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Image Classification of Leukemia Cancer Using Wavelet Deep Neural Network

Abstract. *Classification of blood cell images, through color and morphological features, is essential for medical diagnostic processes. This paper proposes an efficient method using LeGall5/3 wavelet transform (LeGall5/3WT) based on Convolutional Neural Network (CNN) for leukemia cancer image classification. The proposed algorithm is applied on 108leukemia images, including 49 blast cell images and 59 healthy cell images. All these images are obtained from the acute lymphoblastic leukemia image database for image processing (ALL-IDB). The data augmentation technique provided 7776 images, including3528 blast cell images and 4248 healthy cells. LeGall5/3WT feature extraction results are used as inputs to the CNN for leukemia cancer classification. The network system architecture contains three convolutions, three aggregate layers, a fully connected layer, a Soft Max layer, and an output layer with two classes. The proposed algorithm achieves accurate results (accuracy of 100%, sensitivity of 100%, specificity of 100%) for ALL-LDB1 database.*

Streszczenie. *Klasyfikacja obrazów krwinek pod kątem cech kolorystycznych i morfologicznych jest niezbędna w procesach diagnostyki medycznej. W artykule zaproponowano wydajną metodę wykorzystującą transformatę falkową LeGall5/3 (LeGall5/3WT) opartą na konwolucyjnej sieci neuronowej (CNN) do klasyfikacji obrazów raka białaczki. Proponowany algorytm jest stosowany na 108 obrazach białaczki, w tym 49 obrazach komórek blastycznych i 59 obrazach zdrowych komórek. Wszystkie te obrazy uzyskano z bazy danych obrazów ostrej białaczki limfoblastycznej do przetwarzania obrazów (ALL-IDB). Technika powiększania danych dostarczyła 7776 obrazów, w tym 3528 obrazów komórek blastycznych i 4248 zdrowych komórek. Wyniki ekstrakcji cech LeGall5/3WT są wykorzystywane jako dane wejściowe do CNN w celu klasyfikacji raka białaczki. Architektura systemu sieciowego zawiera trzy sploty, trzy warstwy agregatów, warstwę w pełni połączoną, warstwę Soft Max i warstwę wyjściową z dwiema klasami. Zaproponowany algorytm pozwala uzyskać dokładne wyniki (dokładność 100%, czułość 100%, specyficzność 100%) dla bazy danych ALL-LDB1. (**Klasyfikacja obrazu raka białaczki za pomocą głębokiej sieci neuronowej Wavelet**)*

Keywords: Artificial intelligence, Convolutional neural network, Image classification, LeGall5/3wavelets transform, Leukemia.
Słowa kluczowe: Sztuczna inteligencja, Konwolucyjna sieć neuronowa, Klasyfikacja obrazu, Transformacja falkowa LeGall5/3, Białaczka.

Introduction

Blood cells (BC) are one of the most critical cells in the human body. Under the microscope, one can see that they are made up of red blood cells (RBC), white blood cells (WBC), and platelets. Recently, various reports and statistics in the world, especially in the African continent indicate frightening figures for Leukemia [1, 2]. Four main types of Leukemia exist: Chronic Lymphocytic Leukemia (CLL), Acute Myeloid Leukemia (AML), Acute lymphocytic leukemia (ALL), and Chronic Myeloid Leukemia (CML)[3]. To diagnose Leukemia, many well-known methods and traditional tests are used, such as physical examination, blood test, immunophenotype, cytogenetic, bone marrow biopsy, a complete blood count (CBC). Radiography, an x-ray image, ultrasound, or MRI, may be used. These tests are used to detect damage to bones (x-rays), brain (MRI), kidneys, spleen, or liver (ultrasound) [4]. A computerized tomography scan (CTS) can be used to examine the lymph nodes in the chest. Although these methods are used to diagnose whether the patient is infected or healthy, some people are undiagnosed. The reason for this is the misdiagnosis of the significant similarity of cells and symptoms with other diseases. In addition, manual segmentation and classification of blood cells are very laborious and time-consuming due to their irregular shape and size, and their accuracy directly affects the medical diagnostic process. For all these reasons, researchers resort to other, more accurate solutions based on the use of artificial intelligence (AI) in diagnosing Leukemia and distinguishing between its different types [5]. In recent years, researchers have revealed that AI can help predict and detect Leukemia, especially Acute Myeloid Leukemia using AI, scientists fed data that include information about whether or not the sample came from a patient with or without myeloid Leukemia. Then the algorithms search for a copy of the disease-specific models, through machine learning [6]. And based on the identification of pathological patterns, more data are analyzed and classified by algorithms into samples with and without myeloid Leukemia. Overall, the main contributions of this paper can be summarized as follows:

- A new method based mainly on wavelet transform to isolate regions of interest and on deep neural network to extract features for the purpose of classification.
- The ability to process large amounts of data accurately with reduced latency.
- Benchmarking of different deep learning algorithms and datasets together with discussions on open research questions related to improving the efficiency of feature extraction.

Related work

In recent years, researchers have proposed several Deep Learning (DL) algorithms for Leukemia image classification. To detect the disease, various morphological, textural, and color characteristics are considered. In [7], the CNN was used for 3504 images of Acute promyelocytic leukemia (APL). The CNN in [8], is used to recognize the subtypes of Leukemia (Acute and chronic) from microscopic blood cell images. The data source is obtained from ALL-IDB and American society of hematology (ASH) Image Bank. The decision tree (DT), support vector machine (SVM), naive Bayes (NB), and k-nearest neighbor (KNN) have been explored to prove the efficiency of the suggested approach. In [9], the authors used a semantic segmentation method based on a DL network (DeepLabv3+ ResNet-50) to segment leukocytes.

The accuracy achieved is 96.1%. In [10], an automation system based on the YOLOv4 algorithm has been introduced to predict leukemic cells from the ALLIDB1 and CNMC2019 datasets as either blast cells (ALL) or healthy cells (HEM). The highest Mean Average Precision values were for the CNMC2019 dataset (98.7%). In [11], Discrete Wavelet Transform (DWT) and the Stacked Autoencoder

algorithm are used to reduce the size of data and classification of the cancer genome, respectively. In [12], the CNN-RNN framework is proposed to automatically diagnose and classify blood cells. In [13], CNN and RNN discriminate between immature lymphoblasts and normal cells. In [14], DBM has been applied to diagnose AML. In [15], the study focuses on recognizing ALL to classify normal and blast cells based on the generative adversarial optimization algorithm. To improve the efficiency of the proposed algorithm, it is compared with respect to the Naïve Bayes classifier, the k-nearest neighbor, the backpropagation neural network, and the SVM. In [16], a deep convolutional generative adversarial network (DC-GAN) and a residual neural network (ResNet) is used to augment data and classify WBC. In [17], the k-means clustering algorithm is used to extract the region of interest (ROI) of ALL images. Even if all these approaches give acceptable results, we believe that improvement is still possible. Hence, in this paper, we propose an efficient method using LeGall5/3WT for feature extraction and DNN architecture based on CNN algorithm to discriminate between normal and cancerous cells. In addition, data augmentation (DA) is used to train the model and to test the efficiency of the proposed method. This distinguishes directly our proposal from the cited works. Regarding the relevant works discussed in this section, they have suffered from many constraints and limitations, including: (1). The performance needs further improvement. (2). Low detection and classification performance under the proposed method. (3). Cannot support real-time applications. (4). A weak base datasets (5). The rare cells were fewer. (6). Use only CNN architecture or another DNN type.

Proposed method

In this section, we propose an algorithm for the classification of medical images. The algorithm is divided into five essential parts. (i). Pre-processing: is performed to prepare the images for the ROI extraction and feature extraction steps. (ii). Data augmentation: is applied to increase the number of medical images to improve the learning process. (iii). ROI extraction: region of interest extraction based on wavelets is applied to Leukemia images to clear different geometric. (iv). Feature extraction: is performed using CNN layers. (v). Classification: the images are classified by the last layer of CNN to determine normal and abnormal cells and differentiate between them. In recent years, the wavelet transform has been used in many medical imaging applications for its efficiency in extracting features of images [18, 19, 20, 21, 22, 23]. Among the numerous wavelets family available, LeGall5/3 wavelets [24] were used in this study. The 5/3 biorthogonal wavelets are art of the Cohen-Daubechies-Feauveau (CDF) family of symmetric biorthogonal wavelets employed for their characteristic of reversibility and loss lessness. They are so named because of the support width of their low-pass filters, detailed in Table. 1, is p=5 samples at analysis and p=3 at synthesis.

The idea of wavelet decomposition (WD) is shown in Fig. 1. Which can be used to compute the wavelet coefficients.

Table 1. Coefficients of symmetric impulse responses of the analysis low-pass filter h(n) and the synthesis low-pass filter h(n)* associated with the legall5/3 wavelet.

N	H(n)	h(n)*
0	1.06066017177982	0.70710678118655
1	0.35355339059327	0.35355339059327
2	-0.17677669529664	-

This wavelet has two filters High-Pass (HP) and Low-Pass (LP) filters defined using the following expression [25]:

$$H_0(z) = 1/8(-z^2 + 2z + 6 + 2z^{-1} - z^{-2}) \quad (1)$$

$$H_1(z) = 1/2(-z + 2 - z^{-1}) \quad (2)$$

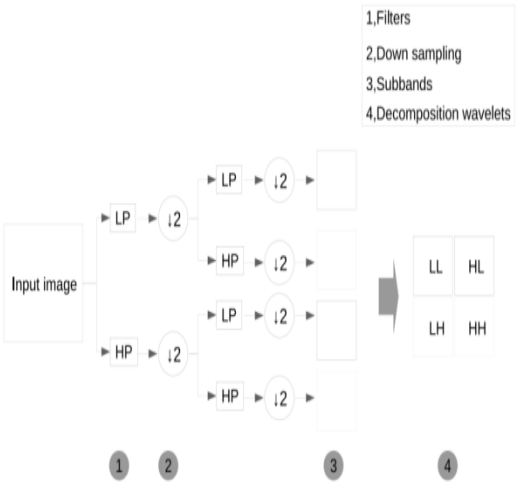

Fig. 1. An example of the one-level wavelet decomposition.

Fig. 2.

Where H_0 (z): Low-pass filter H_1 (z): High-pass filter. After convolution with the filter, the original signals are divided into HP and LP, which are known as approximate and detail coefficients. Moreover, they have N=N˜=2 zero moments because of their relative simplicity and the symmetry they offer. The wavelets of this family are also called CDF (N, N˜), where N denotes the number of zero moments of the analysis wavelet ψ and N˜ is equivalent in synthesis. As for the Daubechies wavelets, it is possible to show that the CDF wavelets have minimal support for a given number of zero moments (N, N˜). In general, image analysis techniques involve the automatic extraction of shape, color and texture properties which are then used in the subsequent classification between normal and abnormal cells based on AI algorithms such as the CNN model, which is included in the list of deep-learning algorithms [26, 27, 28]. The CNN is the most required model for image classification, where it is based on many layers for classification. (1) Convolutional layer is responsible for the extraction and detection of various features in the input images. (2) Max-Pooling layer is responsible for reducing the dimensions of the filtered image and thus focusing on the ROI. (3) Flatten Layer allows obtaining a one-dimensional array of the max-pooled matrix. (4) Fully connected networks consist of layers that are fully interconnected between each neuron in each layer. The CNN parameters are shown in Table. 2. In this paper, the output results of LeGall5/3WT were used as inputs of CNN architecture were composed of ten layers, three convolution layers (Conv Layer1, Conv Layer2, Conv Layer3), three max pool layers (pool layers1, pool layers2, pool layers3), one fully-connected layer and one SoftMax layer to classify Leukemia images into two cases blast cells and healthy cells. The computational complexity of CNN models depends on the number and size of filters and layers. The proposed model is presented in Fig. 2. The Leukemia dataset is divided into a training set and a testing set (see Table. 3.).

Table 2. CNN parameters used during the training.

NL	LN	Att	NF	FS	Str	Padd	FMS	NP
0	Input	125	-	-	-	-	15625	0
1	C1	125	8	3	1	1	125000	80
2	P1	62.5	8	2	2	0	31250	-
3	C2	62.5	16	3	1	1	62500	1168
4	P2	31.25	16	2	2	0	15625	-
5	C3	31.25	32	3	1	1	31250	4640
6	P3	14.625	32	2	2	0	6844.5	-

Number of layer (NL), Layer Name (LN), Attribute (Att), Number filter (NF), Filter size (FS), Stride (Str), Padding (Pdd), Feature map size (FMS) and Number of Parameters (NP).

Table 3. Distribution of Leukemia dataset in our dataset.

	BC	HC	TOTAL
TRAINING SET	39.2	47.2	86.4
TEST SET	9.8	11.8	21.6
TOTAL	49	59	108

We used 80%of the data as a training set (6220.8 images), and the other 20% was left (1555.2 images). The model makes two possible predictions. One is blast cells, and the other is healthy cells. The model trains on the training set and learns the characteristics that differentiate the two classes of cells (blast and healthy cells). Learning is performed by varying the number of epochs. When leukemia images are given to the layers of the proposed model, it goes through pre-processing, convolution, and pooling layers, and the final class prediction is based on the learning of specific features in each layer.

Results and discussion

This section presents the results of the proposed approach together with its comparison to existing ones.

The input dataset

Herein, we rely on databases of medical images of blood cells obtained through microscopic imaging. It contains about 39000 blood elements.The images are taken with different magnifications of the microscope ranging from 300 to 500, which have been captured with an optical laboratory microscope coupled with a Canon PowerShot G5 camera. All images are in JPG format, with a resolution of 2592x1944. Table. IV summarizes the details and specifications of devices used for image acquisition.To ensure the robustness of the proposed algorithm, our algorithm has been tested on other databases ALL-IDB2, BCCD, Cell a vision and JTSC respectively.

Table 4. Details of image acquisition

Device		Specification
Resolution		2592×1944
Microscope	OLYMPUS	300-500
CX31		Canon Power Shot
Camera		G5
Image format		JPG
Colour depth		24 bit RGB Colour

Data augmentation

To extract new samples and increase the efficiency of the proposed model and due to the lack of data from the original images and to avoid the saving process, techniques have been used to increase their size, especially in the field of DL. The process of increasing the image field, for example, depends on rotation, translation vertical, translation horizontal, rescale, flip, noise and shear. Generating several secondary images from the original images leads to reducing the error rate and allows accurate and satisfactory results. In this study, because of the limited number of Leukemia images (108 images), each Leukemia image was increased by 7 images compared to the original images to contribute a total of 864 images, including 392 BC images and 472 HC images (Fig. 3) to improve the learning efficiency of the various features of the proposed model and to avoid overfitting problems caused by the limited number of training samples. Table. 5, demonstrates the distribution details of the Leukemia DA source.

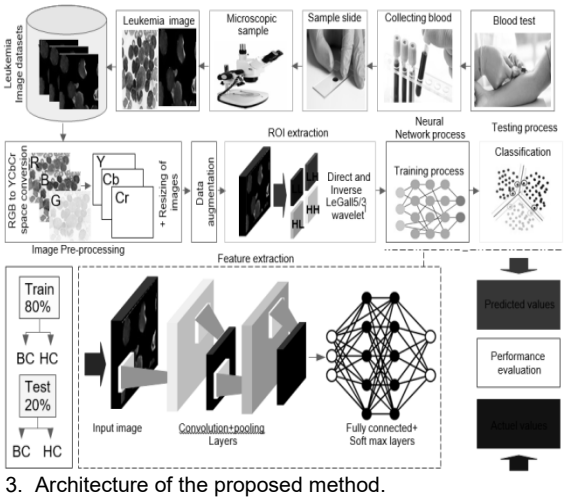

Fig. 3. Architecture of the proposed method.

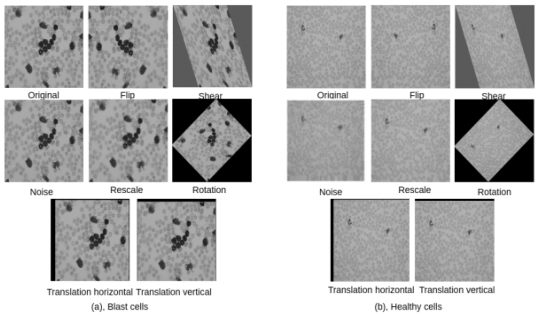

Fig. 4. Example of ALL-IDB1 augmented data image.

Fig. 5.

Table 5. Distribution of Leukemia DA in our dataset

	BC	HC	Total
Training set	313.6	377.6	691.2
Test set	78.4	94.4	172.8
Total	392	472	864

4.3 The evaluation criteria

The performance measures are tabulated in Table. 6.

Table 6. Details of used metrics

Metrics	Definitions
Accuracy (ACC)	(TP+TN)/(TP+FP+TN+FN)
Sensitivity (SEN)	TP/(TP+FN)
Specificity (SPE)	TN/(TN+FP)
F1 Score (F1)	2TP/(2TP+FN+FP)

Results

1) The LeGall5/3WT+CNN algorithm versus CNN algorithm

The proposed work employs LeGall5/3 wavelet transform (LeGall5/3WT) to extract texture features from the leukemia images. When LeGall5/3WT is applied to an image size of 125×125, it gives a feature matrix of 125×125 coefficients, and each coefficient is considered a feature for decomposition level. The use of LeGall5/3WT in the ROI extraction phase of the medical images helped the algorithm to be fast and, therefore, reduced the undesirable features and improved the performance of the proposed method in image classification. LeGall5/3WT decomposition is shown in Fig. 4. The proposed model was trained and tested on images considering the size and shape of cells and image intensities. The model was trained for 150 iterations. An example of the impact of decomposition level for LeGall5/3WT to improve the quality of the databases

before the training processes is shown in Table. 7. Therefore, the obtained results indicate that the decomposition level should be set at 6. The matrix confusion of the model is represented in (Fig. 5).

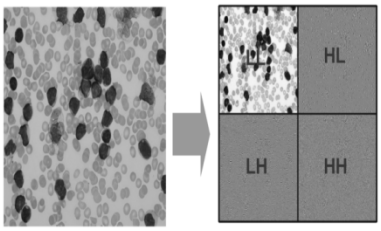

Fig. 6. LeGall5/3WT decomposition.

Table 7. The impact of decomposition level for ALL-IDB1 database

Decomposition level	2	3	4	5	6
ACC	99.57	99.71	99.13	99.86	100
SEN	99.68	100	99.68	100	100
SPE	99.47	99.47	98.69	99.74	100
F1	99.36	99.36	98.41	99.68	100

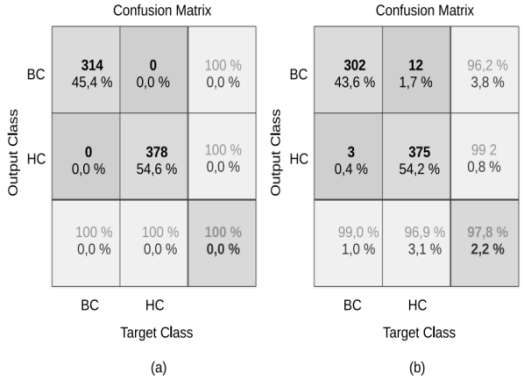

Fig. 7. The confusion matrix for the ALL-IDB1 database: (a). LeGall5/3WT+CNN algorithm, (b). CNNalgorithm
Fig. 8.

The confusion matrix shows the results of the testing part where the model predicted 314 correct cases out of 314 abnormal cases (blast cell) and predicted 378 correct cases out of 378 normal cases (healthy cell), and it can be concluded that these are good results. However, the model of CNN predicts 302 correct cases out of 302 blast cells and predict 375 correct cases out of the healthy cell. The train loss curve (or loss function) where represents the error rate between the actual value and the predicted value. From (Fig. 6), this function decreases rapidly from1 iteration to 50, where the loss is close to 0% starting with 50 iterations and then stabilizes at about 0 after iteration 100 until the last value it takes. For the test loss, it takes some time to reach 0, but after 50 iterations, it settles at 0 until the end of the training. According to the accuracy curves (Fig. 7), it is clear that the accuracy curve increases rapidly from iterations 1 to 50 except for some perturbations and stabilizes above 98%, similar to the test curve from iteration 1 to 50 and then stabilizes around 98%. Also, when the training process, there is no underfitting and overfitting from the first iteration and last iteration, which means the performance of the suggested model is high.

2) Comparison according to the number of epochs

In this part, we vary the number of epochs from 10 to 60 and calculate the evaluation parameters.

The best results are obtained for several epochs equal to 30, as shown in theTable. 8. The timerequired to obtain these important results when applying our proposed method is equal to 15m16sec. This training time is acceptable considering the number of epochs, the level of decomposition, thenumber of images, the size of the images, the nature of the images, the number of layers of CNNnetwork, number of the attribute, the number of filters, number of operations of the algorithm, andcomputer characteristics. All these parameters have been taken into consideration so that they do notdirectly influence the complexity of our proposed algorithm.

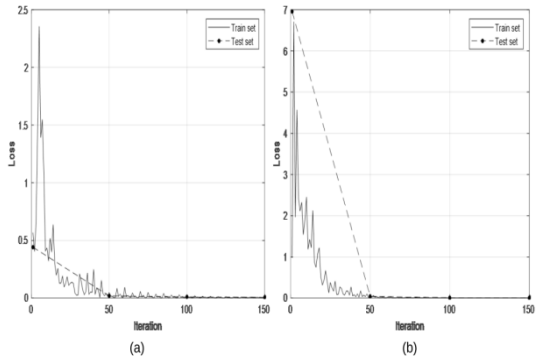

Fig. 9. The Loss function for ALL-IDB1: (a). LeGall5/3WT+CNN algorithm, (b). CNN algorithm.

Table 8. The impact of epochs for ALL-IDB1 DATABASE.

Epochs	10	20	30	40	50	60
ACC	99.57	99.57	100	99.86	99.71	99.42
SEN	100	99.68	100	100	99.68	99.36
SPE	99.21	99.47	100	99.74	99.78	99.41
F1	99.04	99.36	100	99.68	99.65	99.34

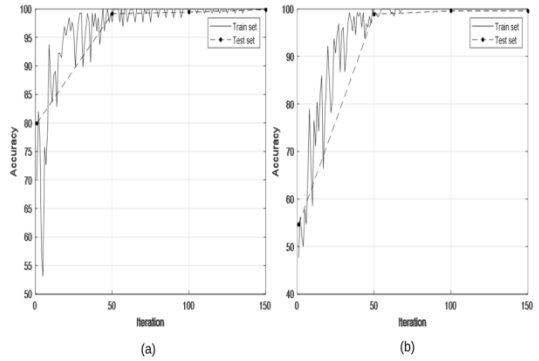

Fig. 10. Loss Accuracy function for ALL-IDB1: (a). LeGall5/3WT+CNN algorithm, (b). CNN algorithm

3) *Comparison with existing methods*

Several methods have been used to diagnose Leukemia using datasets in terms of performance parameters such as accuracy, sensitivity, specificity, and F1-score. Some of these approaches, which give excellent results, are presented and compared with the proposed model. Table. 9 illustrates the quantitative comparison between the previous studies and the suggested method. As illustrated by the analysis of these tables, the proposed model was employed to solve the issue of leukemia detection more efficiently. The suggested model is more efficient than the existing methods, where the value of metrics achieves 100%.

Finally, some limitations related to the processing of this type of digital medical images, such as optimal color accuracy, brightness, and contrast, must be worked out so as not to affect the accuracy of the proposed model. However, a precise and complete diagnosis and classification can be obtained with the large number of images **used.**

Table 9. Comparison between our method and state-of-the-Art methods.

Ref.	Year	Datasets	Used method	Leukemia types	ACC (%)	SEN (%)	SPE (%)
Our model	2023	ALL-IDB	LeGall5/3WT +CNN	Leukemia	100	100	100
[29]	2022	ALL-IDB	BE	ALL,AML	97.04	96.99	98.52
[30]	2022	ALL-IDB	TL	ALL,AML	95.00	-	-
[31]	2021	ALL-IDB	YOLOv4	ALL	98.70	-	-
[32]	2021	ALL-IDB	CNN	ALL	91.10	-	-

Bagging ensembler (BE), Transfer learning (TL).

Conclusion

To detect the Leukemia disease, we presented in this study a new method of detection of this disease based mainly on the process of classification of Leukemia through microscopic images of a blood smear. For this purpose, we have proposed to use the LeGall5/3 wavelet on blood sample images, followed by the CNN algorithm. The proposed method can help in the early diagnosis of Leukemia. To increase the accuracy and efficiency of the proposed method, we relied on the application of DA techniques that help avoid overfitting problems. Through this method, we were not only satisfied with the detection of leukemia, but we obtained more than that because we were able to classify the BC affected by this incurable disease in the types known to specialized doctors, which guarantees the accuracy of the doctor and save time in the process of medical diagnosis. As a result, we also showed that our model outperforms other machine learning algorithms by achieving 100% accuracy for leukemia classification. The proposed method avoided us falling into a situation of underfitting or overfitting. This method helped medical specialists in their clinical examination to diagnose and classify these diseases with high precision. In our future work, we plan to generalize the application of our approach to the diagnosis and classification of other types of cancers in order to provide better decision-making to physicians in their examination process. This will be the subject of a collaboration with several anti-cancer centers in our country and throughout the world.

REFERENCES

[1] The Global Cancer Observatory, Available online: https://gco.iarc.fr/, accessed: 2023-0303.

[2] Z. Gao, A. Mao, K. Wu, Y. Li, L. Zhao, X. Zhang, J. Wu, L. Yu, C. Xing, T. Gong et al., "Childhood leukemia classification via information bottle-neck enhanced hierarchical multi-instance learning," IEEE Transactions on Medical Imaging, 2023.

[3] N. Bibi, M. Sikandar, I. Ud Din, A. Almogren, and S. Ali, "Iomt-basedautomated detection and classification of leukemia using deep learning,"Journal of healthcare engineering, vol. 2020, pp. 1–12, 2020.

[4] G. R. Spinner, C. Federau, and S. Kozerke, "Bayesian inference using hierar-chical and spatial priors for intravoxel incoherent motion mr imaging in the brain: Analysis of cancer and acute stroke," Medical image analysis, vol. 73,p. 102144, 2021.

[5] A. Bodzas, P. Kodytek, and J. Zidek, "Automated detection of acute lymphoblastic leukemia from microscopic images based on human visual perception," Frontiers in Bioengineering and Biotechnology, vol. 8, p. 1005, 2020.

[6] J.-N. Eckardt, M. Bornh¨auser, K. Wendt, and J. M. Middeke, "Applicationof machine learning in the management of acute myeloid leukemia: current practice and future prospects," Blood Advances, vol. 4, no. 23, pp. 6077–6085, 2020.

[7] N. Ouyang, W. Wang, L. Ma, Y. Wang, Q. Chen, S. Yang, J. Xie, S. Su,Y. Cheng, Q. Cheng et al., "Diagnosing acute promyelocytic leukemia byusing convolutional neural network," Clinica Chimica Acta, vol. 512, pp.1–6, 2021.

[8] N. Ahmed, A. Yigit, Z. Isik, and A. Alpkocak, "Identification of leukemiasubtypes from microscopic images using convolutional neural network," Diagnostics, vol. 9, no. 3, p. 104, 2019.

[9] R. M. Roy and P. Ameer, "Segmentation of leukocyte by semantic segmen-tation model: A deep learning approach," Biomedical Signal Processing andControl, vol. 65, p. 102385, 2021.

[10] R. Khandekar, P. Shastry, S. Jaishankar, O. Faust, and N. Sampathila,"Automated blast cell detection for acute lymphoblastic leukemia diagnosis,"Biomedical Signal Processing and Control, vol. 68, p. 102690, 2021.

[11] S. Patil, G. Naik, R. Pai, and R. Gad, "Stacked autoencoder for classificationof glioma grade iii and grade iv," Biomedical Signal Processing and Control,vol. 46, pp. 67–75, 2018.

[12] G. Liang, H. Hong, W. Xie, and L. Zheng, "Combining convolutional neuralnetwork with recursive neural network for blood cell image classification,"IEEE access, vol. 6, pp. 36 188–36 197, 2018.

[13] S. Shah, W. Nawaz, B. Jalil, and H. A. Khan, "Classification of normal andleukemic blast cells in b-all cancer using a combination of convolutional and recurrent neural networks," in ISBI 2019 C-NMC Challenge: Classificationin Cancer Cell Imaging: Select Proceedings. Springer, 2019, pp. 23–31.

[14] M. Hess, S. Lenz, T. J. Bl¨atte, L. Bullinger, and H. Binder, "Partitionedlearning of deep boltzmann machines for snp data," Bioinformatics, vol. 33,no. 20, pp. 3173–3180, 2017.

[15] M. Tuba and E. Tuba, "Generative adversarial optimization (goa) foracute lymphocytic leukemia detection," Studies in Informatics and Control,vol. 28, no. 3, pp. 245–254, 2019.

[16] L. Ma, R. Shuai, X. Ran, W. Liu, and C. Ye, "Combining dc-gan withresnet for blood cell image classification," Medical & biological engineering& computing, vol. 58, pp. 1251–1264, 2020.

[17] S. Kumar, S. Mishra, and P. Asthana, "Automated detection of acuteleukemia using k-mean clustering algorithm," in Advances in Computer andComputational Sciences: Proceedings of ICCCCS 2016, Volume 2. Springer, 2018, pp. 655–670.

[18] Y. Habchi, A. F. Aimer, M. Beladgham, and R. Bouddou, "Ultra low bitrate retinal image compression using integer lifting scheme and subbandencoder," Indonesian Journal of Electrical Engineering and Computer Sci-ence (IJEECS), vol. 24, no. 1, pp. 295–307, 2021.

[19] Y. Habchi, M. Beladgham, A. MOULAY LAKHDAR, A. Bassou, and T.-A.Abdelmalik, "Low bit-rate medical video coding using dwt." Electrotehnica,Electronica, Automatica, vol. 63, no. 1, 2015.

[20] Y. Habchi, M. Beladgham, H. Benlabbes, and A. T. Abdelmalik, "Hybriddct-dbt algorithm for medical video compression," Electrotehnica, Electronica, Automatica, vol. 64, no. 2, p. 97, 2016.

[21] B. Sdiri, M. Kaaniche, F. A. Cheikh, A. Beghdadi, and O. J. Elle, "Efficient enhancement of stereo endoscopic images based on joint wavelet decompo- sition and binocular combination," IEEE transactions on medical imaging,vol. 38, no. 1, pp. 33–45, 2018.

[22] E. Kang, W. Chang, J. Yoo, and J. C. Ye, "Deep convolutional framelet denosing for low-dose ct via wavelet residual network," IEEE transactions on medical imaging, vol. 37, no. 6, pp. 1358–1369, 2018.

[23] J. Shi, Y. Zhao, W. Xiang, V. Monga, X. Liu, and R. Tao, "Deep scatteringnetwork with fractional wavelet transform," IEEE Transactions on SignalProcessing, vol. 69, pp. 4740–4757, 2021.

[24] A. P. D. G. Savi´c, M. Prokin, V. M. Rajovi´c, and D. Prokin, "Memory efficient hardware architecture for 5/3 lifting-based 2-d

forward discrete waveletransform," Microprocessors and Microsystems, vol. 87, p. 104176, 2021.
[25] L. Ding and W. Chen, "The analysis and research of lifting scheme based onwavelet transform," in Cyber Security Intelligence and Analytics. Springer,2020, pp. 1377–1382.
[26] M. Shaban, R. Awan, M. M. Fraz, A. Azam, Y.-W. Tsang, D. Snead, and N. M. Rajpoot, "Context-aware convolutional neural network for grading of colorectal cancer histology images," IEEE transactions on medical imaging, vol. 39, no. 7, pp. 2395–2405, 2020.
[27] R. Gu, G. Wang, T. Song, R. Huang, M. Aertsen, J. Deprest, S. Ourselin, T. Vercauteren, and S. Zhang, "Ca-net: Comprehensive attention convolutional neural networks for explainable medical image segmentation," IEEE transactions on medical imaging, vol. 40, no. 2, pp. 699 711, 2020.
[28] D. Karimi and S. E. Salcudean, "Reducing the hausdorff distance in medical image segmentation with convolutional neural networks," IEEE Trans- actions on medical imaging, vol. 39, no. 2, pp. 499–513, 2019.
[29] R. Baig, A. Rehman, A. Almuhaimeed, A. Alzahrani, and H. T. Rauf, "Detecting malignant leukemia cells using microscopic blood smear images: Adeep learning approach," Applied Sciences, vol. 12, no. 13, p. 6317, 2022.
[30] A. Abhishek, R. K. Jha, R. Sinha, and K. Jha, "Automated classification ofacute leukemia on a heterogeneous dataset using machine learning and deeplearning techniques," Biomedical Signal Processing and Control, vol. 72, p.103341, 2022.
[31] R. Khandekar, P. Shastry, S. Jaishankar, O. Faust, and N. Sampathila,"Automated blast cell detection for acute lymphoblastic leukemia diagnosis,"Biomedical Signal Processing and Control, vol. 68, p. 102690, 2021.
[32] M. Zakir Ullah, Y. Zheng, J. Song, S. Aslam, C. Xu, G. D. Kiazolu, andL. Wang, "An attention-based convolutional neural network for acute lymphoblastic leukemia classification," Applied Sciences, vol. 11, no. 22, p.10662, 2021.