Leukemia Identification from Blood Smear Images Using Dense Skip Connection Net

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Abstract — Conventional diagnostic techniques for acute lymphocyte leukemia (ALL), also known as a potentially lethal haematological malignancy, depend on manual assessment, which is both labour-intensive and capable of causing delays in critical treatment decisions. To address this challenge, researchers are progressively employing advanced technologies that include deep learning (DL) techniques. To expedite and enhance the diagnosis of ALL, deep learning models employ artificial intelligence to analyse intricate patterns and characteristics in medical images and data. To address this modified dense network Utilizing pictures of blood specimens, Skip Association Based Thick Organization (DSCNet) are explicitly engineered to identify Acute Lymphoblastic Leukemia (ALL). Through the hardship of KL difference, progress is attained, guaranteeing accurate predictions. Dropout regularization is employed to mitigate overfitting during training, hence enhancing the robustness of component representations. The proposed DSCNet has superior performance compared to competing methods, exhibiting significant enhancements in accuracy, sensitivity, specificity, F-score, and the area under the curve of 98.25%, 97.88%, 98.41, and 96.54%, respectively.

Keywords — deep learning, skip connections, dense network, data augmentation, diagnosis, medical imaging.

I. INTRODUCTION

A further analysis of the figures indicates that ninety percent among children and 31 to 41% of adults are affected [1]. The study forecasts the identification of 6,151 instances of ALL. Nonetheless, several factors such as age, experience, mental condition, and weariness may render human assessment of screening findings using microscopic blood samples subjective. Consequently, in these critical situations, automated techniques may be essential in minimizing errors. Acute lymphoblastic leukemia is able to averted with early detection. Dizziness, dyspnea, hyperpigmentation, recurrent or chronic viral infections, influenza or diaphoresis, arrhythmias, petechiae, heightened bleeding tendencies, diminished appetite, musculoskeletal pain, and lymphadenopathy with bulging or thrombosis are indicative of acute lymphoblastic leukemia (ALL). Given the absence of early detection procedures for ALL, it is imperative to monitor any dubious indicators in body language. You will be promptly evaluated if you inform a licensed physician of these suspected symptoms [3].

Further examination is necessary, as the majority of the above signs are not exclusive to ALL. Three architectures—EfficientNet, VGGNet, and LeNet—are employed for filtering and retrieve attributes from the input image. To ascertain that the output is classified as malignant, these functions are allocated to completely integrated layers, and categorization occurs concurrently. As a result, cell deformation is accurately and swiftly assessed utilizing the Deep Learning methodology.

Various challenges constrain the efficacy of existing deep learning models for acute lymphoblastic leukemia diagnosis in actual environments. A significant difficulty is the scarcity of complete and diverse datasets, necessitating the compilation of extensive and accurate information for training purposes [4]. Comprehensive validation and performance assessment are essential to ensure model generalizability across diverse patient populations and real-time implementation. The model's quality and reliability are greatly influenced by the management of data augmentation, preparation, and class imbalance. Collaborative efforts are necessary to improve the clinical application and feasibility of DL models, hence enhancing all diagnoses and prognoses [5]. Despite their advantages, DL-based ALL diagnostic models encounter obstacles related to computational expense, hyperparameter sensitivity, and the management of noisy or low-quality input pictures.

II. LITERATURE SURVEY

Acute lymphoblastic leukemia has been identified or categorized utilizing several machine learning along with deep learning methodologies. A series of studies are employed to identify ALL. Rezayi et al. investigated the utilization of deep learning methodologies rooted on artificial intelligence to facilitate the rapid diagnosis of Both. They distinguished leukemic cells against healthy cells using microscopic images utilizing two prominent deep learning networks, ResNet-50 along with VGG-16. The proposed convolutional network including machine learning methods for the classification of all types exhibited encouraging results, suggesting their use for leukemia diagnosis [6]. Abunadi and Senan created hybrid and deep learning-based multi-method diagnostic instruments for the early diagnosis of acute lymphoblastic leukemia (ALL). Genovese et al. proposed a deep learning algorithm and adaptive unsharpening method for ALL identification [7]. The method employed deep learning (DL) along with algorithms for image processing to enhance the clarity of blood sample images. A sophisticated CNN was employed to assess the methodology on a publicly available image database.

In-depth CNN employs unsupervised data training methodologies to facilitate precise classification and accurate identification of images. The automated categorization of camera-based microscopy images exhibited significant domain shift degradation when evaluated on several datasets on which it was trained [8]. The issue confronting CNN is addressed through unsupervised domain adaptation (UDA). Access to unannotated target data is essential for Unsupervised Domain Adaptation (UDA). They offer a hypothetical closets clone which can be trained absent target data. The UDA achieves a 92% accuracy rate through the implementation of both the ResNet-50 as well as VGGNet-16 architectures.

Leukemia is classified as a disease, as indicated by studies conducted by A. Shah, S. S. Naqvi, K. Naveed, N. Salem, M. A. U. Khan, and K. S. Alimgeer [9]. It induces the rapid production of atypical white blood cells. It affects both the blood vessels and the bone marrow. Consequently, hemoglobin is diminished. A full blood count, or CBC, can detect it. These manual operations are time-consuming and lack reliability. Leukemia is discovered and classified automatically by a computer-aided diagnostic method. Methods such as contrast stretching along with histogram equalization are employed to preprocess leukemia cells. The thresholding segmentation approach of Utah is implemented here. Features are extracted using shape, area, rotation, and the perimeter. The method known as KNN is utilized for classification. An accuracy of 93% was achieved.

Hui et al. devised a sophisticated classification method for acute leukemia utilizing blood samples stained with Wright-Giemsa. The approach utilized morphological techniques, color thresholding, image pre-processing, and deep learning models (AlexNet and Google Net) for classifying white blood cells [10]. Atteia et al. developed a Bayesian-optimized convolutional neural network, termed BO-ALLCNN, to detect acute lymphoblastic leukemia in micro blood smear images. The Bayesian-optimized CNN surpassed other optimized deep learning models in the classification of all images [11]. Morphological approaches were employed in the second phase to enhance accuracy by distinguishing amongst foreground

and background colors. Khandekar et al. employed the YOLOv4 technique to automate blast cell detection through artificial intelligence.

The average accuracy for picture-level classification of HI on the BreakHis dataset was 84.89% for AlexNet, 93.5% for GoogLeNet, 94.13% for VGGNets, and 94.35% for ResNet. The classification accuracy of the deep networks ResNet101 and DenseNet121 is reported as 91.43% along with 96.74% in the BreaKHis dataset, as well as 91.53% and 96.38% with the BACH-2018 dataset [12]. Uncertainty in entity assessment is measured by Bayesian deep learning [13], [29]. The belief theory-based classification fusion (BCF) method, in conjunction employing pre-trained CNN along with SVM classifiers, achieved an average rate of accuracy of 96.91% with regard to feature differentiation. This study presents a skip connection network specifically engineered for acute lymphoblastic leukemia diagnosis utilizing peripheral blood smear images to tackle these issues. The skip connectionNet design enhances performance and generalization with the integration of dropout regularization, KL convergence loss, custom image filtration, and skip connections.

II. PROPOSED METHOD

The 93% accuracy rate with a 7% error margin were observed when evaluating the Sequence Model, VGGNet, alongside LeNet. VggNet exhibits a 34% accuracy and an overall 66% error rate. It necessitates additional time for computation. It operates efficiently with extensive datasets. LeNet has an accuracy rate of 95.75% and an error rate of 4.25% [14]. It yields optimal outcomes, features the most compact architecture, and processes data with more speed. LeNet has been determined to be the most appropriate design following the comparison. The proposed approach involves developing an automated system to assist healthcare practitioners in accurately diagnosing acute lymphoblastic leukemia. Acute lymphoblastic leukemia is classified into two categories: malignant and benign. Pro-B, early pre-B, and pre-B represent the three subgroups of malignant neoplasms. Convolutional Neural Networks (CNN) are employed during data classification, identifying features, and image analysis. The input consists of a tiny image of the blood cell. Kaggle supplied the input dataset for acute lymphoblastic leukemia. The images were obtained from peripheral blood smears of 89 people. Acute manifestations of lymphoblastic leukemia have been seen in 64 individuals. The benign label is assigned to the other 25 healthy individuals.

A. *Dataset*

The recognition of acute lymphoblastic leukemia, also known as ALL, proves difficult due to the time-consuming and invasive nature of the tests. The initial screening is facilitated by smears of peripheral blood (PBS) images; but, due to the vague nature of ALL symptoms, diagnostic mistakes persist. This dataset was compiled at Taleqani Hospital of Tehran, Iran, comprising 6,512 PBS images taken from 89 patients suspected of having ALL. The images, processed and stained by skilled laboratory personnel, depict malignant lymphoblasts along with benign hematogones indicative of the Initial Pre-B along with Pro-B ALL subtypes. Images were captured with a Zeiss microscope cameras at a resolution of 100x and saved as JPG files.

A specialist employed flow cytometry to reliably identify cell types by utilizing segmented pictures derived from color thresholding-driven separation in the hue space of the HSV [15]. The dataset of the study is categorized into two equal groups: malignant and regular (non-cancerous). Subsequently, it is categorized into 4 classes—Early, Pre, then Pro—each comprising three separate kinds of cancer. The initial 3256 of the 6512 total cell images are categorized into four groups: benign images (504), early images (985), pre-images (963), along with pro-images (804), facilitating a 50:50 ratio for training and testing, respectively.

B. Deep skip dense network

The Deep Skip Connections-Based Dense Network (DSCNet) employs peripheral blood smear images to offer innovative approaches for the detection of acute lymphoblastic leukemia (ALL). The model design employs dropout regularization, KL convergence loss, skip connections, along with unique image filters to enhance efficiency and generalization [16]. The image filtering layer, as the preliminary stage, improves the input images through a specific image filtering technique. Pre-processing improves the accuracy of input information as it highlights significant elements. The model subsequently traverses several layers, encompassing dense or convolutional blocks, as shown in Figure 1. Convolutional blocks employ a non-linear activation function (e.g., ReLU) subsequent to the convolution of filtered images.

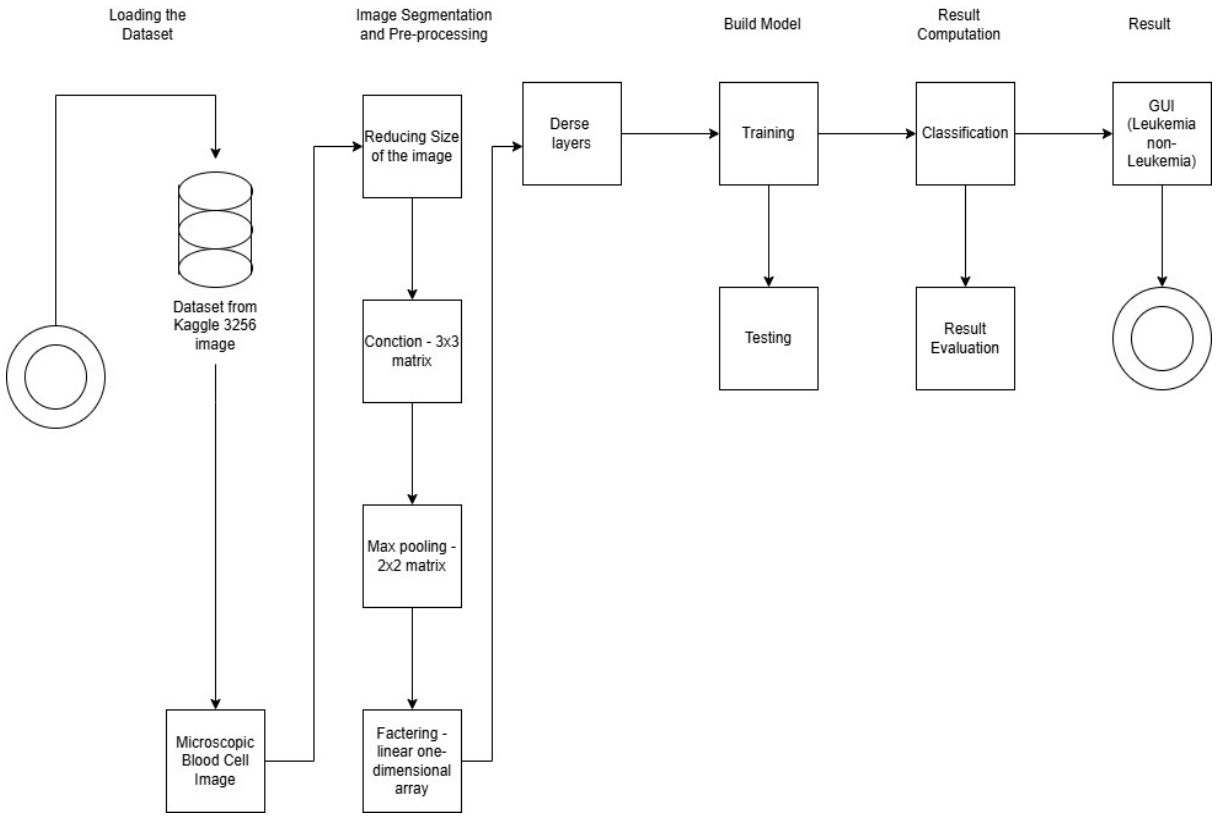

Figure 1. Proposed DSCnet model to detect ALL

Utilizing skip connections facilitates the seamless transfer of information across several network layers, addressing the vanishing gradient problem and enabling the model to record long-range dependencies, hence enhancing overall performance. The KL divergence loss, essentially quantifies the disparity between the actual distribution of all types and the expected probability distribution, serves as the objective function in modelling optimization. The model generates precise predictions by reducing the variance of KL [17]. Dropout regularization, essentially randomly deactivates a portion of neurons in every learning iteration, is employed to mitigate overfitting during training. This approach improves generalization to unfamiliar data and promotes more resilient feature representations.

A softmax classifier is employed to complete the model, generating a probability distribution across all subtypes for each input image. The model can classify images into certain diagnostic categories and allocate probability to each category. The integration of these approaches enhances the speed, accuracy, and robustness of the deep dense model in recognizing ALL using peripheral blood smear images [18]. The model enhances its capability to address challenges such as noisy data, intricate feature interactions, as well as overfitting with the implementation of skip connections, specialized image filtering, KL

divergence loss, with dropout regularization. The primary objective is to furnish an effective tool for the early and accurate diagnosis of ALL, hence enhancing patient outcomes and advancing leukemia recognition in the medical domain.

C. *Training Process of DSCNet*

A training dataset comprising image-label pairs, each depicting a smear of peripheral blood for acute lymphoblastic leukemia (ALL) diagnosis, is utilized to initiate the training procedure to develop a deep skip connection network aimed at ALL diagnosis [19]. The KL divergence loss has been chosen as the optimization objective, and the parameters of the model, including the biases and weights, are randomly initialized.To minimize memory consumption and accelerate convergence, training occurs over multiple epochs, with data segmented into mini-batches throughout each epoch.
In each epoch, the model performs a forward pass over its architecture, which comprises convolutional layer dense blocks and skip connections following image filtering to enhance input images. The predicted probabilities for the smaller batch are derived from this sequence. Gradients are computed after the backward pass by back-propagation, and the Kullback-Leibler divergence loss comparing the anticipated and actual label distributions is determined. To minimize loss and enhance the model's diagnostic precision for ALL, an optimizer uses algorithms to adjust the model's parameters. The deep dense model is ultimately enhanced to accurately identify Most on peripheral blood smear imaging as this training iteration progresses for the specified number of epochs.

III. EXPERIMENT RESULT

A. Experimental setup

The current investigation was implemented using Python routines in Jupyter Notebook. The studies utilized an Intel(R) Core(TM) i5-8250U CPU operating at 1.60GHz and 1.80GHz, accompanied by 8 GB of RAM, a single GPU, and a 64-bit Windows 10 operating system on an x64-based processor. The model is trained using the Keras framework that includes a sequential API and a TensorFlow backend. The ALL dataset has 20,000 photographs divided into four categories, each containing 5,000 images. This balanced dataset ensures a comparable variety of samples for each class.

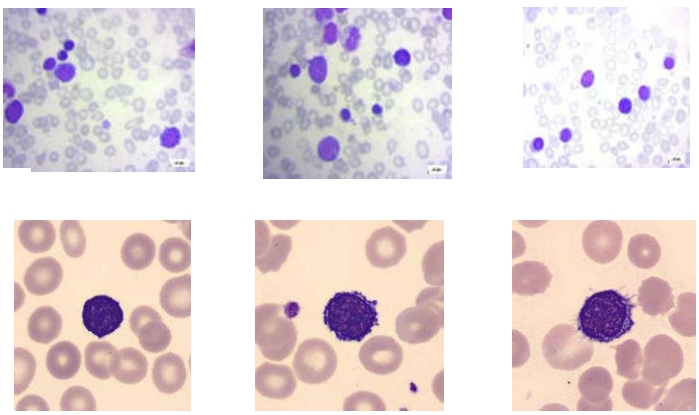

Figure 2. Samples of ALL and non-ALL images

Table 1 lists the input parameters for the suggested skip connection model, which is used to run the model for the epoch series in order to identify the ALL.

Parameters	Values
Input shape	224×224×3
Batch size	20
Number of epochs	20
Number of training samples	6875
Number of testing samples	256
Output classes	4
Class mode	Categorical
Optimizer	Adam
Learning rate	0.000
Activation function	ReLU, Leaky ReLU
Dropout	0.1

TABLE 1: INPUT PARAMETERS FOR DEEP SKIP DENSE NETWORK

Metrics (in %)	Different classes of Leukemia			
	Accuracy	Precision	Recall	F1 Score
VGG-16	90.00	90.00	90.00	89.55
YOLO-V3	92.50	92.74	90.00	92.31
Proposed model	99.85	98.87	96.55	98.21
Support image	504	985	963	804

TABLE 2: PERFORMANCE METRICS OF DEEP SKIP DENSE NETWORK

B. Evaluation criteria

Multiple evaluation metrics for assessing algorithm performance include confusion matrices, efficiency, F1-score, recall, along with precision. In the provided equations, TP, TN, FP, and FN represent True Positive, True Negative, False Positive, and False Negative, respectively; confusion matrices visually illustrate model performance.

$$\text{Accuracy} = (TP+TN)/(FP+TP+FN+TN)$$

$$\text{Precision} = TP/(FP+TP) \quad \text{Recall} = TP/(TP+FN)$$

$$\text{F1 Score} = (2 * R*P)/(R+P)$$

The program accurately identifies leukemia samples and predicts positive outcomes in the presence of leukemia. Conversely, TN accurately identifies non-leukemia samples by denoting negative predictions in a lack of malignancy.

False positives (FP) are erroneous positive predictions that misclassify non-cancerous samples as malignant. FN refers to a false negative prediction that erroneously categorizes cancer specimens as non-cancerous despite the presence of cancer.

Table 2 presents the performance characteristics for VGG-16, YOLO-V3, and the proposed Deep Skip connection network. The accuracy, accuracy, recall, and F1 score of VGG-16 utilizing the deep dense network are 90.00 each. The Yolo V3 model achieves an accuracy of 92.50 due to its restricted grid cell predictions, however the low density of the layers resulting in an accuracy of 90. The proposed model, due to its substantial layers, surpasses limitations and identifies all instances with 99.85% accuracy.

C. Accuracy and loss representations

Training as well as validation graphs were generated following the training of the Bayesian model via the Bayesian variational estimation method; these are illustrated in Figures 1 and 2 respectively. The model achieved a training accuracy of 94.78% with an error rate of 0.1467. The validation accuracy was 98.28% with an error rate of 0.0619.

Figure 4's confusion matrix indicates that our model accurately classified all images in the dangerous class. Exceptional performance is evidenced by achieving an average weighted precision, recall, with F1-score above 95% across all four categories. Our model attained an overall weighted average precision of 98.5, an overall recall of 97.5, and an average F1-score of 98.2 for dividing the types of leukaemia into benign, early pre, and pro stages during validation.

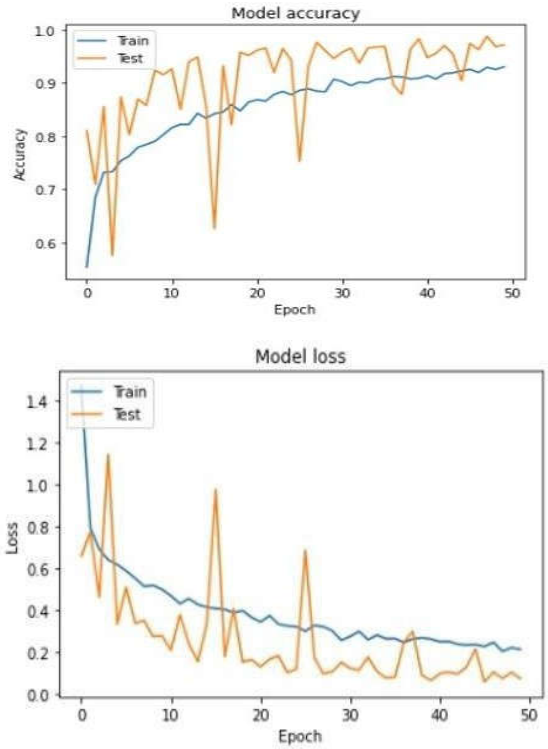

Figure 3. Accuracy and Loss of the DSCnet model

Among the different models, DSCNet distinguished itself with a unique architecture specifically tailored for comprehensive diagnosis. By including dense blocks, skip connections, with distinctive image filtering, DSCNet demonstrated enhanced efficacy in detecting various stages of ALL using peripheral blood smear images. The input data quality was markedly enhanced by the distinctive image filtering process, and precise predictions were facilitated through optimization of KL divergence loss, ultimately resulting in an improved diagnostic model. Figure 4 presents the confusion matrix.

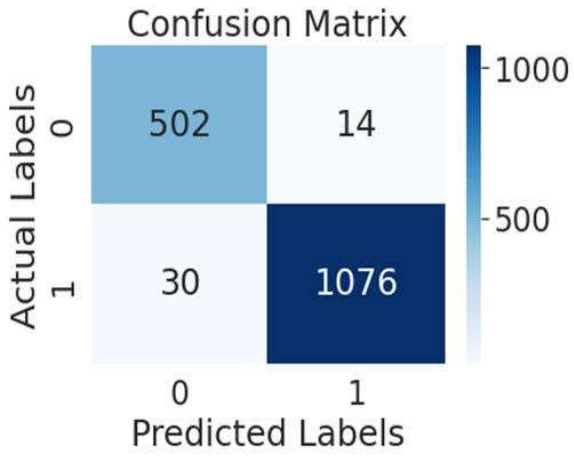

Figure.4 Confusion matrix of DSCnet model

The matrix of confusion in Figure 4 illustrates the quantity of diagnoses and misunderstandings of the specimens pertaining to matching losses. The anticipated and actual labeled samples are displayed against one another. Certain benign images are erroneously classified as belonging to the "early" and "pre" categories, as indicated by the subject's confusion matrix. The uncertainty and visual resemblance present in these medical images result in this misclassification. Nonetheless, for the majority of supplied photographs, the model accurately identifies the provided image as indicative of leukemia.

V. CONCLUSION AND FUTURE SCOPE

This study introduces a deep learning methodology utilizing DSCnet to identify ALL, which can also be applied to seismic facies, remote sensing, diverse medical imaging tasks, including human movement categorization. undetected acute lymphoblastic leukemia poses significant risks, underscoring the critical necessity for a highly precise and reliable diagnostic approach. A poll of various techniques for blood cancer identification and monitoring indicates that individuals prefer Deep Learning over traditional diagnosis due to its efficacy, precision, and cost-free availability [21]. LeNet is the superior choice among the three assessed designs: Sequential, VGGNet, and LeNet. LeNet achieves an impressive accuracy rate of 95.75% with a loss of 4.75%. A Bayesian CNN enhances the traditional CNN architecture by employing Bayesian inference approaches to account for uncertainty in network weights, so rendering predictions more robust and reliable, especially in contexts characterized by significant uncertainty or limited data.

The proposed DSCNet effectively generated precise probability distributions for all subtypes by employing KL divergence loss during optimization methods, hence enhancing diagnostic accuracy. The successful use of dropout regularization diminished overfitting, ensuring the model's robustness. Moreover, data augmentation techniques enhanced DSCNet's generalization ability. The experimental results unequivocally demonstrated DSCNet's superiority over competing models, revealing significant enhancements with regard to accuracy, sensitivity, specificity, F-score, and overall AUC, with respective improvements of 99.85, 98.87, 96.65, and 98.21.

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