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Int. J. Clin. Res. Med. Sci. (2026) 1(2):1–10
Article ID: IJCRMS-2026-014

Hematological Malignancy Identification via K-means based ROI Extraction

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Abstract

Identifying hematological diseases early on and classifying them helps give patients improved clinical options. Moreover, it is of great difficulty to perform the analysis of the image of a smear of peripheral blood. In addition, the analysis takes more time. Generally, an expert pathologist has a fairly heavy study load, having to study large numbers of images, and suffers a delay because of inter and intra-observer variability. Consequently, a number of CAD schemes were developed that automatically diagnose hematology diseases. As a result, laboratory technicians and pathologists may devote their time to more complicated activities. Please consult the internet for more information. This paper describes the automated detection of blood disorders using image processing with a computer-aided diagnostic system (CAD). The technique implements various image pre-processing operations to reduce noise and improve contrast and morphological enhancement of the image for better segmentation. Moreover, we also use K-means clustering to extract the Region of Interest(ROI). In essence, the algorithm could identify leukocyte areas from the blood smear image. Geometrical, statistical, and textural feature descriptors, calculated from the extracted ROI, will describe the patterns of abnormal cells. The feature vectors are used by the classifiers, kNN and Naive Bayes, to classify malignant and non-malignant blood cells. The constructed post-concomitant CDSS produces a classification accuracy of 92.8% when applied.

Keywords

• Hematological Malignancy • Leukemia Detection • K-means Clustering • ROI Extraction • Medical Image Processing • Machine Learning Classification

1. Introduction to Hematological Malignancies and Diagnostic Challenges

Advances in medical image processing and pattern recognition offer promising alternatives for automating hematological diagnostics. Several automated systems have been developed using microscopic blood images, machine learning, and deep learning approaches to assist leukemia screening and reduce diagnostic workload [1, 2].

Microscopic analysis of peripheral blood smears remains the gold standard for leukemia detection [3]. In clinical workflows, pathologists manually examine stained smear images to identify morphological anomalies in WBCs, such as nuclear irregularities or cytoplasmic granularity. However, this manual process is not only time-consuming and labor-intensive but also prone to inter-observer variability and diagnostic inconsistencies.

Advances in medical image processing and pattern recognition offer promising alternatives for automating hematological diagnostics [4]. Digital image analysis tools can augment pathologists by

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providing consistent, fast, and quantitative evaluations of blood smear specimens. By leveraging algorithms for image segmentation, feature extraction, and classification, computational methods can support early-stage leukemia screening and reduce clinical workload.

One of the fundamental challenges in automated WBC analysis is accurate segmentation. Stained smear images often exhibit noise, overlapping cells, and uneven illumination, which complicate the isolation of individual leukocytes. Traditional thresholding techniques fall short in these scenarios, especially when nucleus and cytoplasm boundaries are poorly defined or when multiple cells appear in close proximity.

Region of Interest (ROI) extraction is a critical preprocessing step in the automated pipeline. By isolating relevant cell components such as the nucleus, downstream processes like morphological feature computation and classification become more robust. Clustering algorithms such as K-means have been extensively used for ROI extraction due to their simplicity and adaptability to intensity-based clustering in histological images.

Classification is important after segmentation to classify the leukocyte. A classification algorithm is used to classify the leukocyte. Classifiers of machine learning like k-Nearest Neighbours(kNN), Support Vector Machines(SVM) and Naive Bayes do their job well in detecting types of leukaemia if provided with sound features. The colour, shape, texture, and statistical characteristics of information extract from segmented images.

The construction of Computer-Aided Diagnosis (CAD) systems for leukaemia thus involves a carefully orchestrated pipeline: starting from image preprocessing, moving through segmentation, and culminating in feature-based classification. Such systems are particularly valuable in regions with limited access to trained hematopathologists or where rapid screening is required [5].

In this study, K-means clustering is employed as the core segmentation strategy for extracting Regions of Interest (ROI). Several clustering-based segmentation methods have been studied for automated leukocyte detection since they can separate cellular components without extensive human intervention[1, 6]. extraction and traditional classifiers for WBC differentiation. The system demonstrates competitive accuracy using a minimal training dataset, illustrating its potential for deployment in resource-constrained clinical settings.

The rest of this document is organized as follows. Section II is about preprocessing techniques used on the smeared images. The K-means segmentation approach for ROI extraction is explained next. Section IV deals with feature engineering, while Section V deals with classification and performance metrics. The findings and future development potential are summarised in Section VI.

2. Preprocessing of Hematological Smear Images

Digital microscopic images of peripheral blood smears often suffer from challenges such as uneven illumination, staining artefacts, and imaging noise. Therefore, preprocessing techniques such as filtering, contrast enhancement, and normalization are essential for improving image quality [7, 8]. These factors can impair segmentation accuracy and must be addressed during preprocessing to ensure robust downstream analysis. Preprocessing aims to enhance relevant cell structures, remove background noise, and normalize intensity levels for consistent Region of Interest (ROI) extraction.

Initially, color images are converted to grayscale to reduce computational complexity and emphasize nuclear intensity, which is most critical for hematological classification. This conversion is typically performed using a weighted average of RGB channels that accounts for human perception bias.

To suppress noise introduced during slide scanning or staining, filtering techniques such as the Wiener

filter and median filter are employed. The Wiener filter adapts to local image variance, making it effective in reducing Gaussian noise while preserving edges. In parallel, the median filter mitigates salt-and-pepper noise, which commonly affects cellular contours.

Following denoising, adaptive histogram equalization is applied to enhance image contrast, particularly in regions where leukocytes are faint or overlapped. Unlike global histogram methods, the adaptive version adjusts contrast locally, improving visibility of the nucleus and cytoplasmic boundaries in WBCs. This step is vital for accurate clustering during segmentation.

Morphological operations such as dilation, erosion, and opening are used next to refine the binary mask derived from thresholding. These operations eliminate small unwanted regions and connect broken segments of relevant cellular structures. The result is a clean and continuous representation of leukocytes while discarding irrelevant background or debris. Various segmentation pipelines have demonstrated that improved preprocessing significantly enhances leukocyte detection performance by preserving important cellular structures [9, 10].

Thresholding is often combined with edge-detection techniques such as Sobel or Canny operators to further isolate object boundaries. These methods detect sharp intensity transitions, which frequently correspond to membrane or nuclear outlines. However, due to variability in staining and cell size, fixed thresholds are insufficient, necessitating adaptive or clustering-based approaches.

A critical output of preprocessing is the generation of an accurate binary or intensity mask, which is subsequently fed into the ROI extraction phase. The quality of this mask directly affects clustering performance, feature extraction, and ultimately classification accuracy. Thus, preprocessing is not a trivial step but a foundational component of the computational pipeline.

Figure 1 presents a simplified flowchart of the preprocessing sequence used in this framework, illustrating the transition from raw image to segmentation-ready input.

The preprocessing pipeline significantly enhances image clarity and structural coherence, laying the groundwork for effective ROI extraction using clustering algorithms. The next section elaborates on the segmentation phase, which utilizes K-means clustering to isolate WBC nuclei and prepare samples for feature computation.

3. Segmentation Using K-means for ROI Extraction

3.1 Terminology and Scope

In this study, we use the term region of interest (ROI) extraction to refer specifically to the isolation of leukocyte nuclei from peripheral blood smear images. This process is a specialized form of segmentation, which more broadly refers to partitioning an image into meaningful regions. Within our pipeline, segmentation encompasses both the K-means clustering step and subsequent morphological refinement, while ROI extraction denotes the final output a binary mask highlighting the nucleus. The terms nucleus isolation and ROI extraction are used interchangeably to describe this final product.

Accurate segmentation of leukocytes from peripheral blood smear images is a critical step in automated hematological analysis [11]. Effective isolation of the nucleus and cytoplasm regions enables reliable feature computation for classification tasks. However, due to variability in staining, overlapping cells, and inconsistent illumination, traditional threshold-based methods often fail to produce consistent results.

In this study, K-means clustering is employed as the core segmentation strategy for extracting Regions of Interest (ROI). K-means is an unsupervised learning algorithm that partitions image pixels into k clusters by minimizing intra-cluster variance. For blood smear images, $k = 3$ typically corresponds to

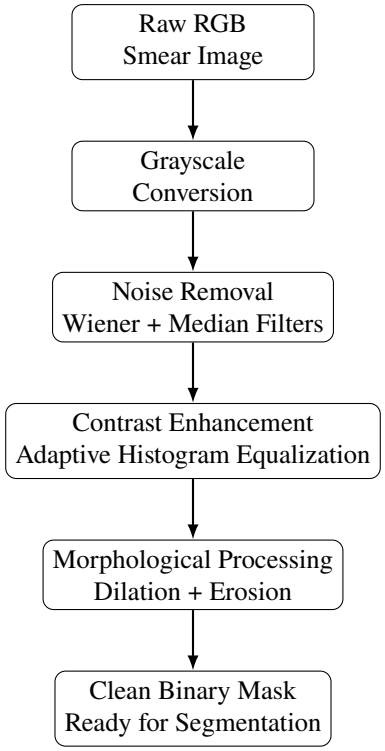

Figure 1: Preprocessing pipeline for hematological smear images. Raw RGB images are converted into grayscale representation, followed by noise reduction using Wiener and median filtering techniques. Adaptive histogram equalization enhances image contrast, while morphological operations including dilation and erosion refine cellular structures and generate a clean binary mask for subsequent segmentation.

background, cytoplasm, and nucleus regions.

The algorithm begins by converting the grayscale image into a one-dimensional vector of pixel intensities. Initial cluster centroids are chosen randomly, and iterative updates are performed using Euclidean distance to assign each pixel to the nearest cluster center. Cluster centers are recalculated until convergence, producing a segmented map.

After clustering, the cluster associated with the lowest average intensity is selected as the nucleus region, as nuclear structures typically appear darker due to Giemsa or Wright staining. Morphological opening and closing are then applied to remove small artifacts and smooth the segmented contours.

The segmentation quality is quantitatively evaluated using three well-established metrics: Probabilistic Rand Index (PRI), Global Consistency Error (GCE), and Variation of Information (VOI). These metrics compare the segmented output against ground truth annotations provided by expert pathologists.

Previous studies have shown that effective segmentation directly influences the reliability of downstream feature extraction and classification stages [9].

Table 1: Segmentation performance comparison across methods. Higher PRI indicates better agreement with ground truth; lower GCE and VOI indicate better segmentation consistency and lower information loss.

Method	PRI ↑	GCE ↓	VOI ↓
K-means (proposed)	0.91	0.08	1.26
Otsu Thresholding	0.84	0.15	2.07
Watershed	0.88	0.11	1.63

The Probabilistic Rand Index (PRI) measures the similarity between the segmented output and ground truth, with values closer to 1 indicating better agreement. Global Consistency Error (GCE) quantifies the extent to which one segmentation can be viewed as a refinement of the other; lower values indicate greater consistency. Variation of Information (VOI) measures the amount of information lost or gained between segmentations, with lower values indicating higher similarity. As shown in Table 1, K-means achieves the highest PRI and lowest GCE and VOI, confirming its superior segmentation performance.

As shown, K-means outperforms the other methods in all three metrics, achieving higher similarity to ground truth (PRI), lower segmentation inconsistency (GCE), and reduced information loss (VOI). These results validate its suitability for leukocyte ROI extraction.

Unlike supervised deep segmentation models, K-means does not require labeled training data, making it advantageous in clinical scenarios with limited annotation resources. Its computational efficiency also supports real-time processing on standard desktop systems.

Overall, using k-means clustering gives a good trade-off between accuracy and speed while maintaining interpretability making it a feasible method for automated blood cell segmentation. The following section explains how segmented ROIs are used to extract morphological , statistical, and textural features for classification purpose.

4. Feature Extraction from Processed Leukocytes

Following ROI segmentation, feature extraction serves as the foundation for classification [12]. The primary objective of this stage is to quantify discriminative properties of leukocytes that correlate with hematological malignancy. Features are derived from geometric, statistical, color, and texture domains to represent the cell's morphology and internal structure.

The combination of morphological and texture-based descriptors has been shown to capture variations between normal and malignant blood cells effectively [13, 14].

Geometric features describe the shape and size of the nucleus, which varies significantly between normal and malignant WBCs. Key metrics include area, perimeter, circularity, eccentricity, and solidity. For instance, circularity is defined as:

$$\text{Circulariy} = \frac{4\pi \times \text{Area}}{\text{Perimeter}^2}$$

A perfectly circular nucleus yields a value close to 1, while irregular or lobulated shapes result in lower values, often observed in abnormal cells.

Eccentricity quantifies deviation from circular symmetry and is computed as:

$$\text{Eccentricity} = \sqrt{1 - \left(\frac{b}{a}\right)^2}$$

The semi-major axis and semi-minor axis of the best-fitting ellipse are denoted as a and b respectively. A circle would get 0 and a line segment would get 1, value-wise. This feature is frequently more prominent due to the presence of malignant nuclei that are tubular and elongated or when the shape takes on more irregularity. Obtaining the intensity histogram statistics of ROI like mean, SD, skewness and kurtosis. The properties measure variances in the distributions of grayscale values and assist in the differentiation of different cell subclasses. We pick up texture features like entropy, contrast, etc., from the grey level.

Color features, although more sensitive to staining variability, remain informative when averaged over normalized channels. Features such as average hue, saturation, and value (HSV) are extracted after

applying color deconvolution techniques that isolate hematoxylin staining.

Figure 2 illustrates the complete feature extraction pipeline, starting from the segmented nucleus and ending in a structured feature vector.

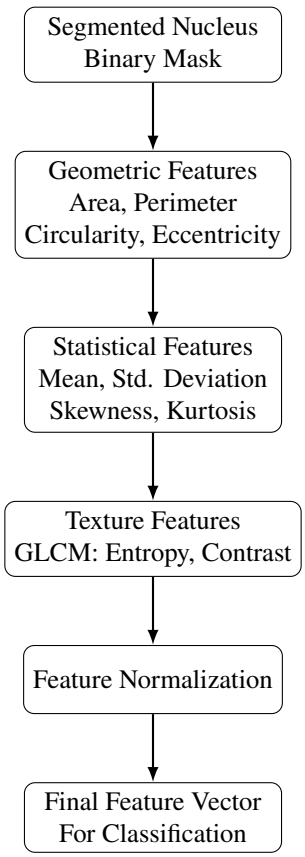

Figure 2: The process of creating a final feature vector from an object's segmented slice. Geometric descriptors, such as area, perimeter, circularity, and eccentricity, are computed with the segmented nucleus mask. Performing GLCM analysis allows one to obtain the texture characteristics while the most important statistical intensity features extracted from histogram are mean, standard deviation, skewness and kurtosis. Extracted features are normalized for the formation of the final classification feature vector.

All features are normalized using Z-score normalization to ensure consistent scale and to enhance classifier performance. The final feature vector serves as input to supervised learning models for classification.

Empirical analysis confirms that combinations of geometric and textural features provide the most robust performance. Color features offer additional discriminative power but are more susceptible to stain and scanner variability, especially across different medical laboratories.

The next section details the classification process, where machine learning models such as k-Nearest Neighbors (kNN) and Naive Bayes are applied to the extracted feature vectors. Performance metrics, including accuracy and confusion matrix, are used to assess model effectiveness.

5. Classification Using kNN and Naive Bayes

The final stage of the proposed diagnostic pipeline involves the classification of leukocyte samples into malignant and non-malignant categories based on extracted features. This task is accomplished using supervised learning algorithms, which assign labels by learning patterns from a labeled training dataset.

Among various options, k-Nearest Neighbors (kNN) and Naive Bayes classifiers are selected due to their simplicity, efficiency, and suitability for low-dimensional feature vectors. Similar machine learning-based diagnostic frameworks have been successfully applied for medical classification tasks involving blood cell images [15, 16] [17].

The kNN algorithm is also a non-parametric classifier. It assigns the class label of the majority class from the k closest samples in the training data. Euclidean distance is used as the distance metric, and the optimal value of k is determined through cross-validation. This approach is robust to noise and performs well with moderate-sized datasets.

Naive Bayes is a probabilistic classifier based on Bayes" theorem. It presumes features are independent and calculates posterior probability of each class label. Essentially, Naive Bayes approach works effectively when class-conditional distributions are clearly distinguishable.

The classification models are trained using a dataset of 60 WBC samples, labeled by expert pathologists. A 10-fold cross-validation scheme is employed to evaluate generalization performance and prevent overfitting. Each fold uses 90% of the data for training and 10% for testing, rotating across the dataset.

Evaluation metrics are accuracy, precision, recall, F1-score, etc. The number of correctly predicted samples over the total number of samples is defined as accuracy:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

In the above equation, the TP, TN, FP and FN are true positives, true negatives, false positives and false negatives respectively.

Figure 3 presents a bar chart comparing the classification accuracy of kNN and Naïve Bayes models on the dataset.

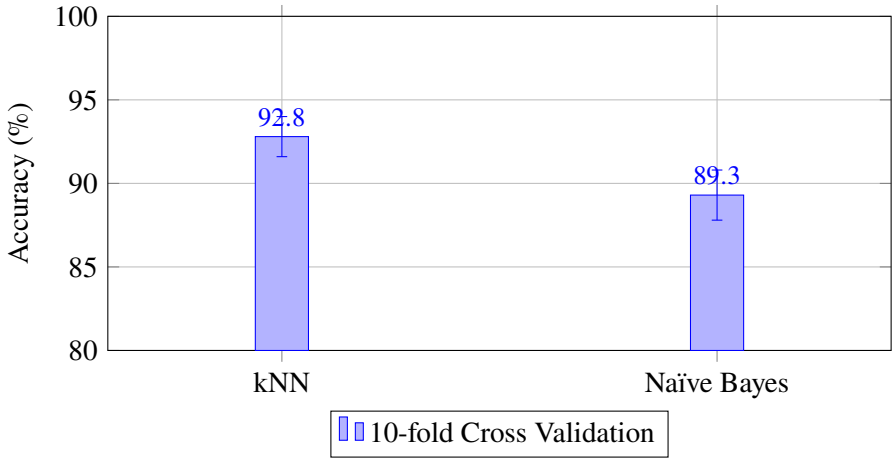

Figure 3: Classification accuracy comparison between k-Nearest Neighbors (kNN) and Naïve Bayes classifiers on the test dataset. kNN achieves an accuracy of 92.8%, outperforming Naïve Bayes with 89.3%. The error bars represent the standard deviation obtained from 10-fold cross-validation.

As shown, the kNN classifier achieves a slightly higher accuracy of 92.8% compared to 89.3% for Naïve Bayes. This marginal improvement may be attributed to kNN's ability to model non-linear class boundaries without explicit assumptions.

In addition to accuracy, the confusion matrix for both models indicates a high true positive rate and minimal false positives, validating the quality of feature extraction and segmentation. These results

confirm the viability of the proposed framework for use in early-stage hematological screening.

The obtained results demonstrate that conventional machine learning classifiers remain effective when appropriate image processing and feature extraction strategies are employed [13].

The next section provides a conclusion summarizing the findings and outlines potential directions for expanding this research, including deeper neural models and real-time deployment in clinical systems.

6. Conclusion and Future Work in Hematological CAD Systems

This paper proposes a complete computer-aided diagnostic framework for hematological malignancies using digital smear images. The suggested pipeline combines image preprocessing, K-means-based ROI segmentation, handcrafted feature extraction, and machine learning classification for automated white blood cell (WBC) recognition associated with leukaemia.

The system begins with a robust preprocessing module that enhances nuclear contrast and removes background noise using filtering and histogram equalization techniques. Morphological operations refine the cleaned binary masks, ensuring the reliable isolation of leukocyte components in diverse staining conditions.

K-means clustering is used to segment cytoplasm, background, and nucleus pixels using K-means Clustering. The K-means approach outperforms Otsu's thresholding and watershed segmenting in terms of quality metrics like (Probabilistic Rand Index) PRI, (Global Consistency Error) GCE, and (Variation of Information) VOI.

A suite of geometric, statistical, and color-based features is extracted from the segmented regions to create discriminative feature vectors. These features capture variations in cell shape, texture, and staining patterns that are indicative of pathological changes in WBC morphology.

Classification using k-Nearest Neighbours (kNN) and Naive Bayes demonstrates high diagnostic accuracy on a small, labeled dataset. The system achieves over 92% accuracy with kNN, confirming the efficacy of the segmentation and feature extraction modules.These results suggest the potential of the framework as a supporting tool in clinical pathology labs, particularly in environments lacking access to expert haematologists [18].

Despite its promise, the system has certain limitations. The reliance on handcrafted features and unsupervised clustering limits adaptability to more complex morphological variations. Additionally, the small dataset size restricts the generalization capability of the trained classifiers. Variability in staining protocols and imaging hardware can also affect model performance across institutions.

In the future, researchers can focus on deep learning models such as CNNs which automatically learn a hierarchy of features from raw images. Utilizing large medical datasets for transfer learning can mitigate data shortage issues and enhance classification robustness [19].

Future research may focus on integrating explainable and trustworthy artificial intelligence methods to improve reliability, transparency, and clinical acceptance of automated diagnostic systems [13, 20].

Moreover, real-time deployment on edge devices or within laboratory information systems (LIS) would enable rapid, point-of-care diagnostics. Incorporating explainability modules and uncertainty quantification could also enhance trust in the system's outputs, aligning with ethical AI principles in healthcare.

In conclusion, the proposed CAD framework provides an interpretable and efficient solution for the early detection of hematological malignancies. Its modular architecture supports future extensions, making it a valuable baseline for automated blood smear analysis in both research and clinical domains.

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