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ACUTE MYELOID LEUKEMIA MULTI-CLASSIFICATION USING ENHANCED FEW-SHOT LEARNING TECHNIQUE

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Abstract. Acute Myeloid Leukemia (AML) is a form of the condition that is fatal and has a high mortality rate. It is characterised by abnormal cells growing rapidly inside the human body. The conventional method for detecting AML seems to be examining the blood sample manually under a microscope, which is a manual and cumbersome task that also requires well-trained medical expertise for efficient identification. On the other hand, considering medical diagnosis, the capacity to classify medical images faster and accurate is essential. The classification of medical images my currently be accomplished using a range of methodologies including Machine Learning (ML), Deep Learning (DL) and Transfer Learning (RL). While these approaches are effective for large datasets, they can take a while and not ideal for small datasets. In recent years, advances in Deep Convolutional Neural Networks (DCNN) have made it possible and produce more accurate and promising outcome while processing a medical image. However, the paradigm that DCNN use for training includes a large number of annotations in order to prevent overfitting and produce promising results. Obtaining large-scale semantic annotations in clinical operations might be problematic in some cases, particularly biological expertise knowledge is needed. It is also regular occurrence in scenarios where only a small number of annotated classes are accessible in some circumstances. At this context, in order overcome the drawback of traditional approach a framework has been developed which comprises of Enhanced Few-Shot Learning Technique integrated Base Classifier (Feature Encoder)-EFLTBC. The proposed model has built using base classifier and meta-learning block, and it optimized the better results. To diagnose AML, the doctor must count the number of white blood cells and red blood cells and see if there are any abnormal health conditions in that using a microscope. However, obtaining an accurate result takes time and effort. To address these issues, the proposed Novel AML detection model employing is used in this study. Base classifier utilizing ResNet-18 pretrained model and meta learning block has computed using the average feature of every samples. Also, the dataset that we used consisting of three classes includes Normal monocytes, Abnormal monocytes, Lymphocyte and Experimental results outperform various existing deep learning technique with the accuracy of 97%, recall of 96.55% F1-Score of 96.65% and precision of 96.60.

Key words: Transfer Learning, Deep Convolutional Neural Networks, Enhanced Few-Shot Learning Technique integrated Base Classifier, Meta learning, base classifier.

AMS subject classifications. 68T05

1. Introduction.

One of the hallmarks of acute myeloid leukemia (AML) is the proliferation of immature progenitors inside the bone marrow, which ultimately leads to a lack of hematopoietic function [1]. While invasion of other organs including the brain and the lungs is rare and observed only in instances with elevated blast numbers in the blood, peripheral blood involvement is perhaps the most frequent tissue affected. At minimum 20% of the myeloblasts in the bone marrow (or plasma) must have myeloid ancestry to qualify as AML, as per the World Health Organization (WHO). As an alternative to greater than 20% threshold, AML can be diagnosed without reference to blast percent in occurrences with Nucleophosmin 1-mutated AML and Acute Promyelocytic Leukemia (APL). Acute undifferentiated Leukemia (AUL) is a kind of Leukemia which has more than 20% blasts absent markers and is often handled as AML [2].

For forecasting survival rates (SR) as well as event-free survival, research have shown that both hereditary and clinical features which are significant. There are three genetic mutations that have been linked to poor outlook and reduced survival rates: RUNX1 (ASXL1), TP53 (ASXL1), and ASXL1. The combination of a TP53 mutant and a complicated karyotype leads in the worst prognosis [3,4]. Typically, it has already been hypothesized that 75 percent of variances are due to genomic instability, and the remaining 25% are due to

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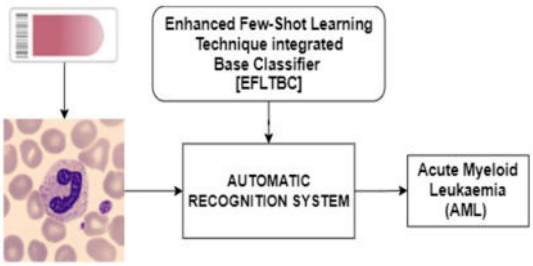

Fig. 1.1: General workflow of Research

clinical, therapeutic, and behavioral characteristics. In the 37 models that have been tested thus far, remission or life span could only be predicted in 76% to 81% of instances [5]. In light of this, it is imperative that we find more accurate prognostic factors.

Forecasting of clinical outcome using machine learning (ML) approaches has grown increasingly common. This method can be used to forecast the prognosis of cancer, for instance [6]. An artificial intelligence technique known as "machine learning" fo- cuses on developing computer algorithms that can be updated as new data comes to light. Because of this, models built from earlier data can be utilized for diagnosis and detection. In this context, Deep learning models also a powerful and robust algorithm that are effectively applied in important research areas like medical im- age analysis, data processing, financial modelling, and spam detection [7, 8]. Deep learning techniques that specialize in visual detection and segmentation include con- volutional neural networks (CNNs) [9]. There are seven different layers in LeNet-5, comprising maximum pooling, convolutional, and fully connected (FC) [10], which is based on CNN. A CNN-based system known as AlexNet employs eight layers, combin- ing maximum pooling and convolution neural networks [11,12]. In the Massive Visual Recognition Problem, AlexNet was stated the best artificial neural model for image classification. Many studies have suggested CNN-based algorithms for the diagnosis of Leukemiain this context, [13-16] focused on the identification of Acute Lymphatic Leukemia (ALL). There were two studies that focused on the detection of Acute Myeloid Leukemia (AML): P. Tiwari [17] and S. Rodrigues et al [18]. According to this study, there has been very little research done on the automatic identification of Acute Myeloid Leukemia (AML). The well deep learning method, AlexNet, can be applied in a variety of fields, including medical image analysis. Medical images including such CT scans, X-rays, MRI, PET, ultrasonic, and hematologic images can be analyzed and detected Alex Net.

2. Background work. Cells that protect the body from illness, infectious diseases, and protozoans, such as bacteria, viruses, and parasites are known as white blood cells (WBCs). In the bone marrow, hematopoietic stem cells produce WBCs. In general, there are five major types of WBC's exists includes neutrophils, monocytes, eosinophils, basophils and lymphocytes. It various one another depends on their physical and functional features. All these has been explained simply as given as follow:

Lymphocytes: It helps to develop antibodies in order to prevent from numerous microorganisms includes bacteria, viruses and different harmful invaders. Also, B cells, T cells and natural killer cells which are its further subcategory.

Monocytes: Bacteria can be broken down more easily because of its longer lifespan. The core purpose of the monocyte cell is to provide a piece of microbe to the T cell so that it can recognise it again in potential attacks.

Eosinophils: Immune responses such as hives and hay fever as well as diseases of the nervous and collagenous systems, the spleen, parasitic inflammation, and other types of allergies are all boosted by it. Nevertheless, parasites like tapeworms and hookworms are their fundamental prey.

Basophils: Antigen and allergic reaction are largely mediated by basophils, which release histamine (a sign of allergy) to dilate blood vessels and aid the immune system.

Neutrophils: Whenever there is a threat of infection, this is the first line of defence. Fungus and bacteria are

the primary targets of their attack. This cell type is commonly found in the early levels of inflammatory response, where its death creates pus in the body.

Types of Leukemia: Leukemia is a haematological illness and form of blood cancer that impairs the immune system of human by producing an excess of malignant WBCs (White Blood Cells) [19]. Acute Myeloblastic (Myeloid) Leukemia (AML), Chronic Myeloblastic (Myeloid) Leukemia (CML), Acute Lymphoblastic (Lymphocytic) Leukemia (ALL), and Chronic Lymphoblastic (Lymphocytic) Leukemia are the four major subtypes of Leukemia(CLL). The following is a brief overview of the four major types of Leukemia[20]: **AML**: This is the most prevalent type of leukaemia, affecting both kids and adults. It has an effect on the human body's WBCs, causing them to develop abnormally. Acute cancers are caused by an excess of unusual WBCs present over the human body.

ALL: Although it is the another very common form of cancer in children, it can affect adults as well. ALL is caused by a rise in lymphocytes (a type of white blood cell) in the human.

CML: It is a type of white blood cell cancer wherein immature white blood cells or blast cell lines form and multiply uncontrolled way in the human body. Adults are primarily affected by CML.

CLL: It is a specific type of cancer that attacks B lymphocytes or B cells. B cells assist the human body in fighting infection; however, cancerous B cells are incapable of fighting infection. CLL is typically found in older adults.

3. Related work and Literature Survey. E. Tuba et al. [20] presented a com- prehensive survey of WBC categorization methods for analyzing fatal diseases includ- ing blood cancer, AIDS, and Leukemia by examining microscopic images of haema- tology reports. Additionally, they highlighted several critical challenges associated with the WBC classification stage, including WBC structure, quality of image, cell differentiation, and time consumption of classification process [21]. J. Su, et al. classified WBCs utilizing neural network models with forward and backward propa- gation. After analyzing two complicated blood cells obtained via extendable images, the neural network was fed the 16 another very crucial components of that cell as input. After segmentation, training has been given with neural network consisting of 50% data and used the remaining data for testing. They classified WBCs with a 96% accuracy. The papers [22-25] noted that identifying WBCs is challenging caused by uneven coloration and anomalous illumination of clinical specimens. They presented a system for WBC classification that incorporates histogram dispersion, K-means clustering, a watershed method, and CNN. They noted a 95.81% accuracy rate for their suggested hybrid approach [27]. Umamaheswari and Geetha provided an overview of leukemia, its sub - types, and the various automated segmentation techniques used during machine learning to detect Leukemiain microscopic examination. They came to two significant conclusions at the conclusion of their reviews, the first among one is Hybrid techniques combining machine learning and image processing may improve Leukemia detection. And the second one is, A benchmark dataset is required to iden- tify periodic advancements to the proposed schemes [28]. Thanh et al. proposed a comprehensive model based on CNNs for the early screening of acute Leukemia disease. The experimental findings for the proposed approach include the first classification process, which represents an impressive result in terms of separating normal and ab- normal cells. Their suggested technique classified Leukemia cells with an accuracy of 96.6% [14]. The methodology based on deep segmentation of CNN for identifying Leukemia blood cells in microscopic examination. Their proposed models were capable of classifying WBCs in blood smear images with an accuracy of 93.94%.

It's suggested a blood cell microscopical classification algorithm based on a combination of CNN and RNN to address the heavily reliant link problem among significant features of an images. They concluded that, the combination of CNN and RNN model is more effective and reliable than other Convolutional neural models. The methodology for detecting blood cells relying on Double Convolutional Layer Deep Neural network and performance in comparison to that of SVM and Naive bayes Classifier models. They demonstrated that their envisaged DCLNN model outperforms SVM and Naive Bayes technique. The envisioned a Decision - Making framework (DMF) based on K-means clustering and panel preference to classify Leukemia cells in microscopic examination. They carried out experiments using a variety of publicly available and benchmark data sources and then validated their findings with expert physicians. They revealed that their proposed model got an accuracy of 99.517 percent [29]. AlexNet is a capable and quite well deep learning technique that is effective in a variety of research areas, most notably medical image processing. AlexNet employs eight distinct layers,

among which are optimum pooling, convolutional, and fully connected layers. AlexNet is capable of analysing and detecting significant features in a variety of medical im- ages, including CT scans, X-rays, MRIs, PET scans, ultrasounds, and hematological images.

This study offers a brand-new approach to categorizing acute myeloid leukemia. As a result of the fact that medical images are by their very nature noisier and more diverse than the original convolutional frame, a convolutional block extracts basic feature knowledge and concentrates on the entire image. [30] With the use of a 1x1 convolutional block, we were able to extract spatial and channel properties from AML blood smears. These changes allow us to give more weight to data that contributes to classification. There are two parts to our strategy. The first is a pre-trained ResNet-18 network enhanced with an additional layer and a meta-learning component that quantifies the averaged feature of every sample before categorizing query set features based on the closest centroid and co- sine metric distance between both. We hope to better grasp the difference between whole-classification and meta-learning by isolating the inconsistencies. After training a classifier just on basis classes, we replace the final FC layer with a 1x1 convolutional layer that is reliant on the base classes. [31] When a new class is being tested, the centroids are obtained by determining the mean immersion of the support samples, and then query samples are assigned to the centroid with nearest cosine distance.

4. Related work and Literature Survey. This research presents a novel method to the classification of Acute Myeloid Leukemia. By nature, medical images are noisier and much more diversified than the original convolutional frame, therefore a convolutional block extracts basic feature knowledge and focuses on the complete image. With the use of a 1x1 convolutional block, we were able to extract spatial and channel properties from AML blood smears. These changes allow us to give more weight to data that contributes to classification. There are two parts to our strategy. The first is a pre-trained ResNet-18 network augmented with an extra layer and a meta-learning component that quantifies the averaged feature of every sample, then classifies query set features are based on the closest centroid and cosine metric distance between both. We hope to better grasp the difference between whole-classification and meta-learning by isolating the inconsistencies. After training a classifier just on basis classes, we replace the final FC layer with a 1x1 convolutional layer that is reliant on the base classes. When a new class is being tested, the centroids are obtained by determining the mean immersion of the support samples, and then query samples are assigned to the centroid with nearest cosine distance. The few-shot learning paradigm we've presented is shown in Figure 1.1.

A. Base Classifier

Here pre-trained ResNet-18 architecture is used as a base classifier. A cosine nearest centroid method is used in few-shot learning technique which helps to training the classifier along with losses has been associated with respect to base classes. In order to obtaining an encoder 'g', fully connected layer is removed from the pretrained model also 1×1 convolutional layer is integrated on top of the pre-trained model. The responsibility of encoder 'g' is to map every input with respect to its embedding which helps to provide training the classifier corresponding to all the base classes along with traditional cross-entropy loss. Let consider the supported set for the few-shot task 'S'. For every class present over the dataset is represented as 't' and the corresponding few-shot samples over the class is taken as 'S_t'. Base classifier determines the average embedding 'X_t' which is known as class centroid and the equation is given as follow:

$$W_t = \frac{1}{|S_t|} \sum_{b \in S_t} g(b) \tag{4.1}$$

In order a provide a sample of query 'b' is used in a few-shot task. It helps to determine the probability of samples present over the class 't' with respect to the cosine similarity along with centroid.

$$p\left(B = t \mid b\right) = \frac{\exp(\langle g\left(b\right), W_t \rangle)}{\sum_{t'} \exp(\langle g\left(b\right), W_{t'} \rangle)} \tag{4.2}$$

The cosine similarity of two vector values in the blood smear image is represented by the value $\langle g\left(b\right), W_t \rangle$. Equation (3) states that cosine similarity is obtained as

$$\langle g\left(b\right), W_t \rangle = \frac{g\left(b\right).W_t}{\|g(b)\| * \|W_t\|} \tag{4.3}$$

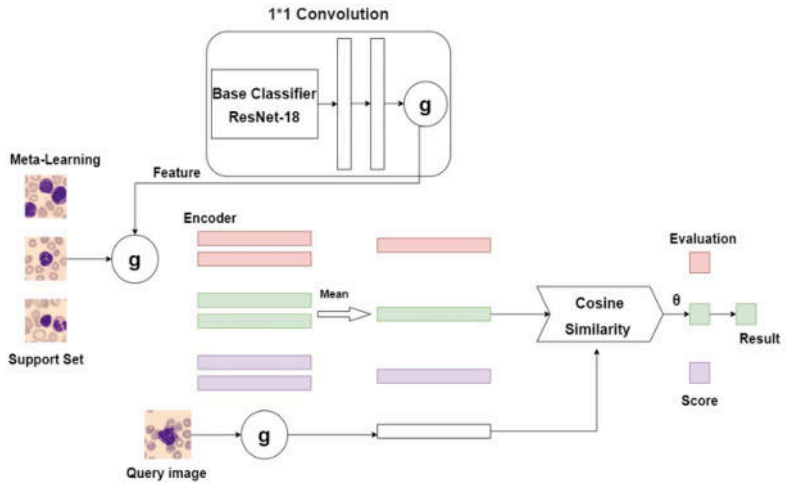

Fig. 4.1: Proposed Workflow

B.Meta-Learning

The Meta-Learning is represented in Figure 4.1. To begin, the classification training stage requires training a base classifier, which entails training a classifier on all possible base classes by removing its last FC layer and replacing it with a 1x1 convolutional layer to achieve the final classifier g [32-33]. The meta-learning stage is the next step in optimizing the model for the pre-trained base classifier evaluation measure. Classification-trained feature encoder f is used to sample from training samples in base classes in order to carry out N-way K-shot tasks (with NxQ query samples). The projected probability distribution for each sample in the query set given in Equation (2) is then used to determine the loss for each task in order to compute the loss for each of the N classes established in Equation(1) using the centroids. When p is used in conjunction with the labels assigned to the samples in the query set, this loss is calculated as a cross-entropy loss. During training, each training batch can contain a number of tasks, with the average loss being calculated for each task.

The confidence interval for cosine similarity is [1, 1], hence when determining logits, it may be useful to normalize the value beforehand employing the SoftMax function throughout training. The cosine similarity and scalar are multiplied by the learnable scalar 'θ' in training to get the prediction of probability.

$$p\left(B = t \mid b\right) = \frac{\exp(\theta . \langle g\left(b\right), W_t \rangle)}{\sum_{t'} \exp(\theta . \langle g\left(b\right), W_{t'} \rangle)} \tag{4.4}$$

To find out if the meta-learning aim is still advantageous when implemented to a comprehensive classification model of classification in Acute Myeloid Leukemia classification, this study sets out to investigate. Using the support set 'S' as input, a few-shot task evaluates the average features for samples of every class and then uses cosine similarity as a proximity metric to classify a specimen in the query set. An additional learnable scalar is provided to adjust the cosine similarity of a basic classifier using Meta-Learning, further optimizing the convergence pre-trained base classifier. To better classify AML, we now have the ability to take into account their spatial and communication channels.

5. Experimentation and Result Discussion.

5.1. Dataset. This study analyzed two distinct datasets, all of which were derived from publicly accessible databases. The first dataset included in this research comprised of 4,000 blood smear acute myeloid test results obtained from two distinct sources which is available in repository [34][1]. Among the dataset, 1000 of which

[1]https://data.mendeley.com/v1/datasets/snkd93bnjr/1

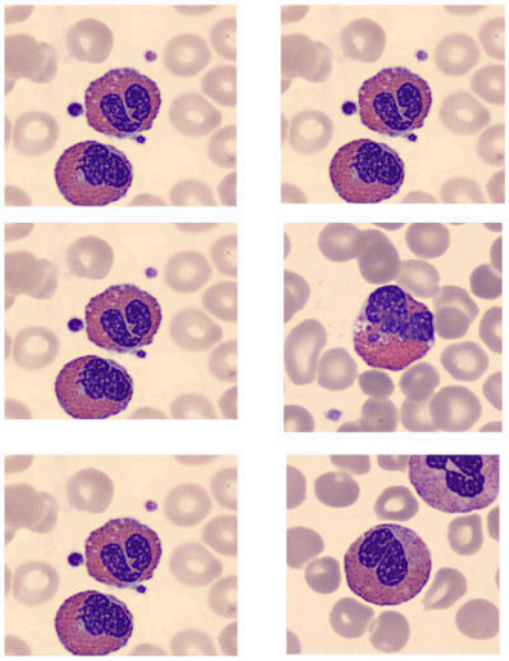

Fig. 5.1: Example of single-cell images taken from peripheral blood smears (includes all the classes).

Table 5.1: Properties of Dataset-1

Properties of dataset	**Respective values**
Image size	960 ×1080 pixel
Nature of image	RGB
Entire classes	3
Lymphocyte	1000
Normal monocytes	1600
Abnormal monocytes	1400

contains lymphocytes, 1600 of which contains normal monocytes and 1400 contains abnormal monocytes. The data has been pre-classified by subject-matter experts. And the second dataset that we have used in our research work which is accesses from publicly available repository. The total dataset consisting of 18,384 images. And the entire images holds both AML infected patients and healthy individuals. Totally Eight classes which are existing in this dataset which includes neutrophil, promyelocyte, metamyelocyte, eosinophil, basophil, erythroblast, smudge cell, lymphocytes. Each class consisting of different number of images. For instance, class neutrophil comprises maximum of 8,583 images and class lymphocytes comprises of only twenty images. The dataset which already reclassified by subject-matter expertise which is publicly available in the repository [35][2].

The datastore is depicted in Fig. 5.1. The dataset's properties are listed in Table 5.1 and Table 5.2 accordingly.

5.2. Implementation. We use ResNet-18 as the grounds classifier, which become trained on the ImageNet database. For training phase of classification, we use the SGD optimizer with such a learning rate of 0.1, a

[2]https://wiki.cancerimagingarchive.net/plugins/servlet/mobile?contentId=61080958#content/view/61080958

Table 5.2: Properties of Dataset-2

Properties of dataset	**Respective values**
Image size	960 ×1080 pixel
Nature of image	RGB
Entire classes	8
neutrophil	8,583
promyelocyte	1630
metamyelocyte	1443
eosinophil	2305
basophil	1440
erythroblast	2326
smudge cell	657
lymphocytes	20

momentum of 0.9, and a decay factor of 0.1. ResNet-18 has a weight decay of 0.0001. For the meta-learning step, we use the SGD optimizer with a momentum of 0.9. We fixed the rate of learning throughout the classification process is 0.001. Also, every training batch includes a small quantity of few shot tasks for the purpose of calculating the average loss. The cosine scaling parameter is initially set to a value of 10. It is crucial to evaluate performance of classification in image classification interrogations in order acquire scientific evidence for the study's findings. Otherwise, the classification study might be abandoned in the classroom, leaving it inadequate.

It is common practice in image classification research to use a variety of performance evaluation criteria that are widely used in other similar studies. There are a number of them, including accuracy, precision, specificity, and sensitivity. Typical performance criteria in image classification investigation are employed in this study to examine the classification reliability and accuracy. It is also used to evaluate models' performance by looking at the AUC of the receiver operation characteristic curve (AUC of ROC). The formulas and related numbers for each of these metrics are provided below.

$$Accuracy = \frac{True\ positive + True\ Negative}{True\ positive + True\ Negative + False\ Positive + False\ Negative}$$

$$Specifity = \frac{True\ Negative}{True\ Negative + False\ Positive}$$

$$Sensitivity = \frac{True\ Positive}{True\ Positive + False\ Negative}$$

$$Precision = \frac{True\ Positive}{True\ Positive + False\ Positive}$$

It is typical practice in few-shot learning to employ the episode training strategy. We use a two-way 25-shot technique for classification-1, using 25 query images for every class in training. The training set is divided into three categories, from which we draw a random sample of twenty images from each. A five-way, 25-shot approach with 25 training images for each class is used to complete the classification-2 task. The training set is divided into nine categories, from which we draw a random sample of twenty images for each.

Table 5.3 depicts the performance of our proposed work. The performance evaluation measures that we used includes accuracy, specificity, precision and sensitivity. Table 5.3 exactly point out that our suggested few shots techniques employ good performance for all the two datasets. In classification task-1, Normal monocytes achieved a 100% accuracy.

Table 5.3: Performance of our Proposed technique

Dataset	**Classes**	**Accuracy (%)**	**Specificity**	**Sensitivity**	**Precision**
Classification task-1	Lymphocytes	99.07632	0.982111	0.979462	0.974312
	Normal monocytes	100	1	1	1
	Abnormal monocytes	97.99993	0.984378	0.963458	0.962361
Classification task-1	Neutrophil	98.0578	0.98635	0.972674	0.973124
	Promyelocyte	97.7366	0.98238	0.931233	0.9165
	Metamyelocyte	97.12548	0.991453	0.923453	0.962375
	Eosinophil	96.82245	0.963446	0.932221	0.887671
	Basophil	97.12492	0.983418	0.911818	0.93116
	Erythroblast	96.22348	0.981353	0.923453	0.962375
	Smudge cell	94.83245	0.973446	0.95341	0.897671
	Lymphocytes	97.14452	0.964418	0.904818	0.94316

Table 5.4: Result Comparison of our proposed model with various existing models

Models	**Classification Task-1**		**Classification Task-2**	
	Accuracy (%)	**AUC**	**Accuracy (%)**	**AUC**
AlexNet	90.13	0.8776	85.13	0.8331
Dual Path Network	88.91	0.8745	84.54	0.8469
ResNet-50	93.97	0.9348	77.23	0.8212
VGG-16	87.29	0.9356	89.67	0.8908
DenseNet169	87.23	0.8613	90.99	0.9122
Constellation Net	84.38	0.8575	92.33	0.9332
Proposed Model	**97.87**	**0.9696**	**94.76**	**0.9793**

We make a comparison between our approach and that of transfer learning. Models from AlexNet [33], VGG16, ResNet-50 and DenseNET169 [33] are modified with the final classification layer and then used. Furthermore, our proposed methodology outperformed the constellation Net [32], an approach based on a few shots. A summary of results from two datasets is shown in Table 5.4.

It is shown in Figures 5.2 and 5.3 that classification task-1 has an accuracy and loss value. The testing set's loss is diminishing over time, as can be shown. Though there is a difference in training and test accuracy between epochs 20 and 40, it improves after 50. Results for classification task 2 are shown in Figures 5.4 and 5.5.

To train and evaluate our classifiers on the AML dataset, we start with the pretrained ResNet-18 as a foundation classifier. Examining Table 5.4, it is obvious that our proposed model is more accurate than other models. Comparing our approach to pre-trained models, the findings show that it has enormous benefits. In the case of pre-trained models, the ImageNet dataset is frequently used as the training dataset. However, the natural images on ImageNet differ from the medical ones, resulting in disappointing results on a regular basis. It was built on top of an already-trained model and retrained via meta-learning. Relatively poor outcomes are obtained when using the Dual Path Network, which combines ResNeXt and DenseNet. This may be due to the medical image's features and the embedding module used. The result of this is that our model performs better ever more densely connected networks.

Graphical representations of the accuracy comparison between two datasets are depicted in Figures 5.6 and

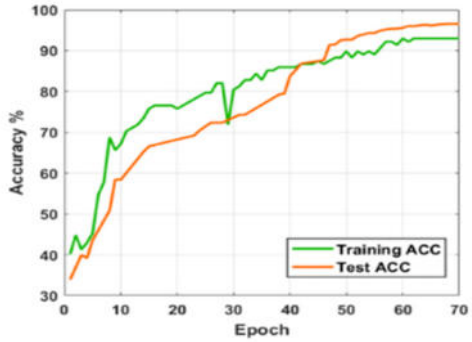

Fig. 5.2: Classification task-1 Accuracy

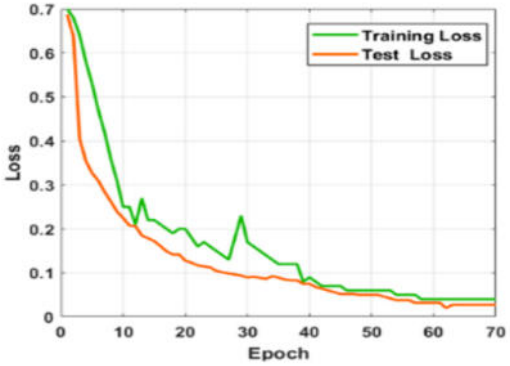

Fig. 5.3: Classification task-1 Loss

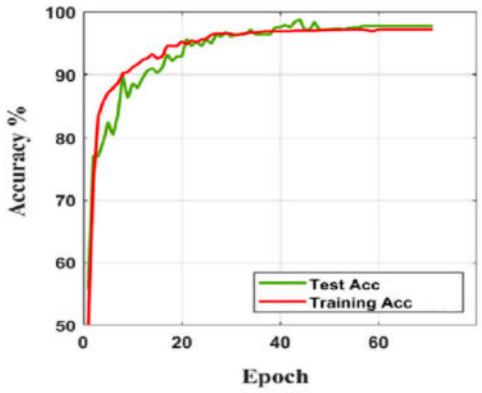

Fig. 5.4: Classification task-2 Accuracy

5.7. We can clearly see that our proposed model outperforms another model in this trial. In order to increase nonlinear features without sacrificing resolution, we use 1x1 convolution. It could also be used to alter the size

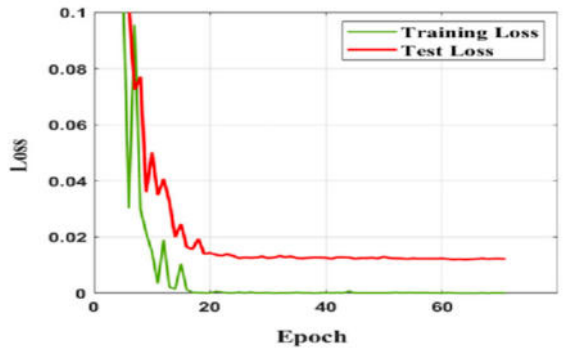

Fig. 5.5: Classification task-2 Loss

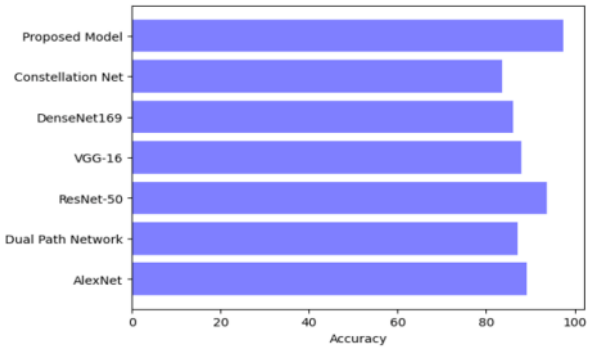

Fig. 5.6: Comparison results for Classification task-1

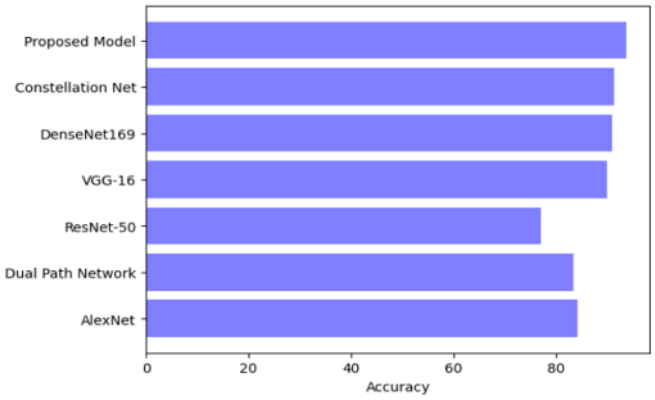

Fig. 5.7: Comparison results for Classification task-2

of an object, making it smaller or larger. During the feature extraction process, it makes it easier to take into account spatial and channel information.

6. Conclusion. When the white blood cells (WBCs) in the blood become can- cerous, it is known as acute myeloid leukemia (AML). We use the few-shot learning approach to solve the problem of classifying AML-impacted blood sample images. We proposed a framework based on a combination of pre-trained base classifiers and meta-learning. It is significantly easier and more convenient than other approaches. Incorporating a basic classification top on the pretrained ResNet-18 and 1x1 convolution kernel to the base module significantly improves the model's presen- tation potential. Our investigations are based on the AML dataset, which we use to compare two datasets. From the experimentation outcome, our proposed model achieves the classification accuracy of 97.87% and 94.76% in both classification tasks respectively. When building our model, we use the cosine similarity distance to esti- mate how far off the trained meta-learning model and the query image are from each other. This distance keeps spatial and channel information in blood smear samples intact. We will experiment with various distance metrics in order to conduct future research.

REFERENCES

[1] Pollyea D.A., Kohrt H.E., and Medeiros B.C., Acute myeloid Leukemiain the elderly: a review. British journal of haematology, 2011, p. 524–542.

[2] Estey E.H., Acute myeloid leukemia: 2019 update on risk-stratification and management. American Journal of Hematology, 2018, p. 1267–1291.

[3] Arber D.A., et al., The 2016 revision to the World Health Organization classification of myeloid neoplasms and acute leukemia. Blood, 2016, p. 2391–2405.

[4] Do ner H., et al., Diagnosis and management of AML in adults: 2017 ELN recommendations from an international expert panel. Blood, 2017, p. 424–447.

[5] Kourou K., et al., Machine learning applications in cancer prognosis and prediction. Computational and structural biotechnology journal, 2015. 13: p. 8–17.

[6] Omondiagbe, D.A., S. Veeramani, and A.S. Sidhu. Machine Learning Classification Techniques for Breast Cancer Diagnosis. in IOP Conference Series: Materials Science and Engineering. 2019. IOP Publishing.

[7] E. Nazari, A. H. Farzin, M. Aghemiri, A. Avan, M. Tara, and H. Tabesh, "Deep learning for acute myeloid leukemia diagnosis," Journal of Medicine and Life, vol. 13, pp. 382–387, 2020.

[8] P. Mamoshina, A. Vieira, E. Putin, and A. Zhavoronkov, "Applications of deep learning in biomedicine," Molecular Pharmaceutics, vol. 13, no. 5, pp. 1445–1454, 2016.

[9] P. Bharati and A. Pramanik, "Deep learning techniques-RCNN to mask R-CNN: a survey," in Proceedings of the Computational Intelligence in Pattern Recognition, pp. 657– 668, Springer, Xiamen, China, May 2020.

[10] C.-W. Zhang, M.-Y. Yang, H.-J. Zeng, and J.-P. Wen, "Pedestrian detection based on improved LeNet-5 convolutional neural network," Journal of Algorithms & Computational Technology, vol. 13, 2019.

[11] M. Z. Alom, T. M. Taha, C. Yakopcic et al., "The history began from alexnet: a comprehensive survey on deep learning approaches," 2018.

[12] A. Krizhevsky, I. Sutskever, and G. E. Hinton, "Imagenet classification with deep convolutional neural networks," Communications of the ACM, vol. 60, no. 6, pp. 84–90, 2017.

[13] N. Kumar, N. Kaur, and D. Gupta, "Major convolutional neural networks in image classification: a survey," in Proceedings of International Conference on IoT Inclusive Life (ICIIL 2019), pp. 243–258, Chandigarh, India, June 2020.

[14] T. T. P. Thanh, C. Vununu, C. Vununu, S. Atoev, and S.-H. Lee, "Blood cell image classification using convolutional neural network," International Journal of Computer eory and Engineering, vol. 10, no. 2, pp. 54–58, 2018.

[15] S. L. a. S. Daware, "Analysis of white blood cell segmentation techniques and classification using deep convolutional neural network for leukemia detection," HELIX, vol. 8, pp. 4519– 4524, 2018.

[16] G. Liang, H. Hong, W. Xie, and L. Zheng, "Combining convolutional neural network with recursive neural network for blood cell image classification," IEEE Access, vol. 6, pp. 36188–36197, 2018.

[17] P. Tiwari, J. Qian, Q. Li et al., "Detection of subtype blood cells using deep learning," Cognitive Systems Research, vol. 52, pp. 1036–1044, 2018.

[18] S. Rodrigues, B. Majhi, and P. K. Sa, "Texture feature-based classification on microscopic blood smear for acute lymphoblastic leukemia detection," Biomedical Signal Processing and Control, vol. 47, pp. 303–311, 2019.

[19] S. Mishra, B. Majhi, P. K. Sa, and L. Sharma, "Gray level cooccurrence matrix and random forest based acute lymphoblastic leukemia detection," Biomedical Signal Processing and Control, vol. 33, pp. 272–280, 2017.

[20] E. Tuba, I. Strumberger, N. Bacanin, D. Zivkovic, and M. Tuba, "Acute lymphoblastic leukemia cell detection in microscopic digital images based on shape and texture features," in Proceedings of the International Conference on Swarm Intelligence, pp. 142–151, 2019.

[21] J. Su, S. Liu, and J. Song, "A segmentation method based on HMRF for the aided diagnosis of acute myeloid leukemia," Computer Methods and Programs in Biomedicine, vol. 152, pp. 115–123, 2017.

[22] S. Agaian, M. Madhukar, and A. T. Chronopoulos, "Automated screening system for acute myelogenous leukemia detection in blood microscopic images," IEEE Systems Journal, vol. 8, no. 3, pp. 995–1004, 2014.

[23] H. Kutlu, E. Avci, and F. Ozyurt, "White blood cells detection and classification based on regional convolutional neural networks," Medical Hypotheses, vol. 135, Article ID 109472, 2020.

[24] V. Lights, Leukemia, 2019, https://www.healthline.com/ health/leukemia.
[25] K. AL-Dulaimi, J. Banks, V. Chandran, I. Tomeo-Reyes, and K. Nguyen Thanh, "Classification of white blood cell types from microscope images: techniques and challenges," Microscopy Science: Last Approaches on Educational Programs and Applied Research, vol. 8, pp. 1–10, 2018.
[26] M. Z. Othman, T. S. Mohammed, and A. B. Ali, "Neural network classification of white blood cell using microscopic images," International Journal of Advanced Computer Science and Applications, vol. 8, pp. 99–104, 2017.
[27] L. Lin, W. Wang, and B. Chen, "Leukocyte recognition with convolutional neural network," Journal of Algorithms & Computational Technology, vol. 13, 2018.
[28] D. Umamaheswari and S. Geetha, "Review on image segmentation techniques incorporated with machine learning in the scrutinization of leukemic microscopic stained blood smear images," in Proceedings of the International Conference on ISMAC in Computational Vision and Bio-Engineering, pp. 1773–1791, 2018.
[29] A. S. Negm, O. A. Hassan, and A. H. Kandil, "A decision support system for acute Leukemiaclassification based on digital microscopic images," Alexandria Engineering Journal, vol. 57, no. 4, pp. 2319–2332, 2018.
[30] S. Q. Salih, H. K. Abdulla, Z. S. Ahmed, N. M. S. Surameery, and R. D. Rashid, "Modified alexnet convolution neural network for covid-19 detection using chest x-ray images," Kurdistan Journal of Applied Research, vol. 10, pp. 119–130, 2020.
[31] S. Lu, S.-H. Wang, and Y.-D. Zhang, "Detection of abnormal brain in MRI via improved AlexNet and ELM optimized by chaotic bat algorithm," Neural Computing and Applications, vol. 99, pp. 1–13, 2020.
[32] Weijian Xu, yifan xu, Huaijin Wang, and Zhuowen Tu. Constellation nets for few-shot learning. In International Conference on Learning Representations, 2021.
[33] Chen, Y., Li, J., Xiao, H., Jin, X., Yan, S., Feng, J.: Dual path networks. In: Guyon, I., et al. (eds.) Advances in Neural Information Processing Systems 30: Annual Conference on Neural Information Processing Systems 2017, Long Beach, CA, USA, 4–9 December 2017, pp. 4467–4475, 2017.

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