 9% higher than the average among the architectures under consideration, while the difference between the worst and best value of the F1 metric is 0.23).

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