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Original Article

Improving Sickle Cell Anaemia Classification in Nilgiri Tribes through Multimodal RBC Spot Extraction Using Optimized Deep Stacking Network Algorithm

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Abstract *- Sickle Cell Anemia (SCA) is a prevalent genetic blood disorder that disproportionately affects the health of the Nilgiri tribes. Early and accurate diagnosis is pivotal for effective management of the disease. This research proposes an innovative approach to Multimodal RBC Spot Extraction using Optimized Deep Stacking Network (MRSE-ODSN) Algorithm to classify SCA diagnosis within this community by harnessing the synergies of multimodal Red Blood Cell (RBC) image analysis. The MRSE-ODSN framework begins with acquiring diverse RBC images encompassing brightfield microscopy, phase-contrast imaging, and fluorescence microscopy. Each imaging modality captures distinctive aspects of RBC morphology and function. The sample data were collected from the NAWA-Nilgiri Adivasi Welfare Association in Nilgris, which contains data from 300 patients with 14 features related to SCA that were acquired. Rigorous preprocessing and augmentation techniques ensure data quality and resilience. A sophisticated architecture tailored for sequential feature extraction from multimodal RBC images. ODSN expertly integrates with CNN to classify sickle cell anemia efficiently within the Nilgiri tribes. The proposed model obtained 98.01 percent accuracy. By employing MRSE-ODSN, healthcare practitioners can potentially offer timely interventions, personalized treatments, and enhanced disease management strategies, thereby positively impacting the health and well-being of the Nilgiri tribes.*

Keywords *- Sickle Cell Anemia, Classification, Red Blood Cell, Multimodal RBC Spot Extraction, Optimized Deep Stacking Network, Convolution Neural Network, Nilgiri tribes.*

1. Introduction

Sickle cell anemia is a genetic blood disorder marked by the occurrence of defective hemoglobin, the protein that transports oxygen through the body. This inherited condition primarily affects Red Blood Cells (RBCs), causing them to assume a characteristic sickle or crescent shape [1]. These deformed RBCs are less flexible and have a reduced ability to flow smoothly through blood vessels, leading to various health complications [2]. A Genetic blood disorder that varies in occurrence among different populations, including indigenous communities [3]. Among these communities, the Nilgiri tribes stand out due to their unique genetic makeup and historical isolation. Understanding and addressing the prevalence of sickle cell anemia within the Nilgiri tribes is essential for providing targeted healthcare interventions and raising awareness about this hereditary condition [4].

The Nilgiri tribes residing in the Nilgiri Hills of India represent a distinctive population with their own cultural practices and genetic heritage. The prevalence of sickle cell anemia within this community is important because of its potential influence on the health of the tribe's members [5]. There are several types of sickle cell anemia, each caused by specific genetic mutations [6, 7]. The foremost types of sickle cell anemia include:

Hemoglobin SS Disease (HbSS): This is the most prevalent and dangerous form of sickle cell anaemia. It happens when a person inherits two copies of the hemoglobin S gene (HbS) - one from each parent. People with HbSS experience frequent and severe symptoms, including pain crises, anemia, and organ damage.

Hemoglobin SC Disease (HbSC): Hemoglobin SC disease consequences from getting one HbS gene and one hemoglobin C gene (HbC) from each parent. It causes milder symptoms compared to HbSS but can still lead to anemia, pain, and organ complications.

Hemoglobin Sβ-Thalassemia (HbSβ-Thalassemia): This type occurs when a person inherits one HbS gene and one β-thalassemia gene from their parents. β-thalassemia is a condition that affects the invention of beta-globin chains of hemoglobin. The severity of symptoms varies based on the specific type of β-thalassemia gene inherited.

Hemoglobin SD Disease (HbSD): Hemoglobin SD disease is a less common type that occurs when an individual inherits one HbS gene and one hemoglobin D gene (HbD) from each parent. The symptoms are generally milder compared to HbSS or HbSC.

Other Variants and Subtypes: There are additional less common variants and subtypes of sickle cell anemia resulting from different combinations of hemoglobin mutations, such as hemoglobin SE disease and hemoglobin SO-Arab disease.

Genetic counseling and medical guidance are crucial for individuals and families affected by sickle cell anemia to understand their specific type and make informed decisions about their healthcare [8].

Understanding and addressing the prevalence of sickle cell anemia within the Nilgiri tribes is of utmost significance due to its potential effect on the health and happiness of these communities [9]. The unique genetic characteristics of the tribes, combined with challenges in healthcare access and cultural factors, necessitate innovative approaches for accurate diagnosis and classification.

The key challenges are the varying severity of sickle cell anemia and the genetic diversity among different subgroups of Nilgiri tribes, which present challenges for accurate classification.

Limited healthcare resources and remote geographical locations can hinder timely and accurate medical interventions [10]. Cultural beliefs and practices may influence individuals' attitudes towards medical procedures and interventions.

The primary objective of this study is to enhance the classification accuracy of sickle cell anemia in Nilgiri tribes through the integration of multimodal RBC spot extraction and an optimized deep stacking network algorithm.

1.1. Expected Outcomes and Impact

The novelty of this work lies in combining multiple imaging modalities (brightfield, phase-contrast, and fluorescence microscopy) with the Optimized Deep Stacking Network (MRSE-ODSN) for enhanced RBC feature extraction, which hasn't been explored in previous SCA studies. Unlike single-modality approaches, our method achieves a 98.01% accuracy, outperforming traditional techniques in diagnosing SCA in the Nilgiri tribes. This study is expected to yield several impactful outcomes:

1.1.1. Enhanced Accuracy

Integrating multimodal data and an optimized deep stacking network is anticipated to improve accuracy in sickle cell anemia classification.

1.1.2. Targeted Healthcare

The enhanced classification accuracy can contribute to more targeted healthcare interventions for individuals affected by the disease.

1.1.3. Cultural Empathy

Integrating cultural values and sensitivities fosters better acceptance and participation in medical procedures within the Nilgiri tribes.

1.1.4. Empowered Decision-Making

Accurate classification and severity assessment enable informed medical decisions and genetic counseling.

Through the innovative fusion of multimodal data and advanced machine learning techniques, this study endeavors to revolutionize the classification of sickle cell anemia in Nilgiri tribes, ultimately improving these communities' health outcomes and quality of life.

Sickle Cell Anemia (SCA) significantly impacts the Nilgiri tribes, but early diagnosis is hindered by limited resources and single-modality imaging. This research proposes a Multimodal RBC Spot Extraction using an Optimized Deep Stacking Network (MRSE-ODSN) Algorithm, combining diverse imaging techniques for precise SCA classification and improved disease management.

2. Related Works

This section presents various methods available from existing sources that are mainly helpful in identifying sickle cell disease. Various researchers have tried to identify sickle cell disease in the early stages.

Medical professionals use machine learning algorithms to identify sickle cell abnormalities in patients in order to aid in the process of early identification of sickle cell anaemia. For the purpose of diagnosing sickle cell illness, the authors of this study [11] created a canny edge and double threshold method to identify overlapping red blood cells.

SCD is one of a number of diseases that are difficult to diagnose and treat in many of the countries that are located in this region of the globe due to a lack of crucial diagnostic and therapeutic tools. As a consequence, there is an urgent need to develop methods that are both affordable and susceptible to control for the identification and diagnosis of SCD. This research [12] proposes innovative strategies for the diagnosis of SCD that make use of Plain Convolution Neural Networks.

After the image has been subjected to the appropriate image analyzing technique for better improvements, the techniques are used and issued to morphological processing in order to lessen the noise in the image; it is then subjected to the classifier technique, which is a sort of ML in which an algorithm examines the area and perimeter of a cell to discover the different types of cells that need to be classified [13]. The image collected from the subjects is then applied to the classifier method.

DNN analysis was used in this research [14] to provide a novel automated approach for counting pitted RBCs. The second step was to evaluate the stability of fixed RBCs for pitting RBC numbers throughout the course of time. An oil-

immersion objective was used to examine the cells after they had been fixed in paraformaldehyde, and microscopy images were captured.

A single random phase encoding biosensor that is small, field portable, lensless, and present in this study [15] was provided for the purpose of automating the differentiation of healthy human red blood cells from those affected by sickle cell disease. A lensless method is used to identify diseases by having healthy and sickle cell disease-affected human donors' entire blood samples on microscope slides. The healthy donors' blood samples were not affected by sickle cell disease.

This study [16] includes AI models evaluated on clinical data acquired by utilizing five distinct classifiers. These models were tested using data collected by the hospital. Analyzing the models with regard to the accuracy of kappa statistics and the classification time allowed for the selection of the classification strategy that proved to be the most effective.

The findings of this research suggest the development of a model capable of accurately categorizing these images as either healthy RBC or SC images. Comparative analysis was performed on the results produced by five different Deep Learning models using two distinct optimizers. According to the findings of the research [17], transfer learning using the VGG16 model helped obtain features from images in order to do the classification.

A potential and affordable measure for monitoring the clinical condition of sickle cell disease patients is the percentage of RBC that adopt a certain motion when exposed to low shear flow. The purpose of this research [18] was to propose a two-stage end-to-end machine learning pipeline capable of automatically classifying cell movements in films with a large class imbalance. The dataset and the scripts were made available to the public.

This study [19] offered a unique and efficient deep-learning strategy for identifying sickle cell anaemia. This approach was developed by the authors of this work. From the publicly available database, around nine hundred images of human RBC under a microscope are retrieved. Each of the images has been scaled down to the same dimensions. Additionally, the sickle cell trait may be identified with the use of a conventional InceptionV3 model by using the SoftMax layer.

In this work [20], transfer learning of a pre-trained AlexNet model is presented for the categorization of illness versus trait instances. The suggested approach has the greatest classification accuracy possible, which is 95.5%.

For the purpose of this study [21], de-identified patient data from 12 years' worth of SCA patients were collected legitimately from the hospital and then tested in connection to SCA patients' medical records. A text mining framework was used in this study to analyze and forecast the duration of stay of SCA patients using three different machine learning models.

This article [22] provided a new image processing-based technique that can be readily implemented into a smartphone together with low-cost imaging equipment. It has been determined that the distortion generated by haemoglobin may be mapped to the geometric features of the sickle form.

Recent studies have explored deep learning models for automated SCA classification, but many rely on a single imaging modality, limiting their accuracy and robustness. Furthermore, multimodal imaging has been underexplored in SCA detection despite its potential to provide a more comprehensive understanding of RBC morphology. This research fills these gaps by combining multiple imaging techniques with an optimized deep learning architecture, improving classification performance and diagnostic accuracy.

3. Proposed Model

The overall architecture of classifying sickle cell anemia, as shown in Figure 1, can be divided into four main steps: The first step is to acquire an image of the blood cells. This can be done using a microscope. The next step is to preprocess the image to remove noise and improve the contrast. This can be done using techniques such as noise filtering and data augmentation. The third step is to extract features by Multimodal RBC Spot Extraction from the image that can be used to classify the blood cells. These features can be based on the blood cells' shape, size, and texture. The final step is to classify the blood cells as either sickle cells or healthy cells. This can be done by using an optimized Deep Stacked CNN Model.

3.1. Data Acquisition and Preprocessing

The dataset utilized for assessment in this study is real-time data. This dataset comprises information from 300 patients with 14 SCA-related characteristics. The data set was divided into 60% for training and 40% for testing for performance analysis. This real-time data was gathered from the NAWA-Nilgiri Adivasi Welfare Association in the Nilgiris district. A total of 300 samples were obtained, including 187 female and 113 male samples. The patients' ages range from 3 to 72. Acquire images of blood samples using different imaging modalities. Each modality might highlight different features of the red blood cells, such as size, shape, or presence of specific molecules. Apply preprocessing techniques to enhance the quality of the images and remove noise, as shown in Figure 2.

Convert color images to grayscale to simplify the data while retaining important structural information.

If I_{color} is the original color image, H x W x C, where H is height, W is width, and C is the number of color channels (usually 3 for RGB images); then the grayscale image I_{gray} is obtained by averaging color channels:

$$I_{gray}(x,y) = \frac{1}{C}\sum_{c=1}^{C} I_{color}(x,y,c) \qquad (1)$$

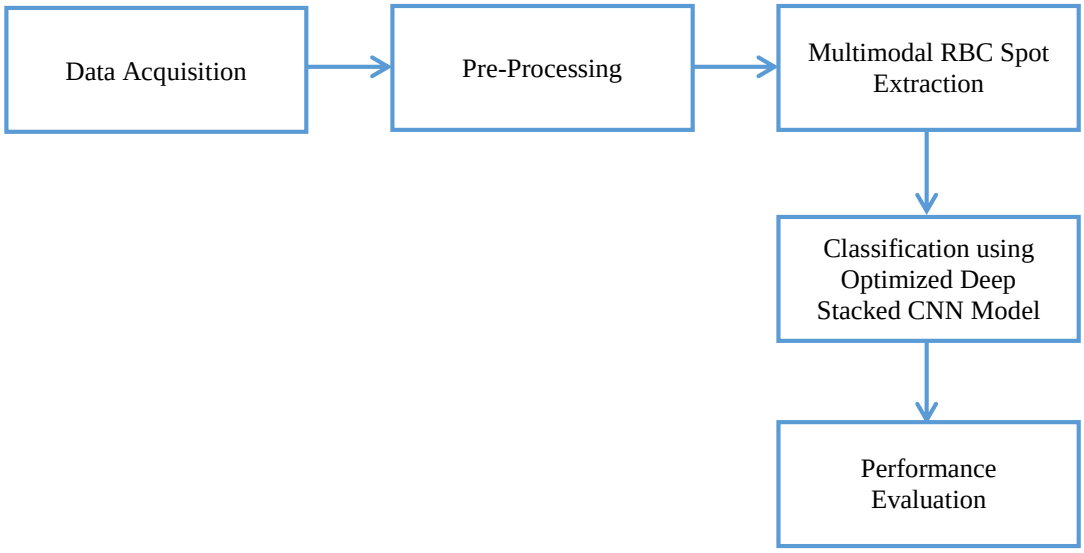


Fig. 1 Overall architecture of proposed work

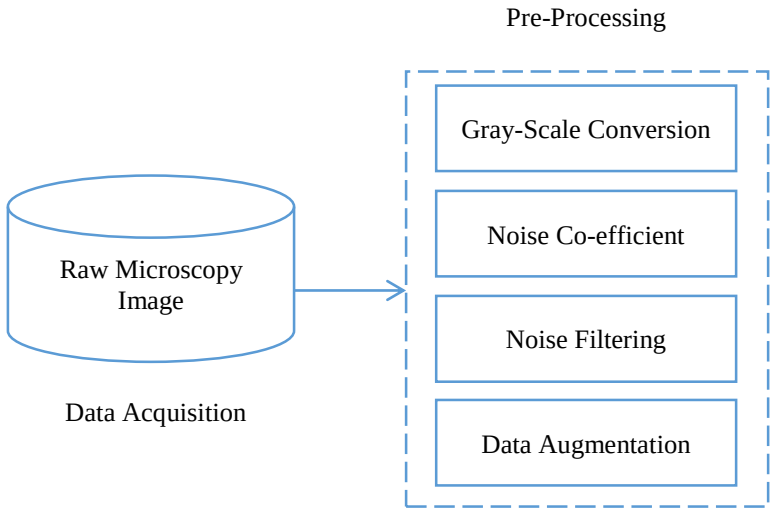


Fig. 2 Data acquisition and preprocessing

For contrast stretching, if I_{input} has pixel values in the range [0, 255], the enhanced image $I_{enhanced}(x, y)$ can be obtained using:

$$I_{enhanced}(x,y) = \frac{255}{I_{max} \cdot I_{min}} . I_{input}(x,y) - I_{min} \quad (2)$$

Gaussian noise reduction using a convolutional filter involves applying a Gaussian kernel to an image to reduce noise while preserving important features. The Gaussian kernel is a weighted matrix that assigns more weight to the central pixel and gradually reduces weight away from the center. This technique is effective for reducing random noise in an image.

Generate a Gaussian kernel based on the desired filter size and standard deviation. The kernel should have odd dimensions to maintain a central pixel.

Given a kernel size k x k and standard deviation σ, the Gaussian kernel G is calculated as follows:

$$G(i,j) = \frac{1}{2\pi\sigma^2} \cdot exp\left(-\frac{i^2 + j^2}{2\sigma^2}\right) \quad (3)$$

Where G(i, j) is the Gaussian kernel.

Convolve the Gaussian kernel with the noisy image using a convolution operation.

Given a noisy image I_{noisy} and the Gaussian kernel G, the filtered image $I_{filtered}$ can be obtained using convolution:

$$I_{filtered}(x,y) = \sum_{i=-k}^{k} \sum_{j=-k}^{k} I_{noisy}(x+i, y+j) , G(i,j) \quad (4)$$

3.1.1. Data Augmentation

Data augmentation is the process of applying different changes to images in order to generate fresh training examples. Data augmentation is a method used in image processing that applies different changes to existing images. Data augmentation in the context of Red Blood Cell (RBC) images might assist in enhancing the resilience and

generalization of machine learning models by exposing them to a broader variety of variations that might occur in real-world scenarios.

Flip the image horizontally or vertically to simulate different orientations of RBCs.

1. Horizontal Flip:
$$I_{flipped}(x,y) = I(x, image\_width - y - 1) \quad (5)$$

2. Vertical Flip:
$$I_{flipped}(x,y) = I(x, image_{height} - x - 1, y) \quad (6)$$

Rotate the image by a certain angle (e.g., 90 degrees, 180 degrees) to simulate variations in cell orientation.

$$I_{rotated}(x,y) = I(rotate\_center(x,y,\theta)) \quad (7)$$

Apply zoom-in or zoom-out transformations to mimic images captured at different magnifications.

- Zoom-In: Horizontal Flip:
$$I_{zoomed}(x,y) = I\left(\frac{x}{zoom\_factor}, \frac{y}{zoom\_factor}\right) \quad (8)$$
- Zoom-out:
$$I_{zoomed}(x,y) = I(x \times zoom_{factor}, y \times zoom\_factor) \quad (9)$$

Adjust the brightness and contrast of the image to simulate varying lighting conditions.

- Brightness Adjustment:
$$I_{bright}(x,y) = I(x,y) + brightness_{factor} \quad (10)$$
- Contrast adjustment: $I_{contrast}(x,y) = contrast_{factor} \times (I(x,y) - mean\_pixel\_value) + mean\_pixel\_value$ (11)

Pseudocode for Data Augmentation Process

```
procedure apply_data_augmentation(image: Image, augmentation_type: String, params: Dictionary) -> Image
    if augmentation_type == "horizontal_flip":
        augmented_image = flip_horizontally(image)
    else if augmentation_type == "vertical_flip":
        augmented_image = flip_vertically(image)
    else if augmentation_type == "rotate":
        angle = params["angle"]
        augmented_image = rotate_image(image, angle)
    // Add more cases for other augmentation types
    return augmented_image
end procedure
```

Data augmentation is typically applied during the training phase of a deep learning model. Training the model on both the original and augmented images makes it more capable of recognizing patterns and features in a wider range of scenarios, leading to improved generalization of unseen data.

3.2. Multimodal RBC Spot Extraction

Multimodal RBC Spot Extraction is the process of extracting relevant features and information from different imaging modalities to analyze red blood cell (RBC) spots. In the context of medical research, especially in fields like haematology and diagnostics, multimodal RBC spot extraction involves utilizing various imaging techniques to capture different aspects of RBCs' morphology, structure, and function. The term multimodal refers to multiple imaging modalities, such as brightfield microscopy, phase-contrast imaging, fluorescence microscopy, or other specialized techniques. Each modality provides unique information about RBCs, such as cell shape, size, texture, and internal components. Integrating data from these modalities can enhance the accuracy of analyzing RBCs and diagnosing various blood-related disorders.

Furthermore, since sickle cells are usually diverse in form and sometimes touch or overlap, employing a constant pixel size might make it impossible to gather all single RBC patches. We created a multimodal RBC spot extraction approach for our research to address the aforementioned issues. Multimodal RBC spot extraction refers to the process of extracting red blood cell spots from images acquired through multiple imaging modalities, such as brightfield microscopy, fluorescence microscopy, etc. The general steps involved in multimodal RBC spot extraction are shown in Figure 3.

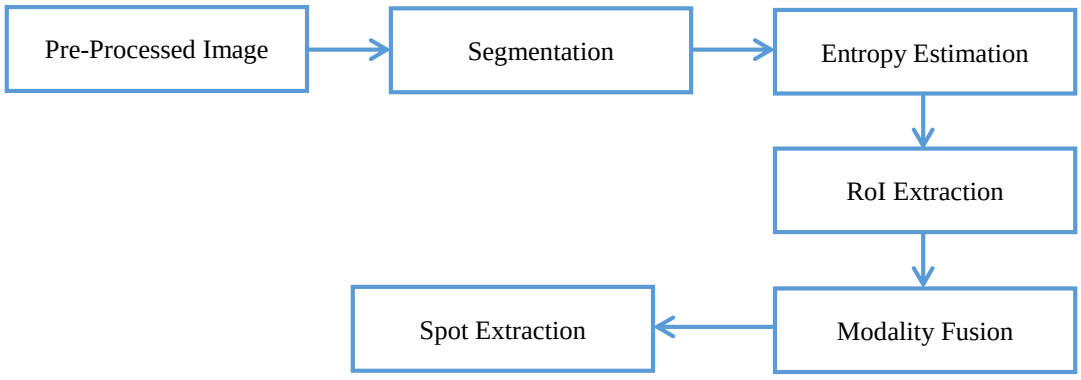


Fig. 3 Multimodal RBC spot extraction

3.2.1. Segmentation

Cell segmentation is performed to separate individual RBCs from the background and other cells. Different segmentation techniques might be used based on the characteristics of the images and the imaging modalities.

3.2.2. RoI Extraction Using Entropy Estimation

Extract relevant features from each segmented cell. These features might include size, shape, texture, intensity, and modal-specific features. Different modalities of RoI might yield different sets of features. Entropy estimation can be used to extract ROIs from RBCs by dividing the image into small blocks and then calculating the entropy of each block. Blocks with low entropy are more likely to contain RBCs. This information can then segment the image and extract the RBC spots.

3.2.3. Modality Fusion

Our research in multimodal cellular imaging focuses on integrating features from diverse imaging modalities to create a comprehensive representation of cells. Selecting fusion strategies and rigorously evaluating their performance aims to enhance understanding of cellular systems and advance biomedical research and healthcare practices. Fusion techniques could involve simple concatenation, weighted averaging, or more advanced techniques like feature-level fusion.

3.2.4. Spot Extraction

Determine the regions or locations on the cells corresponding to specific spots of interest. These spots could be related to certain molecules or markers. This step might involve using domain-specific knowledge to identify the spots based on the features extracted in the previous steps.

The raw RBC images are preprocessed using the techniques mentioned earlier, and cell segmentation is performed to separate individual RBCs. Entropy estimation is used to identify regions of the image that are likely to contain RBCs. The calculation for entropy is given in eq 12.

$$E = -\sum_{h=1}^{g} Prob_i log P_i \quad (12)$$

Where g is the value of grey-scale conversion, $Prob_i$ is the possibility of occurrence for every intensity range, and the calculation may be performed by splitting the count of the ith histogram h(i, j) through the analysis of the pixel count in each image, as shown in Eq 13 below:

$$Prob_i = \frac{h(i,j)}{N^2} \quad (13)$$

There are some steps to extract ROI from RBCs using entropy estimation, which includes:

1. Divide the image into small blocks, 2. Calculate the entropy of each block. 3. Identify the blocks with low entropy. 4. These blocks are likely to contain RBCs. 5. Extract the ROI from these blocks.

The size of the blocks used for entropy calculation is an important parameter. If the blocks are too small, the entropy estimation may not be accurate. If the blocks are too large, the ROI extraction may not be accurate. RBCs are typically more homogeneous in terms of their intensity than the surrounding tissue, meaning they have lower entropy. This means that regions of the image with low entropy are more likely to contain RBCs.

3.3. Deep Stacking Network Model

A Deep Stacking Network Model" typically refers to a model that involves stacking multiple layers of neural networks or other machine learning models to create a more complex and powerful predictive system. This approach combines the concepts of deep learning and ensemble learning.

3.3.1. Base Models

These are individual models that make up the first layer of the network. They could be neural networks, decision trees, support vector machines, or machine learning models.

3.3.2. Intermediate Layers

These are additional layers of models that take the outputs of the base models as input features. They might involve transforming the features, combining them, or generating new features.

3.3.3. Meta Model

This is the final layer of the network that takes the outputs from the intermediate layers and produces the final prediction. It's often a simple model like logistic regression, but it can also be a neural network or any other suitable classifier.

The general process involves training each layer sequentially. The base models are trained independently on the input data. Then, the intermediate layers are trained on the outputs of the base models. Finally, The Meta model is trained using the intermediate layer outputs. The goal of this structure is to enable the network to learn hierarchical data representations. Each layer develops the ability to capture various degrees of abstraction and complexity. Combining the predictions yields the strengths of multiple layers, potentially leading to better overall performance compared to using just a single model.

Let X be the input features matrix, and Y be the corresponding labels.

Train individual base models. $M_1, M_2, \ldots, M_k$ using different algorithms on the same dataset X;

$$\left.\begin{aligned} M_1: f_1 &= M_1(X) \\ M_2: f_2 &= M_2(X) \\ M_k: f_k &= M_k(X) \end{aligned}\right\} \quad (14)$$

Concatenate the predictions from the base models to create a stacked features matrix F:

$$F = [f_1, f_2, \ldots, f_k] \quad (15)$$

Train an intermediate meta-model G (can be a neural network or any other suitable model) using the stacked features F and the true labels Y:

$$G: h = G\ (F, Y) \quad (16)$$

If desired, train a final meta-model H on the intermediate meta-model's predictions h and the original labels Y:

$$H: \hat{y} = H\ (h, Y) \quad (17)$$

- For a new input X_{new}, pass it through the base models to get their predictions $f_1, f_2, \ldots, f_k$
- Stack these predictions to form F_{new}.
- Pass F_{new} through the intermediate meta-model G to get h_{new}.
- Optionally, pass h_{new} through the final meta-model H to get the final prediction $\hat{y}_{new}$.

3.4. Optimized Deep Stacked CNN Model

The optimized Deep Stacked CNN approach employs a multi-layered convolutional neural network architecture designed to learn intricate features and patterns within microscopic images of RBCs, as shown in Figure 4. Unlike traditional methods, which often require expert intervention, the Deep Stacked CNN automates the classification process, enabling quick and reliable diagnosis.

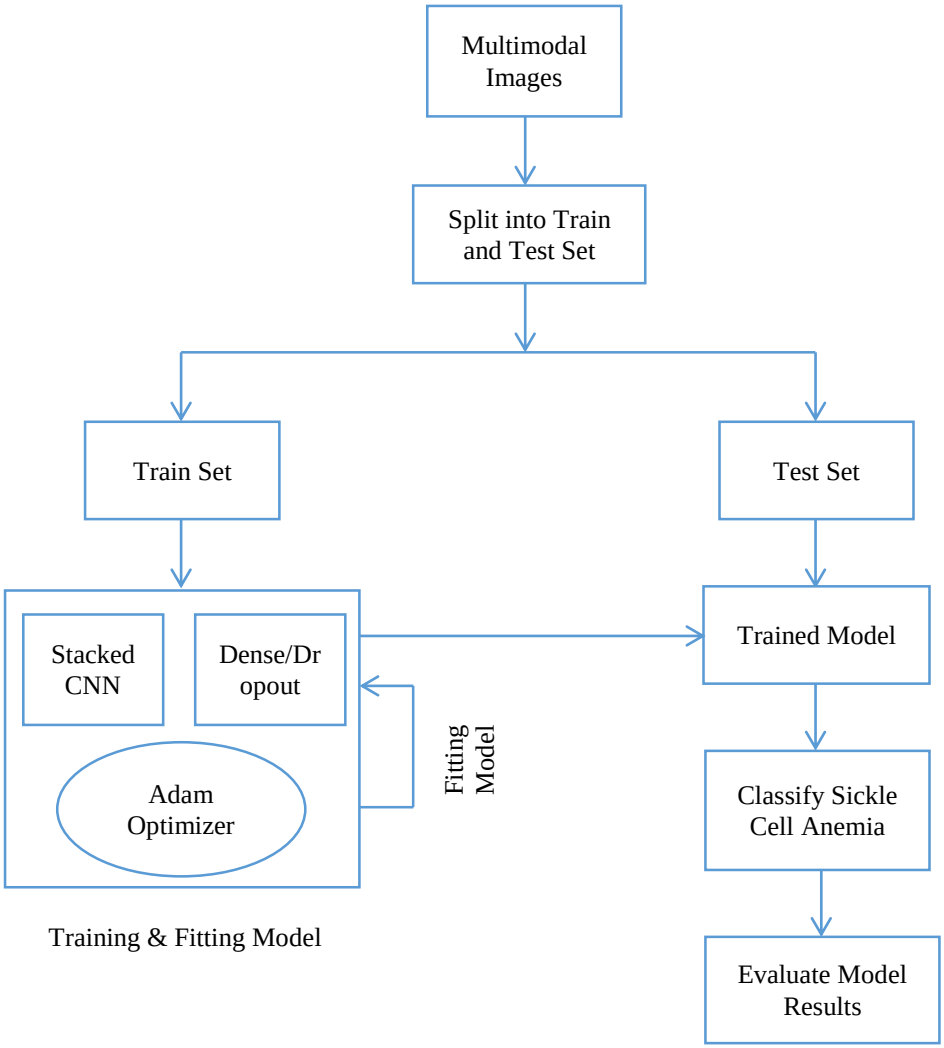


Fig. 4 Optimized deep stacked CNN model

The architecture of the Deep Stacked CNN is meticulously designed to extract progressively abstract features from RBC images. The Adam optimizer is an adaptive optimization algorithm commonly used in training neural networks. It computes adaptive learning rates for each parameter, adjusting them based on the first and second moments of gradients. This adaptive nature enables faster convergence and better performance, making it widely utilized in deep learning tasks. By combining techniques like momentum and RMSProp, Adam offers efficient gradient descent. He is suitable for various neural network architectures, including convolutional neural networks like the Deep Stacked CNN used for analyzing microscopic images of RBCs. Stacking multiple convolutional and pooling layers enables the network to automatically learn relevant representations of the input data. Creating a mathematical representation of an optimized Deep Stacked CNN for classifying sickle cell anemia using RBC images

involves describing the model's architecture, operations, and components. Let's denote:

X is the input RBC image data, Y is the corresponding label (normal or sickle cell anemia), N is the number of training examples, C is the number of classes (2 in this case: normal and sickle cell), H is the height of the input image, W as the width of the input image, D as the number of channels in the input image (e.g., 3 for RGB images).

The architecture can be represented as a series of layers:

A convolutional layer applies a set of learnable filters to the input image to extract features.

Let W_i represent the i-th filter, b_i the bias term, and σ the activation function (e.g., ReLU).

$$Z_i = \sigma\,(W_i * X + b_i) \quad (18)$$

Pooling layers reduce computation by downsampling the spatial parameters of the feature maps and introducing translational invariance.

Let P represent the pooling operation (e.g., max pooling) and s the stride.

$$P_i = P(Z_i, s) \quad (19)$$

The flattening layer converts the pooled feature maps into a 1D vector.

$$F = Flatten\,(P_i) \quad (20)$$

Fully connected layers process the flattened feature vector.

$$A_i = \sigma\left(W_{fc_i}F + b_{fc_i}\right) \quad (21)$$

The output layer produces the class probabilities using softmax activation.

$$\hat{Y} = softmax\left(A_{output}\right) \quad (22)$$

The cross-entropy loss measures the discrepancy between predicted probabilities and actual labels.

$$Loss = -\frac{1}{N}\sum_{i=1}^{N}\sum_{j=1}^{C} Y_{ij}\log\left(\hat{Y}_{ij}\right) \quad (23)$$

The model is optimized by updating the learnable parameters (weights and biases) to minimize the loss function using an optimization algorithm like gradient descent.

Pseudocode for ODSN

```
# Define hyperparameters

learning_rate = 0.001

batch_size = 32

num_epochs = 50

num_classes = 2

# Build the Deep Stacked CNN architecture

model = Sequential()

model.add(Conv2D(filters=32, kernel_size=(3, 3), activation='relu', input_shape=(height, width, channels)))

model.add(MaxPooling2D(pool_size=(2, 2)))

model.add(Conv2D(filters=64, kernel_size=(3, 3), activation='relu'))

model.add(MaxPooling2D(pool_size=(2, 2)))

model.add(Conv2D(filters=128, kernel_size=(3, 3), activation='relu'))

model.add(MaxPooling2D(pool_size=(2, 2)))

model.add(Flatten())

model.add(Dense(128, activation='relu'))

model.add(Dense(num_classes, activation='softmax'))

model.compile(optimizer='adam',
loss='categorical_crossentropy', metrics=['accuracy'])

# Split dataset into training, validation, and test sets

X_train, Y_train, X_val, Y_val, X_test, Y_test
                = split_dataset()

model.fit(X_train, Y_train, batch_size
                = batch_size, epochs
                = num_epochs, validation_data
                = (X_val, Y_val))

test_loss, test_accuracy
                = model.evaluate(X_test, Y_test)

predictions = model.predict(X_test)
```

This pseudocode outlines creating a Deep Stacked CNN model, training it on RBC image data and visualizing the training history.

4. Results and Discussions

The suggested model was developed and tested using the PYTHON tool version 3.7.12. During the study, the participants used a PC equipped with 8 GB of RAM, an Intel Core i7-10700 processor operating at 4.8 GHz, and a 64-bit Windows 10-OS installation.

4.1. Experimental Analysis

Table 1 provides the step-by-step process with its outcomes of results using Multimodal RBC Spot Extraction using an Optimized Deep Stacking Network algorithm, and the final classification is shown in Figure 5.

The given input RBC sample is classified as Thalassemia type of sickle cell anemia.

Table 1. Output for SCA using MRSE-ODSN

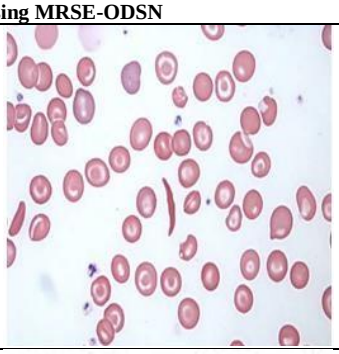
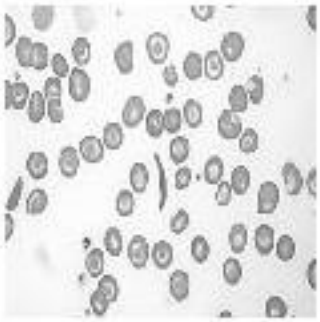
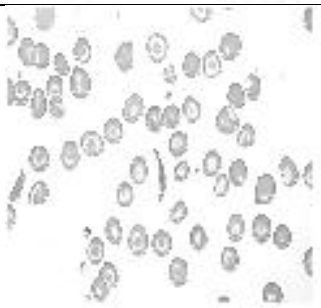
Input Image	
Gray-scale Image Conversion	
Noise Coefficient Data	
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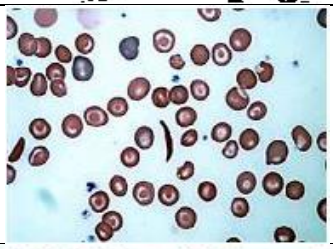
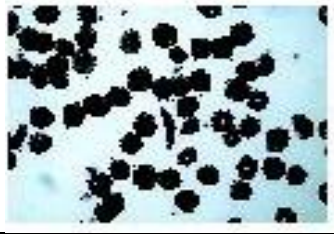
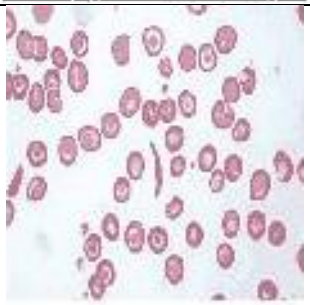
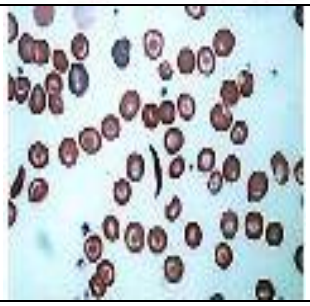
Image Enhancement	
Segmentation	

RoI Extraction using Entropy Estimation	
Modality Fusion	
Multimodal Spot Extraction	

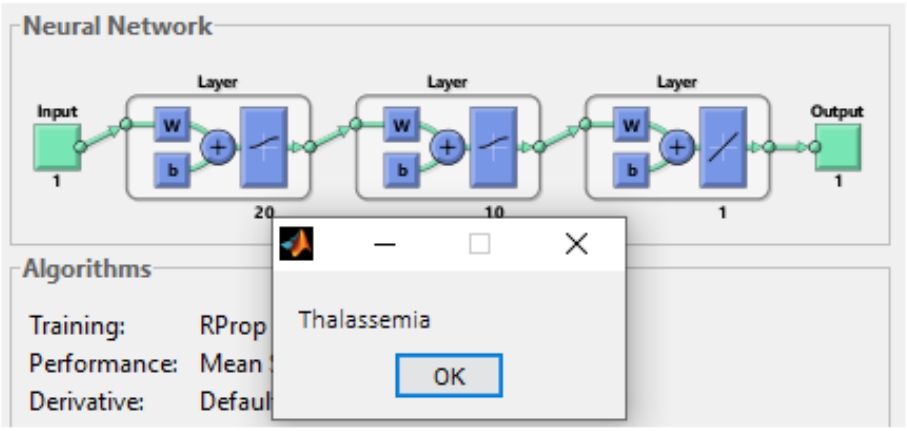


Fig. 5 Classification results of SCA

4.2. Performance Metrics

Performance metrics are essential for evaluating the effectiveness of assessing the quality of your sickle cell anemia classification model:

1. Accuracy: Accuracy is intended to separate the number of successfully predicted cases by the total number of occurrences in the dataset.

$$Accuracy = \frac{Number\ of\ correct\ Predictions}{Total\ number\ of\ predictions} \quad (24)$$

2. Precision: Out of all positive events predicted, precision is the percentage of correct predictions. The purpose is to determine whether optimistic predictions are accurate.

$$Precision = \frac{True\ Positives}{True\ positives + False\ Positives} \quad (25)$$

3. Recall: The percentage of accurately predicted positive events out of all real positive instances is measured by recall. It emphasizes the capacity to record good events.

$$Recall = \frac{True\ positives}{True\ positives + False\ Negatives} \quad (26)$$

4. F1-Score: The harmonic mean of accuracy and recall is the F1-score. It strikes a stability between accuracy and recall.

$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (27)$$

5. Specificity: The percentage of accurately predicted negative events out of all actual negative illustrations is measured by specificity.

$$Specificity = \frac{True\ Negatives}{True\ Negatives + False\ Positives} \quad (28)$$

Matthews Correlation Coefficient (MCC): The MCC considers true and false positives and negatives and provides a balanced performance metric.

$$MCC = \frac{(TP \times TN) - (FP \times FN)}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \quad (29)$$

Table 2. Performance analysis comparison of proposed model

Models	Accuracy	Precision	Sensitivity	Specificity	PPV	NPV	MCC
BFO-SVM	92.93	92.04	92.07	93.83	91.28	93.48	87.23
PCA-DNN	92.16	92.45	93.36	94.96	93.55	94.86	92.16
PSO-kNN	93.90	93.21	91.05	92.65	93.26	94.16	88.17
LM-RF	95.58	95.32	94.76	94.16	94.78	94.85	92.02
Proposed Model	98.01	97.89	97.56	98.04	97.76	97.15	94.54

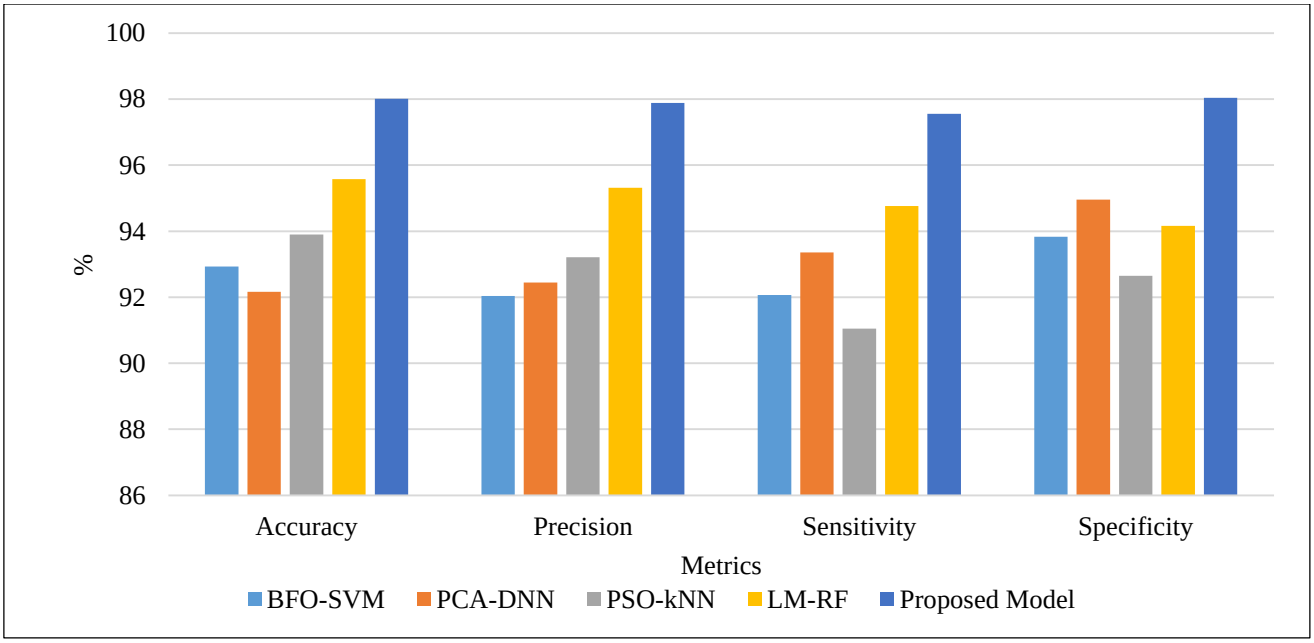


Fig. 6 Performance metrics comparison

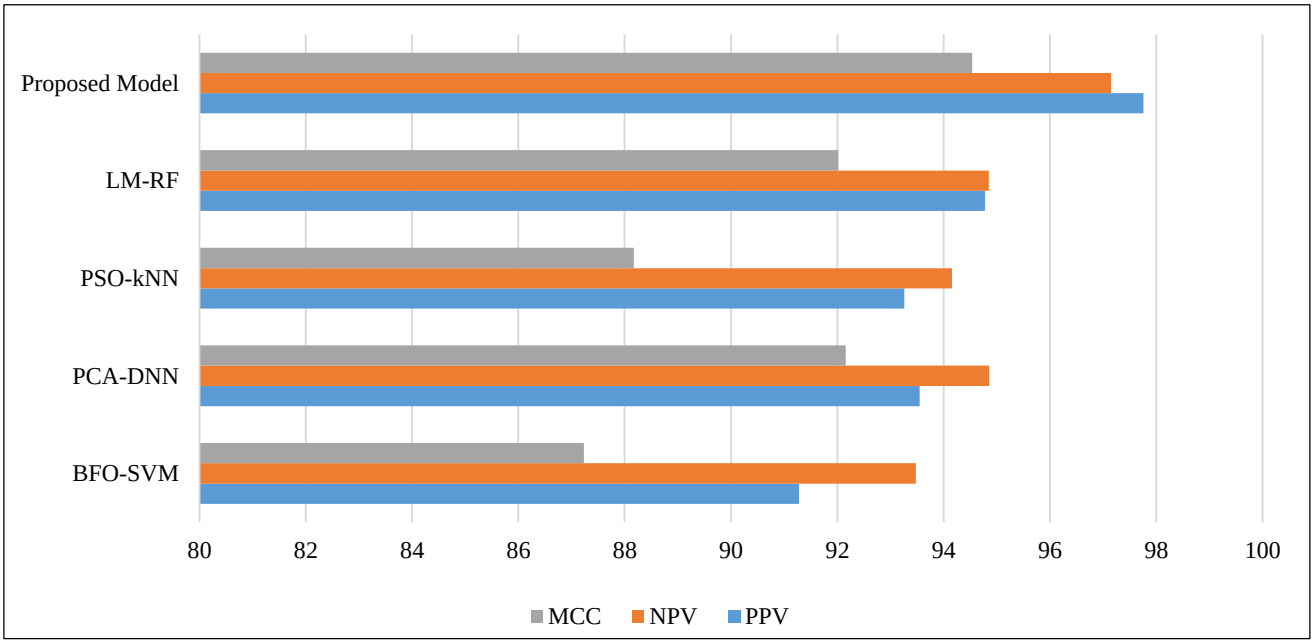


Fig. 7 Comparison of performance analysis

Integrating multimodal data and deep learning models has shown the potential to achieve 98.01% accuracy in SCA classification, which is higher than other existing methods, as given in Table 2, Figures 6 and 7. This approach not only detects the presence or absence of SCA but also has the potential to identify specific subtypes or causes of SCA, which is crucial for tailored treatment strategies.

5. Conclusion

This research proposes an approach for improving sickle cell anemia classification within the Nilgiri tribes through the innovative integration of multimodal RBC spot extraction and an optimized deep stacking network algorithm. The primary objective was to improve the accuracy, efficiency, and cultural sensitivity of sickle cell anemia diagnosis within this indigenous community. A dataset was acquired for review from the NAWA-Nilgiri Adivasi Welfare Association in the Nilgiris area. The dataset comprised a collection of sickle cell anaemia test results from tribal people living in various locations of the Nilgiris region. This dataset comprises information from 300 patients with 14 SCA-related characteristics. The utilization of multimodal data, including microscopic RBC images and clinical information, has led to a substantial improvement in the accuracy of sickle cell anemia classification. The optimized deep stacking network algorithm's ability to effectively leverage the strengths of diverse modalities has contributed to more robust and reliable predictions. The results of the classification model demonstrate a significant improvement in accuracy of 5.32% compared to traditional classification methods.

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