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A New Computerized Method of Detecting Leukemia

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Abstract

Currently, blood problems are diagnosed by looking at tiny images of blood cells. The classification of certain blood-related ailments can be aided by identifying blood abnormalities. This report describes a preliminary investigation into the development of a method for detecting leukaemia kinds using microscopic images of blood samples. Image analysis is crucial because diseases may be recognised and diagnosed more quickly. Other disease control, surveillance, and prevention methods can then be implemented.

I. INTRODUCTION

White blood cells come in a variety of shapes and sizes. Leukemia is a blood cell malignancy in which the number of immature white cells increases and these immature cells destroy other cells. Experts examine microscopic images of blood in the manual method of Leukemia identification; this is a lengthy and time-consuming process that requires specialist abilities. As a result, the correctness isn't guaranteed. The ratio of white blood cells to red blood cells in human bodies is 1000:1. It signifies that there is one white blood cell for every 1000 red blood cells. As a result, if the quantity of white blood cells in the body increases dramatically, the person will get leukaemia. There are two types of leukaemia: acute and chronic.

II. OPERATION

The automated leukemia detection system is built for experts and students to learn about how the leukemia cells are in a blood cancer sample. This system is built using python and opencv with image processing techniques. A total of 350 images were collected in order to train the machine learning model where it will classify when a test sample given is cancerous or not cancerous. The graphical user interface built will help the experts in order to visualize the cells better by segmenting the given image where the final image only consists of the cancer cells if they are present. The graphical user interface consists of operations such as selecting image to be segmented and classified, image processing tools such as enhancement of the image, grayscale conversion, smoothing the image, thresholding the image after gray scale conversion and finally classifying the image. When the user presses the classify button, a new window pops up where the segmentation process results can be seen and a message telling the user that the model has detected cancer or not. The fundamental steps taken in the implementation of this model were image acquisition, image preprocessing, image segmentation, feature extraction and classification.

A. Image Acquisition.

The images were obtained from kaggle, UCI referential and cancer image archives. A total of 370 images were obtained

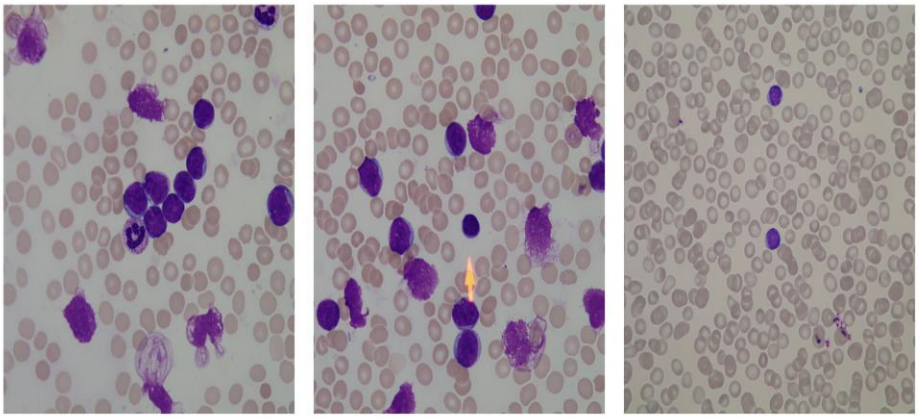

Fig 1 Sample Image

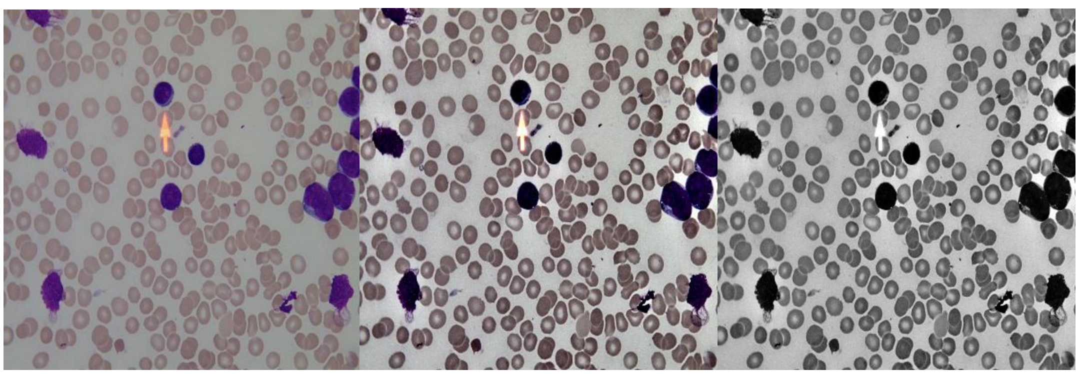

Fig 2a Normal Image ***Fig 2b Enhanced Image***

Fig 2c Grayscale Image

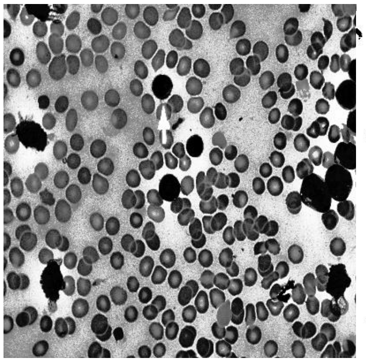

Fig 2d Histogram Equalization

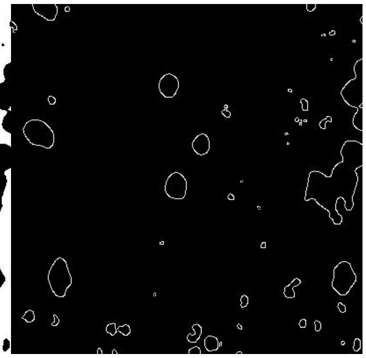

Fig 2f Canny Edge detection

Fig 2e Negative and Median Blur

Fig 2g Sobel Edge detection

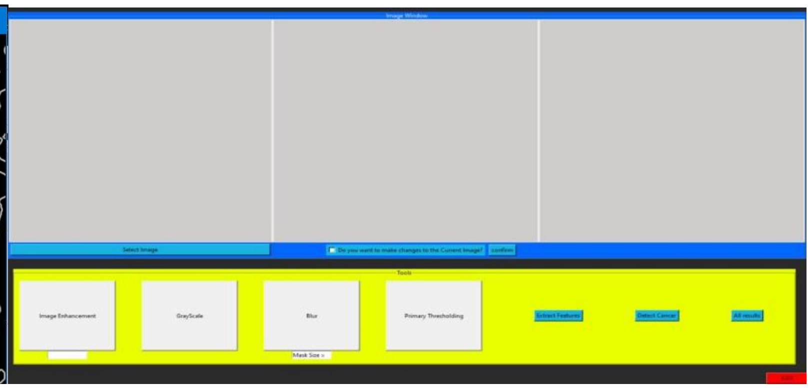

Fig 2h Graphical user interface

Image Pre-processing

The images collected needed processing such as resizing because the images were large, that is 1200x1200 pixels. The images were resized to 500X500 pixels. After resizing the images were improved using a non-photorealistic image rendering method where the results were promising for the next step in the process. The images were then converted to grayscale for methods such as thresholding and other feature extraction processes. Then the images were smoothed in order to remove any aberrations.

B. *Image Segmentation*

Image segmentation is a process in which only the ROI is extracted from the pre-processed images. In microscopic images, the area of interest (ROI) is the cells in a purple spot that are acute lymphoblastic cells. We implemented our algorithm using a bunch of filters like blur filters, accentuation filters, and morphological operations to clear the image. Blur was widely used to remove aberrant values after the last segmentation step. Two thresholding steps were performed to segment the picture. Segmentation results are white dots on the picture that are the ALL cells from which the functions are extracted.

C. Feature Extraction

Extracting functions is an important step in the classification of an image. A total of 10 features(Table 1) have been extracted when those features are statistical interpretations of images. These characteristics are then scaled using a standard scaling procedure to inform the machine learning model. The retrieved characteristics were the standard deviation and mean of all images at each stage of segmentation. Finally, the number of breath cells was calculated and this was one of the main characteristics of the classification process.

Region Mean
Region Standard deviation
Threshold Mean
Threshold Standard Deviation
Canny Mean
Canny Standard Deviation
Gaussian Mean
Gaussian Standard Deviation
Sobel Mean
Sobel Standard Deviation
White Pixel Count

Table 1 Features Extracted

D. Classification

In machine learning, classification refers to a predictive modeling problem where a class label is predicted for a given input data. Our model is a binary classification model in which the given image may be classified as cancerous or non-cancerous. A total of 3 machine learning models were used to validate the efficacy of our model a)KNN classifier, b)Support vector machine and, c)Random forest classifier. Out of three machine learning models, Random forest Classifier gave the highest accuracy.

Machine Learning Algorithm	Precision (%)	f1-Score	Accuracy
KNN Classifier	TP - 84 TN - 64	TP - 84 TN - 64	71
SVM	TP - 92 TN - 60	TP - 68 TN - 73	71
Random Forest Classifier n = 300	TP - 82 TN - 88	TP - 85 TN - 84	85

Fig 3 Different Machine learning models implemented

F. *Validation*

Initially, the data was split 80% as training and 20% as testing, for which our machine learning model gave an accuracy of 87%. Next, fifteen unseen images from another dataset were fed to the machine learning model and got 95% as our accuracy.

G. Graphical User interface

The final phase of the project involved building a front-end application so that users could use our model to easily classify leukemia. With the help of libraries like Tkinter, we built a GUI to make it user-friendly.

III. FLOWCHART OF THE BACKEND CODE.

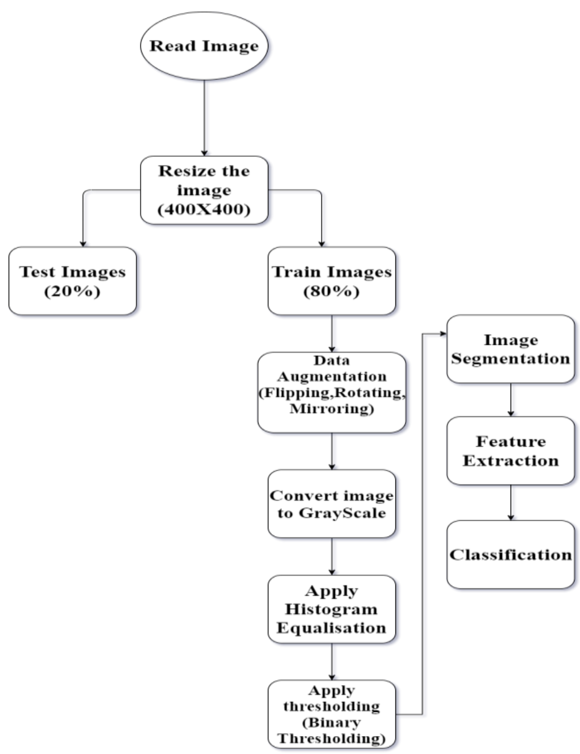

Fig 4 Flowchart

IV. THE FLOW OF WORKING.

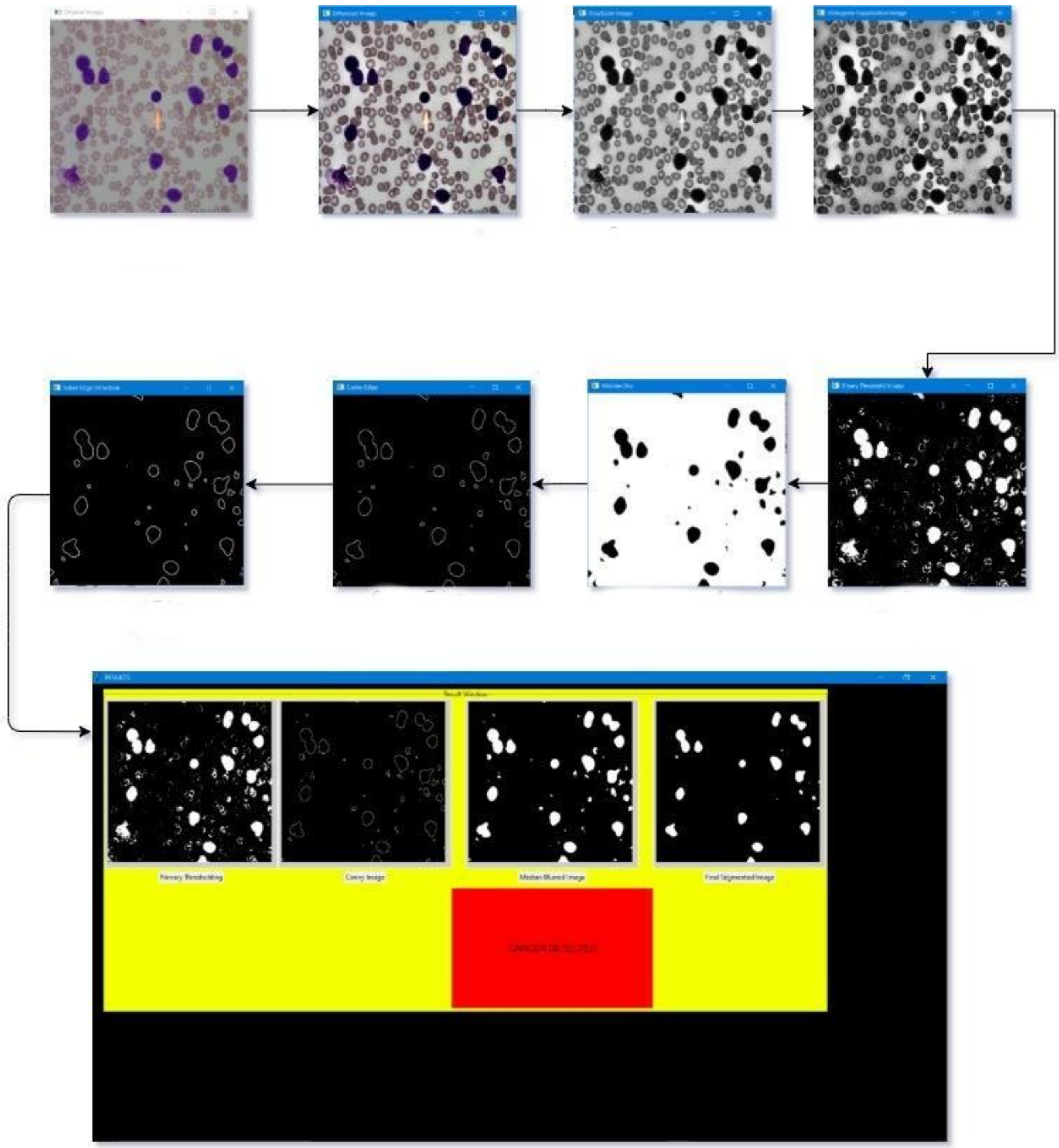

Fig 5 The flow of working

An input image that is to be tested is added to the GUI (Graphical user interface) by the user. Once the image is fed to the model a series of outputs are displayed along with the classification result.

V. RESULT

With a 92% average accuracy, 90% selectivity, and 88% sensitivity our model works perfectly when classifying test images. The graphical user interface is user-friendly and it eventually performs all the pre-processing, segmentation, and feature extraction and Classifies the image.

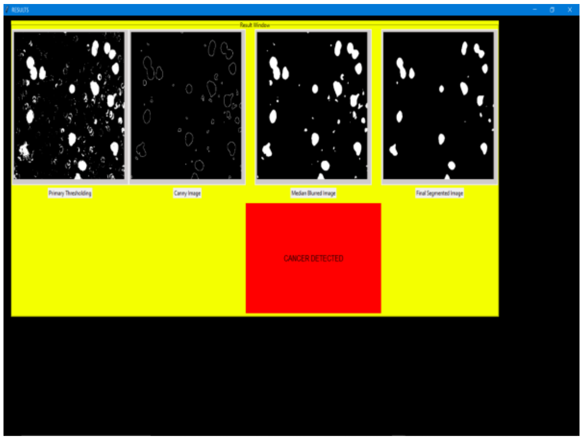

Fig 6a Cancer Detected

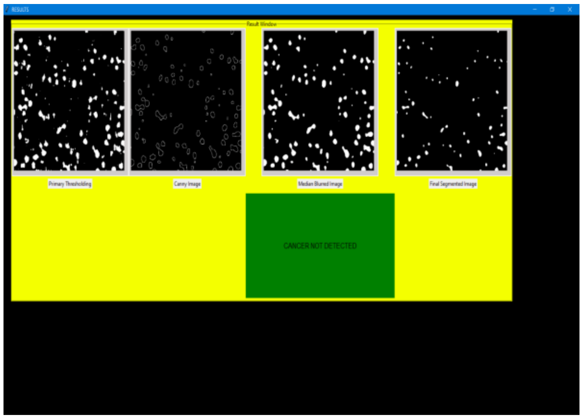

Fig 6b Cancer not Detected

VI. CONCLUSION

Leukemia is dangerous cancer that affects white blood cells and bone marrow and affects the immune system of the human organism. One of the most commonly used diagnostics is a microscopic analysis of blood cells (blood swabs). In this study, we presented a new approach to diagnosing leukemia from microscopic blood images using random forest classifiers capable of identifying cancerous or non-cancerous cells. Our model has demonstrated the capability to process a small number of image samples. As a result, 91% accuracy, 90% specificity, and 88% sensitivity for binary classification of acute lymphoblastic leukemia were achieved. We also used cross-validation in all experiments and achieved good results.

VII.APPLICATION

- User-friendly application.
- Computationally efficient software.
- Rapid results have made it possible to diagnose acute lymphoblastic leukemia.
- High-quality enhanced results.

VIII. ADVANTAGES

a)Overcomes the disadvantages of traditional diagnosis of leukemia that include CBC, bone marrow aspiration whose results take a long time to get results.
b)Our method may be one of the diagnostic methods where the doctor may consider diagnosing leukemia. c)In this method, we separate blastic and normal cells.

IX.FUTURE SCOPE

Going forward, we plan to expand our experiments using a hybrid deep learning approach using convolutional neural networks with recurrent neural networks to enhance performance. In addition, we plan to expand our dataset by adding new samples and using new data-raising techniques. We also plan to implement equipment with the aid of a microscope with a raspberry pi camera module.

X. ACKNOWLEDGEMENT

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