

Original Article

Enhanced Segmentation Algorithms for Improving Acute Lymphocytic Leukemia Diagnosis from Blood Microscopic Images

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Abstract - The application of Digital Image Processing on medical images could greatly help doctors to identify the disease in an early phase before it starts spreading. In this research work, the segmentation steps needed to find out the leukemic blood cells are being discussed and elaborating some of the important segmentation steps have been carried out. The resultant images will also be given for visual analysis. Some of the important Segmentation steps associated with the leukemic blood cell images will be given with the results. The major aim of this research work is to detect malignant leukaemia at the earliest so that it would improve the chances of survival of the patients. This research work has combined two enhanced segmentation algorithms to carry out the segmentation process, and also it has been proved that it works well when compared with the conventional segmentation algorithms.

Keywords - Segmentation, Blood cell Images, Enhanced Algorithms.

1. Introduction

Extraction of white blood cells from the microscopic image is the most important and challenging task in ALL(Acute Lymphoblastic Leukemia) detection and classification. The challenges arise mainly because of the high variations of cells in shape, size, edge, and position. Each microscopic blood cells image has three main colors,

- Blue, which Indicates White Blood Cells (WBC)
- Red, Indicates red blood cells
- Gray-white, Indicates the background

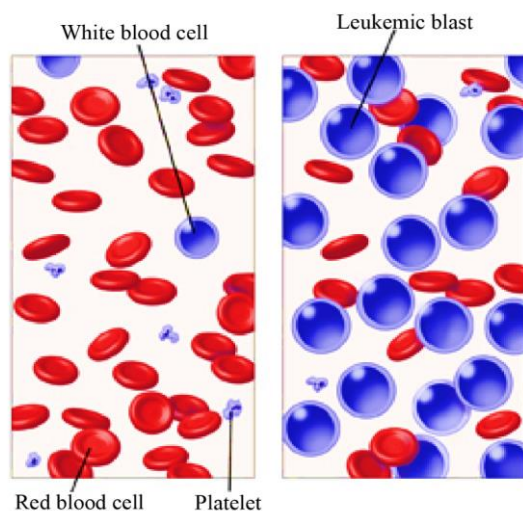


Fig. 1 Sample Microscopic Blood Cell Image

Separating these three cells is vital and is performed using image segmentation algorithms. Segmentation is defined as a task that partitions an image into disjoint and homogeneous regions based on some image characteristic. The main objective here is to create stable segments less sensitive to parameter changes.

Various types of segmentation methods are there in Image processing. Some of those methods existing are,

- Thresholding techniques in which, it will be done by changing the pixels of an image in order to make the image mor easier to analyze.
- Boundary-based segmentation will be used to determine the boundaries between the light and the dark pixels.
- Region-based segmentation, the similarity between the pixels will be identified based on the color, intensity etc.
- Hybrid techniques will combine boundary and region-based methods.

Each of the above algorithms has its own merits and demerits, and when applied to the same image, each may portray a different performance. No single segmentation algorithm can be considered universal to produce stable and accurate segmentation. In this research work, two widely used algorithms are enhanced and combined to improve the accuracy of the segmentation process. The two algorithms used are the Enhanced Watershed Algorithm and the Enhanced K-means Clustering Algorithm. An Integration of



both enhanced algorithms was done to fetch the Segmentation results.

2. Literature Survey

A method was investigated by Xiang Li et al. (2018) for human blood cell classification, distinguishing white cells and red cells. Their method made use of deep convolutional neural networks.

A unique framework was identified by Hong Zhao et al. (2018) for classifying the heterogeneous shapes present in the images of blood by making use of deep convolutional networks for classification based on convolutional networks. Their approach has provided robust predictions to identify certain hematological diseases.

A new method was introduced by T. Markiewicz et al. (2018) in which they exploited features in images of blood cells resembling geometry, texture and statistical analysis. They have focused on the feature selection and generation of features. W. Qiang et al. (2015) have proposed an algorithm named reinforcement learning algorithm for blood cell detection in order to classify the four different types of leukemia.

Khot s et al. (2013) used Support Vector Machine. They extracted the features from the images and applied them to the classifier.

Himali et al. (2015) have identified that when compared with watershed transform, histogram equalizing methods, and k means clustering, the shape-based features are more accurate for counting leukemic cells. The accuracy of their method was 97.8%. They used shape-based features to detect different cells like basophils, monocytes, eosinophils and lymphocytes. Finally, they diagnosed the disease based on the immature cell count.

Emad A. Mohammed and Mostafa M.A. Mohammed et al. (2017) have adopted a method for the cell segmentation of leukaemia cells. In their research work they have used the otsu method by using an optimal threshold value. They have also performed canny edge detection. The dilation and erosion were also carried out, the isolated pixels were eliminated, and they derived a segmented nucleus.

Subrajeet Mohapatra, Dipti Patra and et al. (2017) have examined a method known as color-based clustering to segment the images of blood. They have compared the performances of some of the standard clustering techniques. The clustering techniques were k Means, FCM and FPCM. They have also used contour signature and hausdorff dimension to find the irregularities of the boundary of the nucleus. SVM classifier has been used to derive the results.

Sonal G. Deore and Prof. Neeta Nemade et al. (2015) have proposed a method in which they extracted the lymphocyte cells, then extracted morphological indexes, and then classification was done. They have identified the single cells by enhancing the input image. The filter used was adaptive pre-filtering. The second step of their research

work was identifying the white cells by separating them from other blood components. The third step was identifying the lymphocytes associated with the other white cells. The accuracy of their research work was 93.63%

3. Methodology

This research proposes a methodological segmentation design that attempts to find a perfect combination of algorithms instead of comparing the performance of various segmentation algorithms to find an effective method. The motivation behind this methodology is that it is possible to obtain benefits from combining the strengths of multiple segmenting algorithms. For this purpose, this research applies two enhanced segmentation algorithms to build a combined algorithm that forms final segments that is more stable and accurate. This algorithm is termed as 'Combined Segmentation Algorithm for WBC Identification or CSA_WBC'.

3.1. Steps in CSA-WBC

The CSA-WBC is designed using two synergistic segmentation algorithms to produce an accurate grouping of blood cells.

The first algorithm enhances the watershed algorithm, while the second is a clustering-based algorithm.

- Steps Involved in CSA-WBC

Input: Microscopic Image, I

- Step 1: Segment the input image using the enhanced watershed algorithm and perform region merging
- Step 2: Segment input image using enhanced clustering algorithm and perform region merging
- Step 3: Combine segment results to produce a single set of segments
- Step 4: Identify Lymphocytes
- Step 5: Use a post-processing procedure to refine the segmented result further

Output: Three Segments

3.2. Step 1- Enhanced Watershed Algorithm

The proposed algorithm uses an amalgamation of sequential methods to segment microscopic images. This algorithm uses edge, color and shape information to segment and identifies WBCs.

The EWS algorithm is designed using

- Color Intensity
- Otsu's Threshold Algorithm
- Enhanced Watershed Segmentation Algorithm
- Region Merging Algorithm
- Pruning Algorithm

The proposed algorithm is termed as 'Enhanced Watershed Segmentation Algorithm to Identify WBC or EWS_WBC'.

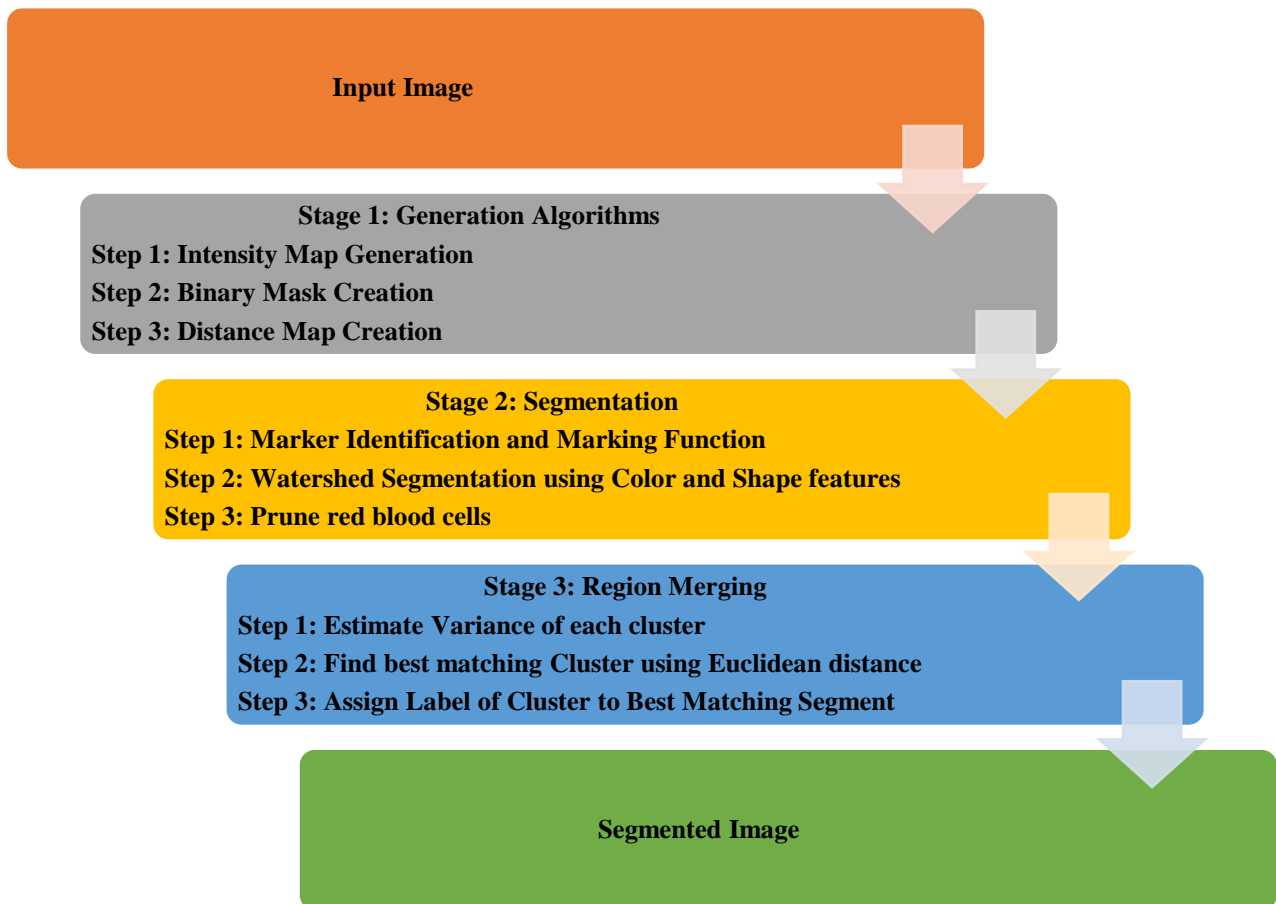


Fig. 2 Methodology

Stage 1 of the Enhanced Watershed Segmentation Algorithm is Intensity Map Generation, Binary Mask Creation and Distance Map Creation. In the segmentation phase, the marker regions will be identified using the marker function, followed by watershed segmentation using colour and shape features. Finally, the pruning of the red blood cells will be done. In the region merging phase, the Variance of each cluster will be estimated, and the best matching cluster will be found using the Euclidean distance. The final step is to assign the cluster label to the Best matching segment.

3.3. Step 2: Enhanced K-Means Algorithm

The K-Means clustering algorithm which it will divide an image into k clusters, and the means of the clusters will be kept at a distance from one another. The data points in each cluster will be related to the nearest mean, and they will belong to one of the clusters.

Although k-means has the great advantage of being easy to implement, it has some drawbacks. They are,

- Mandatory requirement that the number of clusters should be known prior to clustering
- Sensitive to initial centroid selection
- Huge number of computations are involved during similarity calculation

The proposed K-Means clustering algorithm aims to solve the above three issues of the conventional counterpart, and the solutions have been given below

-As the microscopic image has to be divided into three regions, background, white blood cells and red blood cells, K is set to 3.

-A subtractive clustering method is used to obtain a set of optimal center points.

-A computation reduction algorithm is proposed to reduce the number of computations, thus reducing time complexity.

The proposed K-Means algorithm is termed as 'Parameter less Fast KMeans Clustering (PFKM) Algorithm'.

Steps in PFKM

Input: Microscopic Image M

Step 1: Assign $K=3$

Step 2: Estimate K initial seeds (c_j) using Subtractive Clustering Algorithm

Step 3: Repeat

a. For each pixel of an image, calculate Euclidean Distance d , between the centre and each pixel of an image using the equation given below

$$D = |p(x,y) - c_k|$$

b. Find the closest centre c_j and assign pixels to cluster j

c. Store the label of cluster centre j along with the distance and store them in an array Cluster [] and Distance [], respectively

d. Set cluster[i] = j (j is the nearest cluster)

e. Set Dist [i] = D_{ij} (Distance between x_i to the closest centre c_i)

f. Recalculate Cluster Centres

g. Compute New Distance to new cluster centres

h. Calculate D with all the cluster centres assign cluster $i =$ cluster j ,

$$\text{Distance} = D_{\text{new}}$$

End if

Until Convergence

Step 4: Output clustered results

3.4. Step 3: Combine Segment Results

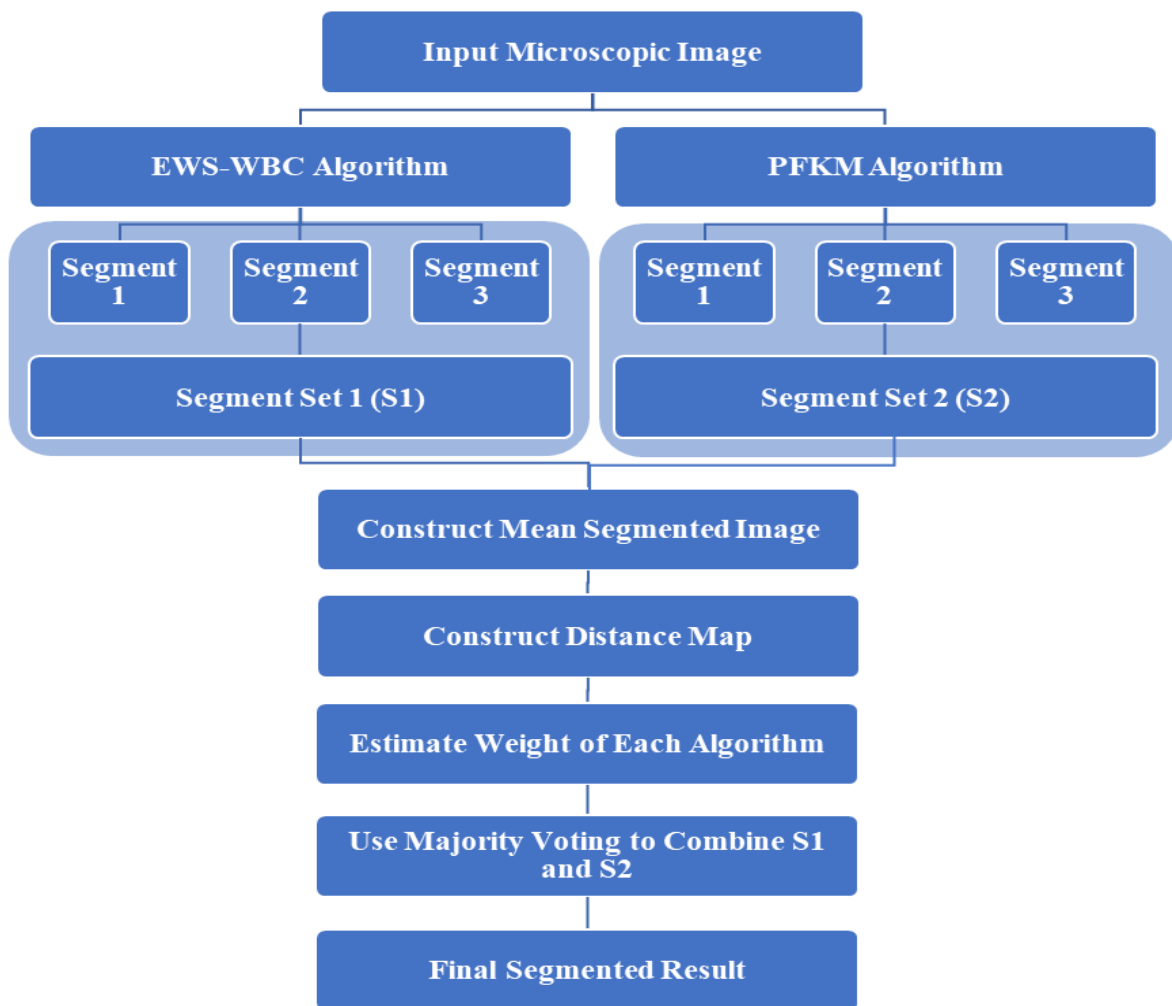


Fig. 3 Combine segment result

The combining of segmentation results has been done by using segment set 1 from EWS-WBC and segment set 2 from PFKM for the Input microscopic image. Both the segment sets will then be combined to construct the mean segmented image, followed by distance map creation. Then the weight of each algorithm will be estimated, and majority voting will be used to combine S1 and S2. The resultant image will be the final segmented result.

3.5. Post-Processing

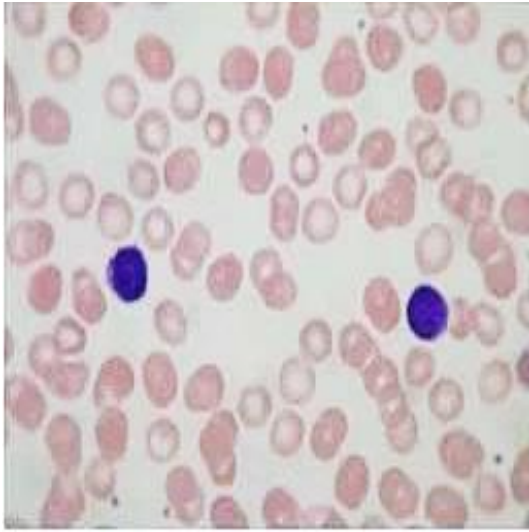
To further improve the perceptibility and visuality of the combined clustering results, morphological filtering is applied. The following operations were performed.

- Edge Enhancement
- Dilation - To connect separated points in a better manner using a 2 x 2 structuring element
- Hole Filling - The internal holes were filled using the hole-filling method.

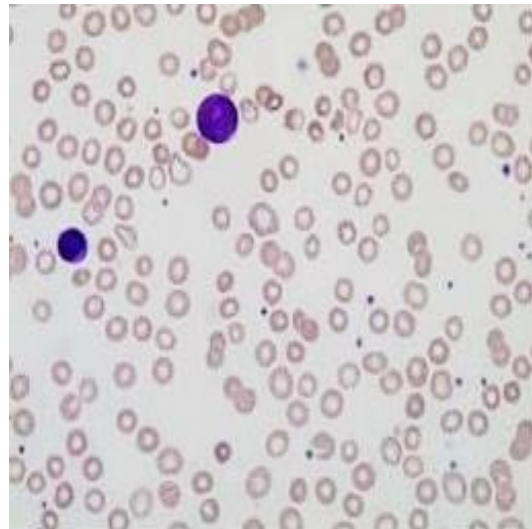
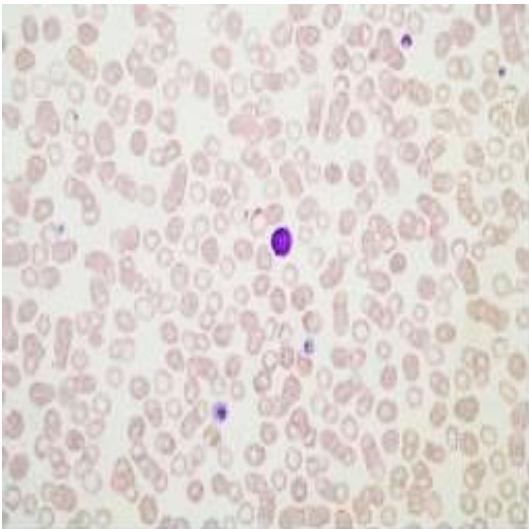
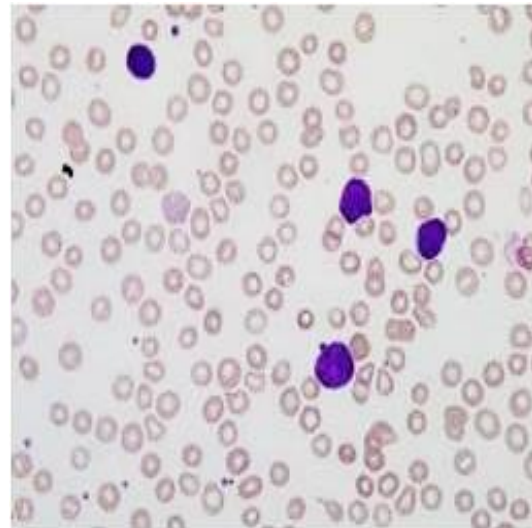
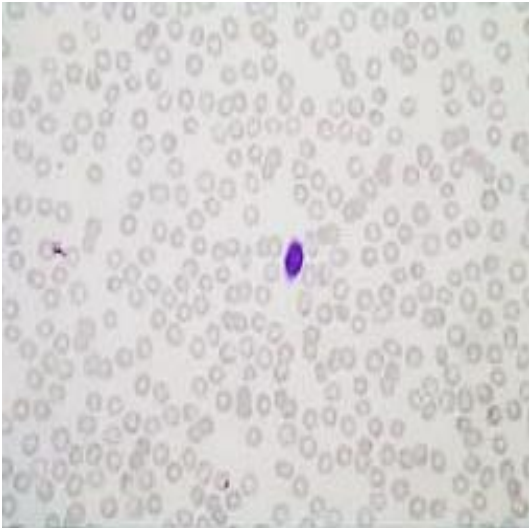
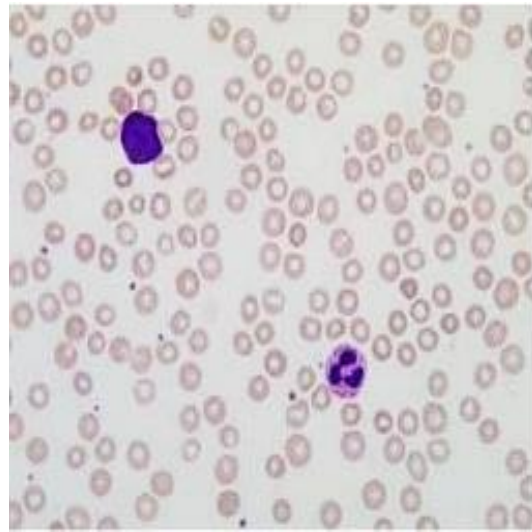
4. Results and Discussions

Some of the test images are shown below,

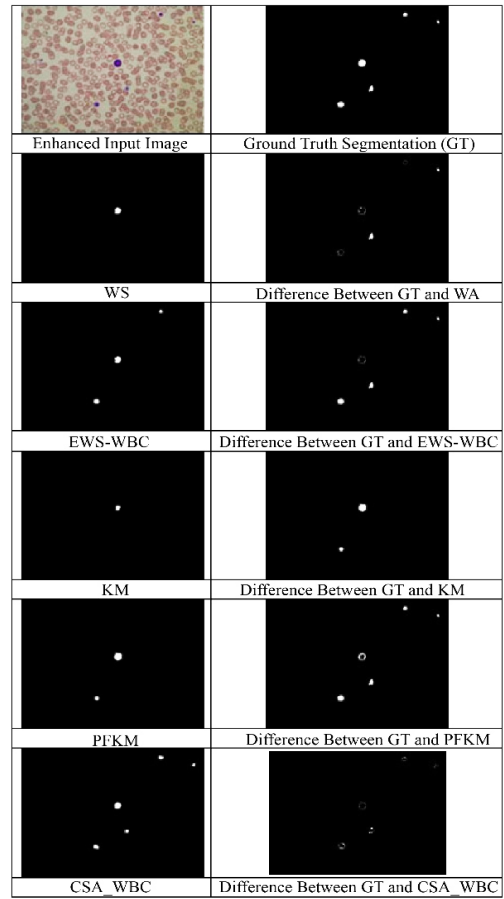
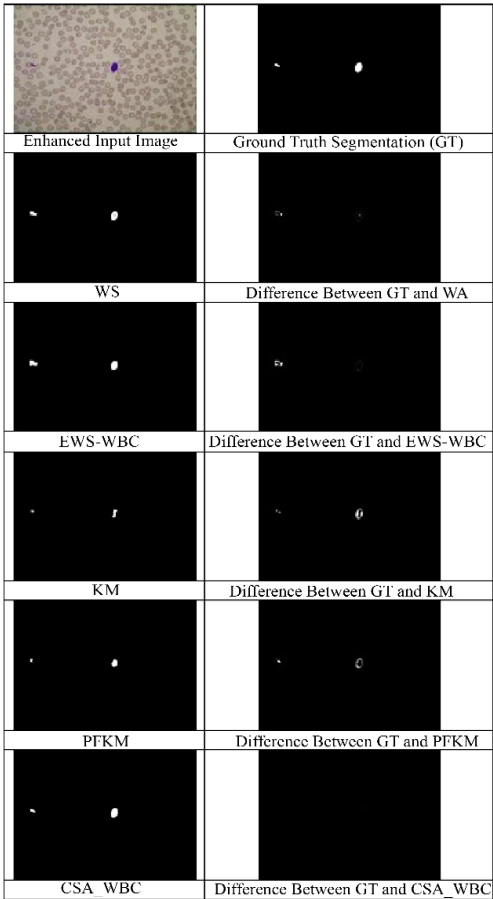
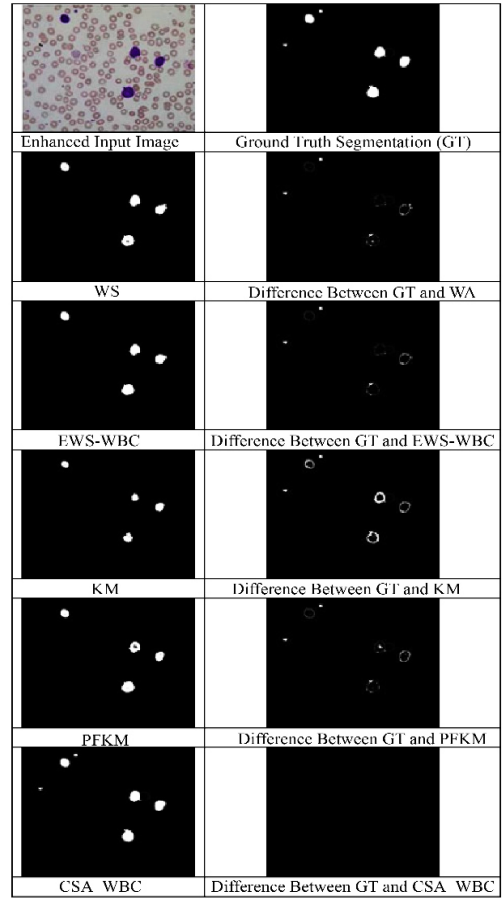
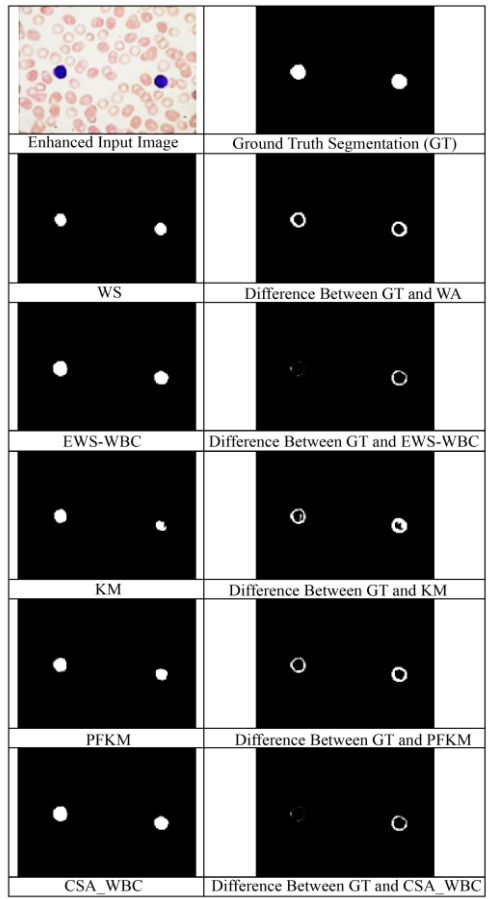
Images with Healthy Cells

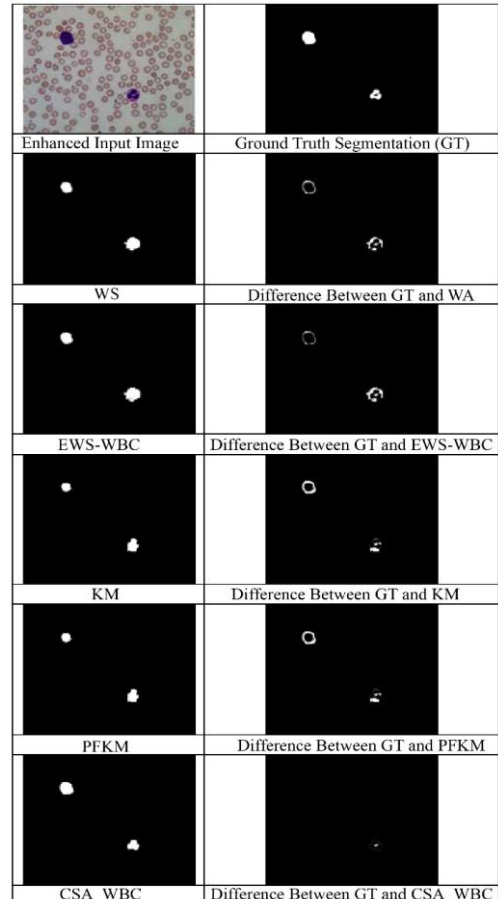
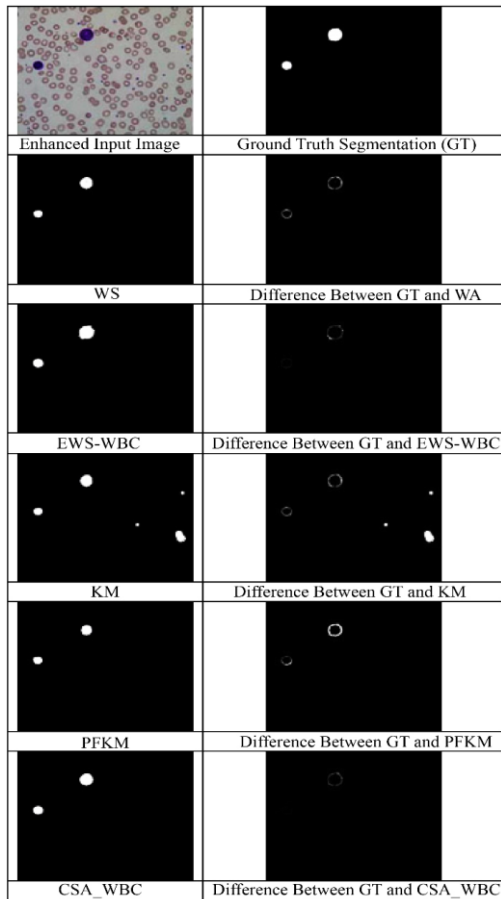


Images with Probable Lymphoblasts



Visual Results of Images are shown below,





5. Findings

The novelty of the proposed research work is that,

- From the results, it can be seen that both enhanced segmentation algorithms work better than their conventional counterparts.
- However, the proposed algorithm that combines the results of the two enhancement algorithms finds white blood cells most efficiently.
- This is proven by both quantitative and visual analysis.

6. Conclusion

In this research paper, the segmentation process has been elaborated, and the corresponding images have been

shown. The paper has described the methodology adopted in carrying out the segmentation process. The results and discussions have been given with the resultant images when the segmentation methods were applied. A comparison has been made by combining two of the efficient segmentation methods, as Enhanced Watershed Algorithm and the Enhanced K-Means Algorithm. Rather than comparing various segmentation algorithms, this research work has used a combination of two efficient segmentation algorithms, which have been enhanced to carry out the segmentation process. This has been adopted to improve the efficiency of the process. The methods were applied, and the performance was compared on the dataset images. Some of the test images and the visual results have been shown to prove both quantitative and visual analysis.

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