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An Efficient System for Detection and Classification of Acute Lymphoblastic Leukemia Using Semi-Supervised Segmentation Technique

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Abstract: Acute lymphoblastic leukemia (ALL), sometimes referred to as hematopoietic cancer or blood cancer, is a group of cancers that impact lymphocytes, which are white blood cells. Improving patient outcomes and developing efficient treatment plans depend on early and precise blood cancer diagnosis. The lack of labelled data makes it difficult to segment lymphoblast cells from microscopic images. Our research aimed to achieve unsupervised approach for precise and accurate segmentation of blasted lymphocyte cells, thereby improving the overall performance of ALL detection and classification into its subtypes L1, L2 and L3. The proposed method employs k-means segmentation, where the parameter k is tuned, and optimal value is determined based on segmentation quality. For better performance, generated segments are evaluated against ground truth image based on Structural Similarity Index Measure (SSIM), Dice similarity coefficient (DSC) and Intersection over union (IoU). The algorithm iterates over different values of k, assesses the segmentation quality, and selects the segment with the highest evaluation score. Customized convolutional neural networks are employed for categorization. The data augmentation technique has been applied to expand the amount of training data in order to enhance model efficiency. The ALL-IDB dataset is used to assess the model's performance, and the experimental results showed that the suggested method can identify blasted cell subtypes with an overall accuracy of 99%. We succeeded in detecting acute lymphoblastic leukemia with 100% accuracy. Our proposed model not only enhances the accuracy significantly but also determines the optimal value of clusters (k) for more effective segmentation.

Keywords: Acute lymphoblastic leukemia, CNN, Classification, Feature Extraction, K-means, Peripheral Blood Smear image, Semi-supervised Segmentation

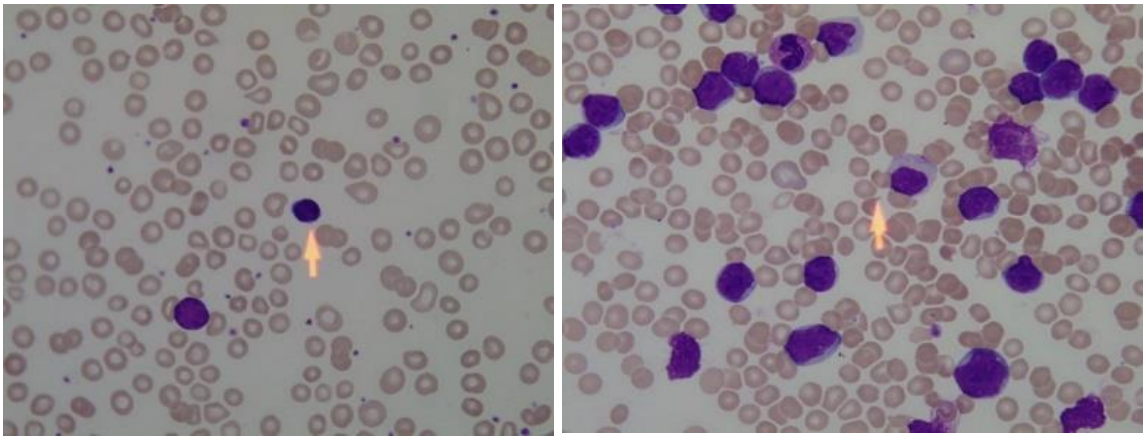
1. Introduction

Blood cell analysis plays a crucial role in diagnosing various blood-related disorders, such as anaemia, leukaemia, malaria and many infections. The principal cells present in the peripheral blood are red blood cells (RBCs), and the white blood cells (WBCs) also called leucocyte. Leucocyte cells containing neutrophil, basophil, eosinophil, lymphocyte and monocyte [1]. White blood cells are a crucial part of the immune system and play a vital role in infections and diseases. White blood cells are segmented and classified into different types based on their appearance, function, and presence of specific cell markers [2].

Acute lymphoblastic leukemia (ALL) is a type of cancer that is related to the lymphocytes in the bone marrow and into the peripheral blood [3]. According to WHO, ALL subtypes are based on whether the precursor cell is a T or B lymphocyte, whereas FAB classification of ALL is based on morphology and histochemical staining and can be L1, L2, or L3 subtypes [4]. Figure 1 shows peripheral blood smear (PBS) image of healthy and ALL patients from ALL-IDB dataset [5].

Leukemia is the most common cancer developed among children (0-14 years). According to estimates, there will be 12.8% more cancer instances in 2025 than there were in 2020 [6]. Early detection and categorization of diseases including cancer, diabetes, COVID-19, and others, traditional machine learning [7], deep learning [8] and transfer learning [9] have been made a substantial contribution to the field of medical science [10]. Medical image analysis involves several steps, including image pre-processing, image segmentation, feature extraction, and classification.

Researchers have analysed PBS images for different purposes in the field of haematology.



a) Healthy patient b) ALL patient

Figure1. a) Healthy cell **b)** Lymphoblast cell (ALL_IDB dataset [5])

One of the primary purposes of analysing PBS images is segmentation and classification of white blood cell [11] for the diagnosis of blood disorder such as acute lymphoblastic leukemia (ALL) [12]. Most popular databases for leukemia diagnosis are ALL_IDB [5] and C-NMC [13]. Other reason is analysis of platelets for malaria diagnosis [14] for that MP-IDB dataset [15] is publicly available. The expert haematologists are required to manually segment the specific cells, which is very tedious and time-consuming job. The accuracy of this manual process directly impacts the medical disease diagnosis and influences doctors' treatment decisions. However, segmenting and classifying white blood cells remains challenging task.

Objective

- We propose precise and efficient segmentation method for segmentation of lymphoblast cells from Peripheral blood smear images.
- Segmentation performance is analysed on ALL-IDB dataset using metrics like Intersection over Union (IoU), Dice similarity coefficient (DSC) and Structural Similarity Index Measure (SSIM).
- With our proposed methodology of segmentation, we provide the optimized value of k to be used in future research for similar application.
- Deep learning-based CNN model is developed for ALL detection and classification into its subtypes L1, L2 and L3
- Model performance is evaluated and compared with existing models on the same dataset

Our work is structured into five sections. Section II provide an overview of related studies on various methods employed by researchers for segmentation and classification of white blood cells. Section III outlines the proposed methodology. Section IV presents the results, discussion and comparison with other state-of-the-at approaches. Finally, section V concludes the manuscript.

2. Related work

White blood cell (WBC) analysis includes cell segmentation followed by feature extraction and classification. Depending on dataset some datasets are already segmented no need to go for segmentation phase like C_NMC_19 or ALL_IDB2 dataset. The segmentation process retains only the area of interest, and all other image components are made part of the background. Segmentation of blood cells in peripheral blood smear (PBS) images is a critical task and plays very important role in improving diagnostic accuracy. WBC is segmented into three different regions: a) nucleus region, b) cytoplasm region, and c) cell region (nucleus and cytoplasm). There are different traditional image processing and machine learning approaches employed by researchers for segmenting blood smear images including thresholding clustering, edge-based, and transform-based. However, threshold-based segmentation methods are used by most researchers [16]. Moreover, k-means and Otsu's methods are used extensively to segment WBC nuclei [17].

Feature extraction consists of extracting features such as texture features, edges, shape features and color features. Feature selection step includes well known algorithms like principal component analysis, chi-squared techniques, etc. It decreases the dimension of extracted feature vectors as well as it also decreases any kind of post-processing time. Finally, classification step, binary classification or multiclassification depending on application [18]. In 2020, Banik et al. introduced novel automated method for WBC classification using two step approach, first color space conversion and k-means based nucleus segmentation, second CNN based classification. Model is evaluated on publicly available BCCD dataset and achieved overall

accuracy of 96%. In this study, the features from the first and last layers were combined to enhance the model performance [19].

Shafique *et al*. (2018), proposed method for detecting ALL and classifying its subtypes L1, L2 and L3 using pretrained deep CNNs. However, it highlighted the challenged posed by domain difference between pretrained datasets (ImageNet) and medical images [20]. Bouchet *et al.* (2020), proposed a new method leukocytes segmentation in Color images based on fuzzy sets algorithm. This approach is particularly effective for handling overlapping cells and varying illumination condition in microscopic images. The proposed model tested on Cella Vision dataset for segmentation and classification of WBC, achieved 99.32% accuracy [21].

Khandekar *et al.* (2021), focuses on an automated system to detect and classify blast cells from microscopic images for diagnosing acute lymphoblastic leukemia (ALL). Using ALL_IDB1 and C_NMC_2019 datasets, the object detection model YOLO4 was trained and evaluated. The C_NMC_2019 dataset has a mean average precision (mAP) of 98.7%, whereas the ALL-IDB1 dataset had a mAP of 96.06% [22].

Deep network model is proposed by Saleem *et al.* (2021) for accurate segmentation and classification of lleukemia cell. The morphological operations based on color thresholding with the deep semantic method are utilized for leukemia cell segmentation. Features are extracted with pretrained model i.e DarkNet-53 and ShufeNet. The semantic segmentation achieved 99.10% and 98.60% for average and global accuracy respectively [23].

Alharbi *et al.* (2022), implemented combination of convolutional neural network (CNN) based ResNet and UNET architecture to effectively segment and classify white blood cells (WBCs). The overall segmentation accuracy of the proposed model was around 96% which was evaluated on across different datasets [24].

Kadry *et.al.* (2022) presented various CNN-based segmentation schemes, such as SegNet, U-Net, and VGG-UNet for WBC segmentation. The authors aim to identify effective CNN scheme for accurate leucocyte segmentation. Study examine and compares the performance of multiple CNN models and concluded that VGG-UNet perform better among all with accuracy 97.73% [25].

Revanda *et al.* (2022), develop a novel approach to improve classification of acute lymphoblastic leukemia (ALL) by leveraging instance segmentation using Mask R-CNN. This approach allows precise detection and segmentation of individual leukemia cell from microscopic images. The results indicate that Mask R-CNN could accurately segment and classify ALL on local dataset with 83.72 % accuracy, 85.17 % precision, and 81.61 % sensitivity [26]. Chen *et al.* (2022) explores the application of deep learning techniques for real time detection of leukemia cells in microscopic images. YOLO5, single stage detector is used for leukemia cell detection. Model is evaluated on ALL-IDB dataset, achieved accuracy of 97.2% [27].

Das *et al.* (2022), introduces deep transfer learning-based method for detecting and classifying leukemia cell. ResNet18 is modified for feature extraction by incorporating optimized orthogonal softmax layer-based classification. Model evaluated on publicly available dataset. The simulation results indicate that the proposed ResNetOSL achieves excellent performance and is faster than other state-of-the-art models [28].

Devi *et al.* (2023), highlights the potential of combining image processing method with machine learning. The authors utilize Gaussian blurring to reduce noise in the microscopic images. HSV technique, being based on simple Color threshold employed for segmentation [29 30]. HSV thresholding limited in its ability to adapt the variations in hue and intensity, which are common in stained images.

Rao *et al.* (2023) prosed computationally efficient deep learning framework for the segmentation and classification of WBCs. The PSP-net based network is used to separate the WBC nucleus from the blood smear image. The shufflenetV2 based network is implemented to classify the WBC into five classes: monocytes, basophils, eosinophils, neutrophils, and lymphocytes. The study faced the problem like inter class similarity, limited labelled data. Raabin-WBC and BCCD datasets are used for performance evaluation achieves 99.19% and 99% accuracy respectively [31]. MoradiAmin *et al.* (2024), developed a novel convolution neural network for automatic classification of ALL cells and the lymphocyte subtype. The study demonstrated the promising result, while addressing the challenge with variations in cell morphology [32].

In the literature, the majority of studies focuses on detecting acute lymphoblastic leukemia. Relatively few addressed the classification of subtype (L1, L2 and L3). Precise segmentation of blasted cell from peripheral blood smear (PBS) images is challenging due to the lack of labelled data in target domain, noisy images and morphological similarity between different cell subtypes. The creation of labelled data requires extensive manual annotation by experts, which is time-consuming and expensive. This limitation can be effectively addressed by using semi-supervised or unsupervised techniques. Traditional machine learning and deep learning-based segmentation techniques have been widely used for segmentation. However deep learning-based models often rely on pre-trained architectures, trained on large-scale datasets like ImageNet, which differ significantly from medical datasets, such as microscopic images. This domain gap leads to reduced efficiency particularly

for unseen images. Unsupervised machine learning approaches, such as clustering algorithms are particularly advantageous as they do not require labelled data for training and can dynamically adapt to variations in cell morphology.

3. Proposed Methodology

The proposed methodology as shown in figure 2 aims to detect and classify subtypes of acute lymphoblastic leukemia using two stage approach: precise segmentation of lymphoblast cells from peripheral blood smear images, followed by their classification. For segmentation, semi supervised approach is employed, utilizing an unsupervised k-means clustering method. The resultant segments are evaluated against corresponding ground truth images to ensure accuracy. Features are then extracted and selected from segmented images for classification, a custom CNN architecture is designed and implemented from scratch.

3.1 Dataset

We used the publicly available ALL-IDB dataset, which was further verified by experts for classes L1, L2 and L3. ALL-IDB dataset consists peripheral blood samples of normal individuals and ALL patients. The ALL- IDB1 consists of 108 images and ALL-IDB2 consists of 260. Figure 3 shows normal and blasted lymphocyte found in ALL patients. Three types of blast are found in ALL patients L1, L2 and L3 blast. L1 type cells are usually small in size and having homogeneous blast. They are of similar shape with little cytoplasm, nucleus is round and well structured. L2 cells are large and heterogeneous blast. The nucleus is irregular in shape. The volume of cytoplasm is variable, but often abundant and may contain vacuoles. L3 blasts are moderately large and have a round or oval nucleus. The volume of cytoplasm is fair with prominent vacuoles [5].

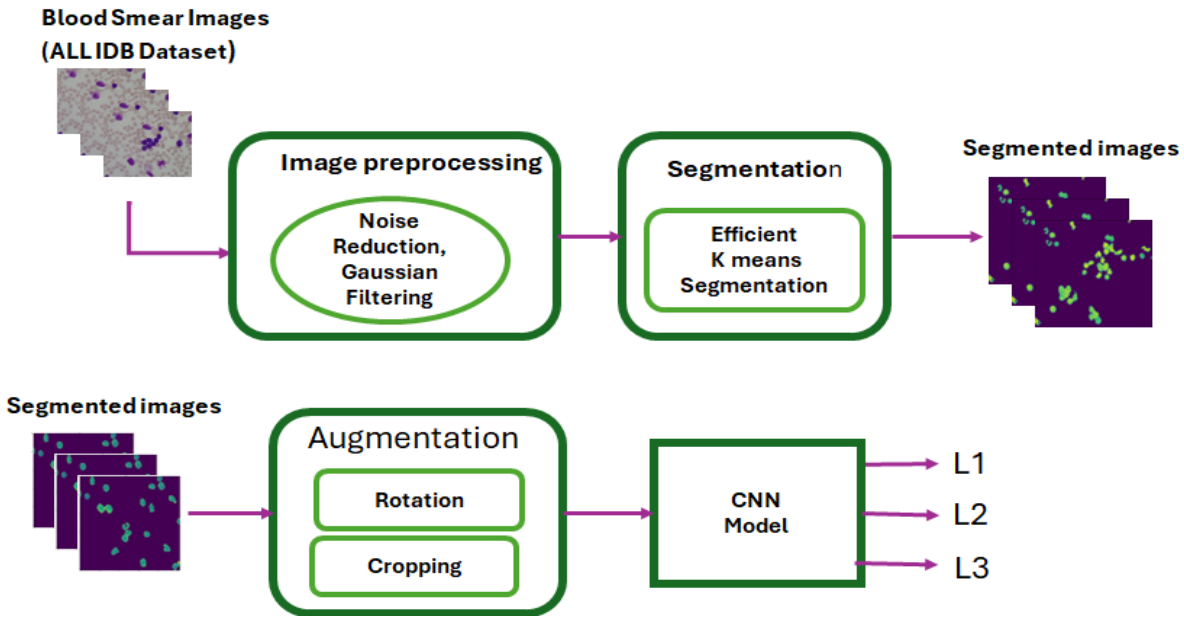


Figure 2. Proposed architecture for segmentation and classification of lymphoblast cell

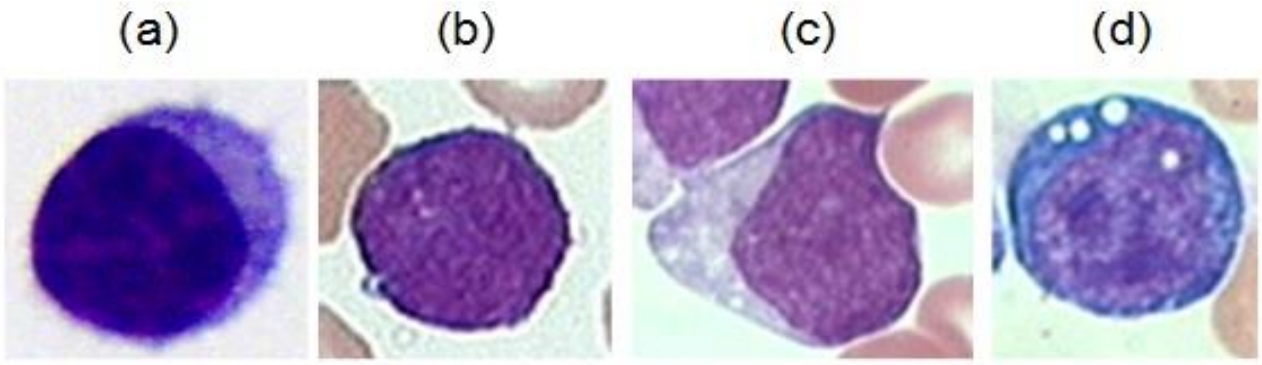


Figure 3. a. Healthy cell, **b.** L1, **c.** L2, **d.** L3 (ALL_IDB Dataset).

3.2 Preprocessing and Segmentation

The images in the dataset contain certain regions that have been colored blue which represent the ALL blasts in that image. Apart from that the other uncolored regions are of less significance. The images have a lot of noise and unwanted information which will not contribute to the classification and needs to be refurbished. Since blue colored regions are more important than the rest of the image, uncolored parts of the image which contribute to the noise should be given less intensity or importance so that the important parts of the image get highlighted. For achieving this, we made use of Gaussian Filtering technique to blur the image. Gaussian Filtering or Blur- ring applies a mathematical function to the image to blur certain parts of it. This reduced the noise in the image making it more suitable for further processing. We use GaussianBlur function of OpenCV with kernel size 5x5, setting standard deviation, $\sigma = 0$ we are instructing OpenCV to automatically compute standard deviation σ based on our kernel size [29].

$$G(x,y) = \frac{1}{2\pi\sigma} e^{\frac{x^2+y^2}{2\sigma^2}} \quad (1)$$

The k-means algorithm is applied as an unsupervised approach for lymphocyte segmentation, with the number of clusters serving as a key hyperparameter. This determines the number of segments into which the image is divided to achieve effective separation. Various values of *k*, ranging from *2* to *6*, are used. Clusters are utilized as masks and applied to original images to segment it effectively. This process helps in localization and identification of regions of interest. *SSIM, DSC & IoU* [33-35] is used to evaluate the similarity between the predicted segment (*x*) and the ground truth image(*y*). SSIM focuses on the structural similarity between the image *x* and *y.* DSC and IoU evaluates the overlap between the image *x* and *y,* IoU is a strict measure of overlap. Each metrics addresses different aspects of segmentation quality. Algorithm1 demonstrates the steps for finding precise segmentation using k-means algorithm.

$$ssim(x,y) = \left(\frac{(2\mu_x\mu_y+C1)\left((2\sigma_{xy}+C2)\right)}{(\mu_x{}^2+\mu_y{}^2+C1)(\sigma_x{}^2+\sigma_y{}^2+C2)}\right) \quad (2)$$

$$DSC = \frac{2*|x\cap y|}{|x|+|y|} \quad (3)$$

$$IoU = \frac{|x\cap y|}{|x\cup y|} \quad (4)$$

where μ_x *and* μ_y *are the means of* x *&*y, $\sigma_x{}^2$ *and* $\sigma_y{}^2$ *are the variances of* x *&* y,

σ_{xy} *is the covariance between* x *&*y, *C1 and C2 are constants.*

Algorithm 1. Steps to find precise and accurate segmentation

input→input ALL image ,corresponding ground truth image

step 1→preprocess input image,noise removal using equation 1

step2→define evalution funcion to compute SSIM, DSC and IoU using equation 2,3 and 4

step3 →create function that compute average of ssim, dsc and IoU

step4→define range of k (0 to 6)

step5→for each k defined in the range

step6→apply k-means clustering to generate k segments

step7→for each segment

step8→call the evaluation function to compute the SSIM, DSC, IoU and average score of the current segmentation against the ground truth image

step9→track the best segmentation by choosing highest average score

step10→return highest average score for given k

step11→return the segment having heighest score among all k

The above algorithm iterates over different values of *k* from 0 to 6, for each value of *k, k* segments are generated using unsupervised k-means clustering algorithm. Resultant segments are evaluated against the corresponding ground truth image using metrics like SSIM, DSC and IoU. Algorithm return the segment having highest average score for given k. We input peripheral blood smear image of ALL patient along with its corresponding ground truth image and applied k means by setting *np.random.seed (42)* for consistent result. We have demonstrated one sample case from class L2 image, the original input image and its ground truth image shown in fig4 a. Step by step segmentation result of same image along with their *ssim, DSC and IoU score* depicted in fig 4b to 4f. Algorithm returns the highest average score for every value of *k* [0,1,2… 6], along with this it also returns precise segment as first segment when *k=4* that achieves the highest average score 0.6505.

Images belonging to each class L1, L2 and L3 are segmented with varying parameter k and each image is evaluated against its corresponding ground truth image to return the best segment along with highest score at given k. Optimized *'k'* is one at which we achieve precise segmentation, can be calculated for future research purpose, if researchers want to segment the images without investigation of parameter *k* using k means algorithm.

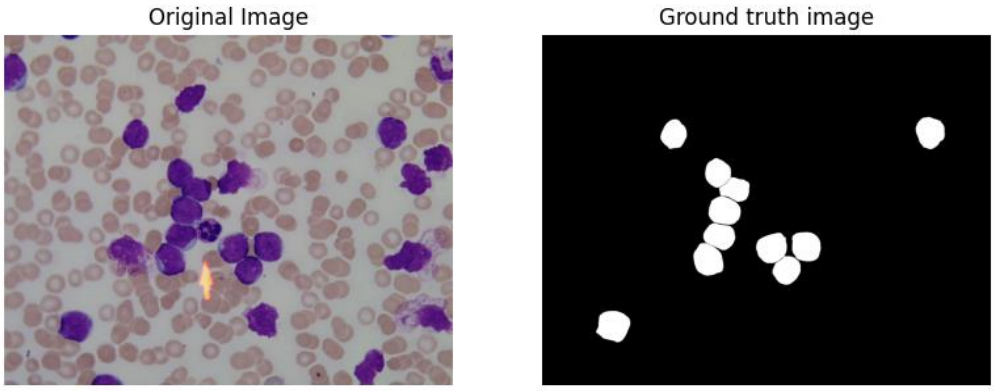


Figure4 (a). Input image and its corresponding ground truth image (ALL-IDB dataset)

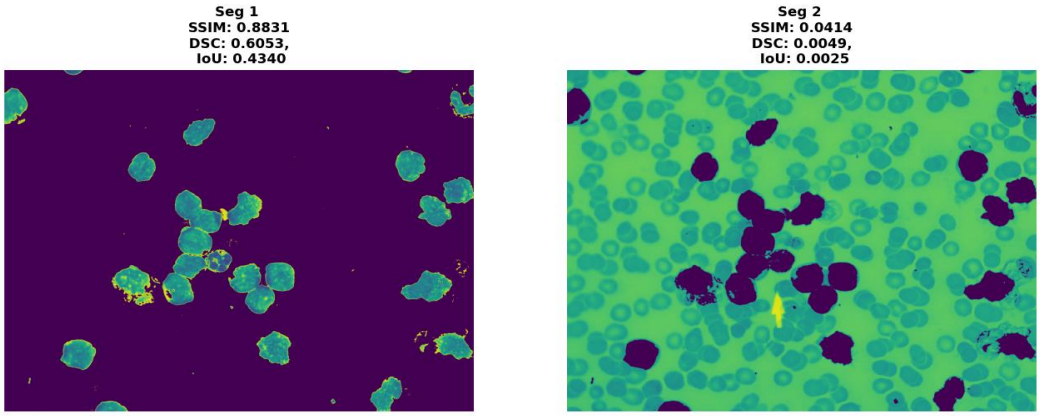


Figure4 (b) k-means segmentation, k=2

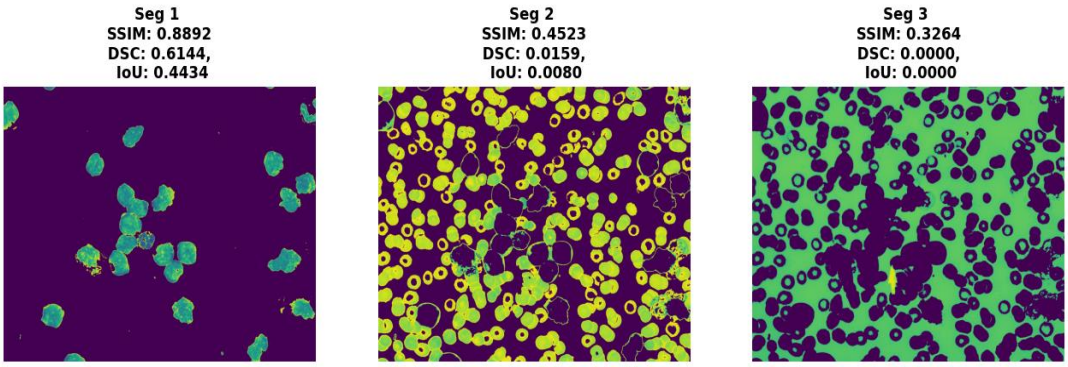


Figure4 (c) k-means segmentations, k=3

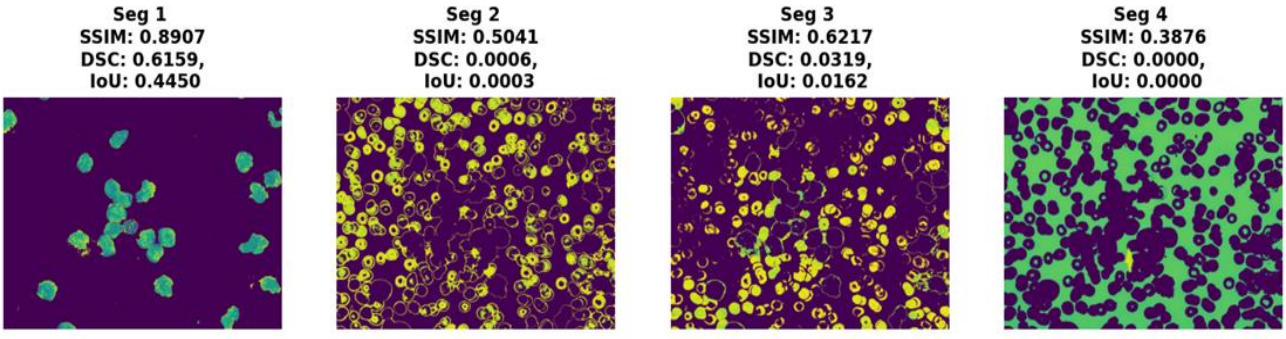


Figure4 (d) K-means segmentations, k=4

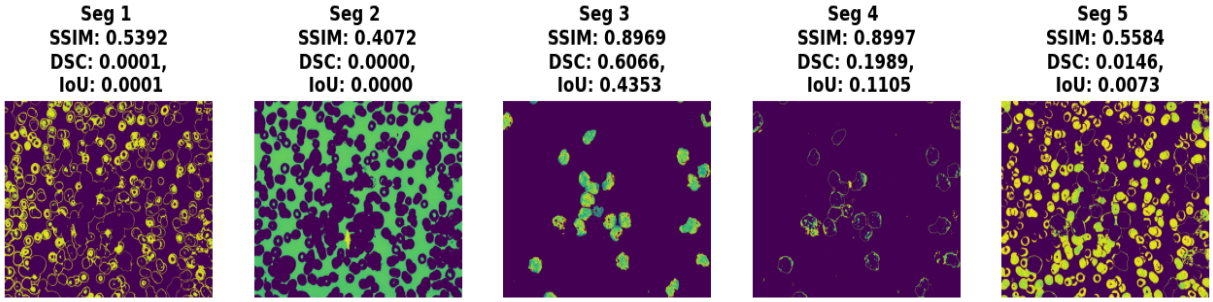


Figure4 (e) K-means segmentations, k=5

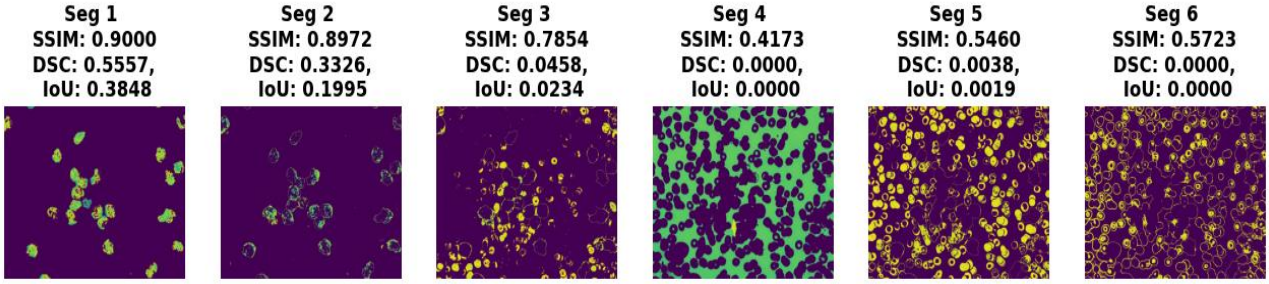


Figure4 (f) K-means segmentations, k=6

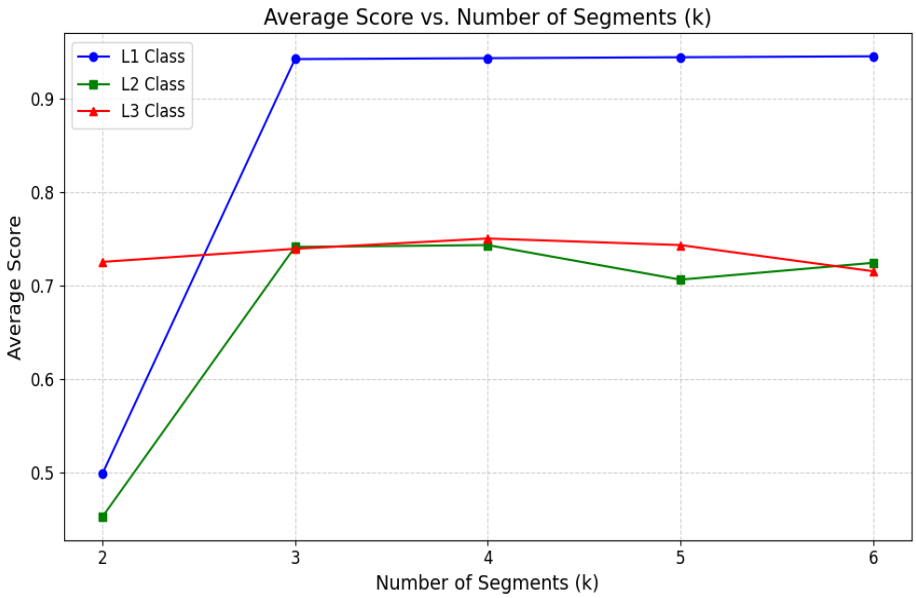


Figure 5. Class wise average score for given k [0 to 6]

Table 1. Average score for k (0 to 6) for L1 class

k	***Average score***
2	0.498
3	0.942
4	0.943
5	0.944
6	0.945

Table 2. Average score for k (0 to 6) for L2 class

k	*Average score*
2	0.452
3	0.741
4	0.743
5	0.706
6	0.724

Table 3. Average score for k (0 to 6) for L3 class

k	*Average score*
2	0.725
3	0.739
4	0.750
5	0.743
6	0.715

To compute optimized value of *k*, class wise score is prepared by averaging returned score for each image at corresponding *k*. Average scores of images from class L1, L2 and L3 is shown in table1, 2 and 3 respectively. From the graph shown in fig 5, precise segmentation can be archived when we chose *k*>=3. Since *k*=3 and *k*=4, approximately yield the same score that separates the most optimal region of interest. We could choose either but selecting the lower *k i*.e. *k*=3 might be preferable for simplicity and potentially reduce the computational complexity.

3.3 Classification using customized CNN

The next step after image segmentation is classification. For classification purpose, we have used a DL based convolutional neural network model shown in figure 6, consisting of total of 8 hidden layers. For feature extraction and selection, we use convolution layer and max pooling layer. We tried several different configurations of the CNN model and came up with the current model that has given the best performance. The input to the convolution layer is a normalized segmented blood smear image having dimension 256 x 256.

The first layer, a convolutional layer with 32 channels that can identify certain patterns in the image, is explained in table 4. In order to save space and minimize calculations, the second layer, a max pooling layer of dimension 2 x 2, replaces the entire region with the maximum value in that region. - Another 64-channel convolutional layer makes up the third layer, while a max pooling layer makes up the fourth. Fifth layer is a flattening layer to flatten multidimensional input to one dimensional for the fully connected layers to process. The sixth and seventh layers are fully connected layers with 196 and 96 neurons respectively and used for processing and learning. The final layer is a softmax layer having 3 neurons corresponding to the 3 categories which we have. It will output the probability of the input image belonging to a particular class. The input image will be classified into 3 categories L1, L2 and L3 which are the stages of ALL. For ALL detection we change final layer to two classes.

Table 4. Architecture details of customized CNN model

Layer	Output shape
Conv2D layer 1	(None, 255 255 32)
Max pooling-1	(None, 128 128 32)
Conv2D layer 2	(None, 125 125 64)
Max pooling-2	(None, 62 62 64)
Dense layer 1	(0,196)
Dense layer 2	(0 96)
Output layer	Softmax layer

4. Experimental Result and Model Evaluation

For acute lymphoblastic leukemia detection, the model was trained and tested using 108 images, including both normal and ALL patients. To build the model for subtype classification, images are divided into three classes resulting in a small dataset that affects model performance.

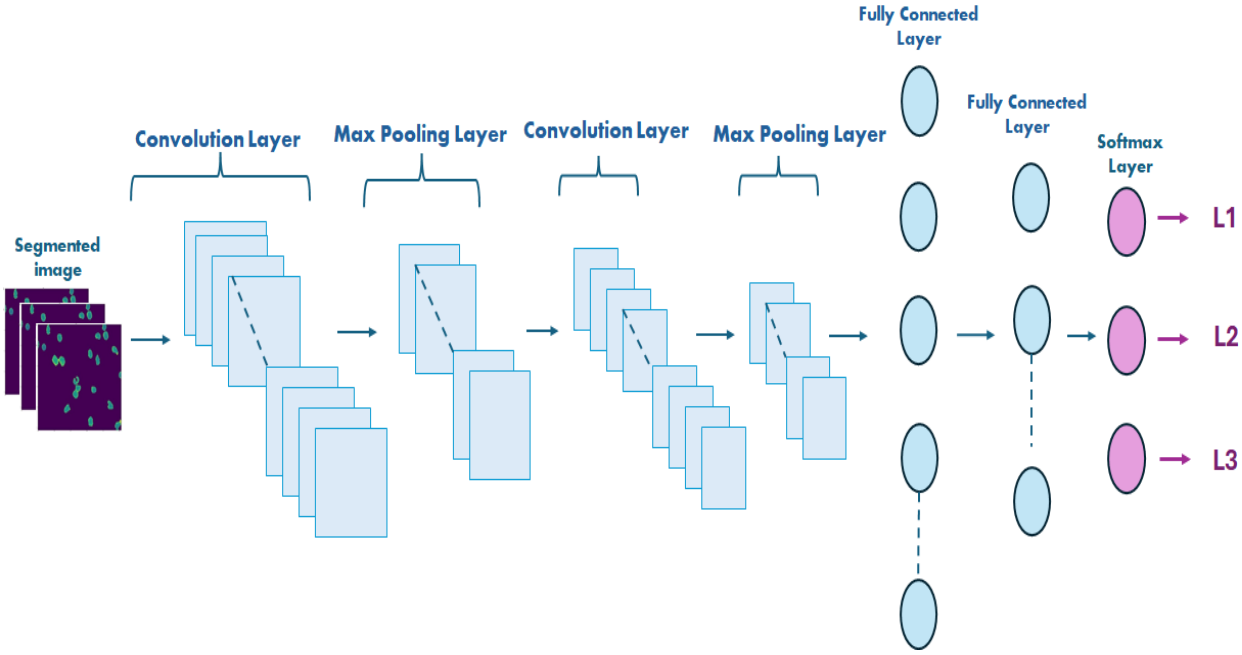


Figure 6. Customized CNN architecture for multiclassification

Table 5. Dataset split for subtype classification

Data categories	L1	L2	L3	TOTAL
Training	150	150	150	450
Testing	42	44	23	109
Validation split	0.2			

Data augmentation techniques are especially valuable when the data is limited, can greatly improve the performance of the model by increasing the diversity of the dataset. Applied augmented technique includes variations like rotations (with angle 90, 180 and 270), cropping, which makes the model more robust to variations it might encounter in real-world scenarios. Following the data augmentation, the model is trained and tested on augmented data comprised 559 images. Table 5 illustrates the distribution across different classes used for training and testing.

We incorporated batch normalization, L2 regularization, and early stopping to avoid overfitting. Figure 7. Display the training vs. validation accuracy and loss plotted against the number of epochs. Training loss steadily decreases, indicating the model has learned the training data well. In figure 7b. Spike in validation loss indicates that initially model struggle to distinguish between different classes

To evaluate the model's performance, metrics such as accuracy, precision, recall, and F1-score—which are calculated using equations 5 to 8—are employed. Precision is defined as precisely predicted positive samples divided by all projected positive samples. Recall is defined as precisely anticipated positive samples divided by actual positive samples. The F1score can be defined as the harmonic mean of precision and recall.

$$Precision = \frac{\text{True Positive}}{(\text{True Positive}+\text{False positive})} \quad (5)$$

$$Recall = \frac{\text{True Positive}}{(\text{True Positive}+\text{False Negative})} \quad (6)$$

$$F1 = 2 * \frac{\text{Precision}*\text{Recall}}{(\text{Precision}+\text{Recall})} \quad (7)$$

$$Accuracy = \frac{\text{True Positive}+\text{True Negative}}{(\text{True Positive}+\text{True Negative}+\text{False Positive}+\text{False Negative})} \quad (8)$$

Figure 8 shows confusion matrix, performance metrics of suggested models on ALL-IDB dataset including precision, recall, f1-score demonstrated in table 6. The model is slightly less precise for class L2. A slight drop in recall for class L3, which leads to lower F1 score. Our approach demonstrates perfect performance for class L1, while performance for classes L2 and L3 is slightly lower, possibly due to inter-class similarity. However, overall accuracy is 99% which indicates the model performs exceptionally well. Macro averaging gives equal weight to each class and weighted averaging accounts for support i.e. no. of true instances.

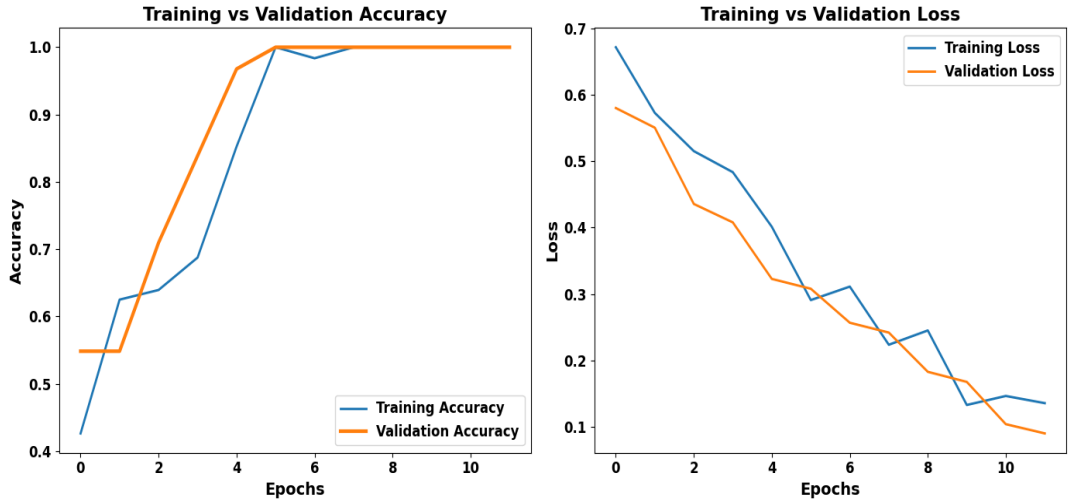


Figure 7a. Training vs validation Accuracy and Loss (ALL detection)

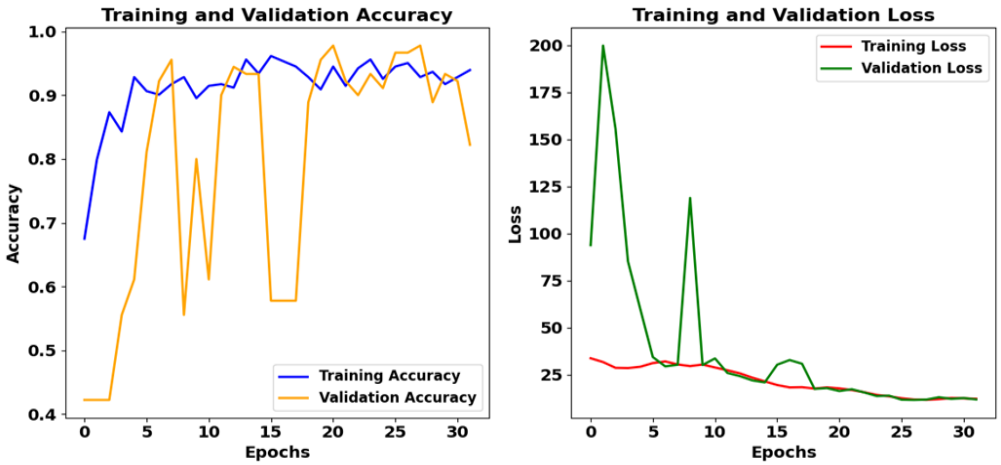


Figure 7b. Training vs validation Accuracy and Loss (Subtype classification)

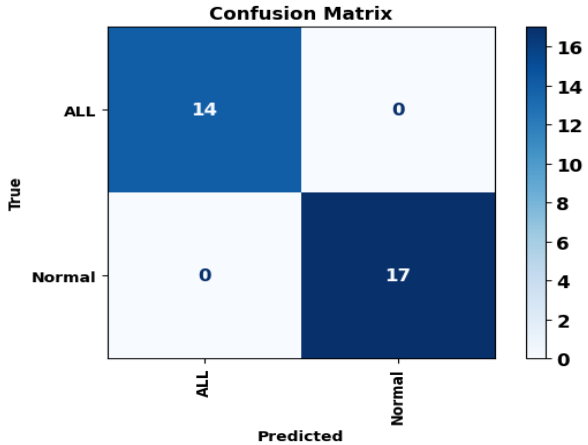


Figure 8a. Confusion matrix (ALL detection)

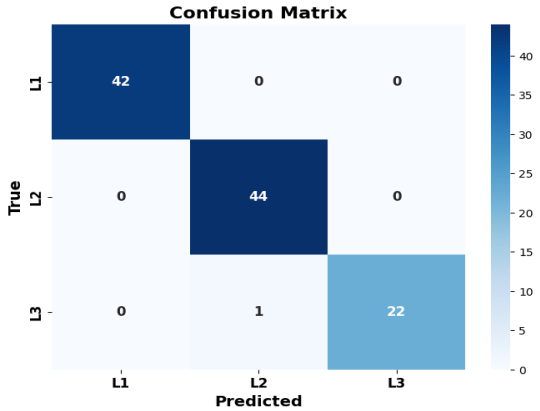


Figure 8b. Confusion matrix (Subtype classification)

Table 6a. Model performance on ALL IDB dataset (ALL detection)

	Precision	Recall	F1-score
ALL	1.00	1.00	1.00
Normal	1.00	1.00	1.00

Table 6b. Model performance on ALL IDB dataset (Subtype classification**)**

	Precision	**Recall**	**F1-score**
L1	1.00	1.00	1.00
L2	0.98	1.00	0.99
L2	1.00	0.96	0.98

Table 7. Classification accuracy comparison with existing model

Author	**Aim**	**Methodology**	**Accuracy**
Shafique *et al.* [20] (2018)	ALL Detection & Subtype classification	Deep CNN using AlexNet	99.5% 96.06%
Das *et al*. [35] (2020)	ALL detection	K-means, SVM	96.00 %
Rahman *et al.* [30] (2021)	ALL Subtype Classification	Threshold based segmentation using HSV color space.	96.8%
Khandekar *et al.* [22] (2021)	ALL detection	YOLO 4	96.06 %
Abed *et al.* [36] (2022)	ALL detection	DenseNet 169	98.93%
Revanda *et.al*.[26] (2022)	ALL subtype classification	Mask R-CNN	83.72%
Devi *et al.* [29] (2023)	ALL Detection	HSV Color space.	95.45%
Ahmed *et al*. [3] (2023)	ALL detection	CNN Model with RF classifiers and XGBoost	98.8%
Moradi Amin *et al.* [32] (2024)	Leukemia Subtype classification	Fuzzy C-means clustering, CNN	97%
Al-Bashir *et al.* [37] (2024)	ALL detection	CNN-based algorithms	99.98%
Proposed Model	ALL detection & Subtype classification	Efficient K-means, CNN	100% 99%

Table 7 represents the comparative analysis of ALL detection and its subtype classification accuracy between the proposed model and existing approaches.

Figure 8 shows confusion matrix, performance metrics of suggested models on ALL-IDB dataset including precision, recall, f1-score demonstrated in table 6. The model is slightly less precise for class L2.

A slight drop in recall for class L3, which leads to lower F1 score. Our approach demonstrates perfect performance for class L1, while performance for classes L2 and L3 is slightly lower, possibly due to inter-class similarity. However, overall accuracy is 99% which indicates the model performs exceptionally well. Macro averaging gives equal weight to each class and weighted averaging accounts for support i.e. no. of true instances. Table 7 represents the comparative analysis of ALL detection and its subtype classification accuracy between the proposed model and existing approaches.

5. Conclusion

An effective automated method for identifying and classifying lymphoblast cells into their L1, L2, and L3 subtypes was presented in this work. The use of unsupervised k-means clustering for segmentation, where the parameter k is tuned based on segmentation quality, is a crucial component of the suggested approach. Our approach identified the optimized value of k, eliminating the need for researchers to rely on trial and error for similar applications. The segment with the highest average scores of SSIM, DSC and IoU is chosen, ensuring improved segmentation reliability and significantly contributing to the total accuracy of the model. The model demonstrated exceptional performance, achieving 100% overall accuracy for ALL detection and 99% for their subtype categorization. The F1-scores for classes L1, L2, and L3 were 100%, 99%, and 98%, respectively, highlights its effectiveness and reliability. This high accuracy and precision suggest that the model could be an effective tool to support medical experts in ALL detection and subtype classification.

Future research will involve evaluating model on more diverse and larger datasets to assess its generalization. Additionally, researchers can apply the same approach for diagnosis of other types of leukemia.

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Data Availability

The data supporting the findings of this study can be obtained from the corresponding author upon reasonable request.

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Yes