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Acute lymphocytic leukemia detection using hybrid deep learning models

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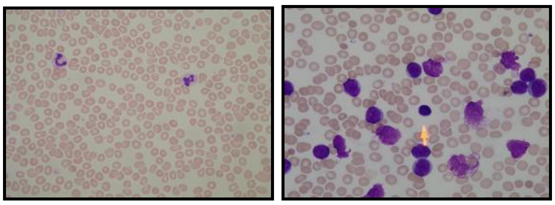
Abstract
Acute Lymphocytic Leukemia is a type of cancer that affects white blood cells and it spreads quickly. This study proposes a computer-aided diagnosis system to detect this type of leukemia from blood microscopic images. We introduce a hybrid machine learning model that uses a ResNet18 encoder to extract latent embeddings from the multi-otsu segmented white blood cells and we feed those embeddings into machine learning classifiers. The random forest and the k-nearest neighbours recorded the best classification accuracy i.e. 98% while misclassifying two samples from the ALL-IDB dataset.

Keywords: Acute lymphocytic Leukemia, deep learning, hybrid CNNs, CADx

Introduction
According to [1], Acute Lymphocytic Leukemia (ALL) is a type of cancer in which the bone marrow makes a large amount of white blood cells specifically lymphocytes.
This study proposed a deep learning hybrid model to detect ALL from blood microscopic images. We fist segment the input image by using multi-otsu thresholding [2] and we only keep the white blood cells. The region of interests (ROI) are fed into a feature extractor, in this case we use a ResNet18 [3] encoder. To predict the label of each image, we input the resulting embeddings into machine learning classifiers i.e. random forest [4] (RF), support vector machines [5] (SVM), and k-nearest neighbours [6] (KNN).
Arif *et al.* [7] used the AlexNet state-of-the-art convolutional neural network model to classify microscopic images from ALL-IDB dataset. This study used filtration and augmentation to pre-process input images. Khandekar *et al.* [8] used Yolov4 object detection model to detect and classify white blood cells as either lymphocyte or normal. Sulaiman *et al.* [9] used hybrid models to classify cells from CNMC dataset. They concluded that the combination of ResNet50 feature extractor, RF as a feature selection technique, and the SVM classifier yields the best performance. Mohamed *et al.* [10] used the watershed algorithm and optimal thresholding to segment white blood cells from microscopic images. Lu *et al.* [11] introduced a WBC-Net which is inspired by the ResNet and the UNet++ models. This study used four Leukemia datasets to train the fully convolutional network to segment white blood cells.

Dataset
ALL-IDB 1 dataset [12] is a publicly available dataset that contains 108 blood microscopic images. 49 images are taken from patient having ALL disease and 59 images labelled as normal. In total, there are 510 lymphocyte labelled by expert oncologists.



(a) (b)

Fig 1: (a) is a normal blood microscopic image and (b) is a blood microscopic image from a patient suffering from ALL.

Materials and Methods

To segment the white blood cells, we used multi-otsu thresholding methods. As shown in Figure 2, when we plot the histogram of a microscopic blood images sample, we notice that there are 3 peaks i.e. The first one is for white blood cells, the second one is for red blood cells, and the third one represents the background. We generate a mask by thresholding the input image using the threshold value representing the first peak.

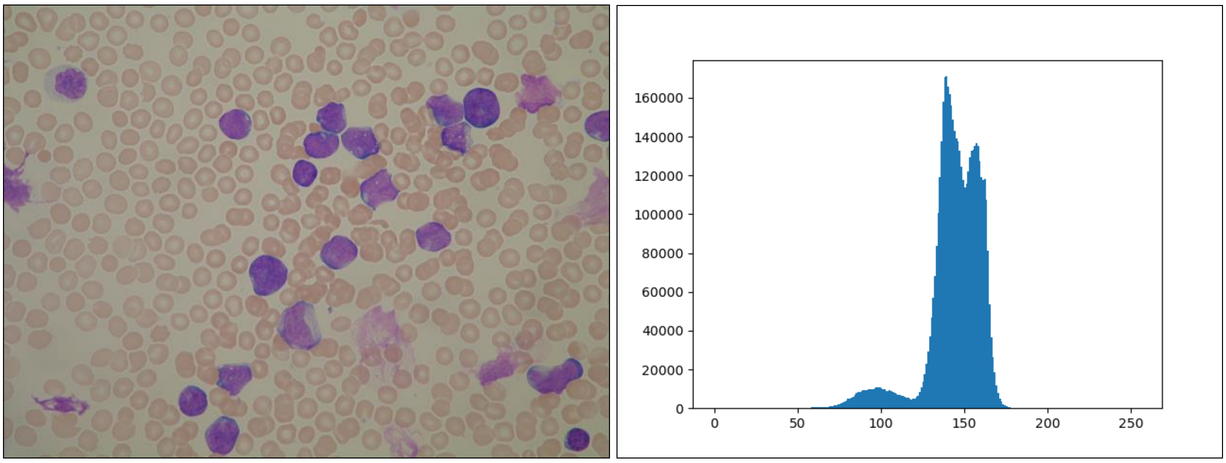


Fig 2: A blood microscopic image and its associated pixel frequency histogram

As shown in Figure 3, we use the ROI extracted from the segmentation step to train a ResNet18 model to extract latent embeddings of size 512. Then, we feed the resulting embeddings into machine learning classifiers i.e. RF, KNN, and SVM with a radial basis function. We use 5-fold cross validation to train the classifier and, to train the ResNet18 model, we use the cross-entropy loss function, an adam optimizer, and 1e-4 learning rate.

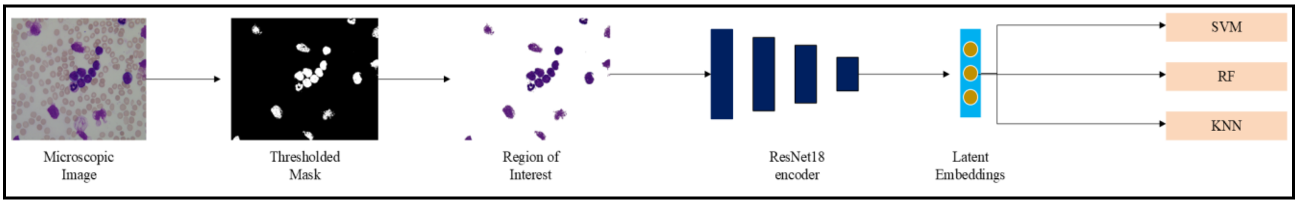


Fig 3. The proposed machine learning pipeline to segment and classify blood microscopic images.

As evaluation metrics, we used the accuracy, the precision, the recall, and the confusion matrix.

Results and Discussion

During this study, we use pytorch and scikit-learn libraries to implement the machine learning models.

Table 1 shows the recorded results using the proposed machine learning classifiers. Both the SVM and the KNN models recorded 98% accuracy while misclassifying two samples from a total of 108 images.

Table 1: The recorded classification results of the proposed machine learning models

Model	Backbone	Accuracy	Precision	Recall
SVM	ResNet18	0.97	0.96	0.96
KNN	ResNet18	0.98	0.98	0.98
RF	ResNet18	0.98	0.98	0.98

Figure 4 shows the confusion matrix of the RF model. The model manages to classify all samples correctly except for two images from a patient suffering from ALL.

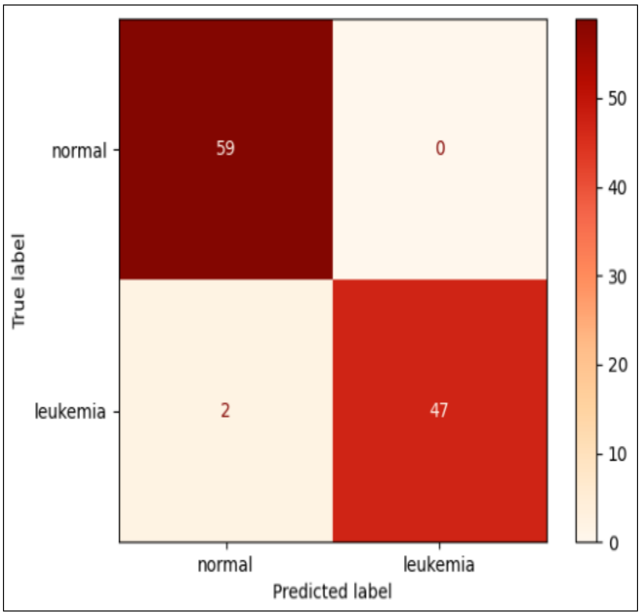


Fig 4: The confusion matrix of the random forest classifier

We further investigate the reason of the false negative values and we notice that the misclassified images have few white blood cells which is common in normal images. (see Figure 5)

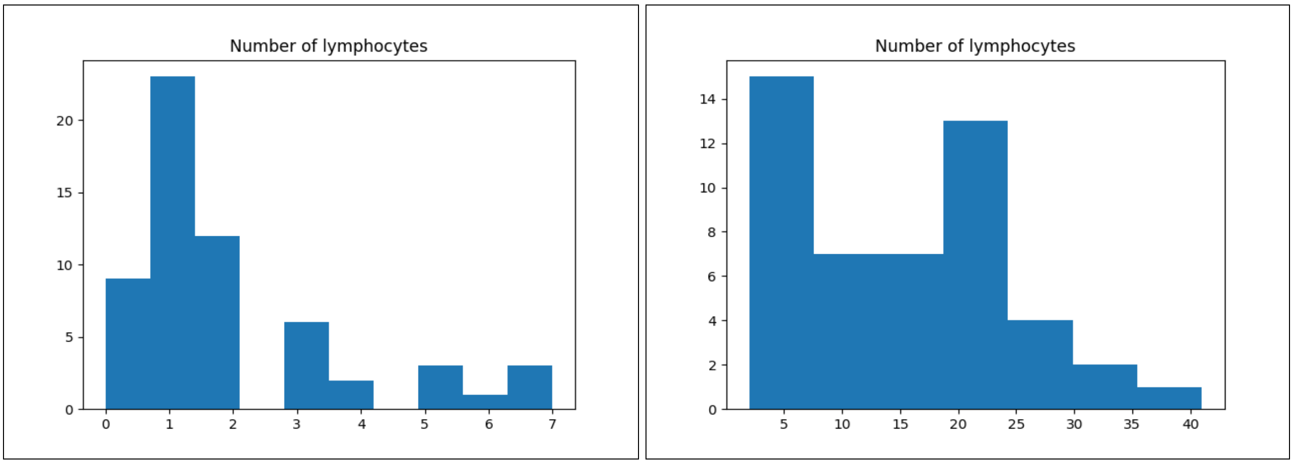


Fig 5: Histograms of the number of white blood cells in normal images and images from patients suffering from acute lymphocytic leukemia

Conclusion

This study introduces a hybrid machine learning model to detect ALL from blood microscopic images. The combination of ResNet18 and RF classifier yield the best accuracy while misclassifying only two samples. We further investigate the cause of this false positive values and we notice that the model is relying on the fact that there are few white blood cells in normal images which is not the case for microscopic images from patient suffering from ALL.

Acknowledgments

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