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LIST OF PUBLICATIONS

International Journals

1. Saranya Vijayan, Dr. V Radha. (2023) "Enhanced Segmentation Algorithms for Improving Acute Lymphocytic Leukemia Diagnosis from Blood Microscopic Images" International Journal of Engineering Trends and Technology, Vol 71, Issue-4, pg.no 483-490, ISSN:2231-5381(**Scopus Indexed**).

2. Saranya Vijayan, Dr. V Radha. (2023) "Classification of Acute Lymphocytic Leukemic Blood Cell Images using Hybrid CNN-Enhanced Ensemble SVM Models and Machine Learning Classifiers", International Journal on Recent and Innovation Trends in Computing and Communication, Vol 11, Issue-8, pg.no 304-314, ISSN:2321-8169 (**Scopus Indexed**).

3. Saranya Vijayan, Dr. V Radha. (2022) "Classification of Acute Lymphoblastic Leukemia using Machine Learning Algorithms", International Journal of Health Sciences, Vol 7, pg. no 5245-5257, ISSN:2550-6978.

4. Saranya Vijayan, Dr. V Radha. (2021) "A Survey on Image processing techniques and Deep learning Algorithm for Blood cell classification", International Journal of computer science and Information Security, Vol:19, pg. no 72-79, ISSN:1947-5500.

5. Saranya Vijayan, Dr. V Radha. (2021) "Comparison of Filters and Edge Detection Methods on Medical Images", Turkish Online Journal of Qualitative Inquiry, Vol:12, Issue 7, pg. no 3790-3797, ISSN no:1309:6591.

International Conferences

1. Saranya Vijayan, Dr. V Radha. (2022) "Pre-processing of Leukemic blood cell Images using Deep learning Algorithms and Image processing techniques", 3rd International Conference on Data Intelligence and Cognitive Informatics -2022" (**Scopus --Taylor and Francis group**)

2. Saranya Vijayan, Dr. V Radha. (2022) "Segmentation of Leukemic Blood cell Images using Deep Learning Algorithm and Image Processing Techniques"," International Conference on Emerging Trends in IoT and Computing Technologies-2022" (**Springer)**

Avinashilingam Institute for HomeScience and Higher Education for Women
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Appendix L2

(Item No 5 of Check List) Details of Research Publications

S.No	Article	Journal	Other Details Vol/No/Page No/ Year	Published in UGC-CARE / Scopus Indexed/ Web of Science
1	Enhanced Segmentation Algorithms for Improving Acute Lymphocytic Leukemia Diagnosis from Blood Microscopic Images	SSRG - International Journal of Engineering Trends and Technology	Volume 71 Issue 4 April 2023 IJETT/V71/I4P24	Scopus Indexed
2	Classification of Acute Lymphocytic Leukemia Blood cell Images using Hybrid CNN - Enhanced Ensemble SVM Models and Machine Learning classifiers	International Journal on Recent and Innovation Trends in Computing and Communication	ISSN: 2321-8169	Accepted for publication.

*Proof of list of Journals from Internet to be attached along with copies of reprints.

Scholar : Saranya

Supervisor : 27/07/23

Checked By:
HoD/Dean of Respective School

The scholar Miss Saranya Vijayan (19PHCSF003) has published her paper in the following journal:

1. SSRG International Journal of Engineering Trends and Technology - is indexed and active in Scopus from 2019 to present and the scholar published her article in Vol 71, No 4, April 2023 and

2. She got acceptance from

International Journal on Recent and Innovation Trends in Computing and Communication - indexed and active in Scopus from 2021 to present.

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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

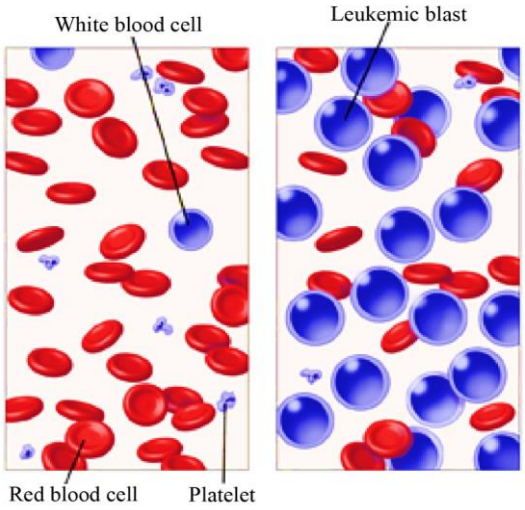


Fig. 1 Sample Microscopic Blood Cell Image

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 outs 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.

SubrajeetMohapatra, DiptiPatraandetal. (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 hausdroff 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'.

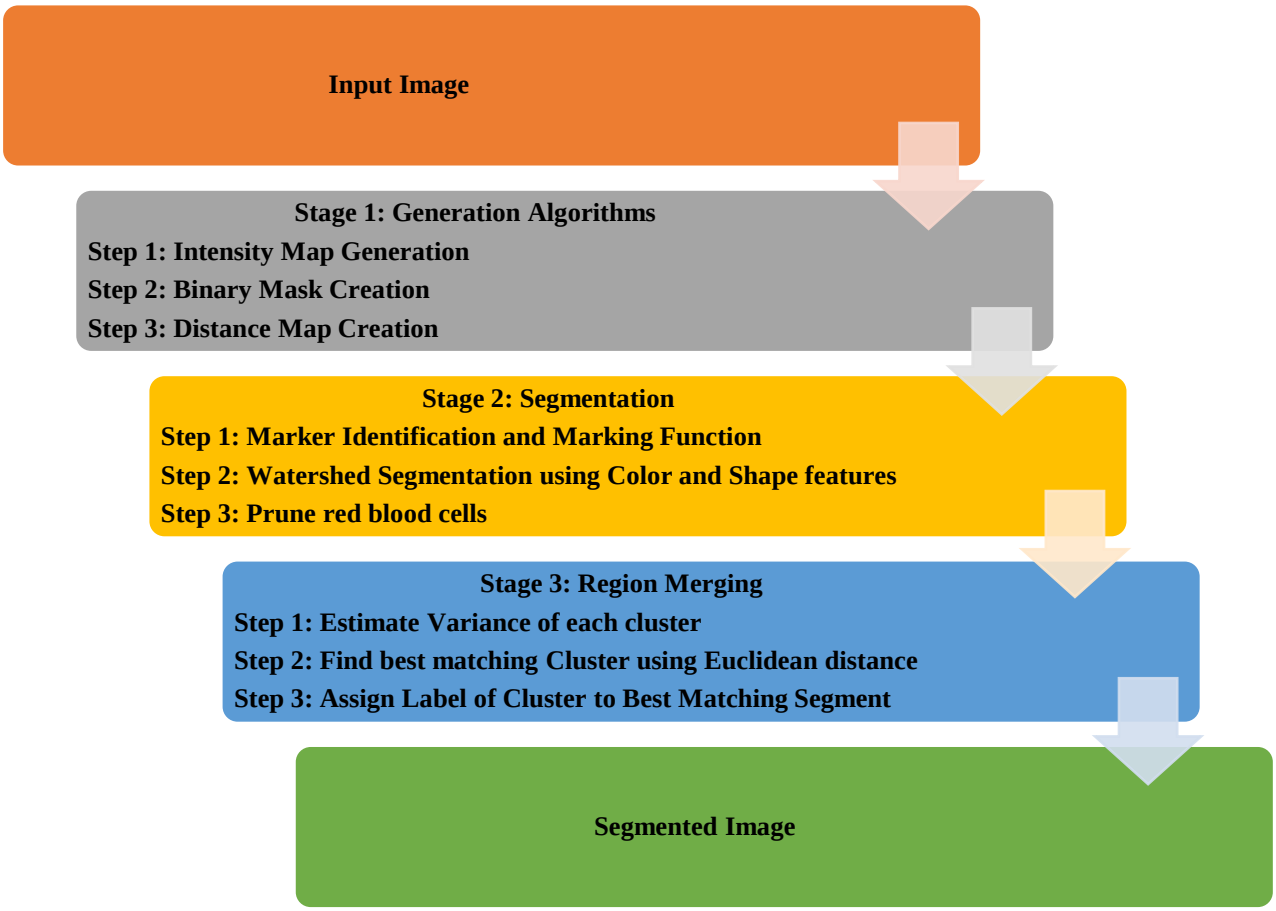


Fig. 2 Methodology

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_i)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,

Distance= D_{new}

End if

Until Convergence

Step 4: Output clustered results

3.4. Step 3: Combine Segment Results

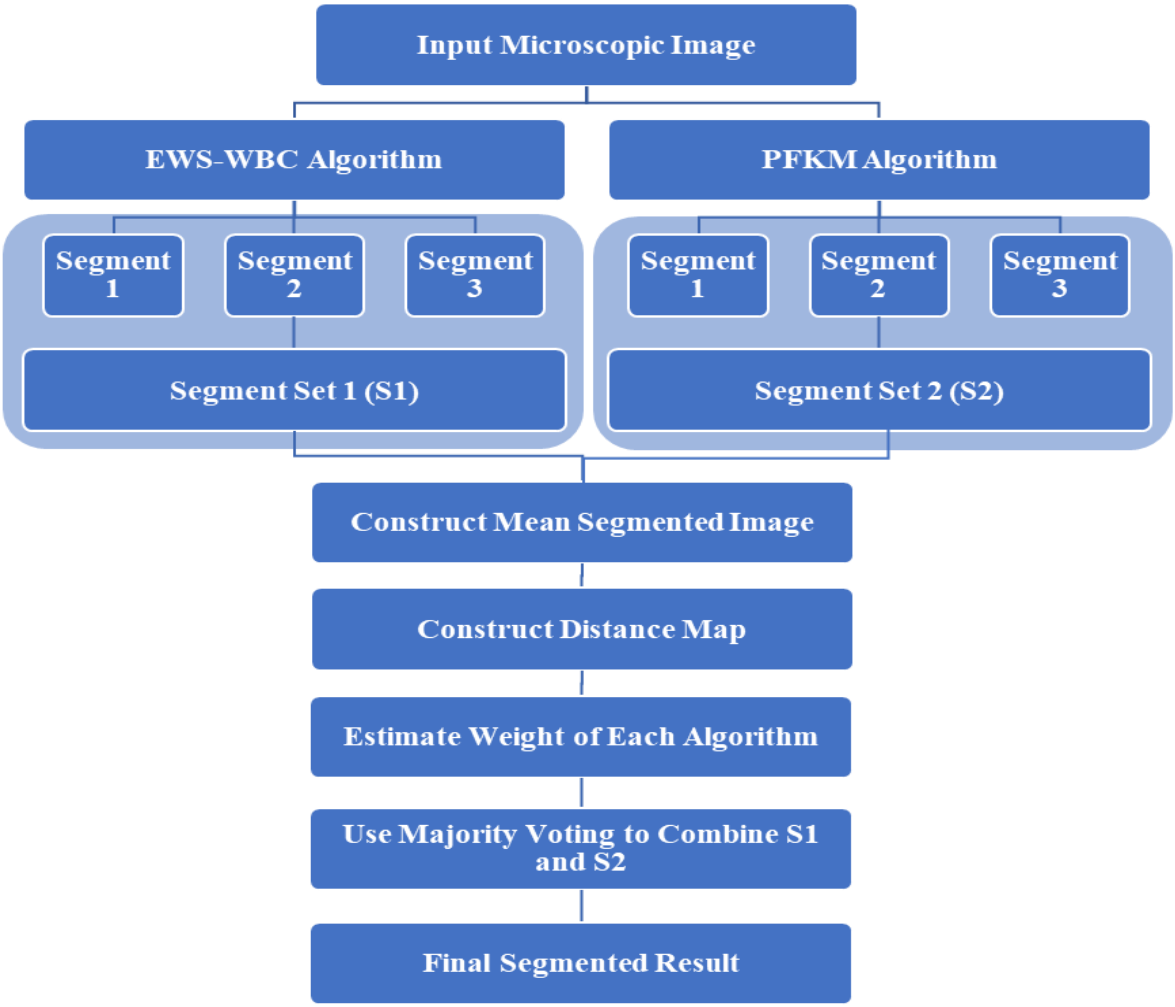


Fig. 3 Combine segment result

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

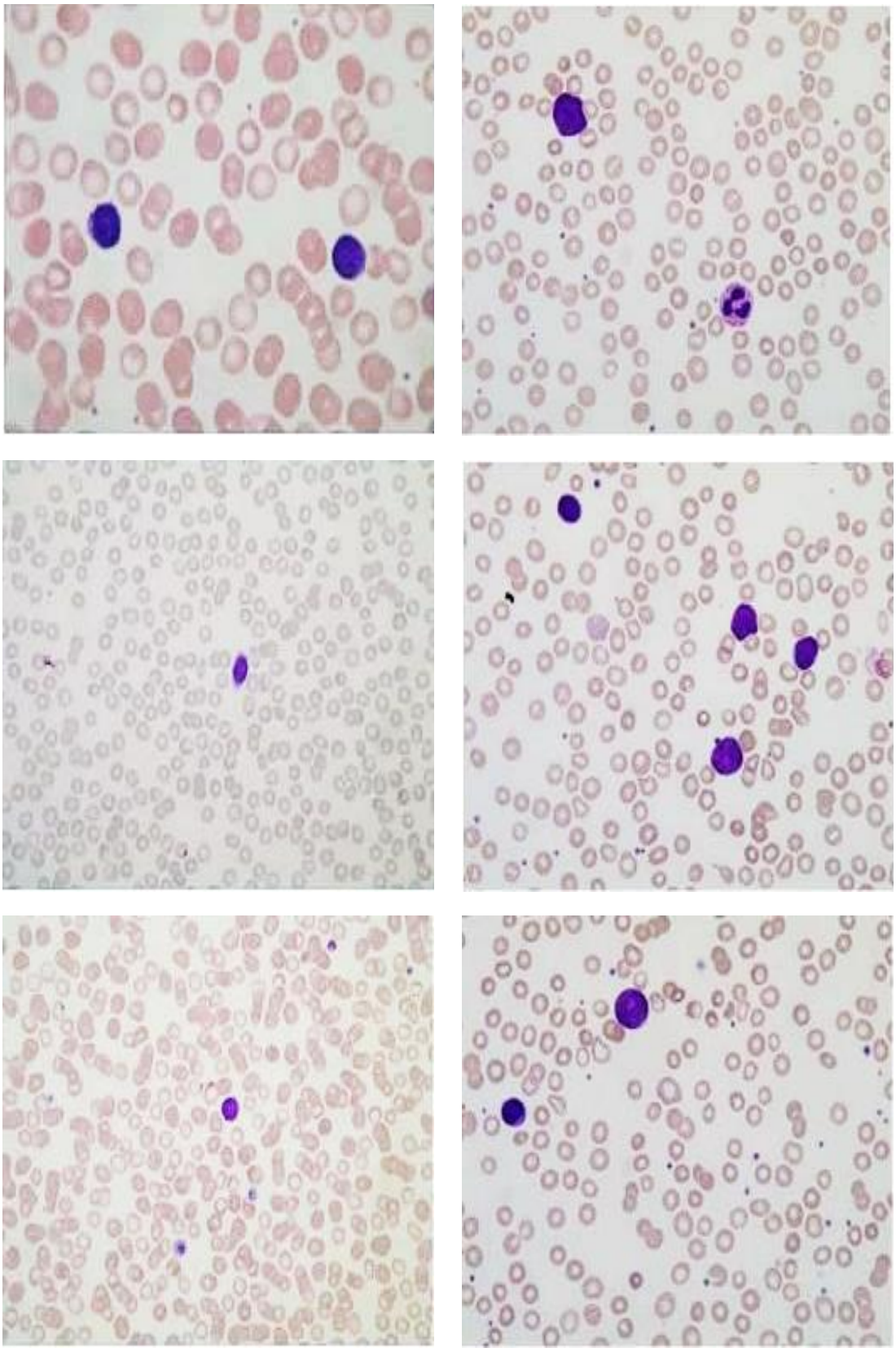
To further improve the perceptibility and visuality of the combined clustering results, morphological filtering is applied. The following operations were performed.

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

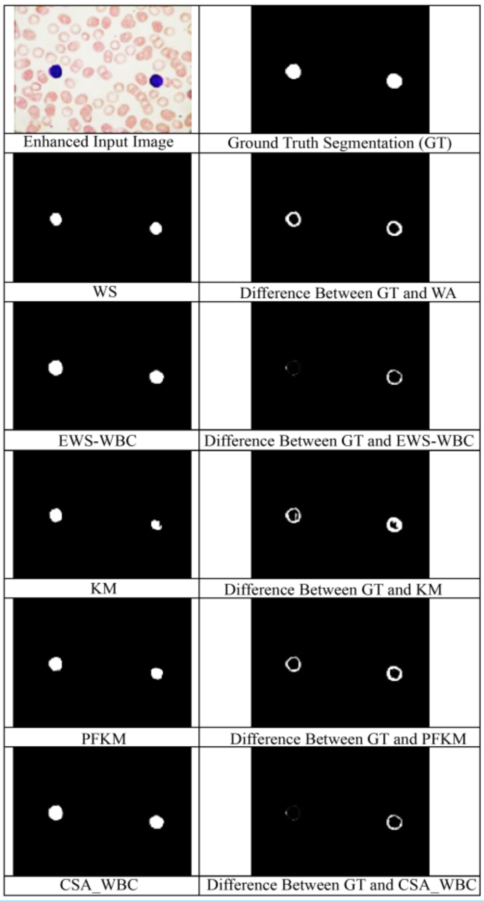
4. Results and Discussions

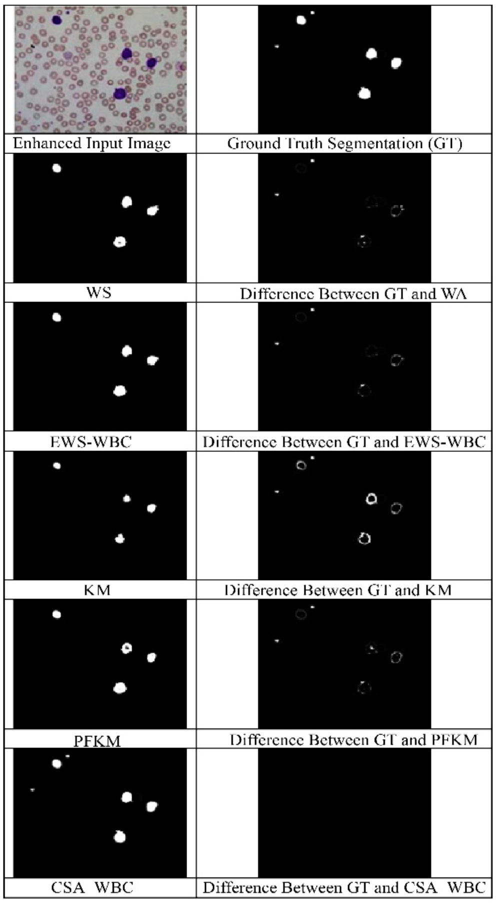
Some of the test images are shown below,

Images with Healthy Cells | **Images with Probable Lymphoblasts**



Visual Results of Images are shown below,


Enhanced Input Image
Ground Truth Segmentation (GT)
WS
Difference Between GT and WA
EWS-WBC
Difference Between GT and EWS-WBC
KM
Difference Between GT and KM
PFKM
Difference Between GT and PFKM
CSA_WBC
Difference Between GT and CSA_WBC


Enhanced Input Image
Ground Truth Segmentation (GT)
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Difference Between GT and WA
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Difference Between GT and KM
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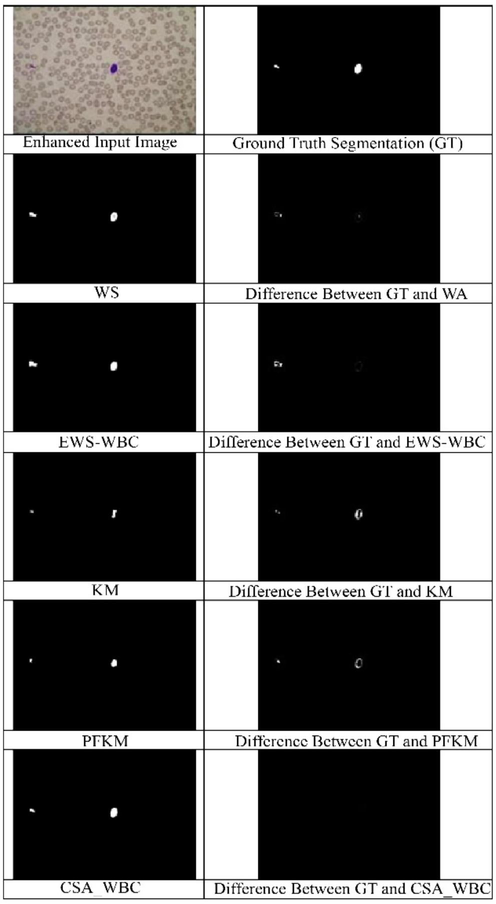
Difference Between GT and PFKM
CSA_WBC
Difference Between GT and CSA_WBC


Enhanced Input Image
Ground Truth Segmentation (GT)
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Difference Between GT and WA
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Difference Between GT and EWS-WBC
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Difference Between GT and KM
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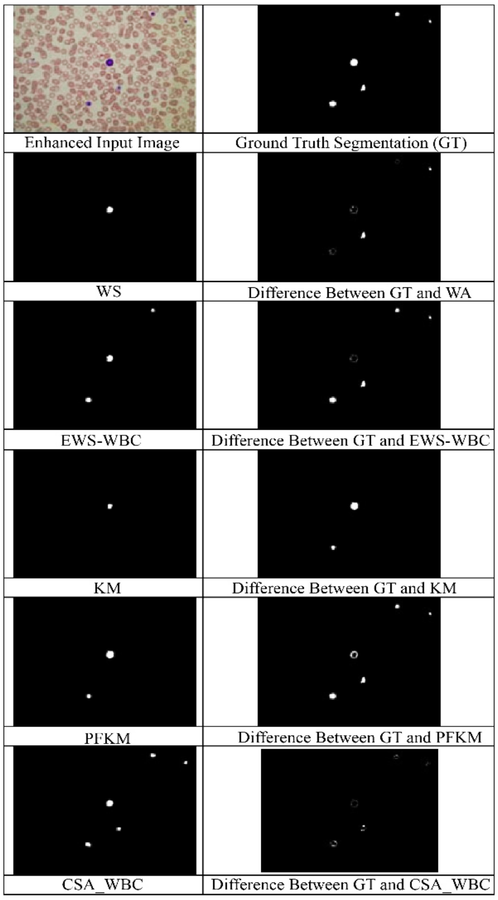
CSA_WBC
Difference Between GT and CSA_WBC


Enhanced Input Image
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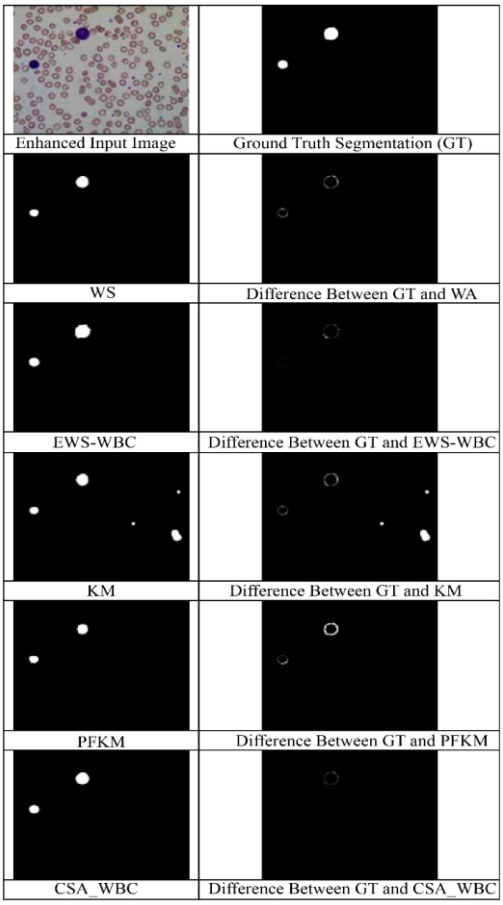
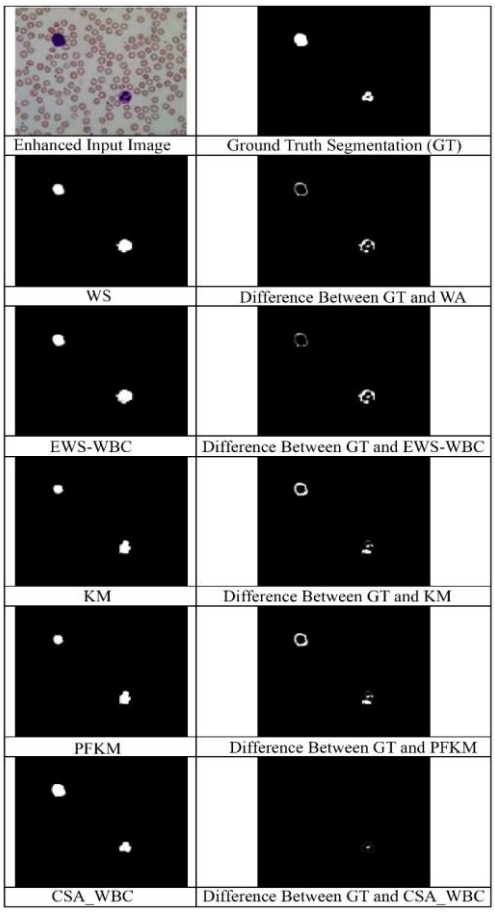
KM
Difference Between GT and KM
PFKM
Difference Between GT and PFKM
CSA_WBC
Difference Between GT and CSA_WBC





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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Classification of Acute Lymphocytic Leukemic Blood Cell Images using Hybrid CNN-Enhanced Ensemble SVM Models and Machine Learning Classifiers.

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Abstract: Acute Lymphocytic Leukemia is a dangerous kind of malignant cancer caused due to the overproduction of white blood cells. The white blood cells in our body are responsible for fighting against infections, if the WBC increases the immunity will decrease and it would lead to serious health conditions. Malignant cancers such as ALL is life threatening if the disease is not diagnosed at an early stage. If a person is suffering from ALL the disease needs to be diagnosed at an early stage before it starts spreading, if it starts spreading the person's chances of survival would also reduce. Here comes the need of an accurate automated system which would assist the oncologists to diagnose the disease as early as possible. In this paper some of the algorithms that are enhanced to detect and classify ALL are incorporated. In order to classify the Acute Lymphocytic Leukemia a hybrid model has been deployed to improve the accuracy of the diagnosis and it is termed as Hybrid CNN Enhanced Ensemble SVM for the classification of malignancy. Machine Learning classifiers are also used to design the system and it is then compared with enhanced CNN based on the performance metrics.

Keywords : Acute Lymphocytic Leukemia , Ensemble System, Hybrid CNN-SVM.

I. INTRODUCTION

Digital Image Processing has been proved for solving many challenging problems in the field of medical images that could greatly contribute in the discovery of diseases and it would provide the physicians with valuable inputs in the process of diagnosing the diseases without any flaws. This paper proposes a hybrid model that uses Enhanced SVM and CNN for the classification of Acute Lymphocytic Leukaemia (ALL) . To identify malformations in white blood cells, generally, a manual inspection is carried out by an expert pathologist. Manual inspection and identification has several drawbacks like being time-consuming, high cost as expert pathologists are expensive and diagnosis accuracy depends on the experience and workload of the expert. To avoid these drawbacks, an automatic system is preferred by pathologists, who use these systems to help them aid in the correct identification of the disease. Moreover, automated systems help to avoid or reduce human intervention during diagnosis and are cost-effective.

Convolutional neural networks is one of the efficient deep neural networks known as CNN. A CNN will extract features automatically without any human intervention. CNNs will eradicate the need for extracting features manually and it removes the need to identify the features that used to classify images. The CNN will directly extract features from images given as input. The features are not pretrained whereas they are learned when the network trains the images thereby making the automatic features extracted by deep learning models are accurate for challenging tasks in image processing.

Leukemia is also known as blood cancer, in which it would result in the rapid overproduction of abnormal white blood cells. Blood cancer occurs when the white blood cells in the bone marrow quickly increase and will eventually end up in destroying normal blood cells. It is considered to be the 11th top cancer type worldwide [Lin *et al.*, 2021]. In order to reduce death related to leukemia, it is important to treat them at the early stage.

An automatic ALL classification (ALL-C) system consists of four steps, namely, preprocessing, identification of white blood cells, feature extraction and classification. [Bukhari *et al.*, 2022; Mustafa *et al.*, 2022]. The proposed system is designed by enhancing the working of each step of the automated system and then combining them to further improve the performance of the ALL-C system.

"To design an Automatic ALL Classification System of the form

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$\mathfrak{R} = DC + EMC$

where $\mathfrak{R}$ is the output indicating the classification of ALL using hybrid deep learning and ensemble machine learning classifiers. The classification operation is of the form

$\mathfrak{R} = \oplus(m_i) \rightarrow \wp(m_i) \rightarrow \varsigma(m_i)$

where $\rightarrow$ denotes the sequential application of operations. The classification output is any one of the pre-defined target label set {Normal, L1, L2, L3} and is to be performed using machine learning and deep learning classifiers."

Extraction of white blood cells from 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, it Indicates red blood cells

-Gray-white ,Indicates background

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

To accomplish this problem statement, the primary research objective was set to strengthen the clinical decision support system by designing an automatic system that enhances the operation of each step involved during ALL-C inorder to increase the overall accuracy and speed of leukemia classification.

II. LITERATURE SURVEY

Xiang li et al. (2018) have investigated a method for the classification of blood cell, to segregate white blood cells and red blood cells. They have used deep convolutional neural networks.

A method was analysed by Khot s et al. (2013) in which they have extracted the features from the images and had applied it to the classifier.

Himali et al. (2015) have investigated that when compared with watershed transform , histogram equalizing methods and k means clustering, the shape based features were more accurate for counting leukemic cells.

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

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

SubrajeetMohapatra, DiptiPatraandetal. (2017) have examined a method known as color based clustering for the segmentation of the images of blood. They have done a comparison on 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 hausdroff dimension for finding out the irregularities of the boundary of the nucleus. SVM classifier has been used to derive the results.

Sonal G. Deore Prof. Neeta Nemade et al. (2015)have proposed a method in which they have extracted the lymphocyte cells followed by extracting 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 to identify the white cells by separating it from other components of blood. The third step was identifying the lymphocytes associated with the other white cells. The accuracy of their research work was 93.63%

Acute leukemia grows rapidly and becomes severe within a short period, while chronic spreads slowly and takes longer to reach the advanced stage. Leukemia Classification is based on the type of white blood cells involving myeloid or lymphoid.

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 made use of shape based features to detect different cells like basophils ,monocytes, eosinophils and lymphocytes. Finally they have diagnosed the disease based on the immature cell count

Xiang li et al. (2018) have investigated a method for the classification of blood cell, to segregate white blood cells and red blood cells. They have used deep convolutional neural networks.

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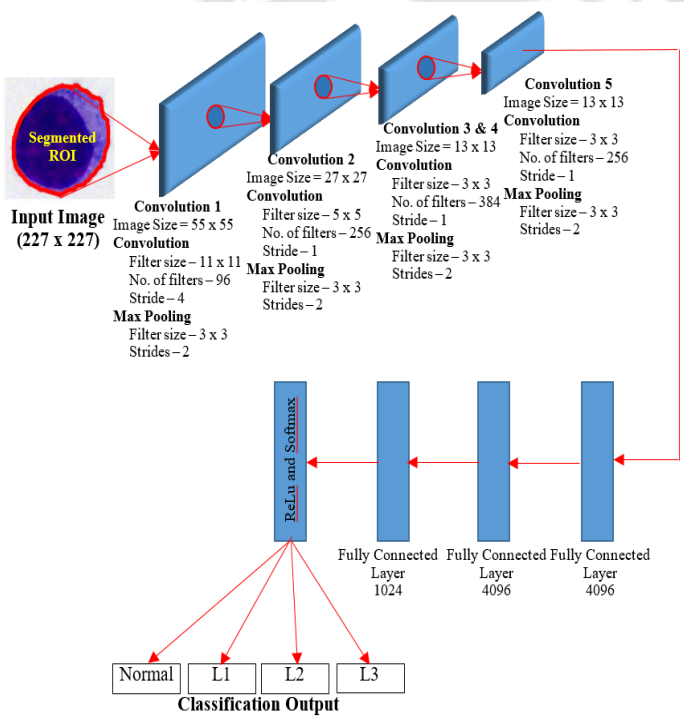
A method was analysed by Khot s et al. (2013) in which they have extracted the features from the images and had applied it to the classifier..

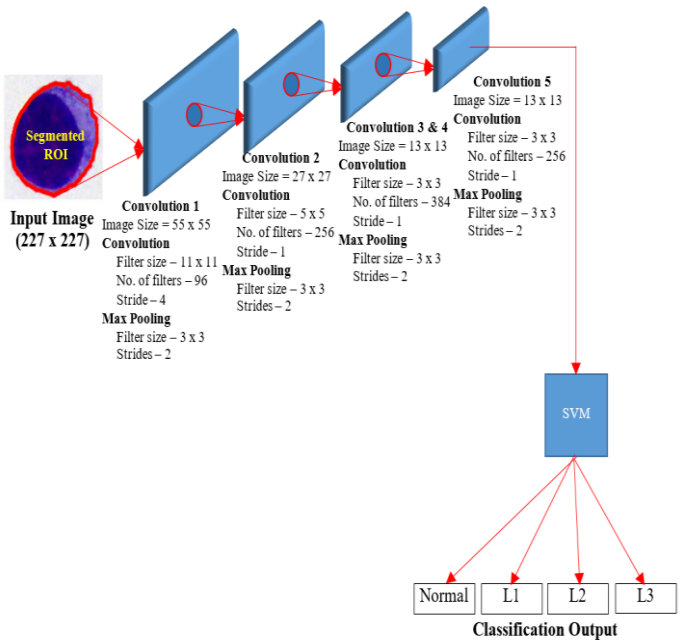
III. PROPOSED METHODOLOGY

The research work has implemented an AlexNet that is pretrained for ALL detection and classification. The concept of transfer learning to retrain the pretrained model with respect to the existing problem was used to design the deep neural network. The RGB images with 227*227 are given as input. The AlexNet Model has got 5 convolutional layers with 3 max polling layers. Each of the convolutional layers have Rectied Linear Unit (ReLU). The last 3 layers such as fully connected layer, softmax layer and classification layer of the pretrained AlexNet were used for Transfer Learning. In the proposed AlexNet architecture the data will be first classified into normal or abnormal. The feature vector size has been reduced by using another fully connected layer with 1024 neurons was added. The layer has been fully connected binary classification (normal, abnormal) probability using softmax function followed by further classifying it into L1, L2 and L3 . In order to further classify it the last fully connected layer is modified from binary classes to four classes output probability by keeping the remaining layers the same.

Transfer learning in machine learning is retraining the pre trained model with respect to the problem. Transfer learning has got advantages such as it is fast as well as effective. The parameters such as the filter size, the number of filters, and stride for each layer are shown in Figure 1.



Through experiments, it was evident that the CNN base model outperforms the conventional SVM-based model in terms of accuracy and its performance is at par with enhanced ensemble SVM from Phase II. However, CNN has more steps hence the time needed to run it is longer than SVM. The CNN models are very good at automatically learning the optimal features. However, its performance is not always the best during classification, as the fully connected layers use parameters that have to be fine-tuned manually. To solve this issue, hybrid models that combine CNN and SVM are proposed by several researchers. These systems use CNN for feature extraction and SVM for classification. This research work, moving in the same path, also combines CNN and SVM and includes procedures that can improve its performance



The proposed hybrid system is designed to combine CNN with ensemble SVM. The base SVM classifiers are created by differing the kernel functions used. The kernel functions used in the proposed system are Linear Kernel, Polynomial Kernel, (RBF), Gaussian Kernel, exponential kernel, Laplacian kernel, Bessel function kernel, Gaussian Radial Basis Function, ANOVA RBF kernel, Laplace RBF and hyperbolic or Sigmoid Kernel. Another point from Phase II is that not all base classifiers in the classification system help with classification. For this purpose, the hybrid CNN-ensemble SVM classifier is enhanced to include the selection step described in Phase II. Thus, Phase III of the research methodology proposes three systems as given below:

- Hybrid CNN-ensemble SVM classifier
- Hybrid CNN-ensemble SVM using DCS
- Hybrid CNN-ensemble SVM using DES

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The proposed hybrid classifiers works in two stages.

In the first stage, the AlexNet CNN extracts the deep features and feeds them to the second stage. The second stage then uses the ensemble SVM classifier to classify the deep feature maps extracted from AlexNet CNNs. The hybrid model proposed replaces the last three fully connected layers of base model by the ensemble SVM classifier. In this stage, dynamic selection methods, DCS and DES, are used, so that only optimal base classifiers are used during classification. Thus, the hybrid model is enhanced by combining CNN with ensemble SVM with DCS/DES method. The DES method selects five optimal classifiers during the construction of the ensemble system.

Aggregation of results, while using ensemble with DES, is done using a weighted ensemble of networks method. In this method, the proposed model considers the performance of each SVM using a weight that denotes its contribution to the final classification. The main aim of this method is to enhance classification system performance by using individual SVM's performance to the result of the respective base classifier. The weights are estimated by first calculating the probability of each class and then using it to calculate an evaluation score. The main advantages of the proposed hybrid system are to reduce the chance of overfitting, number of parameters and the time & process complexities.

3.1 Best Base Classifier Selection Algorithm

- Input

Set of Base Classifiers (S), Classification Accuracy (A)

Output

Set of best performing classifiers (BHC) that are used to construct SVM ensemble

- The Algorithm

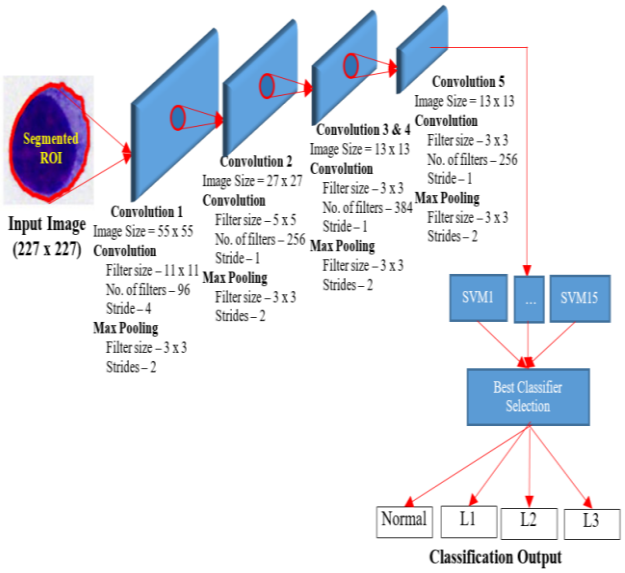
Step 1 : BHC = { }

Step 2 : Arrange base classifiers in S in descending order of its associated accuracy

Step 3 : BHC = BHC + $\{C_1\}$ + $\{C_2\}$ + $\{C_3\}$ + $\{C_4\}$ + $\{C_5\}$

– Step 4 : Return BHC

- The returned BHC has the best performing classifier set



3.2 Classification using Deep Learning Algorithm

The nodes will process the input and the results will be communicated to the next layer of nodes. This process will be repeated until it reaches an output layer. One major problem with ML models is with the feature extraction process, which is hand-crafted. DL models are capable of focusing on the right features by themselves with very little or no human intervention.

To perform early detection of ALL, Phase III proposes a DL classification model based on Convolutional Neural Network (CNN or ConvNet) classifier. This model, called as the base model in this research work, is designed using the AlexNet CNN model based on the transfer learning method, in which deep feature maps were extracted and classified.

CNN will be convolved across the image in the input data and uses convolutional layers for feature extraction. The CNN eliminates the need for human intervention by identifying the features by itself and classifying the images. CNN will extract the features directly from the images. The features are not pre-trained and they will be learned while the network trains on a collection of images. The automatic feature extraction makes deep learning models highly accurate for challenging tasks in Image Processing.

One major issue with CNN is when the size of the training dataset is small, then the issue of overfitting arises (Xiao *et al.*, 2021). To solve this issue, the training set size has been increased through the use of augmentation methods. Data Augmentation methods are implemented through the use of image manipulation methods to increase the size of the training set. Seven manipulation methods were used. They are height shift, width shift, zoom, horizontal flip, vertical flip,

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rotation and shearing. By applying image manipulation methods, the training set size was increased and normalized.

The input for the proposed base model AlexNet are the RGB colored images with 227x227 pixel resolution. The base model is designed with five convolutional layers along with three max polling layers followed by Rectied Linear Unit . Transfer learning was performed using the FCL, softmax layer and classification layer of the pre-trained AlexNet are used. The proposed AlexNet architecture was fine-tuned to perform detection and classification of ALL, where the data is first classified into normal or abnormal.

In the next step, the abnormal category is further classified into L1, L2 and L3 subtype categories. The last fully connected layer is modified from binary classes (normal, abnormal) to four classes classes, while keeping the rest of the layers the same.

Through experiments, it was evident that the CNN base model outperform the conventional SVM-based model in terms of accuracy and its performance is in par with enhanced ensemble SVM from Phase II. However, CNN has more steps, so, the time needed to run it is longer than SVM. The CNN models are very good at automatically learning the optimal features. However, its performance is not always the best during classification, as the fully connected layers use parameters that have to be fine-tuned manually. To solve this issue, hybrid models that combine CNN and SVM are proposed by several researchers (Kang *et al*., 2018; Liu *et al*., 2018). These systems use CNN for feature extraction and SVM for classification. This research work, moving in the same path, also combines CNN and SVM and includes procedures that can improve its performance.

The kernel functions used in the proposed system are Linear Kernel, Polynomial Kernel, (RBF), Gaussian Kernel, exponential kernel, Laplacian kernel, Bessel function kernel, Gaussian Radial Basis Function, ANOVA RBF kernel, Laplace RBF and hyperbolic or Sigmoid Kernel.The hybrid CNN-ensemble SVM classifier is enhanced to include the selection step described in Phase II. Thus, Phase III of the research methodology proposes three systems as given below:

1. Hybrid CNN-ensemble SVM classifier
2. Hybrid CNN-ensemble SVM using DCS
3. Hybrid CNN-ensemble SVM using DES

All three classifiers listed above works in two stages. In the first stage, the AlexNet CNN extracts the features and feeds those features extracted to the second stage. The second stage then uses the ensemble SVM classifier to classify the features extracted from AlexNet CNNs. The hybrid model proposed replaces the last three fully connected layers of base model by the ensemble SVM classifier. In this stage, dynamic selection methods, DCS and DES, are used, so that only optimal base classifiers are used during classification. Thus, the hybrid model is enhanced by combining CNN with ensemble SVM with DCS/DES method.

The DES method selects five optimal classifiers during the construction of the ensemble system. During aggregation of results, while using ensemble with DES, a weighted ensemble of networks method is used. In this method, the proposed model considers the performance of each SVM using a weight that denotes its contribution to the final classification. This method has been used to enhance classification system performance by using individual SVM's performance to the result of the respective base classifier. The weights are estimated by first calculating the probability of each class and then using it to calculate an evaluation score. The proposed hybrid system will reduce the chance of overfitting, number of parameters and the time & process complexities.

In order to meet the above-listed objectives, the research methodology was designed in three phases. Each phase was designed separately to satisfy two points. The first was to improve the performance of the task connected to it, while the second was to integrates these tasks together in a manner that could increase the system's performance of ALL classification. The phases were integrated using a simple I/O (Input/Output) interface, where the output from Phase I was used as input to Phases II and III. The working of each phase along with the optimization methods used is described in the following sections. The first phase, pre-processing, performs two tasks, namely, enhancement and white blood cell identification.

3.1. Noise Removal

Noise in images are visual distortions caused due variations in brightness or color information. The noise in microscopic images is handled by an algorithm that combines the advantages of two frequently used transformation-based algorithms, namely, Discrete Wavelet Transformation (DWT) and K-Singular Value Decomposition (K-SVD).

These issues are solved, in this research work, by proposing a unified algorithm that combines contrast adjustment algorithm with noise removal and edge enhancement algorithms. The contrast variations are corrected using an adaptive histogram equalization algorithm. The distortions in the image is removed using a hybrid DWT and K-SVD algorithm. This algorithm beings with DWT coefficients to obtain LL, LH, HL and HH subbands, The LL subband is then

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divided into edge and non-edge regions using its contrast information. The edge region is enhanced using the sigmoid function, while the noise in the non-edge regions are reduced using K-SVD algorithm.

3.2. ROI-Extraction

The second task of preprocessing phase is the extraction of White Blood Cells (WBC) from the enhanced microscopic image.

The methodology behind the proposed segmentation method involves two steps. The first step enhances the working of two conventional algorithms, whose results are then combined to form a final set of segments in the second step. The two algorithms considered during the design of the proposed algorithm are the watershed algorithm and K-means clustering-based algorithm.

The watershed algorithm is enhanced through the use of a set of techniques, that when applied sequentially can produce accurate segments in a fast manner. The proposed enhanced watershed algorithm is designed using color intensity, Otsu's threshold algorithm, enhanced watershed segmentation algorithm, region merging algorithm and pruning algorithm. The K-means clustering-based segmentation algorithm is enhanced through the use of an automatic technique to determine the initial seeds using a subtractive clustering algorithm. The algorithm sets K as 3 since there are three types of blood cells in microscopic images. The algorithm is further enhanced through the use of a computation reduction algorithm, which can speed up the process of clustering and thus, segmentation. The results of the two enhanced segmentation algorithms are then combined by first generating a mean segmentation image, using which a distance map is constructed. Using this distance map, a weight for each algorithm is estimated. Finally, a majority voting algorithm is used to determine the best segment.

3.3 Steps in CSA-WBC

-The CSA-WBC is designed using two segmentation algorithms, which are combined synergistically to produce accurate grouping of blood cells.The first algorithm enhances watershed algorithm, while the second is a clustering based algorithm.

Steps Involved in CSA-WBC are,

Input : Microscopic Image, I

Step 1 : Segment input image using 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 further refine the segmented result

Output : Three Segments

Input : Microscopic Image M

3.4 Steps in PFKM Algorithm are,

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

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

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

c. Store 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 centre assign cluster i= cluster j,

Distance= D_{new}

End if

Until Convergence

Step 4: Output clustered results

The segmented images are shown below,

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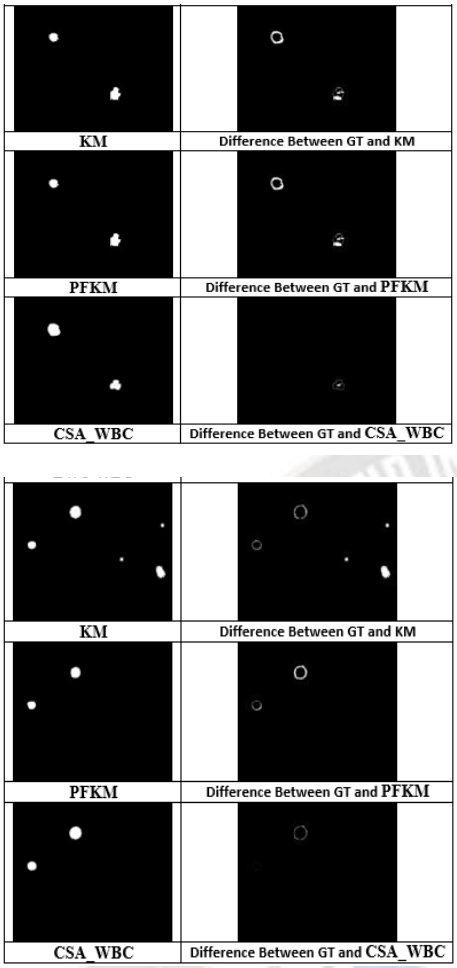

3.3 Classification using Machine Learning Algorithms

Phase II of the research methodology uses the segmented results to classify the identified white blood cells. The steps involved are, feature engineering and classification. Feature engineering consists of two tasks, namely, feature extraction followed by selection of relevant features . In the classification step, the feature vector obtained from feature engineering is used to classify a cell as normal or cancerous. If cancerous, then to classify them into their types L1, L2 and L3.

3.4 Feature Engineering

In this research work, multiple features are extracted from the segmented image. They are, texture features (Energy, Entropy, Contrast, Correlation, Homogeneity), shape features (Area, Perimeter, Eccentricity, Elongation, Compactness, Minor Axis, Major Axis, Solidity, Form Factor, Nucleus-Cytoplasm Ratio), color features (Mean, Standard Deviation) and irregularity of the nucleus boundary (Horizontal Direction, Vertical Direction). Thus, a total of 19 features are extracted.

3.5. Classification

Ensemble systems is used to obtain a more accurate and robust classification by considering multiple views of the same problem. Several researchers have used this idea and proved that multiple classifiers work better than single classifier [Sesmero *et al.*, 2021].

In this research work, the above-described ensemble system is enhanced in two manners, as listed below.

(i) Usage of optimization procedure that pre-treat the training feature set
(ii) Usage of base classifier selection methods.

Dynamic Classifier Selection - It will Select one single best classifier from the set of base classifiers generated

- Dynamic Ensemble Selection –Among the set of base classifiers generated a subset of best classifier will be selected.

This research work, to further enhance the process of classification, proposes two enhanced methods that combine static selection and dynamic selection in order to maximise the performance of the proposed EC system. The proposed hybrid systems are

(i) EC system using static and dynamic classifier selection
(ii) EC system using static and dynamic ensemble selection

The static selection is done using a pruning algorithm that selects optimal classifiers among the base classifiers constructed before the training step. The resultant set of classifiers are then supplied to a dynamic ensemble or dynamic classifier selection method, whose results are reported as the final classification output. The methodology used by the proposed ensemble systems is presented in Figure 1.

In this research work, a static pruning technique is used, as a preprocessing function to reduce optimal candidate classifiers. Static techniques work to construct a subset of base classifiers of fixed size to improve its performance with respect to the full ensemble, removing the rest of the classifiers that do not meet this objective [Margineantu and Dietterich, 1997; Zhang *et al.*, 2006; Munoz *et al.*, 2009]. The reason for using a static pruning technique with the proposed enhanced EC system is to produce a smaller-sized base classifier set, which can produce the same advantages of the full ensemble system with added advantages like low time complexity.

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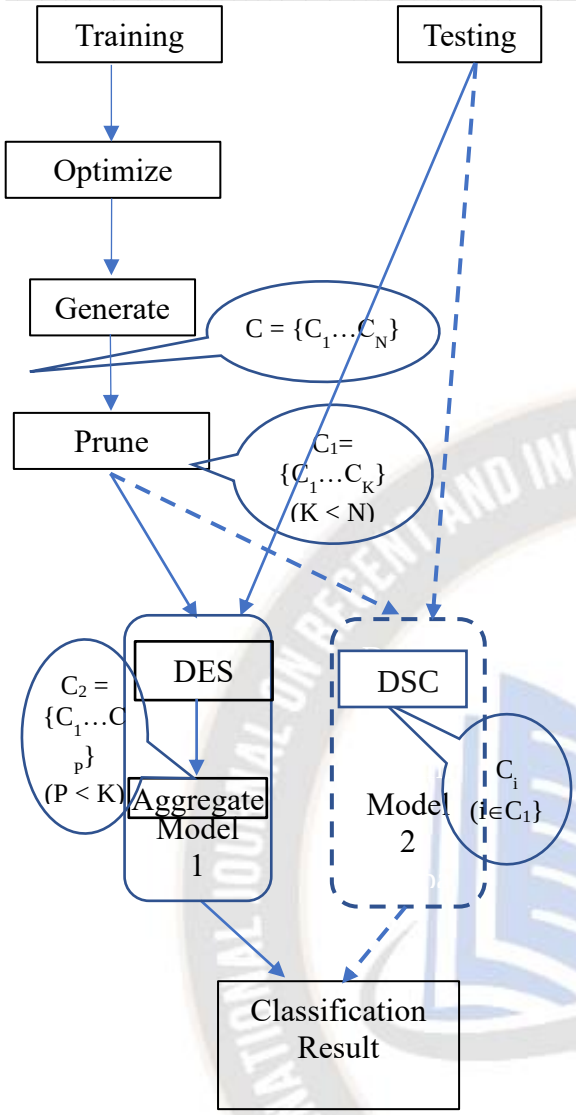

Figure 1 : Proposed Enhanced Ensemble Classification System

The first step selects classifiers that reduce the classification error rate. The rate of error is the percentage of number of classifications that are incorrect by the total number of classifications. The classifiers are then arranged in ascending order of their error rate and this step returns the top 30 classifiers. Let this set be denoted as $\{C_s\}$. In the second step, the kappa statistic pruning technique is used to select the final set of optimal classifiers, $\{C_{ss}\}$.

The kappa statistics returns a value between zero and one, with zero indicating poor agreement and 1 indicating perfect agreement (Landis and Koch, 1977). The resulting set of classifiers is denoted as C_P.

The main aim of the DES is to find a subset of base classifiers, C_O, that can classify a test sample, such that $C_O \subseteq C_P$ and size (C_O) < size (C_P). The classification of test data can be done in three steps.

- Step 1 : Region of Competence Identification. A region surrounding the test data , is used to estimate the base classifier.
- Step 2 : In order to determine the level of the base classifiers Selection Criteria is used in this research work. In this research work, the criteria used is the classification accuracy.
- Step 3 : Determine the selection mechanism, that is, DES or DCS.

That is, all classifiers having the highest accuracy are selected as the most efficient ones, suitable to maximise the performance of the Ensemble system. The number of classifiers selected by DCS is one, while for DES, it is set to 15. The best-performing classifier is selected using an automated procedure that uses the accuracy as the prime metric.

IV. RESULTS AND DISCUSSIONS

Stage 3 experiments focus on the algorithms proposed in Phase III of the research methodology. This stage of experiments also used sensitivity, specificity, accuracy and speed to evaluate the classifiers. The two proposed algorithm CNN-EDCS-SVM and CNN-EDES-SVM were compared with the conventional SVM, conventional CNN and conventional hybrid CNN-SVM classifiers. Figure 4 depicts the accuracy obtained by these classifiers.

The major benefits of the hybrid system proposed is to reduce the chance of overfitting, number of parameters and the time & process complexities.

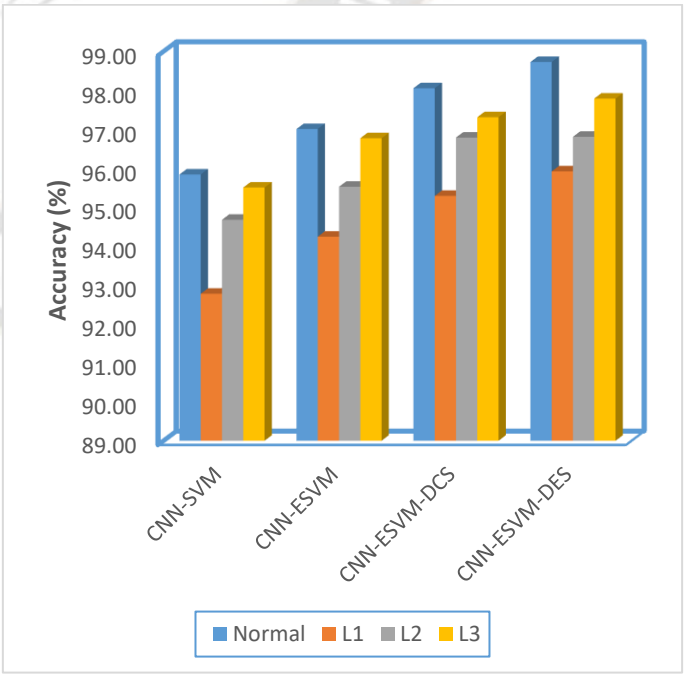

Figure 4 : Accuracy (%) of Hybrid Classifiers

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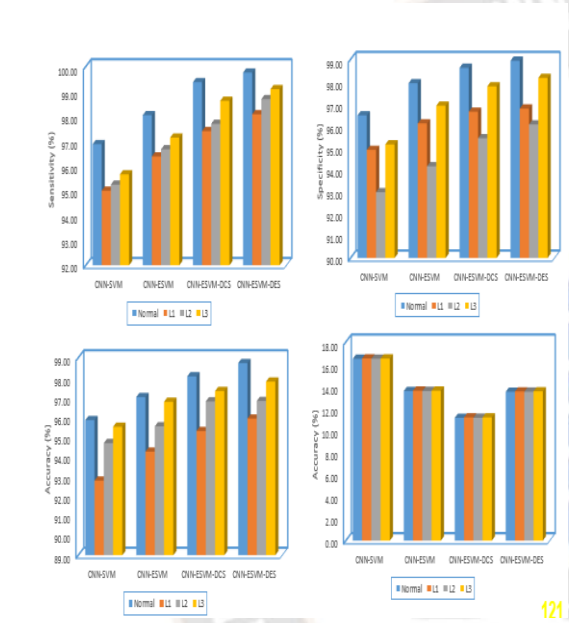
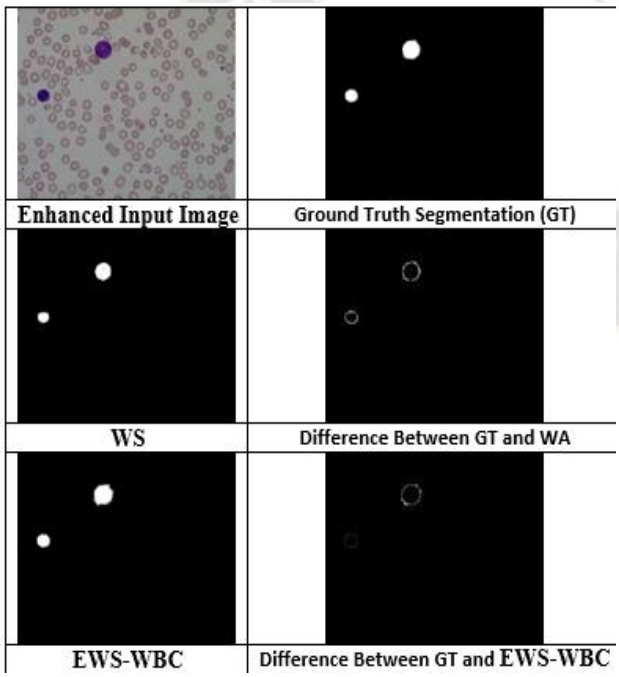
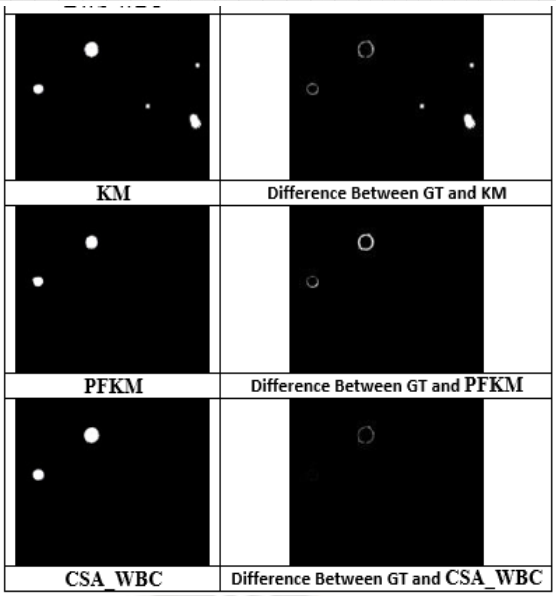
From Phase III experimental results, the hybridization of classifiers have a positive impact on the performance of ALL classification. Comparison of deep and machine learning classifiers showed that CNN outperformed SVM classifier. The proposed hybrid model that used CNN as feature extractor, ensemble SVM with DES for best classifier selection produced maximum advantage during ALL classification. This model produced, on average, a high accuracy of 97.31% accuracy. Thus, from the various results, it could be concluded that the hybrid model that combined CNN with ensemble SVM with dynamic ensemble selection is best suited for ALL classification.







The performance of the proposed algorithms in each phase and its cumulative effect on ALL classification was performed using Acute Lymphoblastic Leukemia Image Database obtained from https://homes.di.unimi.it/scotti/all

The image enhancement algorithms were analysed using four performance metrics, such as PSNR, MSSI, FoM and speed of enhancing a single image in seconds. The proposed unified algorithm was compared with three conventional methods, discrete wavelet transformation, K-singular value decomposition and one existing DWT-KSVD algorithm. From the results, it was proved that the proposed algorithm unified enhancement algorithm outperforms in terms of all the selected performance metrics. Figure 2 shows the PSNR values obtained by five randomly selected test images, where UCED indicates the proposed unified algorithm. This trend envisaged was the same with all the images in the database.

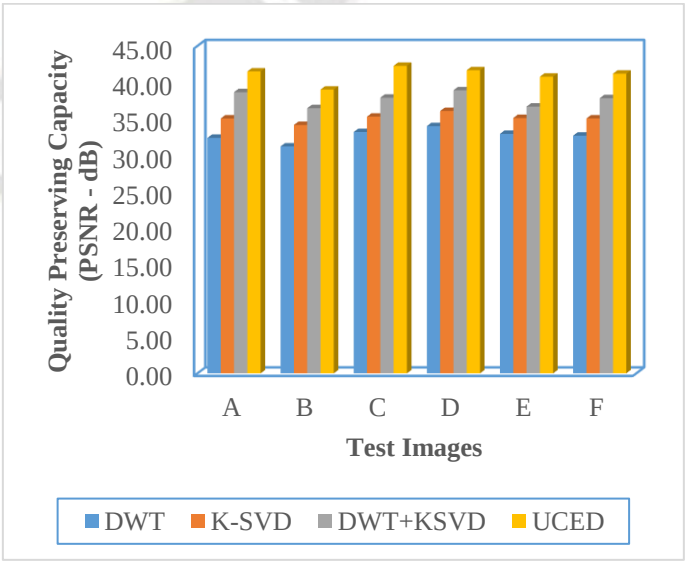


Figure 2 : PSNR (dB) of Enhancement Algorithms

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From the results obtained while evaluating the segmentation algorithms, it could be seen both the enhanced watershed and enhanced clustering-based segmentation algorithms work better when compared with their respective conventional counterparts. However, the proposed algorithm that combines the results of the two enhanced algorithms finds white blood cells in the most efficient manner.

Stage 2 experiments were used to evaluate the machine learning classification algorithm. Four performance metrics, namely, sensitivity, specificity, accuracy and classification speed were used during evaluation. From Phase II experimental results, it could be understood that the proposed ensemble classifiers, enhanced ensemble SVM using dynamic classifier selection (EDCS-SVM) and enhanced ensemble SVM using dynamic ensemble selection (EDES-SVM), were more powerful, when compared to single SVM (SVM) and conventional ensemble classification systems (ESVM). Moreover, comparison between the proposed classifiers showed that enhanced ensemble SVM using dynamic ensemble selection is slightly more efficient than the enhanced ensemble SVM using dynamic classifier selection. The accuracy of the classifiers is shown in Figure 3.

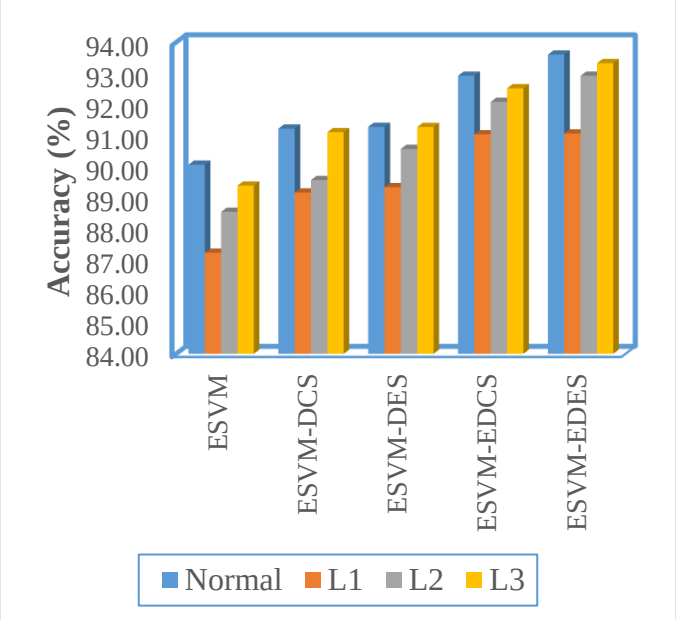

Figure 3 : Accuracy (%) of Machine Learning Classifiers

V. CONCLUSION

From Phase III experimental results, both ensembling of deep learning classifier and hybridization have positive impact on the performance of ALL detection and classification. Comparison of deep and machine learning classifiers showed that CNN outperformed SVM classifier. Among the ensemble models proposed, the CNN-based ensemble model improved ALL classification when compared with SVM-based enhanced ensemble model (EDES-SVM). Stage 3 experiments showed that proposed hybrid model that used CNN as feature extractor, ensemble SVM with best classifier selection as classifier produced maximum advantage during ALL classification. This model produced a high accuracy of 97.31% accuracy. Thus, from the various results, it could be concluded that CNN-EESVM model is best suited for ALL classification.

Machine Learning algorithms have been used in healthcare industries as powerful analytical and diagnostic tool that can assist physicians with maximum efficiency.

The research work was divided into three phases. The first phase focused on preprocessing, which works on improving the visual quality of the input microscopic images and identification of the white blood cells. The enhancement of microscopic images was done using a unified approach that combined contrast adjustment, edge enhancement and denoising into a single algorithm. The second task of Phase I is the extraction of white blood cell regions from microscopic images using segmentation algorithm. The proposed segmentation algorithm merged segments produced by watershed and enhanced K-Means-based clustering algorithm.

Phase II of the research methodology proposed an enhanced SVM based ensemble classifier. The enhancement was achieved by using procedures that reduce the time complexity of ensembling and also to improve its accuracy. The proposed classifier performs classification using two tasks, namely, feature engineering and classification. Feature engineering first extracted four groups of features (texture, shape, color and Irregularity of the nucleus boundary) to form a 19 attribute feature vector. From this feature vector, optimal features were selected using an algorithm namely MRMR algorithm. The constructed ensemble model was enhanced through the use of an algorithm that improved the quality of the training data along with dynamic ensemble selection and dynamic classifier selection algorithms. Apart from this, a pruning algorithm that removed irrelevant base classifiers was also proposed.

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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

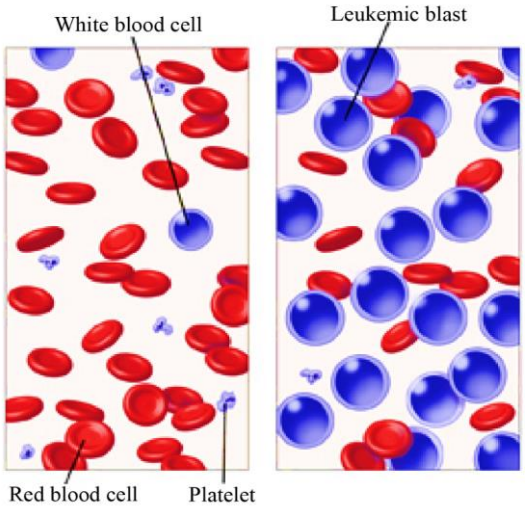

Fig. 1 Sample Microscopic Blood Cell Image

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 outs 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.

SubrajeetMohapatra, DiptiPatraandetal. (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 hausdroff dimension to find the irregularities of the boundary of the nucleus. SVM classifier has been used to derive the results.

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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'.

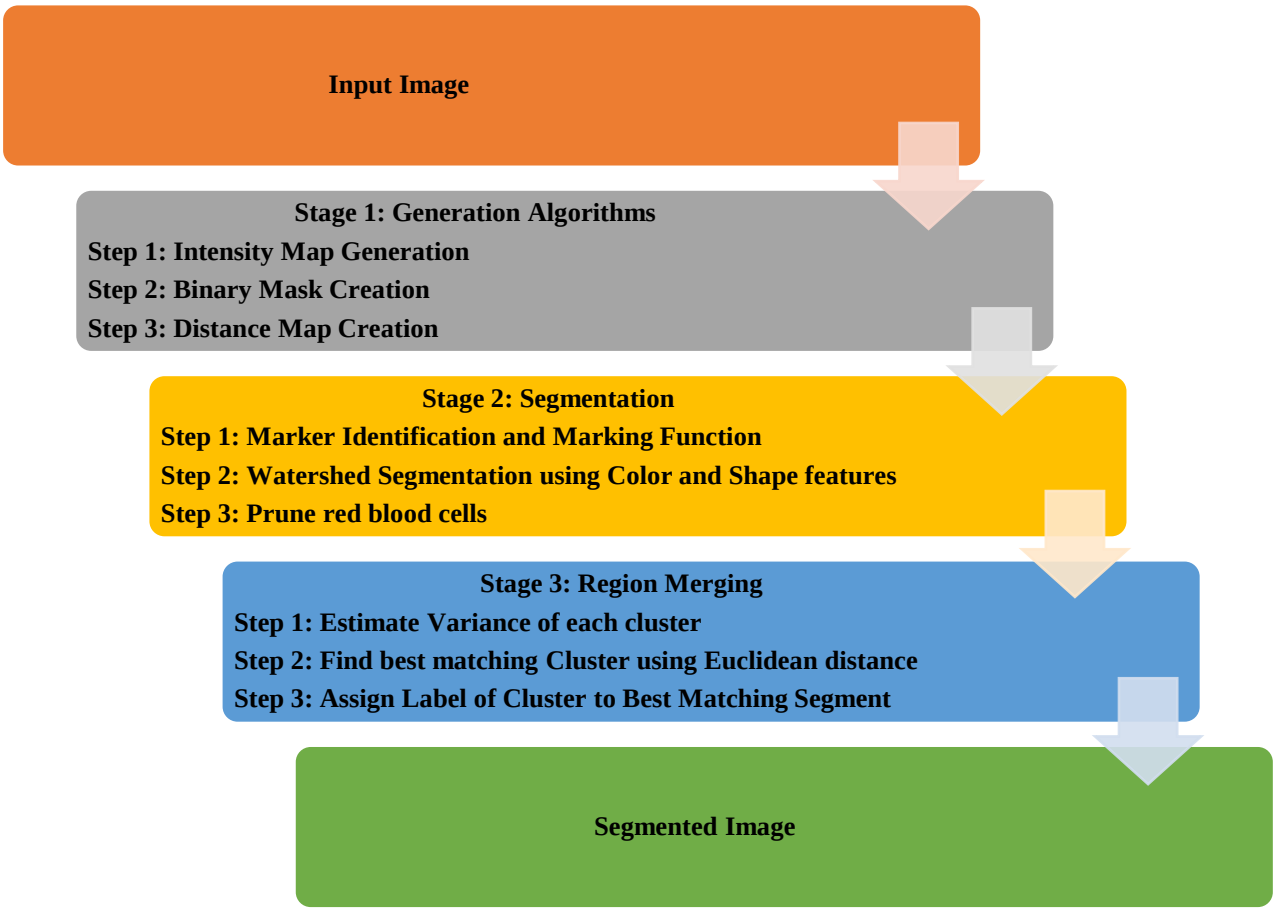


Fig. 2 Methodology

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_i)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,

Distance= D_{new}

End if

Until Convergence

Step 4: Output clustered results

3.4. Step 3: Combine Segment Results

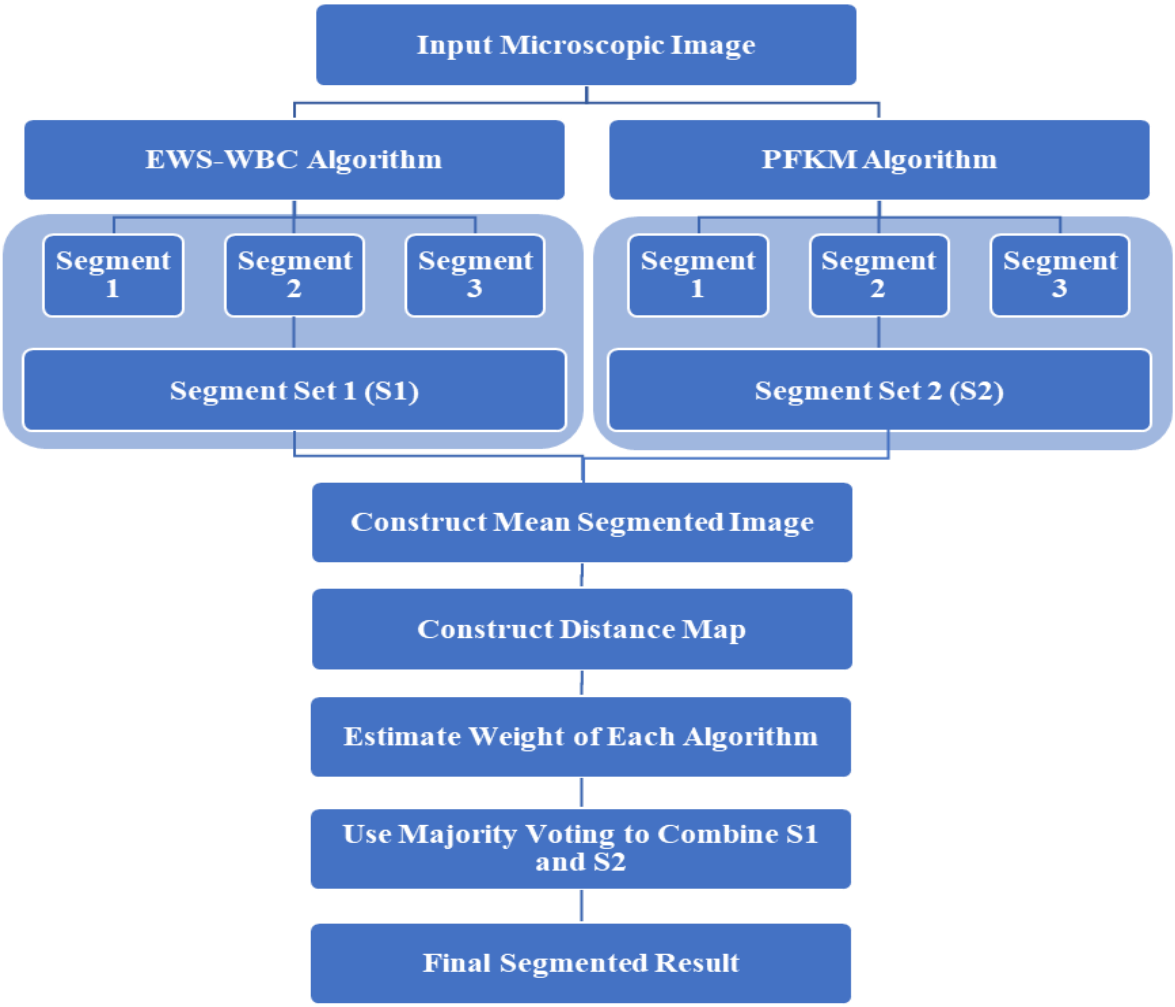


Fig. 3 Combine segment result

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

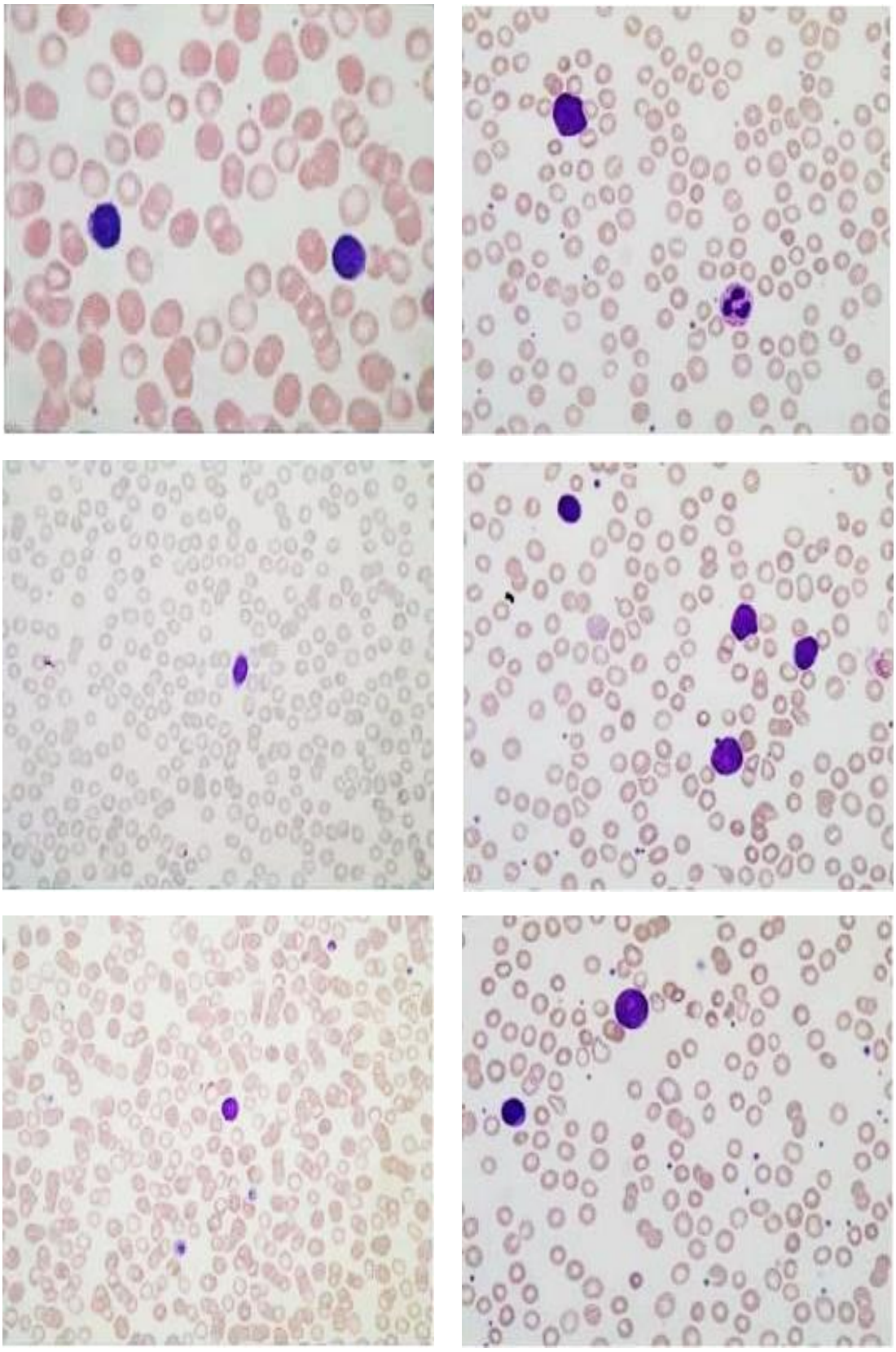
To further improve the perceptibility and visuality of the combined clustering results, morphological filtering is applied. The following operations were performed.

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

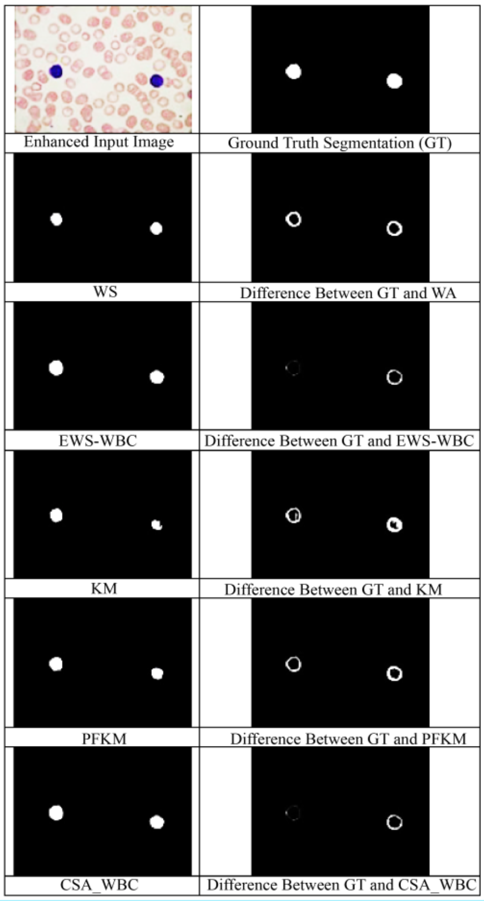
4. Results and Discussions

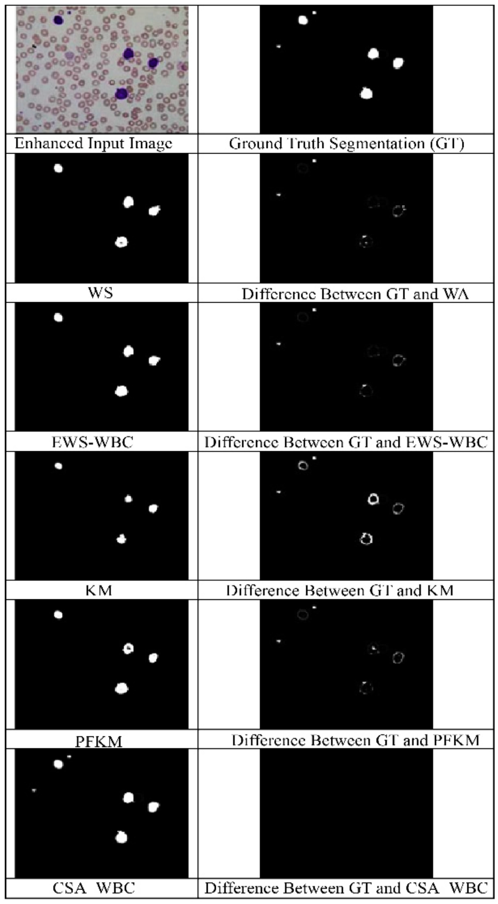
Some of the test images are shown below,

Images with Healthy Cells | **Images with Probable Lymphoblasts**



Visual Results of Images are shown below,


Enhanced Input Image
Ground Truth Segmentation (GT)
WS
Difference Between GT and WA
EWS-WBC
Difference Between GT and EWS-WBC
KM
Difference Between GT and KM
PFKM
Difference Between GT and PFKM
CSA_WBC
Difference Between GT and CSA_WBC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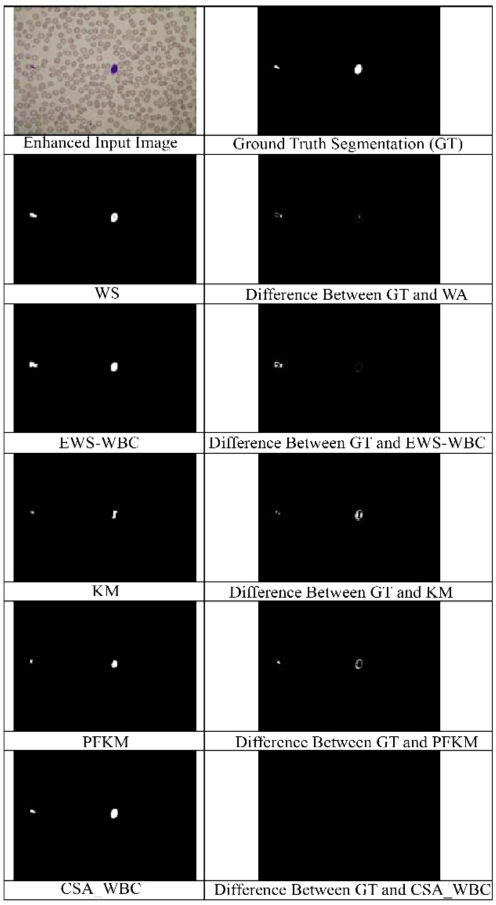
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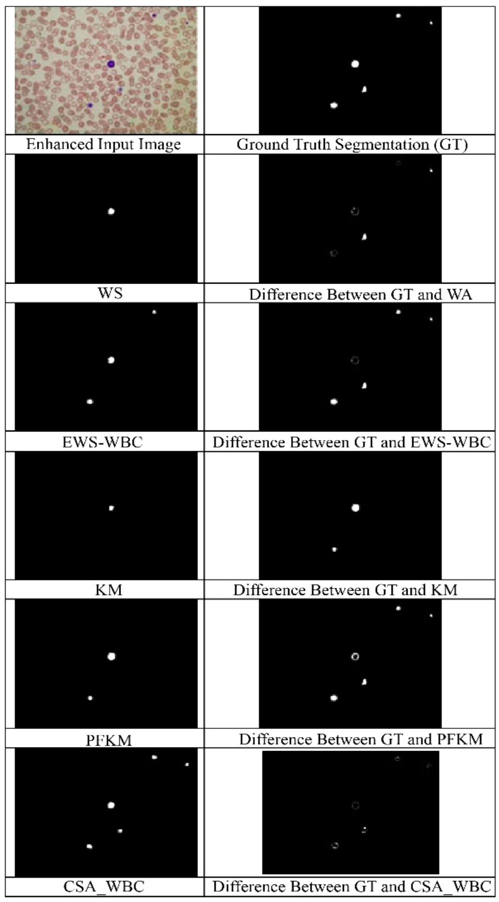
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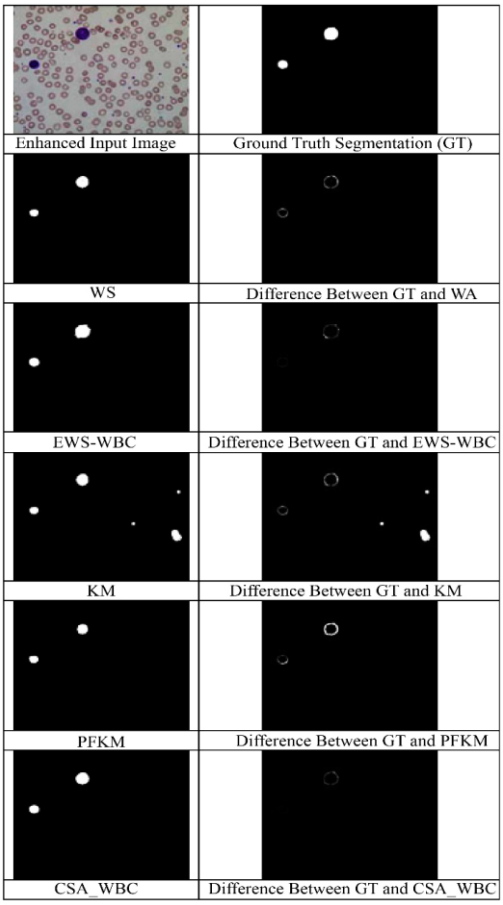

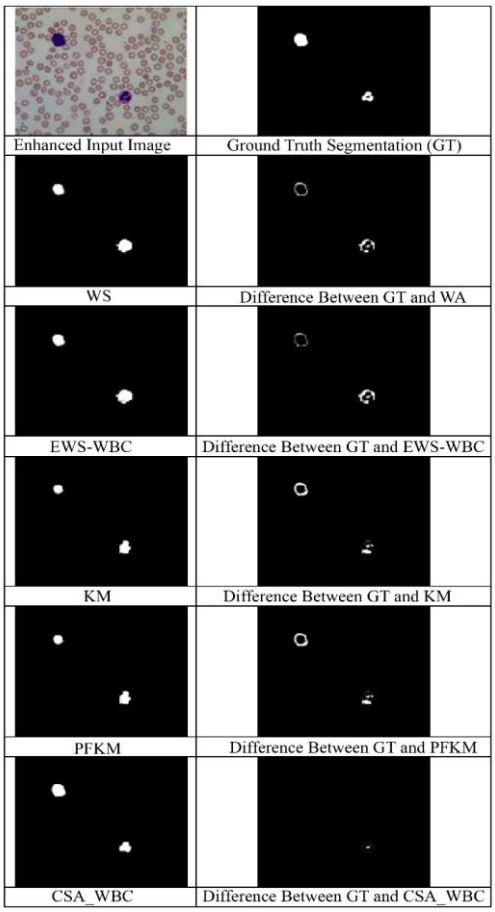

5. Findings

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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Classification of Acute Lymphocytic Leukemic Blood Cell Images using Hybrid CNN-Enhanced Ensemble SVM Models and Machine Learning Classifiers.

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Abstract: Acute Lymphocytic Leukemia is a dangerous kind of malignant cancer caused due to the overproduction of white blood cells. The white blood cells in our body are responsible for fighting against infections, if the WBC increases the immunity will decrease and it would lead to serious health conditions. Malignant cancers such as ALL is life threatening if the disease is not diagnosed at an early stage. If a person is suffering from ALL the disease needs to be diagnosed at an early stage before it starts spreading, if it starts spreading the person's chances of survival would also reduce. Here comes the need of an accurate automated system which would assist the oncologists to diagnose the disease as early as possible. In this paper some of the algorithms that are enhanced to detect and classify ALL are incorporated. In order to classify the Acute Lymphocytic Leukemia a hybrid model has been deployed to improve the accuracy of the diagnosis and it is termed as Hybrid CNN Enhanced Ensemble SVM for the classification of malignancy. Machine Learning classifiers are also used to design the system and it is then compared with enhanced CNN based on the performance metrics.

Keywords : Acute Lymphocytic Leukemia , Ensemble System, Hybrid CNN-SVM.

I. INTRODUCTION

Digital Image Processing has been proved for solving many challenging problems in the field of medical images that could greatly contribute in the discovery of diseases and it would provide the physicians with valuable inputs in the process of diagnosing the diseases without any flaws. This paper proposes a hybrid model that uses Enhanced SVM and CNN for the classification of Acute Lymphocytic Leukaemia (ALL) . To identify malformations in white blood cells, generally, a manual inspection is carried out by an expert pathologist. Manual inspection and identification has several drawbacks like being time-consuming, high cost as expert pathologists are expensive and diagnosis accuracy depends on the experience and workload of the expert. To avoid these drawbacks, an automatic system is preferred by pathologists, who use these systems to help them aid in the correct identification of the disease. Moreover, automated systems help to avoid or reduce human intervention during diagnosis and are cost-effective.

Convolutional neural networks is one of the efficient deep neural networks known as CNN. A CNN will extract features automatically without any human intervention. CNNs will eradicate the need for extracting features manually and it removes the need to identify the features that used to classify images. The CNN will directly extract features from images given as input. The features are not pretrained whereas they are learned when the network trains the images thereby making the automatic features extracted by deep learning models are accurate for challenging tasks in image processing.

Leukemia is also known as blood cancer, in which it would result in the rapid overproduction of abnormal white blood cells. Blood cancer occurs when the white blood cells in the bone marrow quickly increase and will eventually end up in destroying normal blood cells. It is considered to be the 11th top cancer type worldwide [Lin *et al.*, 2021]. In order to reduce death related to leukemia, it is important to treat them at the early stage.

An automatic ALL classification (ALL-C) system consists of four steps, namely, preprocessing, identification of white blood cells, feature extraction and classification. [Bukhari *et al.*, 2022; Mustafa *et al.*, 2022]. The proposed system is designed by enhancing the working of each step of the automated system and then combining them to further improve the performance of the ALL-C system.

"To design an Automatic ALL Classification System of the form

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$\mathfrak{R} = DC + EMC$

where $\mathfrak{R}$ is the output indicating the classification of ALL using hybrid deep learning and ensemble machine learning classifiers. The classification operation is of the form

$\mathfrak{R} = \oplus(m_i) \rightarrow \wp(m_i) \rightarrow \varsigma(m_i)$

where $\rightarrow$ denotes the sequential application of operations. The classification output is any one of the pre-defined target label set {Normal, L1, L2, L3} and is to be performed using machine learning and deep learning classifiers."

Extraction of white blood cells from 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, it Indicates red blood cells

-Gray-white ,Indicates background

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

To accomplish this problem statement, the primary research objective was set to strengthen the clinical decision support system by designing an automatic system that enhances the operation of each step involved during ALL-C inorder to increase the overall accuracy and speed of leukemia classification.

II. LITERATURE SURVEY

Xiang li et al. (2018) have investigated a method for the classification of blood cell, to segregate white blood cells and red blood cells. They have used deep convolutional neural networks.

A method was analysed by Khot s et al. (2013) in which they have extracted the features from the images and had applied it to the classifier.

Himali et al. (2015) have investigated that when compared with watershed transform , histogram equalizing methods and k means clustering, the shape based features were more accurate for counting leukemic cells.

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

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Acute leukemia grows rapidly and becomes severe within a short period, while chronic spreads slowly and takes longer to reach the advanced stage. Leukemia Classification is based on the type of white blood cells involving myeloid or lymphoid.

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 made use of shape based features to detect different cells like basophils ,monocytes, eosinophils and lymphocytes. Finally they have diagnosed the disease based on the immature cell count

Xiang li et al. (2018) have investigated a method for the classification of blood cell, to segregate white blood cells and red blood cells. They have used deep convolutional neural networks.

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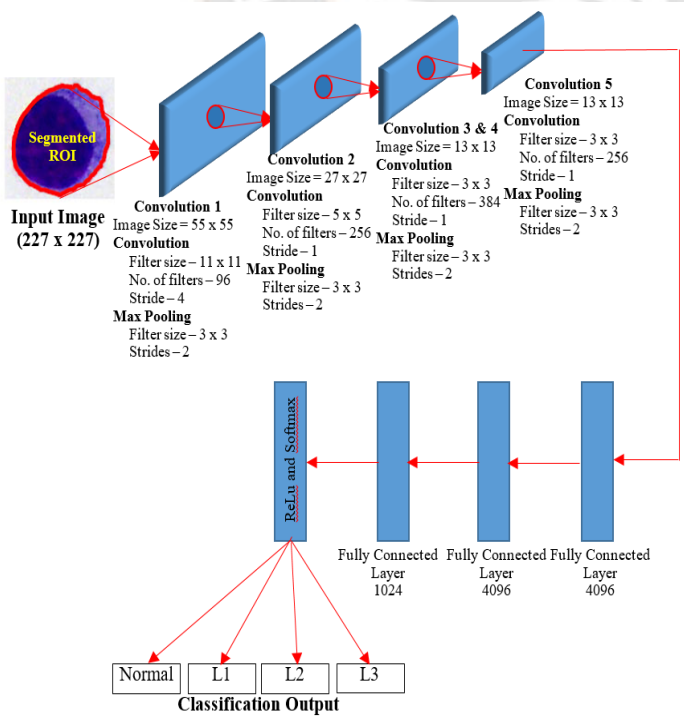
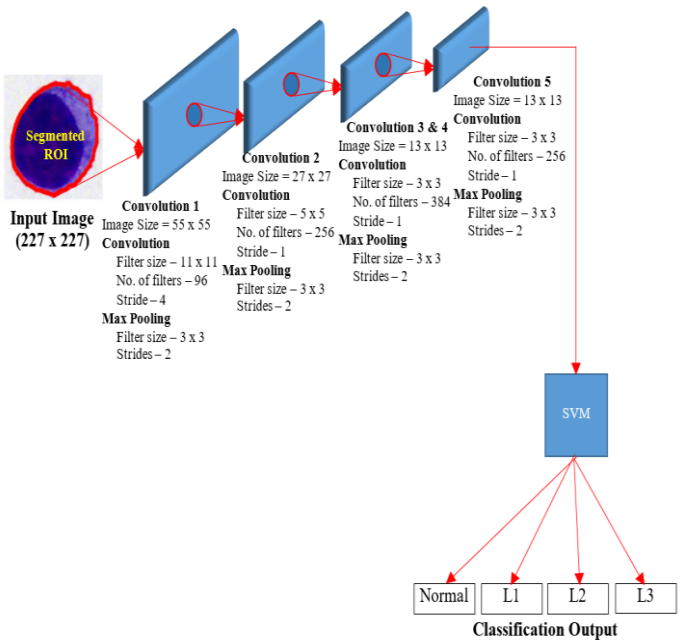
III. PROPOSED METHODOLOGY

The research work has implemented an AlexNet that is pretrained for ALL detection and classification. The concept of transfer learning to retrain the pretrained model with respect to the existing problem was used to design the deep neural network. The RGB images with 227*227 are given as input. The AlexNet Model has got 5 convolutional layers with 3 max polling layers. Each of the convolutional layers have Rectied Linear Unit (ReLU). The last 3 layers such as fully connected layer, softmax layer and classification layer of the pretrained AlexNet were used for Transfer Learning. In the proposed AlexNet architecture the data will be first classified into normal or abnormal. The feature vector size has been reduced by using another fully connected layer with 1024 neurons was added. The layer has been fully connected binary classification (normal, abnormal) probability using softmax function followed by further classifying it into L1, L2 and L3 . In order to further classify it the last fully connected layer is modified from binary classes to four classes output probability by keeping the remaining layers the same.

Transfer learning in machine learning is retraining the pre trained model with respect to the problem. Transfer learning has got advantages such as it is fast as well as effective. The parameters such as the filter size, the number of filters, and stride for each layer are shown in Figure 1.



Through experiments, it was evident that the CNN base model outperforms the conventional SVM-based model in terms of accuracy and its performance is at par with enhanced ensemble SVM from Phase II. However, CNN has more steps hence the time needed to run it is longer than SVM. The CNN models are very good at automatically learning the optimal features. However, its performance is not always the best during classification, as the fully connected layers use parameters that have to be fine-tuned manually. To solve this issue, hybrid models that combine CNN and SVM are proposed by several researchers. These systems use CNN for feature extraction and SVM for classification. This research work, moving in the same path, also combines CNN and SVM and includes procedures that can improve its performance



The proposed hybrid system is designed to combine CNN with ensemble SVM. The base SVM classifiers are created by differing the kernel functions used. The kernel functions used in the proposed system are Linear Kernel, Polynomial Kernel, (RBF), Gaussian Kernel, exponential kernel, Laplacian kernel, Bessel function kernel, Gaussian Radial Basis Function, ANOVA RBF kernel, Laplace RBF and hyperbolic or Sigmoid Kernel. Another point from Phase II is that not all base classifiers in the classification system help with classification. For this purpose, the hybrid CNN-ensemble SVM classifier is enhanced to include the selection step described in Phase II. Thus, Phase III of the research methodology proposes three systems as given below:

- Hybrid CNN-ensemble SVM classifier
- Hybrid CNN-ensemble SVM using DCS
- Hybrid CNN-ensemble SVM using DES

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The proposed hybrid classifiers works in two stages.

In the first stage, the AlexNet CNN extracts the deep features and feeds them to the second stage. The second stage then uses the ensemble SVM classifier to classify the deep feature maps extracted from AlexNet CNNs. The hybrid model proposed replaces the last three fully connected layers of base model by the ensemble SVM classifier. In this stage, dynamic selection methods, DCS and DES, are used, so that only optimal base classifiers are used during classification. Thus, the hybrid model is enhanced by combining CNN with ensemble SVM with DCS/DES method. The DES method selects five optimal classifiers during the construction of the ensemble system.

Aggregation of results, while using ensemble with DES, is done using a weighted ensemble of networks method. In this method, the proposed model considers the performance of each SVM using a weight that denotes its contribution to the final classification. The main aim of this method is to enhance classification system performance by using individual SVM's performance to the result of the respective base classifier. The weights are estimated by first calculating the probability of each class and then using it to calculate an evaluation score. The main advantages of the proposed hybrid system are to reduce the chance of overfitting, number of parameters and the time & process complexities.

3.1 Best Base Classifier Selection Algorithm

- Input

Set of Base Classifiers (S), Classification Accuracy (A)

Output

Set of best performing classifiers (BHC) that are used to construct SVM ensemble

- The Algorithm

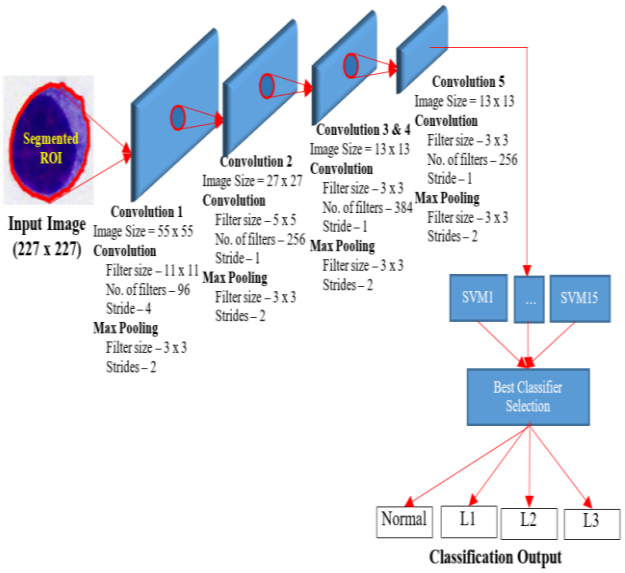
Step 1 : BHC = { }

Step 2 : Arrange base classifiers in S in descending order of its associated accuracy

Step 3 : BHC = BHC + $\{C_1\}$ + $\{C_2\}$ + $\{C_3\}$ + $\{C_4\}$ + $\{C_5\}$

– Step 4 : Return BHC

- The returned BHC has the best performing classifier set



3.2 Classification using Deep Learning Algorithm

The nodes will process the input and the results will be communicated to the next layer of nodes. This process will be repeated until it reaches an output layer. One major problem with ML models is with the feature extraction process, which is hand-crafted. DL models are capable of focusing on the right features by themselves with very little or no human intervention.

To perform early detection of ALL, Phase III proposes a DL classification model based on Convolutional Neural Network (CNN or ConvNet) classifier. This model, called as the base model in this research work, is designed using the AlexNet CNN model based on the transfer learning method, in which deep feature maps were extracted and classified.

CNN will be convolved across the image in the input data and uses convolutional layers for feature extraction. The CNN eliminates the need for human intervention by identifying the features by itself and classifying the images. CNN will extract the features directly from the images. The features are not pre-trained and they will be learned while the network trains on a collection of images. The automatic feature extraction makes deep learning models highly accurate for challenging tasks in Image Processing.

One major issue with CNN is when the size of the training dataset is small, then the issue of overfitting arises (Xiao *et al.*, 2021). To solve this issue, the training set size has been increased through the use of augmentation methods. Data Augmentation methods are implemented through the use of image manipulation methods to increase the size of the training set. Seven manipulation methods were used. They are height shift, width shift, zoom, horizontal flip, vertical flip,

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rotation and shearing. By applying image manipulation methods, the training set size was increased and normalized.

The input for the proposed base model AlexNet are the RGB colored images with 227x227 pixel resolution. The base model is designed with five convolutional layers along with three max polling layers followed by Rectied Linear Unit . Transfer learning was performed using the FCL, softmax layer and classification layer of the pre-trained AlexNet are used. The proposed AlexNet architecture was fine-tuned to perform detection and classification of ALL, where the data is first classified into normal or abnormal.

In the next step, the abnormal category is further classified into L1, L2 and L3 subtype categories. The last fully connected layer is modified from binary classes (normal, abnormal) to four classes classes, while keeping the rest of the layers the same.

Through experiments, it was evident that the CNN base model outperform the conventional SVM-based model in terms of accuracy and its performance is in par with enhanced ensemble SVM from Phase II. However, CNN has more steps, so, the time needed to run it is longer than SVM. The CNN models are very good at automatically learning the optimal features. However, its performance is not always the best during classification, as the fully connected layers use parameters that have to be fine-tuned manually. To solve this issue, hybrid models that combine CNN and SVM are proposed by several researchers (Kang *et al*., 2018; Liu *et al*., 2018). These systems use CNN for feature extraction and SVM for classification. This research work, moving in the same path, also combines CNN and SVM and includes procedures that can improve its performance.

The kernel functions used in the proposed system are Linear Kernel, Polynomial Kernel, (RBF), Gaussian Kernel, exponential kernel, Laplacian kernel, Bessel function kernel, Gaussian Radial Basis Function, ANOVA RBF kernel, Laplace RBF and hyperbolic or Sigmoid Kernel.The hybrid CNN-ensemble SVM classifier is enhanced to include the selection step described in Phase II. Thus, Phase III of the research methodology proposes three systems as given below:

1. Hybrid CNN-ensemble SVM classifier
2. Hybrid CNN-ensemble SVM using DCS
3. Hybrid CNN-ensemble SVM using DES

All three classifiers listed above works in two stages. In the first stage, the AlexNet CNN extracts the features and feeds those features extracted to the second stage. The second stage then uses the ensemble SVM classifier to classify the features extracted from AlexNet CNNs. The hybrid model proposed replaces the last three fully connected layers of base model by the ensemble SVM classifier. In this stage, dynamic selection methods, DCS and DES, are used, so that only optimal base classifiers are used during classification. Thus, the hybrid model is enhanced by combining CNN with ensemble SVM with DCS/DES method.

The DES method selects five optimal classifiers during the construction of the ensemble system. During aggregation of results, while using ensemble with DES, a weighted ensemble of networks method is used. In this method, the proposed model considers the performance of each SVM using a weight that denotes its contribution to the final classification. This method has been used to enhance classification system performance by using individual SVM's performance to the result of the respective base classifier. The weights are estimated by first calculating the probability of each class and then using it to calculate an evaluation score. The proposed hybrid system will reduce the chance of overfitting, number of parameters and the time & process complexities.

In order to meet the above-listed objectives, the research methodology was designed in three phases. Each phase was designed separately to satisfy two points. The first was to improve the performance of the task connected to it, while the second was to integrates these tasks together in a manner that could increase the system's performance of ALL classification. The phases were integrated using a simple I/O (Input/Output) interface, where the output from Phase I was used as input to Phases II and III. The working of each phase along with the optimization methods used is described in the following sections. The first phase, pre-processing, performs two tasks, namely, enhancement and white blood cell identification.

3.1. Noise Removal

Noise in images are visual distortions caused due variations in brightness or color information. The noise in microscopic images is handled by an algorithm that combines the advantages of two frequently used transformation-based algorithms, namely, Discrete Wavelet Transformation (DWT) and K-Singular Value Decomposition (K-SVD).

These issues are solved, in this research work, by proposing a unified algorithm that combines contrast adjustment algorithm with noise removal and edge enhancement algorithms. The contrast variations are corrected using an adaptive histogram equalization algorithm. The distortions in the image is removed using a hybrid DWT and K-SVD algorithm. This algorithm beings with DWT coefficients to obtain LL, LH, HL and HH subbands, The LL subband is then

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divided into edge and non-edge regions using its contrast information. The edge region is enhanced using the sigmoid function, while the noise in the non-edge regions are reduced using K-SVD algorithm.

3.2. ROI-Extraction

The second task of preprocessing phase is the extraction of White Blood Cells (WBC) from the enhanced microscopic image.

The methodology behind the proposed segmentation method involves two steps. The first step enhances the working of two conventional algorithms, whose results are then combined to form a final set of segments in the second step. The two algorithms considered during the design of the proposed algorithm are the watershed algorithm and K-means clustering-based algorithm.

The watershed algorithm is enhanced through the use of a set of techniques, that when applied sequentially can produce accurate segments in a fast manner. The proposed enhanced watershed algorithm is designed using color intensity, Otsu's threshold algorithm, enhanced watershed segmentation algorithm, region merging algorithm and pruning algorithm. The K-means clustering-based segmentation algorithm is enhanced through the use of an automatic technique to determine the initial seeds using a subtractive clustering algorithm. The algorithm sets K as 3 since there are three types of blood cells in microscopic images. The algorithm is further enhanced through the use of a computation reduction algorithm, which can speed up the process of clustering and thus, segmentation. The results of the two enhanced segmentation algorithms are then combined by first generating a mean segmentation image, using which a distance map is constructed. Using this distance map, a weight for each algorithm is estimated. Finally, a majority voting algorithm is used to determine the best segment.

3.3 Steps in CSA-WBC

-The CSA-WBC is designed using two segmentation algorithms, which are combined synergistically to produce accurate grouping of blood cells.The first algorithm enhances watershed algorithm, while the second is a clustering based algorithm.

Steps Involved in CSA-WBC are,

Input : Microscopic Image, I

Step 1 : Segment input image using 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 further refine the segmented result

Output : Three Segments

Input : Microscopic Image M

3.4 Steps in PFKM Algorithm are,

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

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

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

c. Store 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 centre assign cluster i= cluster j,

Distance= D_{new}

End if

Until Convergence

Step 4: Output clustered results

The segmented images are shown below,

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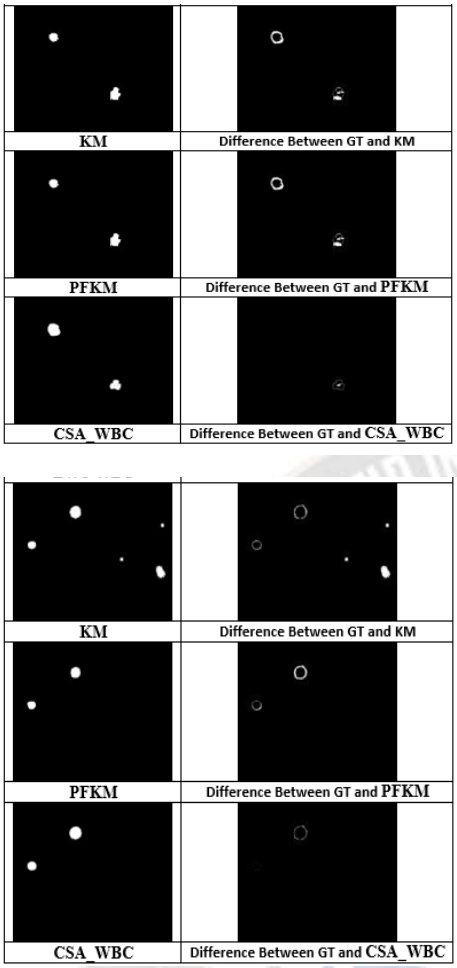

3.3 Classification using Machine Learning Algorithms

Phase II of the research methodology uses the segmented results to classify the identified white blood cells. The steps involved are, feature engineering and classification. Feature engineering consists of two tasks, namely, feature extraction followed by selection of relevant features . In the classification step, the feature vector obtained from feature engineering is used to classify a cell as normal or cancerous. If cancerous, then to classify them into their types L1, L2 and L3.

3.4 Feature Engineering

In this research work, multiple features are extracted from the segmented image. They are, texture features (Energy, Entropy, Contrast, Correlation, Homogeneity), shape features (Area, Perimeter, Eccentricity, Elongation, Compactness, Minor Axis, Major Axis, Solidity, Form Factor, Nucleus-Cytoplasm Ratio), color features (Mean, Standard Deviation) and irregularity of the nucleus boundary (Horizontal Direction, Vertical Direction). Thus, a total of 19 features are extracted.

3.5. Classification

Ensemble systems is used to obtain a more accurate and robust classification by considering multiple views of the same problem. Several researchers have used this idea and proved that multiple classifiers work better than single classifier [Sesmero *et al.*, 2021].

In this research work, the above-described ensemble system is enhanced in two manners, as listed below.

(i) Usage of optimization procedure that pre-treat the training feature set
(ii) Usage of base classifier selection methods.

Dynamic Classifier Selection - It will Select one single best classifier from the set of base classifiers generated

- Dynamic Ensemble Selection –Among the set of base classifiers generated a subset of best classifier will be selected.

This research work, to further enhance the process of classification, proposes two enhanced methods that combine static selection and dynamic selection in order to maximise the performance of the proposed EC system. The proposed hybrid systems are

(i) EC system using static and dynamic classifier selection
(ii) EC system using static and dynamic ensemble selection

The static selection is done using a pruning algorithm that selects optimal classifiers among the base classifiers constructed before the training step. The resultant set of classifiers are then supplied to a dynamic ensemble or dynamic classifier selection method, whose results are reported as the final classification output. The methodology used by the proposed ensemble systems is presented in Figure 1.

In this research work, a static pruning technique is used, as a preprocessing function to reduce optimal candidate classifiers. Static techniques work to construct a subset of base classifiers of fixed size to improve its performance with respect to the full ensemble, removing the rest of the classifiers that do not meet this objective [Margineantu and Dietterich, 1997; Zhang *et al.*, 2006; Munoz *et al.*, 2009]. The reason for using a static pruning technique with the proposed enhanced EC system is to produce a smaller-sized base classifier set, which can produce the same advantages of the full ensemble system with added advantages like low time complexity.

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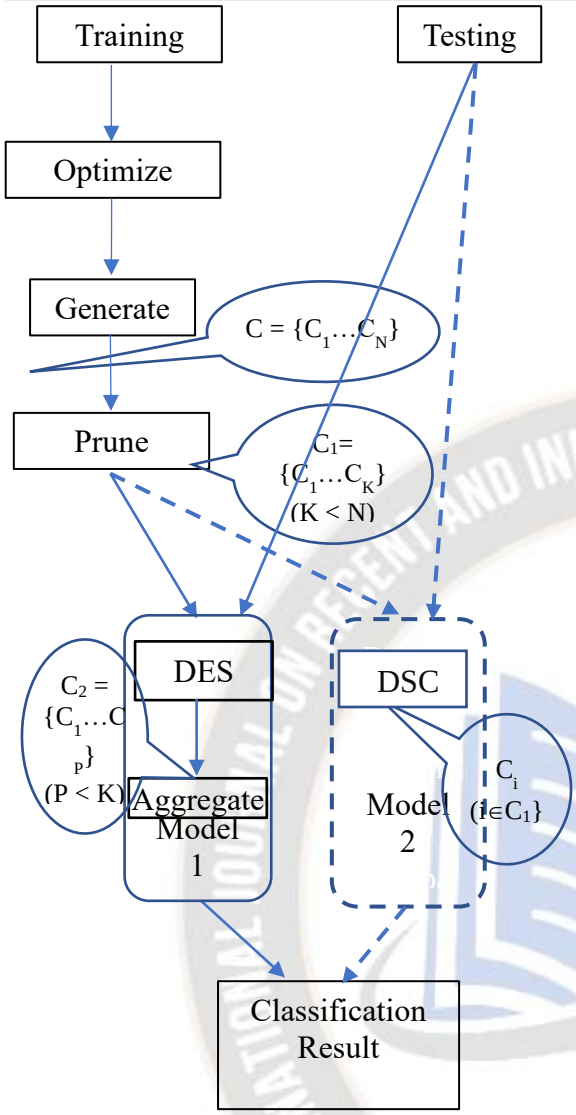

Figure 1 : Proposed Enhanced Ensemble Classification System

The first step selects classifiers that reduce the classification error rate. The rate of error is the percentage of number of classifications that are incorrect by the total number of classifications. The classifiers are then arranged in ascending order of their error rate and this step returns the top 30 classifiers. Let this set be denoted as $\{C_s\}$. In the second step, the kappa statistic pruning technique is used to select the final set of optimal classifiers, $\{C_{ss}\}$.

The kappa statistics returns a value between zero and one, with zero indicating poor agreement and 1 indicating perfect agreement (Landis and Koch, 1977). The resulting set of classifiers is denoted as C_P.

The main aim of the DES is to find a subset of base classifiers, C_O, that can classify a test sample, such that $C_O \subseteq C_P$ and size (C_O) < size (C_P). The classification of test data can be done in three steps.

- Step 1 : Region of Competence Identification. A region surrounding the test data , is used to estimate the base classifier.
- Step 2 : In order to determine the level of the base classifiers Selection Criteria is used in this research work. In this research work, the criteria used is the classification accuracy.
- Step 3 : Determine the selection mechanism, that is, DES or DCS.

That is, all classifiers having the highest accuracy are selected as the most efficient ones, suitable to maximise the performance of the Ensemble system. The number of classifiers selected by DCS is one, while for DES, it is set to 15. The best-performing classifier is selected using an automated procedure that uses the accuracy as the prime metric.

IV. RESULTS AND DISCUSSIONS

Stage 3 experiments focus on the algorithms proposed in Phase III of the research methodology. This stage of experiments also used sensitivity, specificity, accuracy and speed to evaluate the classifiers. The two proposed algorithm CNN-EDCS-SVM and CNN-EDES-SVM were compared with the conventional SVM, conventional CNN and conventional hybrid CNN-SVM classifiers. Figure 4 depicts the accuracy obtained by these classifiers.

The major benefits of the hybrid system proposed is to reduce the chance of overfitting, number of parameters and the time & process complexities.

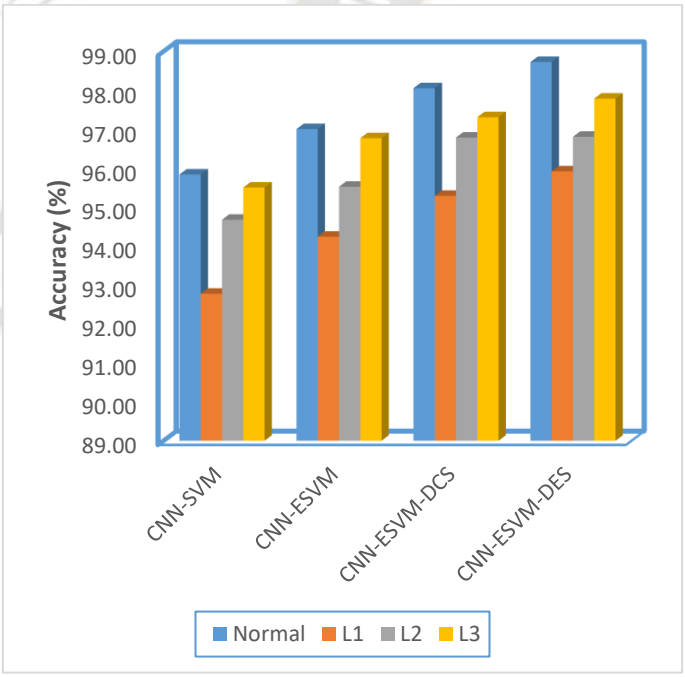

Figure 4 : Accuracy (%) of Hybrid Classifiers

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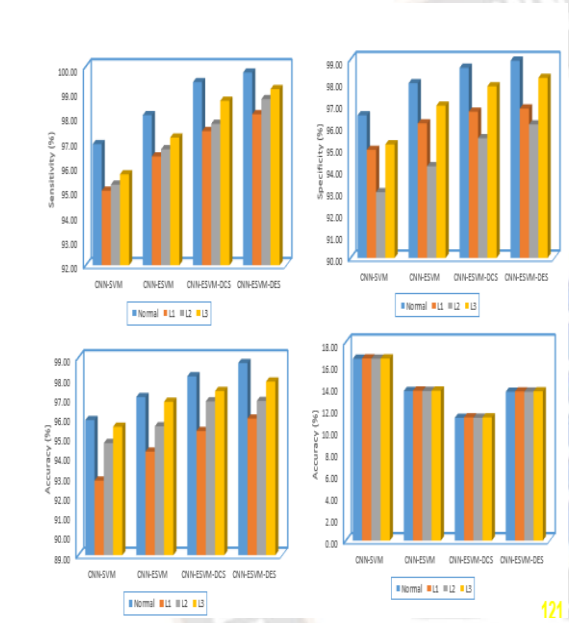
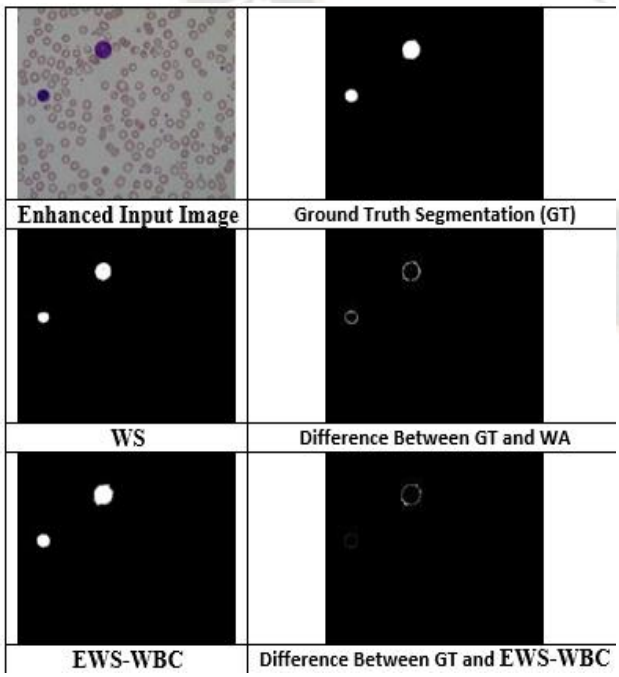
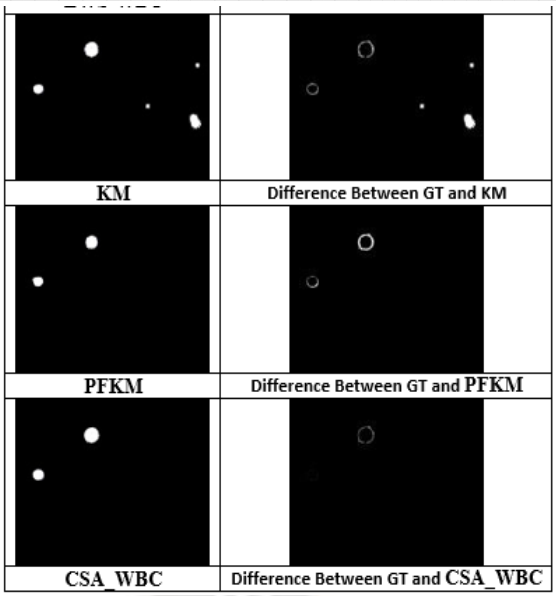
From Phase III experimental results, the hybridization of classifiers have a positive impact on the performance of ALL classification. Comparison of deep and machine learning classifiers showed that CNN outperformed SVM classifier. The proposed hybrid model that used CNN as feature extractor, ensemble SVM with DES for best classifier selection produced maximum advantage during ALL classification. This model produced, on average, a high accuracy of 97.31% accuracy. Thus, from the various results, it could be concluded that the hybrid model that combined CNN with ensemble SVM with dynamic ensemble selection is best suited for ALL classification.







The performance of the proposed algorithms in each phase and its cumulative effect on ALL classification was performed using Acute Lymphoblastic Leukemia Image Database obtained from https://homes.di.unimi.it/scotti/all

The image enhancement algorithms were analysed using four performance metrics, such as PSNR, MSSI, FoM and speed of enhancing a single image in seconds. The proposed unified algorithm was compared with three conventional methods, discrete wavelet transformation, K-singular value decomposition and one existing DWT-KSVD algorithm. From the results, it was proved that the proposed algorithm unified enhancement algorithm outperforms in terms of all the selected performance metrics. Figure 2 shows the PSNR values obtained by five randomly selected test images, where UCED indicates the proposed unified algorithm. This trend envisaged was the same with all the images in the database.

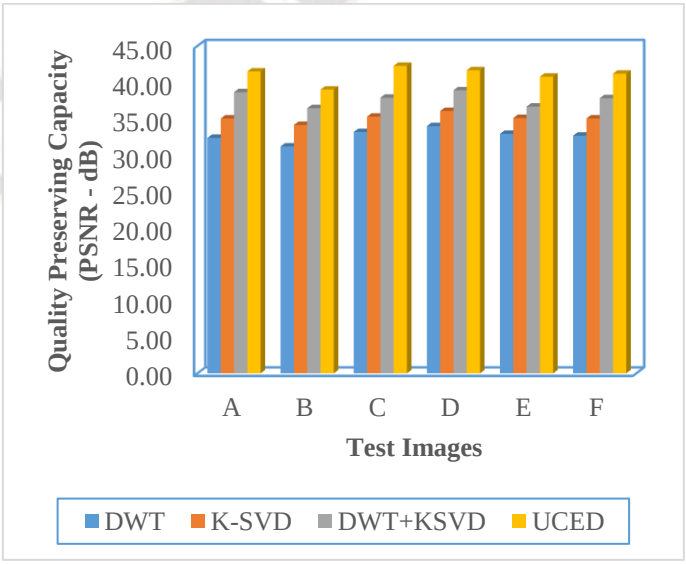


Figure 2 : PSNR (dB) of Enhancement Algorithms

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From the results obtained while evaluating the segmentation algorithms, it could be seen both the enhanced watershed and enhanced clustering-based segmentation algorithms work better when compared with their respective conventional counterparts. However, the proposed algorithm that combines the results of the two enhanced algorithms finds white blood cells in the most efficient manner.

Stage 2 experiments were used to evaluate the machine learning classification algorithm. Four performance metrics, namely, sensitivity, specificity, accuracy and classification speed were used during evaluation. From Phase II experimental results, it could be understood that the proposed ensemble classifiers, enhanced ensemble SVM using dynamic classifier selection (EDCS-SVM) and enhanced ensemble SVM using dynamic ensemble selection (EDES-SVM), were more powerful, when compared to single SVM (SVM) and conventional ensemble classification systems (ESVM). Moreover, comparison between the proposed classifiers showed that enhanced ensemble SVM using dynamic ensemble selection is slightly more efficient than the enhanced ensemble SVM using dynamic classifier selection. The accuracy of the classifiers is shown in Figure 3.

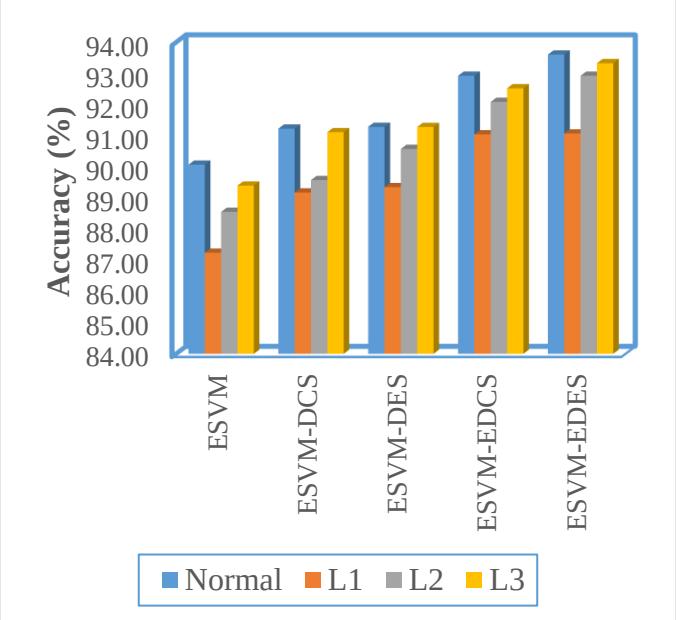

Figure 3 : Accuracy (%) of Machine Learning Classifiers

V. CONCLUSION

From Phase III experimental results, both ensembling of deep learning classifier and hybridization have positive impact on the performance of ALL detection and classification. Comparison of deep and machine learning classifiers showed that CNN outperformed SVM classifier. Among the ensemble models proposed, the CNN-based ensemble model improved ALL classification when compared with SVM-based enhanced ensemble model (EDES-SVM). Stage 3 experiments showed that proposed hybrid model that used CNN as feature extractor, ensemble SVM with best classifier selection as classifier produced maximum advantage during ALL classification. This model produced a high accuracy of 97.31% accuracy. Thus, from the various results, it could be concluded that CNN-EESVM model is best suited for ALL classification.

Machine Learning algorithms have been used in healthcare industries as powerful analytical and diagnostic tool that can assist physicians with maximum efficiency.

The research work was divided into three phases. The first phase focused on preprocessing, which works on improving the visual quality of the input microscopic images and identification of the white blood cells. The enhancement of microscopic images was done using a unified approach that combined contrast adjustment, edge enhancement and denoising into a single algorithm. The second task of Phase I is the extraction of white blood cell regions from microscopic images using segmentation algorithm. The proposed segmentation algorithm merged segments produced by watershed and enhanced K-Means-based clustering algorithm.

Phase II of the research methodology proposed an enhanced SVM based ensemble classifier. The enhancement was achieved by using procedures that reduce the time complexity of ensembling and also to improve its accuracy. The proposed classifier performs classification using two tasks, namely, feature engineering and classification. Feature engineering first extracted four groups of features (texture, shape, color and Irregularity of the nucleus boundary) to form a 19 attribute feature vector. From this feature vector, optimal features were selected using an algorithm namely MRMR algorithm. The constructed ensemble model was enhanced through the use of an algorithm that improved the quality of the training data along with dynamic ensemble selection and dynamic classifier selection algorithms. Apart from this, a pruning algorithm that removed irrelevant base classifiers was also proposed.

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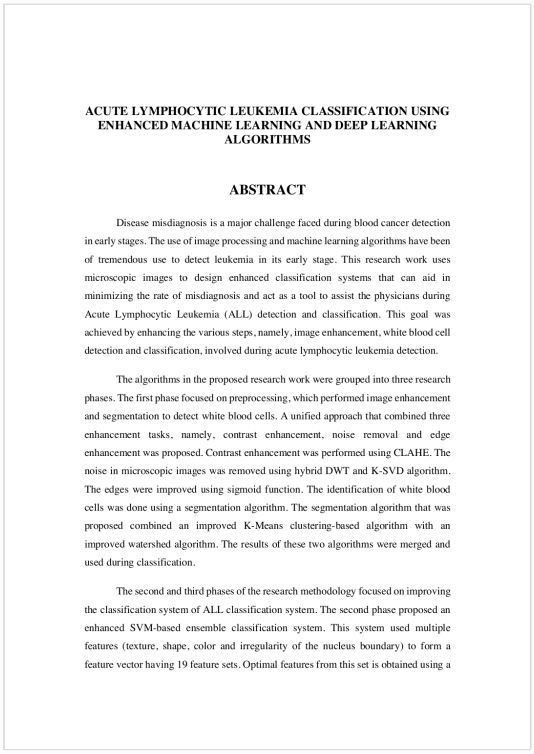

ACUTE LYMPHOCYTIC LEUKEMIA CLASSIFICATION USING ENHANCED MACHINE LEARNING AND DEEP LEARNING ALGORITHMS

ABSTRACT

Disease misdiagnosis is a major challenge faced during blood cancer detection in early stages. The use of image processing and machine learning algorithms have been of tremendous use to detect leukemia in its early stage. This research work uses microscopic images to design enhanced classification systems that can aid in minimizing the rate of misdiagnosis and act as a tool to assist the physicians during Acute Lymphocytic Leukemia (ALL) detection and classification. This goal was achieved by enhancing the various steps, namely, image enhancement, white blood cell detection and classification, involved during acute lymphocytic leukemia detection.

The algorithms in the proposed research work were grouped into three research phases. The first phase focused on preprocessing, which performed image enhancement and segmentation to detect white blood cells. A unified approach that combined three enhancement tasks, namely, contrast enhancement, noise removal and edge enhancement was proposed. Contrast enhancement was performed using CLAHE. The noise in microscopic images was removed using hybrid DWT and K-SVD algorithm. The edges were improved using sigmoid function. The identification of white blood cells was done using a segmentation algorithm. The segmentation algorithm that was proposed combined an improved K-Means clustering-based algorithm with an improved watershed algorithm. The results of these two algorithms were merged and used during classification.

The second and third phases of the research methodology focused on improving the classification system of ALL classification system. The second phase proposed an enhanced SVM-based ensemble classification system. This system used multiple features (texture, shape, color and irregularity of the nucleus boundary) to form a feature vector having 19 feature sets. Optimal features from this set is obtained using a

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