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RESEARCH ARTICLE

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AUTOMATED SICKLE CELL IDENTIFICATION IN DIGITAL BLOOD SMEARS USING FSEF-MOBILENET WITH WOLF BIRD OPTIMIZATION ALGORITHM

Vijayanandh T^{*1}, Santhoshkumar S P², Parvathi R³, Sivaprakash P⁴, Vimala Ithayan J⁵,
Dilip Charaan R M⁶

¹Associate Professor, School of Electrical and Communication, Vel Tech Rangarajan Dr Sagunthala R&D Institute of Science and Technology, Chennai, Tamil Nadu, India.

²Assistant Professor (SG), School of Computing, Vel Tech Rangarajan Dr Sagunthala R&D Institute of Science and Technology, Chennai, Tamil Nadu, India.

³Associate Professor Grade 1, School of Computer Science Engineering and Information Systems, Vellore Institute of Technology, Katpadi, Vellore, Tamil Nadu, India.

⁴Professor, School of Electrical and Communication, Vel Tech Rangarajan Dr Sagunthala R&D Institute of Science and Technology, Chennai, Tamil Nadu, India.

^{5, 6}Associate Professor, School of Computing, Vel Tech Rangarajan Dr Sagunthala R&D Institute of Science and Technology, Chennai, Tamil Nadu, India.

¹<https://orcid.org/0000-0002-6307-4272>, ²<https://orcid.org/0000-0001-8531-759X>, ³<https://orcid.org/0000-0001-7109-134X>,

⁴<https://orcid.org/0000-0002-2777-8889>, ⁵<https://orcid.org/0000-0002-4647-0863>, ⁶<https://orcid.org/0009-0002-1332-4592>

Email: *drvijayanandht@veltech.edu.in, spsanthoshkumar16@gmail.com, 2005.parvathi@gmail.com, sivabtl85@gmail.com,
vimala.ithayan@gmail.com, dilip_charraan@yahoo.co.in

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ABSTRACT

Sickle Cell Disease (SCD), a genetic blood disorder characterised by abnormal red blood cell shape, is sometimes difficult, time-consuming, and susceptible to individual interpretation when inspected under a microscope. To get over these limitations, this study proposes an automated computer-aided diagnostic approach for sickle cell diagnosis from digital blood smear images. The technique begins with preprocessing, which involves resizing and improving images using Adaptive Contrast Limited Adaptive Histogram Equalization (CLAHE) in order to increase the visibility of cellular structures. Red blood cells sometimes be accurately separated from complex smear backgrounds through segmentation using Hierarchical K-Means Clustering. Next, Multi-Scale Gray Level Co-occurrence Matrix (MSGCLCM) features are obtained to capture discriminative textural and morphological patterns across multiple scales. The enhanced features are classified using a special Focal-SE-ECA-Fused MobileNet (FSEF-MobileNet) architecture. This architecture reduces class imbalance and highlights useful features by combining Efficient Channel Attention (ECA) and Squeeze-and-Excitation (SE) techniques with focal loss. Wolf Bird Optimization (WBO), which ensures reduced redundancy and enhanced separation between normal and sickle cells to enhance classification reliability, is used to tune hyperparameter. The proposed approach is analyzed using Python, and the findings indicate that it has a great deal of promise for providing prompt and precise sickle cell disease assistance and achieves an accuracy, precision, recall and FI-score of 97%.



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I. INTRODUCTION

A hereditary disorder known SCD damages the haemoglobin found in red blood cells. Haemoglobin S will develop due to the Haemoglobin Subunit Beta (HBB) gene, which is found on chromosome 11.

A red blood cell's shape is altered by haemoglobin S from a disk to blocking the blood vessels, leading to a sickle. It is less effective at distributing oxygen throughout the body, which result in tissue damage, organ failure, and discomfort [1-3]. Anemia is the result of a lack of blood vessels brought on by sickle cell disease. Other aberrant haemoglobins, like haemoglobin C or haemoglobin F, are produced by SCD patients. A genetic mutation causes the HBB gene, which codes for the beta-globin subunit of haemoglobin, a crucial protein involved in the transportation of oxygen within red blood cells to have a single amino acid substitution at chromosome 11 [4-7]. The aberrant haemoglobin linked to sickle cell disease (SCD), known as haemoglobin S, is created when the amino acid valine takes the place of glutamic acid. Erythrocyte sickling, or the deformation of red blood cells, results from the polymerization of the mutant haemoglobin S into bundles [8]. The World Health Organization (WHO) estimates that, on a typical basis, five percent of people globally are considered to have inherited traits associated with haemoglobin disorders, mainly SCD and thalassemia. In addition, serious haemoglobin abnormalities affect almost 300,000 infants every single year. For SCD, morphological examination of peripheral blood smears (PBS) is an essential diagnostic technique. Infants cannot be diagnosed with SCD using PBS because sickling of cells does not occur until the baby is somewhat older and transitions from generating haemoglobin F to haemoglobin A [9-12]. This is actually the best time to diagnose SCD. As a result, it is only appropriate for diagnosing adults and older children, although it additionally has the potential to track the results of treatment for individuals who have already received a diagnosis. Nevertheless, it is a time-consuming and labor-intensive procedure that cause delays in diagnosis and treatment [13-15]. In order to solve this problem, automated methods for blood sample analysis were developed, which employ machine learning algorithms and image analysis to detect and measure sickle cells. This paper presents an approach for automated SCD in digital blood smears using FSEF-MobileNet integrated with the WBO algorithm. The evaluation process involves preprocessing, segmentation, feature extraction and classification to standardize the image. The process originates with the input image, which undergoes a preprocessing stage where it enhance the quality of input images by removing unwanted distortions, noise and illumination variations [16-18]. A local contrast enhancement method called Adaptive Histogram Equalization (AHE) is used to make features more visible in images with uneven lighting. AHE works on small areas and independently improves contrast in each area.

Because of specialized processing, it also make computations more difficult [19]. Histogram Equalization (HE) enhances overall image contrast by spreading out the intensity levels across the full range. But it fails to handle non-uniform lighting or local contrast variations often present in microscope smear images. To overcome this issue, the proposed system implement resizing and Adaptive CLAHE to ensure uniformity and add contrast limiting to suppress noise and artifacts. The preprocessed image is passed to a segmentation stage where it allows precise isolation and relevant structures. Based on similarities in pixel intensity, texture, or shape properties, red blood cells (RBCs) are able to isolated using the Nearest Neighbour segmentation technique. Nevertheless, it is extremely susceptible to overlapping cells, noise, and uneven illumination, each of which are typical in microscopic blood smear images [20-23]. K-means clustering works by grouping pixels with similar color intensity or texture characteristics into distinct clusters, enabling efficient identification of regions containing potential sickle cells. However, it is sensitive ti the initial selection of centroids which led to inconsistent segmentation results. Therefore, the proposed system uses Hierarchical K-means clustering which is used to achieve more efficient and structured clustering by combining the strengths of hierarchical clustering and K-means. The segmented features are then delivered to feature extraction where it makes easier for the classification model to process and learn from the data. The Gray Level Difference Method (GLDM) determines the absolute gray level difference between a reference pixel and its surrounding pixels at specific orientations and distances. However, as it takes into consideration pixel differences rather than whole co-occurrence patterns, it records only a limited number of spatial interactions, which makes it less informative for complicated textures [24-26]. Gray Level Co-occurrence Matrix helps in capturing textural patterns that differentiate normal RBC from abnormally shaped sickle cells. However, it is computationally intensive, especially for high resolution or color images, as it depends on the number of gray levels and direction angles considered. Therefore, this research proposes a MSGLCM for overwhelmed the confines of the existing methods. Based on extracted features, the automated identification of sickle cells are distinguished between normal and SCD. To classify each cell image, various classification models are illustrated in Table 1.

Table 1: Related works of classification models for Sickle Cell Diagnosis.

SI.NO	Author/Year	Classification	Merits	Demerits	Performance metrics
1.	Sanjeda Sara Jennifer et al [2023] [27]	MobileNet	• Reduce computational complexity. • Highly suitable for real-time based medical image analysis.	• It is sensitive to illumination variations, overlapping cells and dataset imbalance	Attains an accuracy of 96%
2.	Victor Junio Alcantara Cardoso et al [2024] [28]	DenseNet	• It ensure efficient gradient flow during training. • It helps in identifying subtle variations in cell shape and structure.	• Its complex structure make the network less interpretable, which is a concern in clinical diagnostics.	It achieves an accuracy of 96.8%, precision, recall and FI-score of 96.6%
3.	PETER M. DOUGLASS et al [2022] [29]	AlexNet	• It is capable of identifying distinct shape variations and structural irregularities that characterize sickle cells. • It serves as an effective baseline model for medical image classification tasks.	• It requires high computational resources and large labeled datasets for optimal performance.	The performance of AlexNet is 88% of accuracy, 86% of precision, 92% of recall and 89% of FI-score.

4.	Anqi Feng et al [2023] [30]	ResNet-50	- It enables to learn complex and discriminative features that capture subtle morphological differences between healthy and deformed sickle cells - It helps to extract both low-level texture details and high level structural features.	ResNet-50 is sensitivity to noise, uneven illumination and overlapping cells present in microscopic images.	ResNet-50 achieves an accuracy, precision and recall of 95%, 87% and 84%
5.	Amirullah Andi Bramantya et al [2021] [31]	VGG-16-GCN	- VGG-16 efficiently extracts hierarchical spatial and texture features from cell images. - GCN enhances the model's ability to capture relational dependencies among pixel regions. - This hybrid helps in learning both local and global contextual information.	VGG-16-GCN is limited by its high computational demand, training complexity and reduced practical efficiency for real-time biomedical applications.	The combination of VGG-16-GCN achieves the accuracy, precision and recall of 95%, 92% and 97%.

Source: Authors, (2026).

Existing SCD identification have various limitations, hence the proposed FSEF-MobileNet model analyzes the obtained feature representations. This procedure is further improved by the use of the Wolf Bird Optimization Algorithm, which optimizes decision boundaries and adjusts the model's parameters for higher accuracy and faster convergence. The main objectives of this research includes:

- To enhance image quality and for accurate analysis, preprocessing techniques such as resizing and Adaptive CLAHE is executed.
- To segment RBC and allow precise separation of sickled and normal cells, Hierarchical K-means clustering is implemented.
- To capture both global and local intensity relationships of RBC and to extract discriminate texture features, MSGLCM is used.
- To integrate advanced attention and focal mechanism for improved feature representation and to reduce misclassification, FSEF-MobileNet is utilized.
- To optimize hyper-parameters of the classifier and to achieve faster convergence and better classification, WBO algorithm is applied.

II. PROPOSED SYSTEM DESCRIPTION

The proposed approach for Automated SCD in digital blood smears utilizing FSEF-MobileNet with WBO seeks to accurately categorize normal and sickle-shaped red blood cells utilizing an improved image processing and Deep Learning (DL). Figure 1 depicts the block diagram of the proposed model.

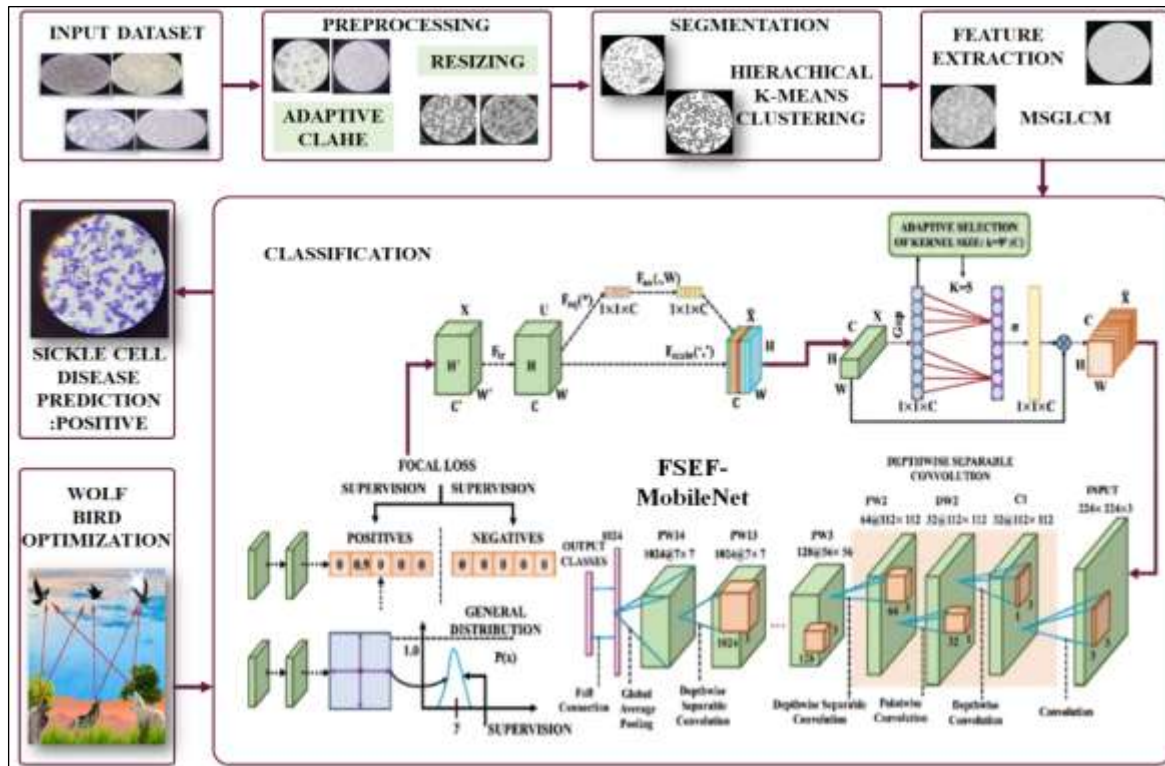


Figure 1: Block diagram of the proposed method.

Source: Authors, (2026).

The process initiates with the preprocessing stage which improves the quality of the input blood smear images by resizing and using Adaptive CLAHE, which improve contrast and eliminate illumination changes, resulting in consistent visual clarity. The improved images are next sent to the segmentation stage, where Hierarchical K-Means Clustering is used to successfully isolate individual red blood cells by grouping pixels according to intensity and spatial distribution. The MSGLCM is used in the feature extraction phase after segmentation to extract complex texture-based characteristics that demonstrate minor structural changes between sickle and healthy cells, such as contrast, correlation, and homogeneity. The FSEF-MobileNet model, which combines MobileNet for lightweight and effective computing, SE and ECA techniques for improving channel interdependencies, and Focal Loss for resolving class imbalance, is used to classify these extracted features. WBO is used to fine-tune hyper-parameters, ensuring optimal convergence and enhanced accuracy, in order to further improve model performance. For early and accurate sickle cell disease identification from digital blood smear images, this integrated framework effectively improves classification precision, lowers computational overhead, and offers a dependable and automated approach.

III. PROPOSED SYSTEM MODELLING

III.1 PREPROCESSING

III.1.1 Resizing

Resizing is a crucial preprocessing step in sickle cell identification from digital blood smear images that ensures consistency and improves detection accuracy. Blood smear images are typically recorded at various magnifications, resolutions, and orientations, resulting in variances in cell size and scale. By resizing all images to a standard dimension, the method ensures that each cell image has a similar scale, allowing the DL network to analyze them evenly. This ensures that the distinguishing characteristics of sickle cells, such as their crescent or elongated form, sharp edges, and uneven curvature, are preserved and precisely documented during feature extraction and categorization.

III.1.1.1 Adaptive CLAHE

Adaptive CLAHE helps to clearly distinguish sickle-shaped cells from normal erythrocytes, which is crucial for accurate classification and segmentation in automated diagnostic systems. The histogram of a digital blood smear image with intensity levels in the range $[0, L-1]$ is represented as a discrete function,

$$h(r_k) = n_k \quad (1)$$

Where, r_k is the k^{th} intensity level and n_k denotes the number of pixels in the image with that intensity. The normalized histogram is expressed as,

$$p_r(r_k) = \frac{n_k}{MN}, \quad k = 0, 1, 2, \dots, L-1 \quad (2)$$

The image dimensions are represented by M and N respectively. The sum of all probability equals 1. Histogram equalization improves global contrast by spreading the intensity values of pixels. By enhancing local variations in texture and shape while reducing background noise, adaptive CLAHE successfully increases the contrast between sickle-shaped and normal red blood cells. Cell boundary visibility, segmentation accuracy, and feature extraction for later classification using models like FSEF-MobileNet architectures are all enhanced as the outcome. Overall, adaptive CLAHE ensures that even in low-contrast areas of the blood smear, the structural details of sickled erythrocytes are visible, allowing for more reliable automated identification and diagnostic decisions.

III.1.1.2 Segmentation- Hierarchical K-Means Clustering

The input blood smear image is first transformed into a feature space, where each pixel is represented as a multi-dimensional vector that includes local shape descriptors, edge magnitude, and grayscale intensity. Every feature vector $s(i, j)$ corresponds to a neighborhood region V_s inside the image. All regions are first regarded as unclassified. Initially, the cluster centroids are initialized at equal distances throughout the intensity or morphological feature range in a coarse clustering step using the K-Means algorithm. Until the intra-cluster variance drops below a predetermined threshold, the initial number of centroids k , is set to one and raised iteratively. This guarantees the clear separation of the three main tissue and cellular regions: sickle cells, normal RBCs, and background. The hierarchical process continues by recursively separating the cluster that corresponds to the aberrant or sickle-like regions, which are distinguished by their elongated shape, low circularity, and intensity variation. Every time the cluster standard deviation surpasses a threshold T_n , the method divides the current cluster into two sub-clusters to refine the division. Adaptively, the threshold is updated as,

$$T_{n+1} = \frac{T_n}{2} \quad (3)$$

This iterative refinement proceeds until the standard deviation of all clusters falls below T_n , ensuring convergence. The K-Means clustering successfully differentiates overlapping and partially distorted sickle cells using this hierarchical method without the need for explicit supervision or pre-labeled data. The process's repetitive structure enables strong adaptation to changes in staining conditions, light, and cell size that are frequently present in microscopic pictures. Additionally, a cluster reliability map that documents the number of splits made during classification is produced by the clustering findings. Higher dependability is indicated by fewer splits, which offers an extra degree of confidence for post-classification refining.

III.1.1.3 Feature Extraction – MSGLCM

To recognize sickle-shaped cells in digital blood smear images, precise identification of RBC borders is required. To improve edge information and reduce microscopic noise, Laplacian operator is used. The Laplacian of a blood smear image (I) can be expressed as,

$$\frac{\partial^2 I}{\partial x^2} + \frac{\partial^2 I}{\partial y^2} \quad (4)$$

The discrete Laplacian at a point $I(x, y)$ is computed as,

$$\nabla^2 I(x, y) = I(x + 1, y) + I(x - 1, y) + I(x, y + 1) + I(x, y - 1) - 4I(x, y) \quad (5)$$

These zero-crossing points correlate to the foreground-background boundary, allowing cell edges to be clearly localized. In the context of sickle cell identification, zero-crossings indicate the sickle-shaped cells' extended or curved borders. To reduce the impact of noise from staining and illumination, the image is convolved with a Gaussian kernel at different scales, minimizing fine-level noise while keeping critical cell borders. At microscopic scales, only prominent structures, such as the primary outlines of sickle cells, are discernible. The spatial link between the gray levels of the identified edge pixel pairs is then examined using the gray-level co-occurrence matrix. MSGLCM components C_θ are described as,

$$C_\theta(m, n) = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} N(I(x, y) = m \& I(x - \sin\theta, y + \cos\theta) = n) \quad (6)$$

Where, if the condition is true, $N(\cdot) = 1$ and if not, it is 0. The combined co-occurrence matrix, taking into account all four directions $(0, \pi/2, \pi, 3\pi/2)$, is represented as,

$$[C] = \frac{1}{4} [C_0 + C_{\pi/2} + C_\pi + C_{3\pi/2}] \quad (7)$$

The modified co-occurrence matrix for edge pixel pair is given in equation 8 and the threshold T used for segmenting sickle and normal RBC is then selected from the MSGLCM is,

$$C_{m,n} = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} N(I(x, y) = m, I(x - \sin\theta, y + \cos\theta) = n), \text{pixel pair is edge} \quad (8)$$

$$T = \arg \max_t \sum_{m=0}^{L-1} \sum_{n=t}^{L-1} c(m, n) \quad (9)$$

The gray-level values of the majority of edge pixel pairs are successfully separated by this threshold, allowing sickle cells which have erratic intensity variations to be distinguished from normal cells, which have smoother, more homogeneous textures. Even in noisy imaging settings, robust identification of sickle cells in digital blood smears can be accomplished using the MSGLCM method.

III.1.1.4 Classification-FSEF-MobileNet

The proposed FSEF-MobileNet is a DL based approach designed to accurately and efficiently detect sickle cells from microscopic images of blood smears. Figure 2 illustrates the diagram of FSEF-MobileNet. The class imbalance between sickled and normal RBC in blood smear pictures is one of the main obstacles to automated sickle cell identification. DL models are typically biased toward the majority class because there are typically significantly more normal cells than sickled cells. The Focal Loss function is used as an enhancement over the conventional Cross-Entropy (CE) loss in order to solve this problem. In binary classification, the CE loss is defined as,

$$CE(p, y) = \begin{cases} -\log(p) & \text{if } y = 1 \\ -\log(1 - p) & \text{otherwise} \end{cases} \quad (10)$$

Where, the ground truth label is represented by $y \in \{0, 1\}$, and the expected probability for the class labeled as $y = 1$ is indicated by $p \in [0, 1]$ and making it easier, we define p_t and rewrite the CE loss as,

$$p_t = \begin{cases} p & \text{if } y = 1 \\ 1 - p & \text{otherwise} \end{cases} \quad (11)$$

$$CE(p, y) = -\log(p_t) \quad (12)$$

However, the CE loss permits many easily categorized normal cells to dominate the total loss in datasets with extreme imbalance, making the model less sensitive to the minority sickled cells. By down-weighting well-classified examples and concentrating the training more on difficult-to-classify or minority cases, the Focal Loss alters this behavior. A modulating factor $(1 - p_t)^\gamma$ is introduced to the CE loss,

$$FL(p_t) = -(1 - p_t)^\gamma \log(p_t) \quad (13)$$

This modification lowers the loss contribution from correctly identified normal cells and shifts attention to challenging or incorrectly categorized sickle cell samples. In doing so, the Focal Loss enhances detection accuracy and resilience even in highly imbalanced datasets by assisting the model in learning more discriminative features for sickle cell identification. The SE block improves the network's attention on the most instructive elements in blood smear images in the proposed automated sickle cell identification system. For a convolutional transformation $Ftr: X \rightarrow U$, with $X \in R^{H' \times W' \times C'}$ and $U \in R^{H \times W \times C}$, let $V = [v_1, \dots, v_C]$ denote the convolutional filters. The output is,

$$u_c = v_c * X = \sum_{s=1}^{C'} v_c^s * x^s \quad (14)$$

Where, convolution is represented by $*$ and v_c^s is a 2D kernel, and the input channel is represented by x^s . By using squeezing and excitation to explicitly describe channel interdependencies, the SE block suppresses unnecessary information while enhancing those that capture sickle cell shape.

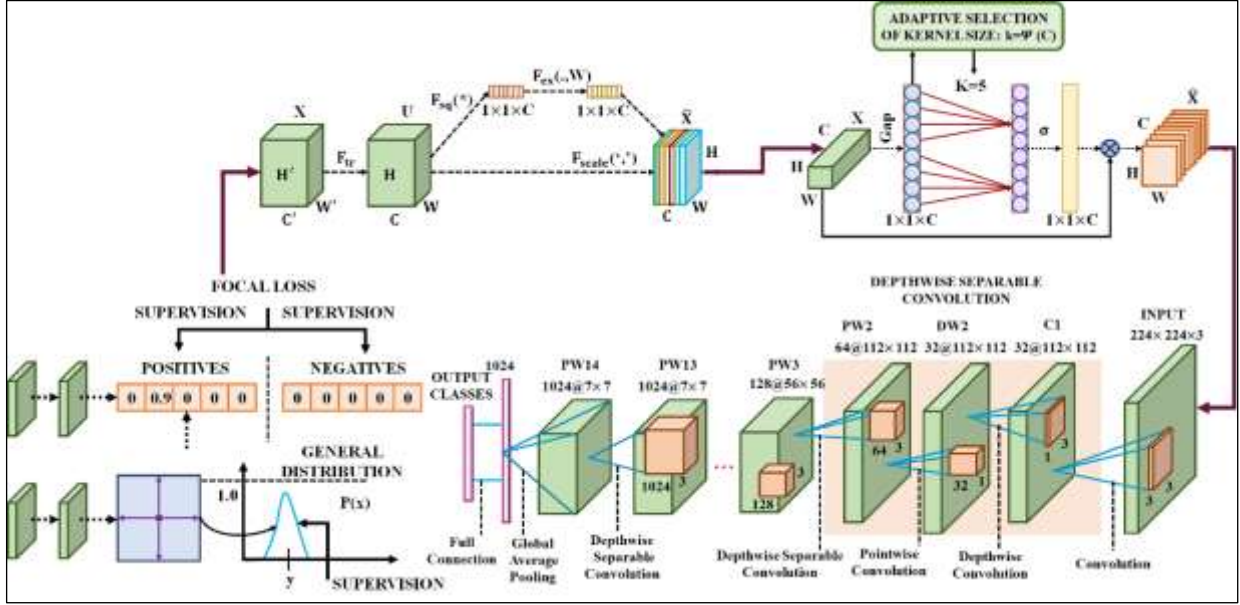


Figure 2: Diagram of FSEF-MobileNet.

Source: Authors, (2026).

This enhances the FSEF-MobileNet's capacity to reliably identify sickle cells in digital blood smears. Without significantly increasing computing costs, ECA enhances the network's capacity to concentrate on important characteristics of red blood cells. In contrast to conventional SE blocks, which employ fully connected layers for channel weighting, ECA uses a lightweight 1D convolution to capture cross-channel interactions, increasing efficiency without sacrificing accuracy. This enables the model to minimize unimportant background elements in blood smear images and give higher weights to channels that capture significant morphological aspects of sickled cells, including elongated or crescent forms. Pseudo-code of FSEF- MobileNet is shown below,

Pseudo-code 1: FSEF-MobileNet.

```

1. Input Layer
Inputs = layers. Input(shape=(224, 224, 3))
Purpose: Accepts RGB images (224x224 pixels, 3 channels).
This is the entry point of your neural network.

2. Rescaling Layer
x = layers. Rescaling(1./255)(inputs)
Purpose: Converts all pixel values from [0, 255] to [0, 1].
Why: Helps the model train faster and perform better numerically (normalization).

3. MobileNetV2 Base Model
base_model = MobileNetV2(include_top=False, input_shape=(224, 224, 3), weights="imagenet")
x = base_model(x, training=False)
Purpose: Pre-trained MobileNetV2 extracts rich features from the image (edges, textures, patterns).
• include_top=False → removes final classification layers of MobileNetV2, keeping only
convolutional feature maps.
• training=False → freezes base layers during initial training.
Output shape: something like (7, 7, 1280) (feature maps).

4. FSEF Block (Feature Squeeze-Excite Fusion)
x = fsef_block(x)
The FSEF Block adds attention mechanisms to highlight important features.
Inside fsef_block():
i. Global Average Pooling
se = layers.GlobalAveragePooling2D()(inputs)
✓ Squeezes spatial info → outputs 1 value per channel (1280 values).
✓ Captures how strong each feature channel is overall.
ii. Fully Connected Layers (Channel Attention)
se = layers.Dense(inputs.shape[-1] // reduction, activation='Relu')(se)
se = layers.Dense(inputs.shape[-1], activation='sigmoid')(se)

```

is.

- ✓ Two dense layers reduce and restore dimensionality.
- ✓ Produces a set of weights (0–1) for each feature channel → “how important” each channel

iii. Reshape + Multiply (Apply Channel Weights)

```
se = layers.Reshape((1, 1, inputs.shape[-1]))(se)
x = layers.Multiply()(inputs, se)
```

- ✓ Reshapes to match feature map dimensions and multiplies — boosting important channels, reducing weak ones.

iv. Spatial Attention (focus on where to look)

```
avg_pool = tf.reduce_mean(x, axis=-1, keepdims=True)
max_pool = tf.reduce_max(x, axis=-1, keepdims=True)
concat = layers.Concatenate(axis=-1)([avg_pool, max_pool])
sa = layers.Conv2D(1, kernel_size=7, padding='same', activation='sigmoid')(concat)
out = layers.Multiply()(x, sa)
```

- ✓ avg_pool + max_pool: capture global spatial context.
- ✓ Conv2D(1, 7×7): learns a spatial attention mask.
- ✓ Multiply: highlights important spatial regions (like focusing the model’s “vision”).

Final output from FSEF block: attention-refined feature map, same size (7, 7, 1280).

5. Global Average Pooling

```
x = layers.GlobalAveragePooling2D()(x)
```

- ✓ Converts (7, 7, 1280) → (1280,).
- ✓ Compresses spatial info into one vector per image.
- ✓ Reduces parameters and prevents overfitting.

6. Dense Layer (Fully Connected)

```
x = layers.Dense(dense_units, activation='Relu')(x)
```

- ✓ Learns nonlinear feature combinations.
- ✓ dense_units (optimized by WBO, e.g., 256–512) controls feature richness.
- ✓ Activation: ReLU adds nonlinearity.

7. Dropout Layer

```
x = layers.Dropout(dropout)(x)
```

- ✓ Randomly drops some neurons during training.
- ✓ Purpose: Prevents overfitting, improves generalization.
- ✓ Dropout rate: optimized by WBO (0.1–0.5 range).

8. Output Layer

```
outputs = layers.Dense(num_classes, activation='softmax')(x)
```

- ✓ Produces final class probabilities (e.g., [0.85, 0.15] for 2 classes).
- ✓ Softmax: ensures probabilities sum to 1.

Source: Authors, (2026).

A lightweight convolutional neural network called MobileNet is perfect for identifying sickle cell disease in digital blood smears. The algorithm can correctly classify cells by fine-tuning it with annotated images of sickle-shaped and healthy red blood cells. It is a useful tool for point-of-care sickle cell identification because of its effective design, which enables quick, real-time analysis on low-resource devices. While the FSEF module improves the model's dimensions to collect fine-grained information and distinguish between normal and sickle-shaped cells, the MobileNet component guarantees a lightweight and computationally efficient model appropriate for real-time medical applications. Combining these methods allows the FSEF-MobileNet to reach great speed and accuracy, which makes it perfect for automated sickle cell disease screening and early diagnosis, particularly in healthcare settings with limited resources.

III.1.1.5 Wolf Bird Optimization

The WBO algorithm, which is based on the cooperative foraging behavior of wolves and ravens, is used to optimize crucial hyper-parameters of the FSEF-MobileNet model, including learning rate, convolutional filter weights, and fusion coefficients, in order to further improve classification accuracy and convergence stability. In the search space, a population of solutions (ravens and wolves) is first randomly initialized as follows,

$$x_i^j = x_{i,min}^j + rand \times (x_{i,max}^j - x_{i,min}^j) \quad (15)$$

Pseudo-code 2: Wolf Bird Optimization (WBO).

WBO Optimization Loop

```
For t = 1 to T do:
  For each particle i in population:
    Calculate wolf_factor (exploration) ∈ [0.4, 0.9]
    Calculate bird_factor (exploitation) ∈ [0.2, 0.7]
    Generate random vector r
    new_position = position[i]
```

```

+ wolf_factor * r * (best_position - position[i])
+ bird_factor * (ub - lb) * (random - 0.5)
Clip new_position within [lb, ub]
Evaluate fitness(new_position)
If fitness(new_position) < fitness(position[i]):
Replace position[i] ← new_position
If fitness(new_position) < fitness(best_position):
Update best_position ← new_position
Print best fitness of current iteration
End For

```

Source: Authors, (2026).

When the complete population (ravens and wolves) is represented by $i = 1, 2, \dots, d$, and the model parameters or dimensions are represented by $j = 1, 2, \dots, d$. The Hunger Level (HL) of each candidate solution is determined by its fitness, which is stated in terms of classification accuracy or loss.

$$HL_i = f(X_i), i = 1, 2, \dots, n \quad (16)$$

In order to do an intelligent local random walk in the area, the algorithm next determines which raven is the hungriest that is the worst-performing solution is represented by equation 17 and $r(t)$ is the random binary vector which is defined in equation 18.

$$X_r(t) = [0, \text{cumsum}(2r(t_1) - 1), \text{cumsum}(2r(t_2) - 1), \dots, \text{cumsum}(2r(t_n) - 1)] \quad (17)$$

$$r(t) = \begin{cases} 1, & \text{if } rand > 0.5 \\ 0, & \text{otherwise} \end{cases} \quad (18)$$

The raven modifies its location in relation to the prey (best parameter region) as follows,

$$\text{New } X_r = X_r + r_1 \times X_p - r_2 \times PCP \quad (19)$$

Where, X_p is the prey position), PCP is the prey center point, and r_1, r_2 are the random coefficients belongs to $[0,1]$ guarantee the diversity of exploration. Next, wolves follow the raven's signal to the best possible prey by,

$$\text{New } X_w = X_w + r_1 \times \text{New } X_r - r_2 \times \frac{X_p}{D_i} \quad (20)$$

Where, D_i is the wolf and raven's Euclidean distance from one another. Other ravens refine local search using Lévy flight-based exploration throughout the exploitation stage, updating their positions as,

$$\text{New } X_{r,k} = X_{r,k} + r_1 \times X_p - r_2 \times PCP, k = 2, \dots, N_r \quad (21)$$

Table 2: Optimized value of WBO.

Hyperparameter	Optimized value
Dropout	0.30
Dense units	255
Learning rate	0.00015 (1.5×10^{-4})
Optimizer	Adam
Base model	MobileNetV2
Attention module	Enabled
Optimization technique	Used
Best validation accuracy	Best accuracy

Source: Authors, (2026).

Table 2 depicts the optimized value of WBO. The WBO algorithm dynamically adjusts the internal parameters of the FSEF-MobileNet model to minimize the objective loss function and maximize classification accuracy through these cooperative and adaptive search procedures. The flowchart of WBO-FSEF-MobileNet is illustrated in Figure 3.

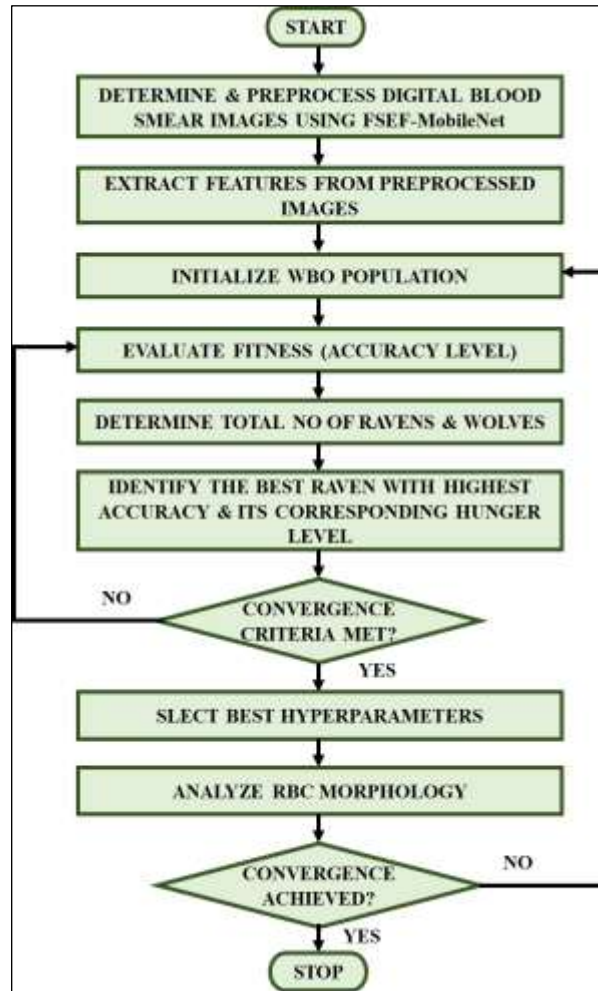


Figure 3: Flowchart of WBO-FSEF-MobileNet.
Source: Authors, (2026).

An excellent synergy between ecological intelligence and DL is demonstrated by the resilient, computationally efficient, and highly accurate system for automated sickle cell identification in digital blood smear images made possible by this biologically inspired optimization method.

IV. RESULTS AND DISCUSSIONS

This work provides a notable explanation of the manner in which FSEF-MobileNet with WBO algorithm is implemented in order to precisely diagnose SCD in digital blood smears. The results produced are then executed in Python, which is utilized to optimally validate the present study. 991 digital blood smear images in the dataset for automated sickle cell detection are separated into two classes: Positive (844 photos) and Negative (147 images). With 675 positive and 117 negative images for training and 169 positive and 30 negative images for testing, it is divided into 80% training and 20% testing sets. Despite the dataset imbalance, sickle cell and normal cells are successfully classified using the FSEF-MobileNet model combined with the WBO algorithm.

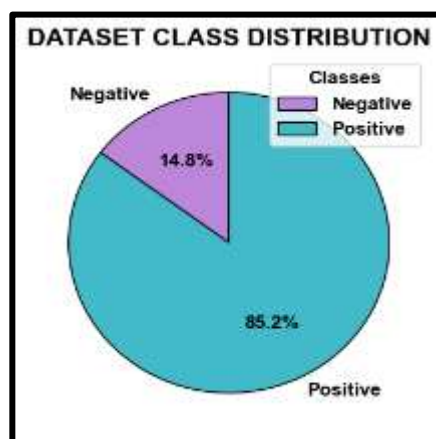


Figure 4: Class distribution of dataset.
Source: Authors, (2026).

Figure 4 shows the pie chart titled Dataset Class Distribution. The Positive class makes up 85.2% of the entire dataset, whilst the Negative class only makes up 14.8%. With a significantly greater number of positive samples than negative ones, this suggests that the dataset is unbalanced. In order to avoid bias against the majority class and guarantee that the model works effectively for both categories, such imbalance should be addressed during model training.

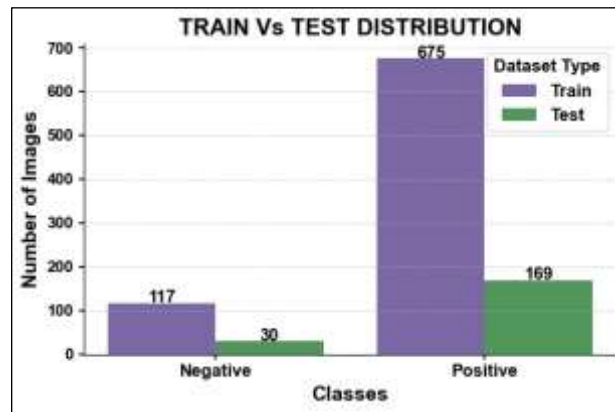


Figure 5: Train vs Test distribution.
Source: Authors, (2026).

Figure 5 shows the number of images in the training and testing datasets for the two classes Negative and Positive. With 675 images in the training set and 169 images in the test set, it demonstrates that the Positive class is more prevalent in both datasets. The Negative class, on the other hand, has 30 testing images and 117 training photos. A class imbalance is evident in this distribution, as the Positive samples much outweigh the Negative ones. Despite this disparity, both classes are represented at every stage of model training and evaluation thanks to the data's proper division into training and testing sets.

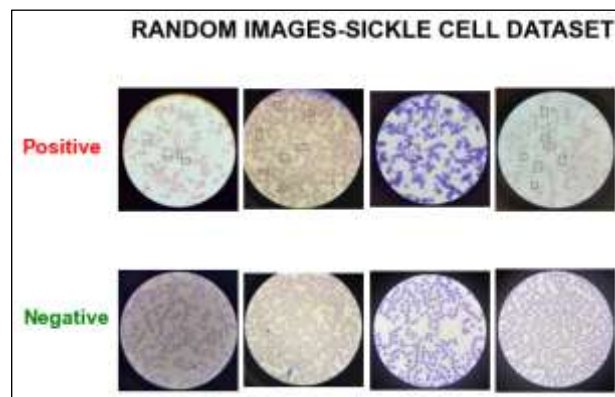


Figure 6: Random images of sickle cell dataset.
Source: Authors, (2026).

Random images of SCD is displayed in the figure 6. Normal, round red blood cells are shown in the Negative images, while abnormal, sickle-shaped red blood cells are indicated with boxes in the Positive images. These visual distinctions aid in the model's accurate learning and classification of sickle cell illness.

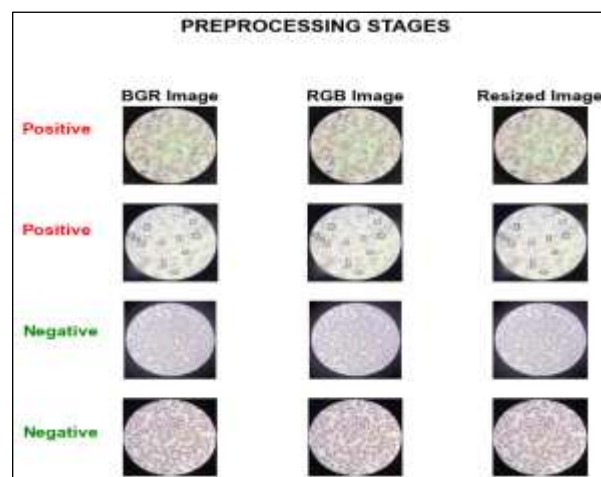


Figure 7: Preprocessing stages.
Source: Authors, (2026).

The sickle cell image processing steps for both positive and negative samples are depicted in the figure 7. Every image is resized to a consistent size appropriate for model input after being converted from the BGR color format to RGB. Normal red blood cells are seen in the negative photos, whereas sickle-shaped cells are highlighted in the positive images. By improving color consistency, scale uniformity, and feature clarity, these preprocessing techniques guarantee efficient input for the DL model.

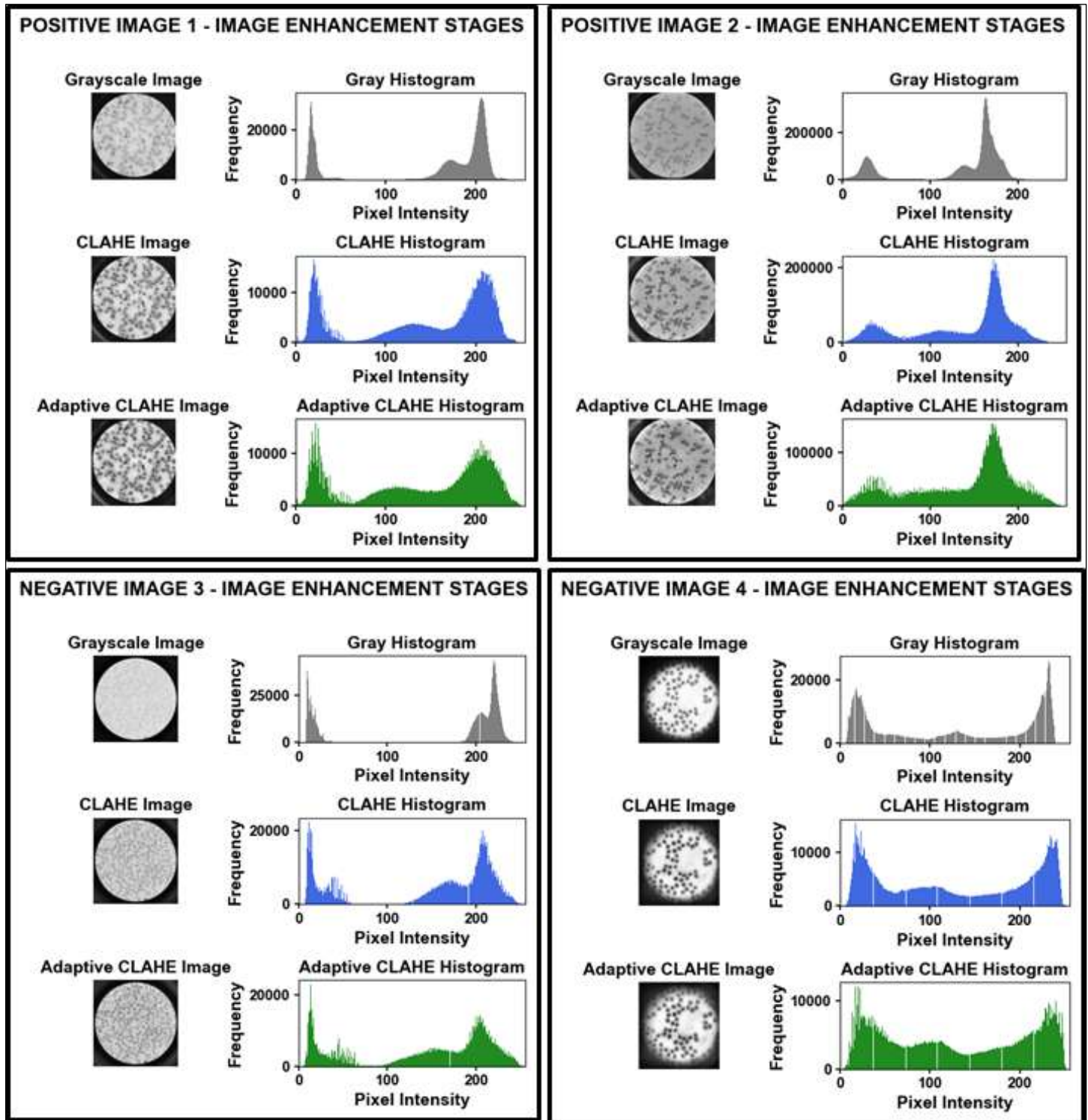


Figure 8: Image enhancement stages for positive and negative samples.
Source: Authors, (2026).

The grayscale, CLAHE, and Adaptive CLAHE image improvement procedures for both positive and negative samples are depicted in Figure 8. The related histograms show how each step enhances contrast and detail visibility, making it easier to discern visual distinctions between positive and negative images.

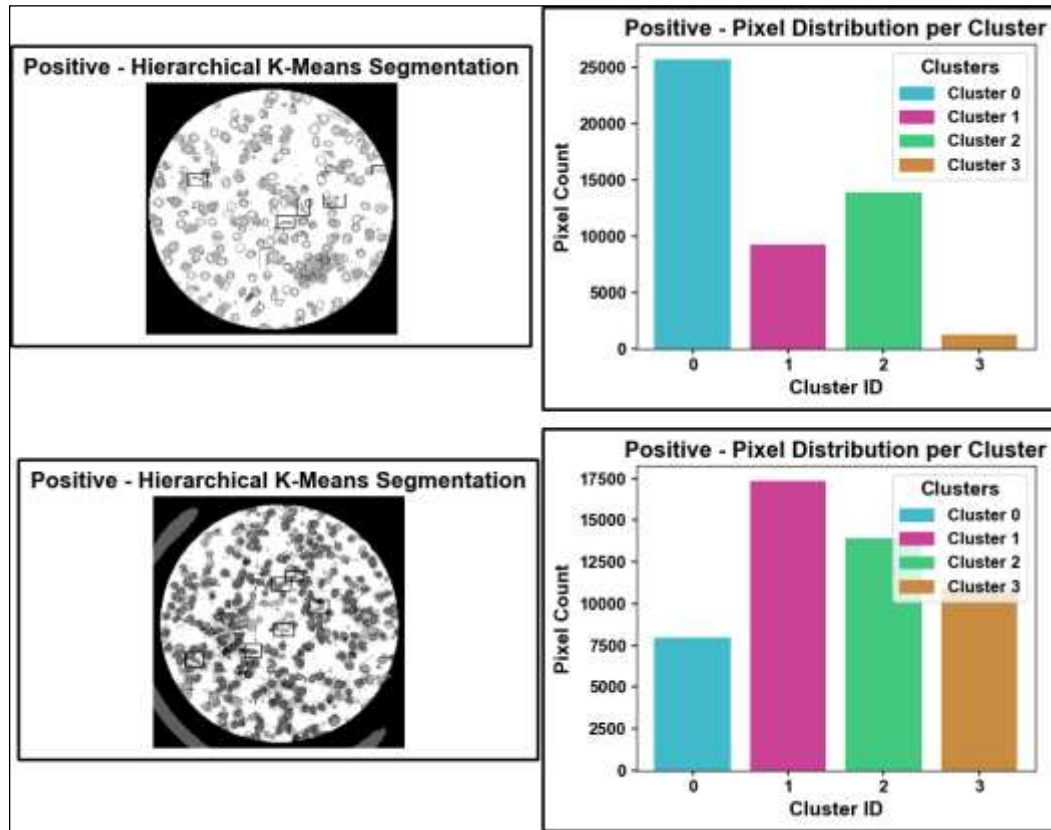


Figure 9: Positive samples of Hierarchical K-means and pixel distribution.
Source: Authors, (2026).

Figure 9 shows the hierarchical K-means segmentation results for two positive samples. The segmented microscopic pictures are separated into four different pixel clusters in the left panels, and the appropriate pixel distribution for each cluster is shown in the right panels. These bar charts illustrate differences in cluster dominance between the two samples by highlighting the relative percentage of pixels in each cluster. Quantitative comparison of structural features within positive samples is made possible by the segmentation, which efficiently distinguishes image regions based on pixel intensity and texture.

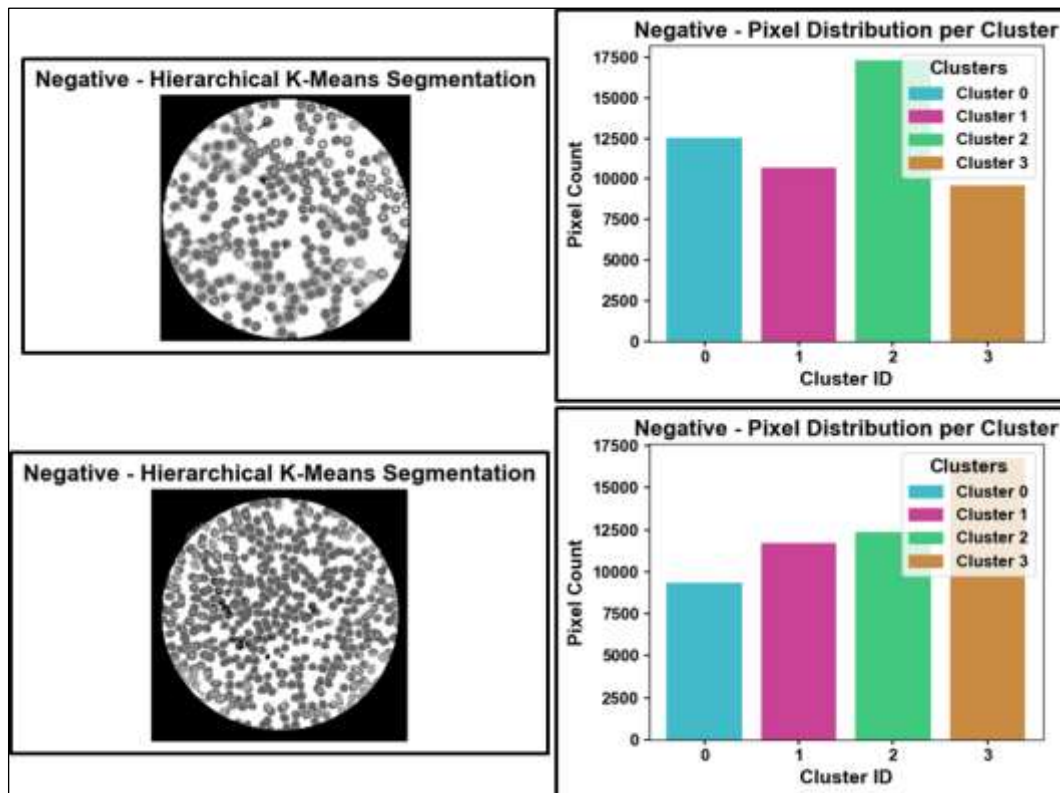


Figure 10: Negative samples of Hierarchical K-means and pixel distribution.
Source: Authors, (2026).

Figure 10 uses Hierarchical K-Means Segmentation to compare two negative samples. A bar chart showing the pixel distribution across four clusters and a segmented microscopic picture are displayed in each row. With Cluster 2 having the most pixels and Cluster 3 having the fewest, both samples show comparable clustering patterns, suggesting consistent segmentation outcomes with minor differences in texture or density.

Table 3: Multi scale GLCM feature.

Scale	Contrast	Correlation	Energy	Homogeneity
1.0	1328.407	0.8766	0.0301	0.1217
0.75	1325.1206	0.8715	0.0098	0.0908
0.5	1833.8721	0.8181	0.0106	0.0795

Source: Authors, (2026).

The texture analysis results at three scales 1.0, 0.75, and 0.5 are displayed in Table 3. It enumerates four characteristics: homogeneity, energy, contrast, and correlation. Contrast rises with decreasing scale, but correlation, energy, and homogeneity typically fall. This indicates that smaller scales capture more texture variation and less uniformity in the image.

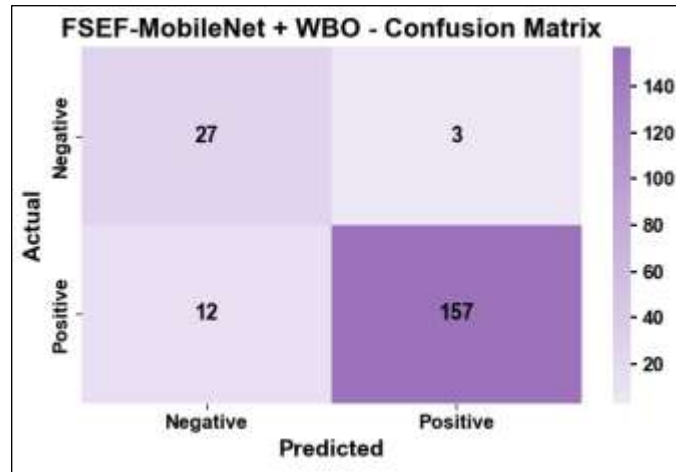


Figure 11: Confusion matrix of FSEF-MobileNet+WBO.

Source: Authors, (2026).

Figure 11 reveals that the FSEF-MobileNet + WBO model accurately identified the majority of samples. This implies excellent accuracy and overall classification performance.

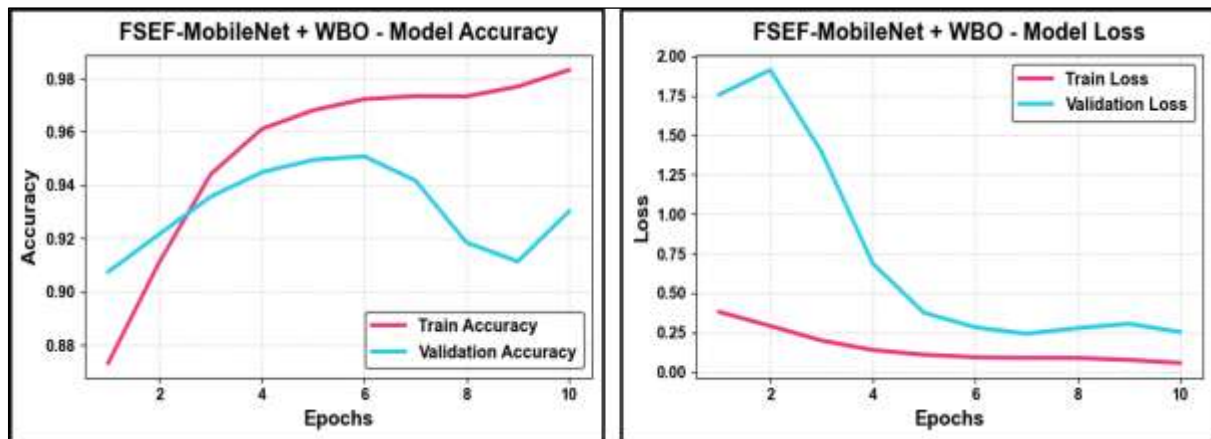


Figure 12: Model accuracy and model loss for FSEF-MobileNet.

Source: Authors, (2026).

Figure 12 depict the training performance of the FSEF-MobileNet + WBO model over ten epochs. The accuracy plot shows that training accuracy progressively grows, reaching about 0.99, whereas validation accuracy peaks around epoch 5 and then gradually drops, indicating modest overfitting. The loss plot demonstrates a steady decline in both training and validation loss, with the validation loss stabilizing after epoch 5, indicating strong convergence and effective model learning.

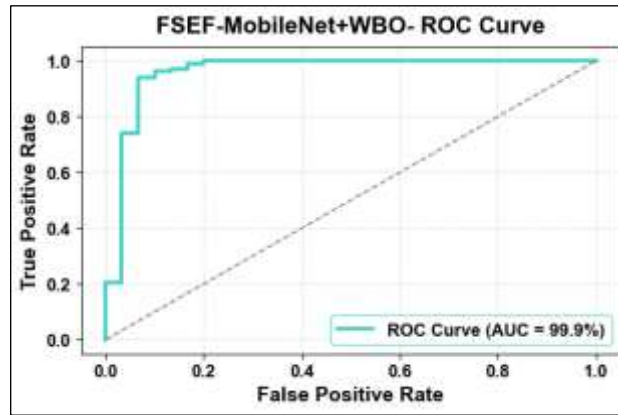


Figure 13: ROC curve of FSEF-MobileNet +WBO.
Source: Authors, (2026).

The ROC curve for the FSEF-MobileNet + WBO model is shown in Figure 13. This shows that the model achieves a high true positive rate while having a low false positive rate, exhibiting great overall discriminative capacity between classes.

Table 4: Comparative analysis of performance metrics.

Model	Accuracy	Precision	Recall	F1-score
DenseNet-121	0.92	0.94	0.92	0.93
CNN	0.94	0.94	0.94	0.93

Source: Authors, (2026).

Table 4 shows the performance comparison demonstrates that both the DenseNet-121 and CNN models produce strong and balanced results across all measures. DenseNet-121 achieves high accuracy, precision, recall, and F1-score, although the CNN model performs slightly better overall, showing more consistent and dependable classification performance across multiple evaluation criteria.

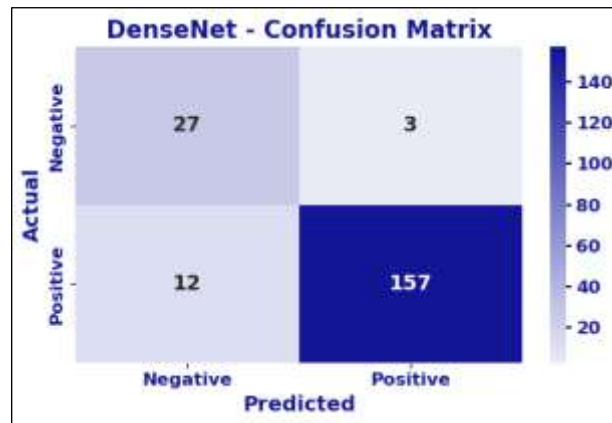


Figure 14: Confusion matrix of DenseNet.
Source: Authors, (2026).

Figure 14 displays the confusion matrix of DenseNet model's performance. It demonstrates that the model accurately predicted 27 negative and 157 positive cases. There were three false positives and twelve false negatives. Overall, the DenseNet model performs well in terms of prediction accuracy.

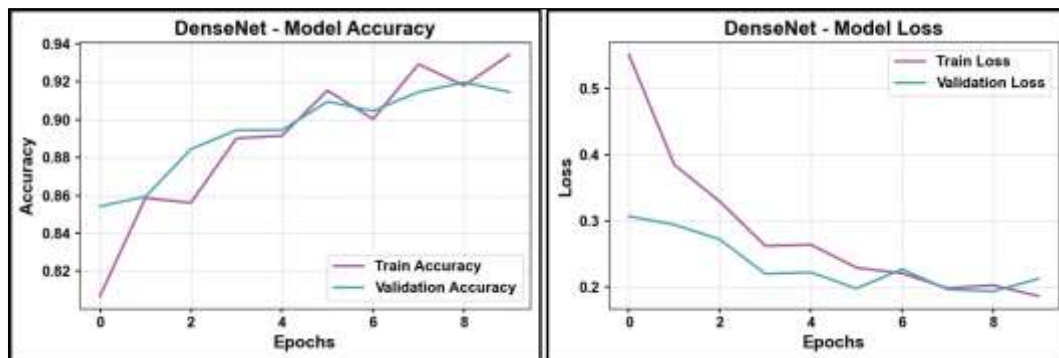


Figure 15: Model accuracy and model loss of DenseNet.
Source: Authors, (2026).

Figure 15 depicts the model accuracy and loss of DenseNet. It improves accuracy and decreases loss over epochs, attaining approximately 94% accuracy with low overfitting, showing good and consistent training performance.

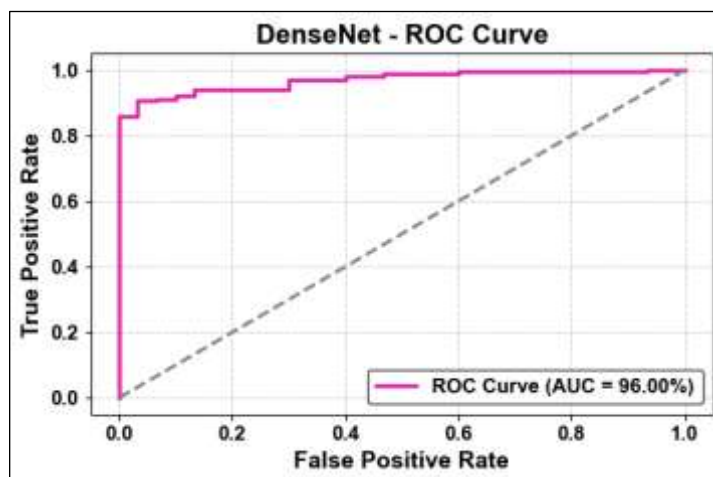


Figure 16: ROC curve for DenseNet.
Source: Authors, (2026).

Figure 16 demonstrates great performance, with an AUC of 96%. The curve remains near to the top-left corner, indicating a high true positive rate and a low false positive rate, implying that the model effectively differentiates between positive and negative classes.

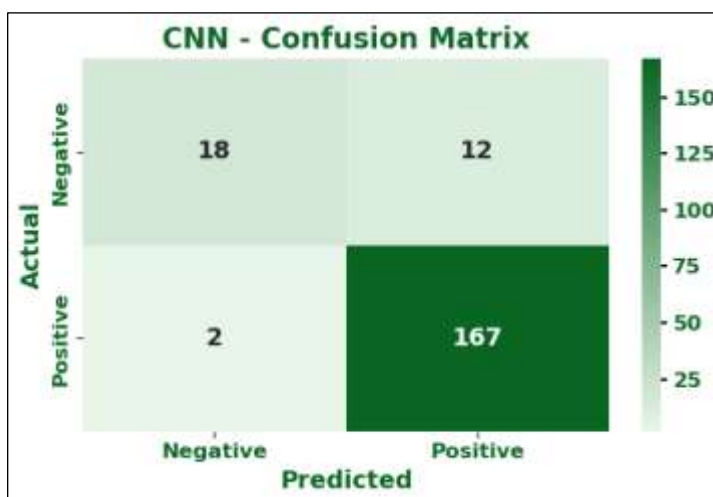


Figure 17: Confusion matrix of CNN.
Source: Authors, (2026).

In Figure 17, CNN model properly categorized 167 positive and 18 negative cases, according to the confusion matrix. Nevertheless, it incorrectly identified two positives as negatives and twelve negatives as positives. With very few misclassifications, the model performs well overall, especially when it comes to recognizing positive cases.

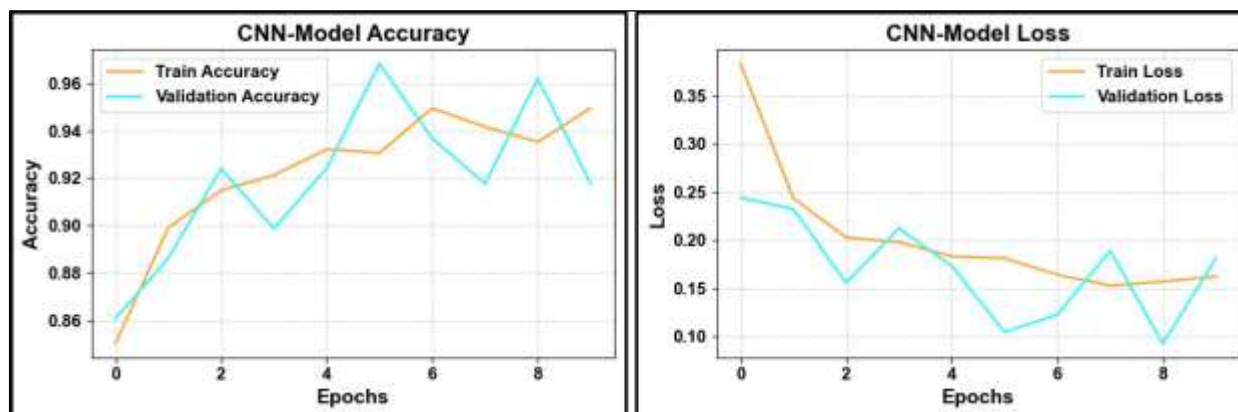


Figure 18: Model accuracy and model loss of CNN.
Source: Authors, (2026).

Figure 18 illustrates the model's training and validation results over ten epochs are displayed in the plots. The accuracy graph shows a consistent increase in training and validation accuracy, reaching approximately 95–97%, indicating successful learning. Both training and validation loss consistently decline, stabilizing after a few epochs, according to the loss graph. Overall, the model exhibits good performance with no discernible overfitting.

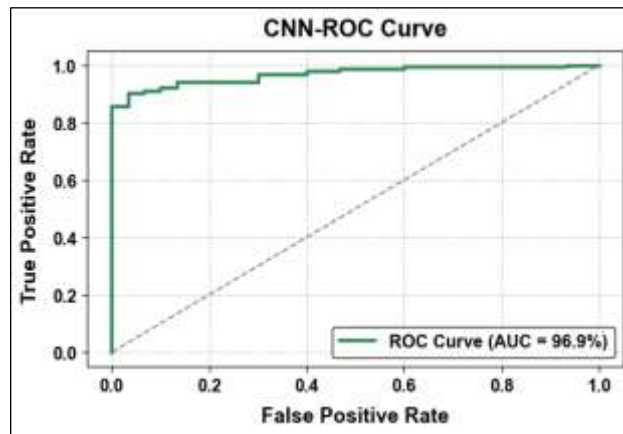


Figure 19: ROC curve for CNN.
Source: Authors, (2026).

Figure 19 demonstrates the ROC curve for CNN which shows outstanding performance. A high genuine positive rate and a low false positive rate are indicated by the curve's continued proximity to the upper-left corner. This implies that the model is quite good at differentiating between positive and negative classes.

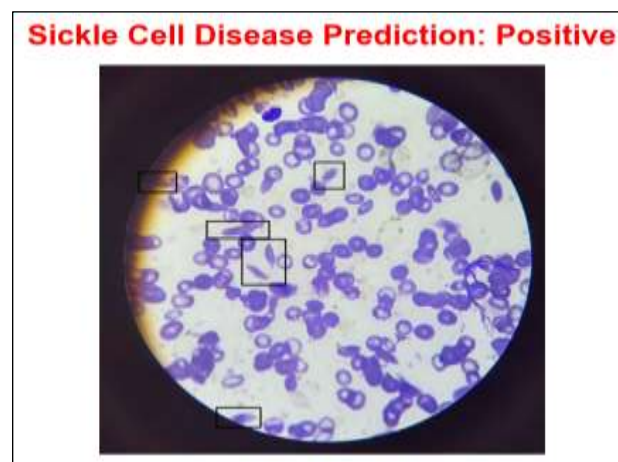


Figure 20: Output prediction.
Source: Authors, (2026).

Prediction of SCD is shown in Figure 20, which displays a microscopic view of blood cells. Black boxes are used to highlight a number of cells, which are red blood cells with an atypical shape (sickle-shaped). Sickle cell disease, a genetic blood condition that damages haemoglobin and causes red blood cells to take on a crescent or sickle shape, is characterized by their uneven forms.

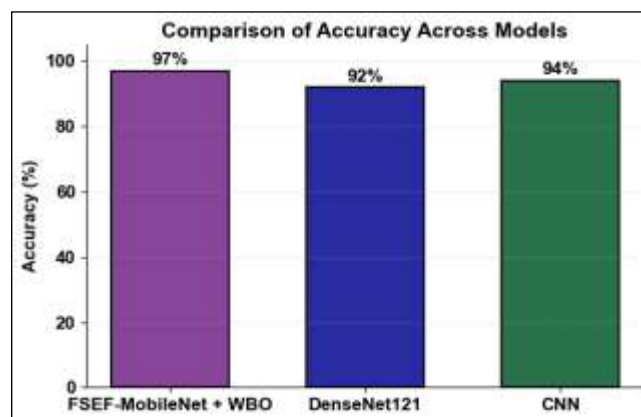


Figure 21: Comparison of accuracy across models.
Source: Authors, (2026).

Figure 21 depicts the bar graph contrasts the accuracy-based performance of three machine learning models. With an accuracy of 97%, the FSEF-MobileNet + WBO model outperformed the CNN model with 94% and the DenseNet121 model with 92%. This suggests that the FSEF-MobileNet + WBO model had better predictive performance than the others.

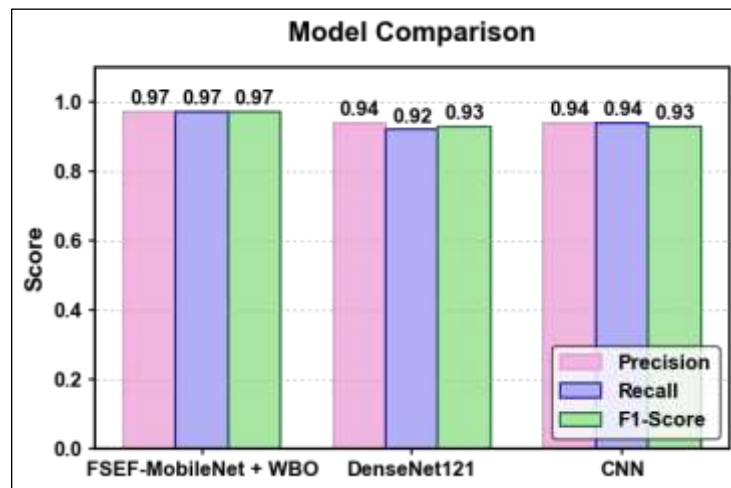


Figure 22: Comparison of models.

Source: Authors, (2026).

The precision, recall, and F1-score for three models FSEF-MobileNet + WBO, DenseNet121, and CNN are displayed in Figure 22. FSEF-MobileNet + WBO performs marginally better than the other two models, although all three exhibit high and closely matched values across the measures. This shows that while all models provide robust and balanced classification performance, the FSEF-MobileNet + WBO model exhibits the highest level of overall consistency.

Table 5: Comparative analysis of accuracy.

Model	Accuracy
DenseNet [28]	96.8
AlexNet [29]	88
VGG-16-GCN [31]	95
PROPOSED	97

Source: Authors, (2026).

The accuracy of various models for a certain task is compared in the Table 5. The accuracy of the DenseNet model was 96.8%, AlexNet was 88%, and VGG-16-GCN was 95%. With the maximum accuracy of 97%, the suggested model outscored all others, proving its better efficacy and dependability in producing more accurate forecasts.

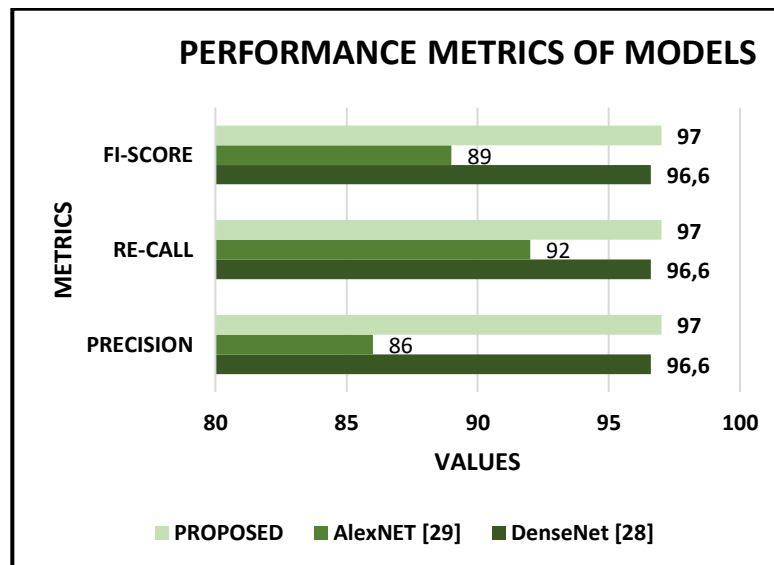


Figure 23: Comparison of models.

Source: Authors, (2026).

The performance of DenseNet, AlexNet, and a proposed model are contrasted in the Figure 23. DenseNet obtained balanced accuracy, recall, and F1-score scores of 96.6. With a moderate F1-score of 89, AlexNet showed lesser precision (86) but higher recall (92). The performance metrics of the proposed system achieves the highest overall value of 97%.

V. CONCLUSION

An extensive and effective process for accurate illness detection is provided by the proposed method for automated sickle cell identification in digital blood smears utilizing FSEF-MobileNet with the WBO algorithm. Preprocessing is the initial phase in the process, where the input blood smear images are improved by resizing and adaptive CLAHE to improve contrast and normalize intensity levels, making red blood cell structures easier to identify. In order to ensure that the research concentrates on relevant cellular regions, segmentation using hierarchical K-means clustering separates individual cells from the background. In order to distinguish sickle cells from normal ones, the MSGLCM is utilized in the process of feature extraction to capture the critical textural and spatial properties of the cells. The WBO approach is then used to modify the extracted features through hyperparameter tweaking, which improves model performance by choosing the best learning parameters. Subsequently the classification is performed by the FSEF-MobileNet model, which uses sophisticated attention mechanisms to detect sickle cells with great accuracy and robustness. Python is used to validate the complete working system, and the results shows the proposed method outperforms other classifiers with an ideal accuracy, precision, recall and F1-score of 97%. Thus, the suggested system simplifies the diagnostic procedure, increasing detection accuracy, decreasing manual intervention, and facilitating quicker and more accurate sickle cell identification.

VI. AUTHOR'S CONTRIBUTION

Conceptualization: Vijayanandh T, Santhoshkumar S P, Parvathi R, Sivaprakash P, Vimala Ithayan J, Dilip Charaan R M.

Methodology: Santhoshkumar S P, Parvathi R, Sivaprakash P, Vimala Ithayan J, Dilip Charaan R M.

Investigation: Vijayanandh T, Santhoshkumar S P, Parvathi R.

Discussion of results: Vijayanandh T, Santhoshkumar S P, Parvathi R, Sivaprakash P, Vimala Ithayan J, Dilip Charaan R M.

Writing – Original Draft: Vijayanandh T.

Writing – Review and Editing: Santhoshkumar S P, Parvathi R, Sivaprakash P, Vimala Ithayan J, Dilip Charaan R M.

Resources: Santhoshkumar S P, Parvathi R, Sivaprakash P.

Supervision: Santhoshkumar S P, Parvathi R, Sivaprakash P, Vimala Ithayan J, Dilip Charaan R M.

Approval of the final text: Vijayanandh T.

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