Research Article

Deep Learning Model Comparison for Sickle Cell Disease Prediction: AlexNet, MobileNetV2, and InceptionResNetV2

Abhishek Tiwari [1*], **Mayank Singh Parihar** [2], **Vanita Jain** [3]
[1] IT&CS Department, Dr. C. V. Raman University, Bilaspur, Chhattisgarh, India
[2] IT&CS Department, Dr. C. V. Raman University, Bilaspur, Chhattisgarh, India
[3] Department of Electronic Science, University of Delhi, Delhi, India

Corresponding Author: * Abhishek Tiwari

DOI: https://doi.org/10.5281/zenodo.17377224

Abstract

Sickle Cell Disease (SCD) continues to be a major challenge to people's health worldwide, especially in areas that lack sufficient resources, where early and accurate diagnosis is of utmost importance for proper clinical management. Automated medical image analysis powered by deep learning has become a highly effective way to improve diagnostic precision and speed. This work is a comparative evaluation of three major convolutional neural network (CNN) architectures, AlexNet, MobileNetV2, and InceptionResNetV2, in the prediction of SCD from microscopic blood smear images. Accuracy, precision, recall, F1-score, and computational efficiency were the metrics used to evaluate the models.

The InceptionResNetV2 obtained the highest accuracy (94%) and also showed the greatest classification robustness; thus, it is very suitable for incorporation into advanced clinical diagnostic systems, according to experimental results. MobileNetV2, with slightly lower accuracy (93%), was highly computationally efficient and had a very short inference time, which makes it very suitable for real-time deployment in healthcare environments with limited resources. On the other hand, AlexNet, a CNN breakthrough, exhibited comparatively lower predictive performance.

Therefore, the findings of this study suggest that the best model choice will depend on the intended use scenario, as a trade-off between diagnostic accuracy and computational constraints. This work moves the field of AI-assisted hematology forward and is a deep learning breakthrough that has enormous potential in the early diagnosis and management of Sickle Cell Disease.

Manuscript Information

- **ISSN No:** 2583-7397
- **Received:** 08-08-2025
- **Accepted:** 30-09-2025
- **Published:** 17-10-2025
- **IJCRM:**4(5); 2025: 381-390
- **©2025, All Rights Reserved**
- **Plagiarism Checked:** Yes
- **Peer Review Process:** Yes

How to Cite this Article

Tiwari A, Prihaar M, Jain V. Deep Learning Model Comparison for Sickle Cell Disease Prediction: AlexNet, MobileNetV2, and InceptionResNetV2. Int J Contemp Res Multidiscip. 2025;4(5):381-390.

Access this Article Online

www.multiarticlesjournal.com

KEYWORDS: Sickle Cell Disease, Deep Learning, Convolutional Neural Networks, AlexNet, MobileNetV2, InceptionResNetV2, Medical Imaging, Comparative Analysis, Computer-Aided Diagnosis.

1. INTRODUCTION

Sickle Cell Disease (SCD) is a gene mutation that regulates blood cells that leading to a change in the gene responsible for the production of haemoglobin (Jain et al., 2022). This variation in genes outcomes in the formation of an unusual type of haemoglobin called HbS (Becking, 2022). Due to mutations in the genes and the abnormal aggregation of haemoglobin, red blood cells display a sickle-shaped phenotype, replacing their usual round and deformable structure (Elendu, 2023; Hassan, 2024). These sickled cells injure blood vessels and can block circulation in small vessels, leading to pain, anaemia, organ damage, and other health complications (Elendu, 2023; Centers for Disease Control and Prevention [CDC], 2025). The disease is prevalent in regions of Africa, India, and Chhattisgarh, where it remains a significant public health challenge (MedlinePlus Genetics, 2024; Hassan, 2024). Early detection is crucial for preventing severe complications and improving the patient's quality of life (MedlinePlus Genetics, 2024). Current diagnostic methods, such as haemoglobin electrophoresis and genetic testing, are accurate but often costly and difficult to implement in low-resource settings (Geraldine, 2001; StatPearls Publishing, 2024).

Deep learning has become a major tool in the medical field because of its speed and accuracy in analysing medical images (Litjens et al., 2017). Convolutional Neural Networks (CNNs), a form of deep learning model, are the fittest to carry out image-based diagnosis (Shen et al., 2017). They do not require human input to pick up distinguishing attributes from blood smear images and identify the sickle-shaped cells, making them a reliable assistant for doctors in detecting SCD, particularly in places lacking advanced laboratories (Das et al., 2022). To a large extent, deep learning methods have been successfully implemented in the medical domain with various CNN models (Esteva et al., 2019). One of the first models to demonstrate deep learning power was AlexNet, introduced in 2012, which pioneered GPU-based training and popularised ReLU activation (Krizhevsky et al., 2012). Created with the aim of computational efficiency, MobileNetV2 allows slim yet accurate predictions, making it especially applicable to telemedicine in hard-to-reach or poorly equipped areas (Sandler et al., 2018). Meanwhile, InceptionResNetV2 combines the strengths of Inception modules and residual connections, enabling deeper feature extraction and high accuracy in complex classification tasks (Szegedy et al., 2017).

Convolutional Neural Networks (CNNs) have been shown to be very effective in predicting sickle cells through various studies. For instance, Das et al. (2022) introduced a CNN-based method for automatic detection of sickle cells from blood smear images. They experimented with different deep learning setups, including ResNet and Inception families, and achieved more than 95% accuracy. Their research emphasized the role of transfer learning and demonstrated that deep learning models could surpass the performance of manual or rule-based methods, thereby showing promise for widespread clinical application (Das et al., 2022). Such studies form the underpinning of the current comparative work of AlexNet, MobileNetV2, and InceptionResNetV2.

Datasets play an important role in building successful deep learning models for SCD prediction. In this research, images were acquired using a brightfield microscope with a 100X/1.4NA objective lens, a motorized x-y stage, and a color camera, and processed with a wavelet-based Extended Depth of Field (EDoF) algorithm to ensure clarity (Olugbara et al., 2020). The ground truth for clinical diagnosis was confirmed through hemoglobin electrophoresis, and the corresponding labels were provided in the file sickle_slides_new_march.txt (Adepoju et al., 2021). The dataset was ethically approved by the Institute for Advanced Medical Research and Training (IAMRAT), University of Ibadan, Nigeria, under permit numbers UI/EC/10/0130 and UI/EC/19/0110 (University of Ibadan, 2019). Although these blood smear images were collected in Nigeria, they exhibit the same morphological characteristics of SCD as those observed in patients from Chhattisgarh, India, making them appropriate for experimental research in regions with high prevalence (Hassan, 2024).

The current study draws from established conceptual frameworks and aims to understand the comparative suitability of AlexNet, MobileNetV2, and InceptionResNetV2 for predicting SCD from blood smear images. The main research question is to what extent each model can be accurate, computationally efficient, and reliable enough for clinical use (Litjens et al., 2017). AlexNet sets the foundation for comparison, being one of the earliest deep CNNs for large-scale image classification (Krizhevsky et al., 2012). MobileNetV2 allows for lightweight deployment and is convenient for mobile devices, making it particularly useful in remote healthcare settings (Sandler et al., 2018). InceptionResNetV2, by combining Inception modules with residual connections, provides extreme versatility for precision-demanding tasks (Szegedy et al., 2017). Both publicly available datasets and clinical collaborations in Chhattisgarh, a region with high disease burden, are considered in this study, where annotated data scarcity and image quality variability remain significant challenges (Hassan, 2024). The anticipated outcome is to identify the most effective model for local implementation and contribute toward quicker, more affordable, and dependable diagnostic practices (Esteva et al., 2019). The study has combined these factors, which allow it to not only review the different deep learning architectures but also to be a step towards the implementation of artificial intelligence in the medical field. Their goal is to enable the provision of diagnostic services in less privileged areas so that detection and treatment of SCD can be easier and more efficient.

2. Related Work

One of the fields that has seen the most accelerated application of Artificial Intelligence (AI) is medical imaging, where the use of deep learning methods has become a cornerstone (Litjens et al., 2017). In earlier years, computer-aided diagnosis relied primarily on conventional machine learning algorithms, which required the extraction of handcrafted features such as texture, shape, and statistical descriptors from microscopic blood smear images (Shen et al., 2017). The next step introduced classifiers such as Support Vector Machines (SVM), k-Nearest Neighbors (k-NN), and Random Forests, which were employed to differentiate between healthy and diseased samples (Chollet, 2018). One of the major drawbacks and performance bottlenecks of these approaches was their dependency on high-quality handcrafted feature engineering, along with their limited ability to generalize across diverse datasets (Esteva et al., 2019). This inadequacy led to the transition toward deep learning models, which can automatically extract multi-level hierarchical features directly from original images, reducing the dependency on manual work and improving generalization performance (LeCun et al., 2015).

It has been a while since Convolutional Neural Networks (CNNs) have held the position of the most successful models in blood image analysis. Choosing to employ CNNs has been backed by numerous experiments where they were used for detecting abnormalities in red blood cells, including malaria, anaemia, and sickle cell disease (Shen et al., 2017). For instance, Rajaraman et al. (2018) applied CNN-based transfer learning to detect malaria parasites in thin blood smear images, achieving a considerable reduction in errors compared to traditional classifiers. Similarly, Das et al. (2020) demonstrated the application of CNNs for identifying morphological changes in red blood cells, showcasing the role of deep learning in haematological diagnostics. Furthermore, CNNs remain among the most effective technologies for predicting SCD, as they can recognize minute shape variations in red blood cells that serve as primary factors for differentiation (Das et al., 2022).

Deep learning methods have been progressively applied to the case of sickle cell disease. For instance, Adegun and Viriri (2021) developed a CNN-based model that achieved notable accuracy in distinguishing between sickled and normal red blood cells, while also emphasizing the importance of intensive preprocessing steps to improve image quality. In another study, Oyelade et al. (2022) explored transfer learning with pretrained architectures, demonstrating that models trained on large-scale datasets such as ImageNet significantly improved classification performance. However, most research in this area has either focused on the development of a single network or failed to conduct systematic comparisons of different models, leaving open the question of whether some architectures may be more suitable than others for real-world applications (Adegun & Viriri, 2021; Oyelade et al., 2022).

A major milestone in deep learning was marked by Krizhevsky et al. (2012) with the introduction of AlexNet, which won the ImageNet Large Scale Visual Recognition Challenge (ILSVRC). With its relatively simple, deep hierarchical architecture of five convolutional layers followed by fully connected layers, AlexNet demonstrated the power of CNNs for feature learning. Although computationally heavy compared to modern architectures, it remains a key reference in CNN evolution, particularly for medical imaging applications. Following this, Sandler et al. (2018) introduced MobileNetV2, representing a shift toward lightweight models optimized for mobile and embedded systems. Through the use of depthwise separable convolutions and inverted residuals, MobileNetV2 significantly reduced parameter count and computational cost without substantial accuracy loss, making it highly suitable for healthcare applications in resource-constrained settings.

Another powerful architecture, InceptionResNetV2, was developed by Szegedy et al. (2017) as a combination of Inception modules and residual connections. This design enables multi-scale feature extraction while addressing the vanishing gradient problem in deep networks, providing accuracy, stability, and depth. InceptionResNetV2 has demonstrated superior performance in medical imaging tasks such as cancer histopathology and retinal disease detection, where identifying subtle features is critical (Szegedy et al., 2017). While these CNN architectures have shown promise in various medical imaging domains, there remains a lack of comparative investigations focusing specifically on AlexNet, MobileNetV2, and InceptionResNetV2 for sickle cell disease prediction. Most existing works employ only one deep learning model or discuss blood disease detection in general without emphasizing SCD, and very few studies address computational efficiency alongside predictive accuracy, an essential factor in low-resource regions where SCD is most prevalent (Adegun & Viriri, 2021; Das et al., 2022).

This research aims to fill the existing gaps in knowledge by comparing these three architectures in a systematic manner across various performance metrics, such as accuracy, precision, recall, F1-score, and computational efficiency. Using medical imaging datasets of red blood cells, the goal of the study is to find out which model is the best for classification, and further to identify the model that would be the most convenient for clinical use. This study, as a result, makes the healthcare' gap between the algorithmic and the practical implementation less wide by providing such a comparative analysis.

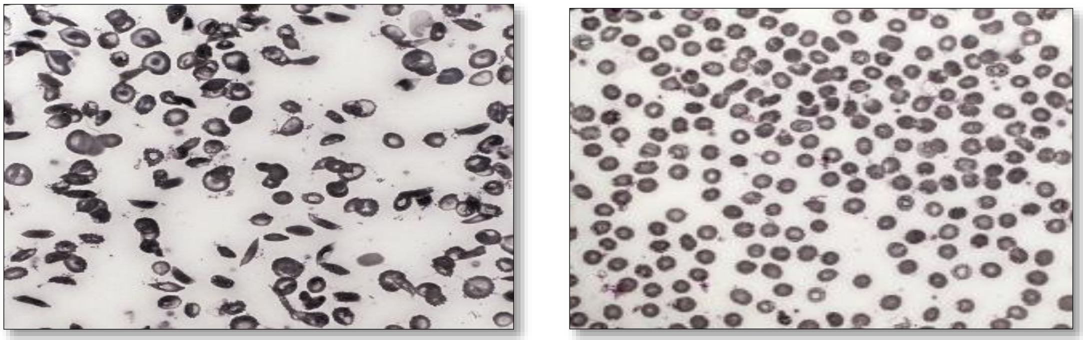
3. METHODOLOGY

The methodological framework of this study is designed to provide a comprehensive comparison of three prominent CNN architectures, AlexNet, MobileNetV2, and InceptionResNetV2, for sickle cell disease (SCD) prediction using medical imaging. The process involves four major stages: dataset acquisition, image preprocessing, model selection and training, and evaluation using performance metrics. Each step has been carefully structured to ensure reproducibility and fairness in model comparison.

3.1 Dataset Acquisition

Images used in this study were obtained from the dataset created at the Institute for Advanced Medical Research and Training (IAMRAT), University of Ibadan, Nigeria. Original blood smear images were captured using a brightfield microscope with a 100X/1.4NA objective lens, motorized x-y stage, and colour camera. To enhance visibility, z-stacks were merged into a single plane using a wavelet-based Extended Depth of Field (EDoF) algorithm (Olugbara et al., 2020). Haemoglobin electrophoresis confirmed clinical ground truth, with diagnostic labels provided in sickle_slides_new_march.txt. Ethical approval was granted under UI/EC/10/0130 and UI/EC/19/0110. The specimens reflect sickle cell morphology also observed in Chhattisgarh, India (Hassan, 2024).

Representative microscopic blood smear images from the dataset are shown in Figure 1, illustrating the quality and morphological characteristics of the samples used for this study.



a. Sickle Cell ***b. Normal Blood Cell***

Fig. 1. Raw full-field microscopic images of red blood cells captured at 100× magnification using a brightfield microscope. Microscopic images showing two categories of red blood cells: (a) sickle-shaped cells with elongated morphology, and (b) normal biconcave red blood cells.

3.2 Image Preprocessing

Due to variations in microscopic imaging conditions, preprocessing was essential to ensure image consistency and enhance model performance. In this study, all blood smear images were resized to 224 × 224 pixels to match the input requirements of standard pretrained CNN architectures. Normalization was then applied by scaling pixel intensity values to the range [0,1], facilitating stable gradient updates during training. To preserve the morphological characteristics of red blood cells while minimizing artefacts, a median filter was employed for noise reduction. Data augmentation techniques, including random rotation (±20°), horizontal and vertical flipping, zooming, and contrast adjustment, were used to enlarge the dataset and improve the model's generalization. These transformations strengthened the system's ability to handle variability in image acquisition. Comparable preprocessing strategies have been widely adopted in medical image analysis, as shown by Das et al. (2022), where resizing, normalization, and augmentation significantly improved CNN accuracy in detecting sickle-shaped cells.

3.3 Model Selection

Choosing the deep learning designs is crucial in predicting SCD from blood smear pictures. To this end, the paper compares three different convolutional neural network (CNN) architectures, i.e., AlexNet, MobileNetV2, and InceptionResNetV2, to find a good trade-off between accuracy, computational efficiency, and clinical usefulness. Basically, each of these models is a turning point in the history of deep learning, providing distinctly different design concepts that could be utilized for medical image processing.

3.3.1 AlexNet

AlexNet is a landmark architecture that significantly advanced deep learning, particularly in computer vision. It consists of five convolutional layers followed by three fully connected layers, employing rectified linear unit (ReLU) activations and max-pooling to introduce non-linearity and spatial invariance (Krizhevsky et al., 2012). Although less deep than more recent networks, AlexNet pioneered the large-scale application of deep convolutional neural networks (CNNs) for image recognition, establishing a foundation for future models.

In this research, AlexNet was adopted as a baseline architecture, enabling comparison of results with contemporary models such as MobileNetV2 and InceptionResNetV2 to evaluate performance improvements.

The convolution operation in AlexNet can be shown mathematically as:

$$Y_{i,j,k} = \sum_{m=1}^{M}\sum_{p=1}^{P}\sum_{q=1}^{Q} \mathrm{v}X_{i+p,\, j+q,\, m} \cdot W_{p,q,m,k} + b_k$$

Here $\left(Y_{i,j,k}\right)$ Is the activation at the spatial position? (i, j) in the k^{th} Feature map, X is the input image, W is the convolutional filter. $P \times Q$ And M is the number of input channels. The bias term is represented by b_k. This specimen expresses how the local receptive fields can get the higher-level features from the images of blood smears and how AlexNet can use these features to get the variations in the morphology that are caused by the different diseases in the blood.

3.3.2 MobileNetV2

MobileNetV2, developed by Sandler et al. (2018), is a pioneering model that changes the fashion trend back to lighter and more efficient CNNs, in particular, those that are usable in mobile and embedded devices. The model introduces depth-wise separable convolutions and inverted residuals, which, in combination, substantially reduce the number of parameters while the accuracy is close to the leading ones. Therefore, MobileNetV2 turns into the optimal choice for healthcare systems that experience a lack of computational resources, where the requirement for speed and efficiency is vital. The depth-wise separable convolution of this model may be depicted as:

$$\left[Y_{i,j,k} = \sum_{p=1}^{P}\sum_{q=1}^{Q} \mathrm{v}X_{i+p,\, j+q,\, k} \cdot W_{p,q,k} + b_k \right]$$

Pointwise convolution was applied to the output of depth-wise convolution:

$$Z_{i,j,m} = \sum_{k=1}^{K} \mathrm{v}Y_{i,j,k} \cdot W_{k,m}^{(1\times1)} + b_m$$

Where X stands for the input, Y is the output of depth-wise convolution, where each channel was consumed independently, and Z is the merged representation after the pointwise convolution. Such a breakdown lowers the computation cost significantly from $O(PQMK)$ to $O(PQM + MK)$ Thus making MobileNetV2 the first choice for large-scale screening tasks. Chowdhury et al. (2020) demonstrated MobileNetV2's effectiveness in medical imaging, achieving high accuracy in blood cell identification while reducing computational time, enabling both local and remote real-time diagnostic applications.

3.3.3 InceptionResNetV2

InceptionResNetV2 combines Inception modules with residual connections, enabling multi-scale feature learning and stable gradient flow, achieving high accuracy and robustness, making it effective for complex medical imaging tasks (Szegedy et al., 2017).

One way to express the residual connection in InceptionResNetV2 is through mathematical representation:

$$\boldsymbol{y} = \boldsymbol{F}(\boldsymbol{x}, \{\boldsymbol{W_i}\}) + \boldsymbol{x}$$

InceptionResNetV2 combines nonlinear operations. $F(x, \{W_i\})$ With residual connections, ensuring efficient gradient flow and stable convergence. Studies, such as Bukhari et al. (2020), confirm its superior performance in medical imaging, highlighting its capability to capture subtle morphological variations, including precise detection of sickle-shaped red blood cells.

3.4 Experimental Setup - All three models were initialized with weights pretrained on the ImageNet dataset and fine-tuned on the Sickle Cell Disease (SCD) dataset, applying transfer learning to adapt general image features for red blood cell classification (Pan & Yang, 2010). To maintain fairness, the The Same training setup was applied across models, using the Adam optimizer with a learning rate of 0.0001 (Kingma & Ba, 2015),

A batch size of 32, binary cross-entropy loss for two-class classification (Goodfellow, Bengio, & Courville, 2016), and 50 training epochs with early stopping to reduce overfitting. Experiments were conducted in a Jupyter Notebook. Environment on an Intel(R) Core i5-10300H CPU @ 2.50GHz, 8 GB RAM (7.87 GB usable), and a 4 GB NVIDIA GPU. For AlexNet, inputs were resized to 227×227 pixels with three RGB channels, consistent with its original design (Krizhevsky et al., 2012) and widely used in biomedical classification tasks (Anwar et al., 2018). InceptionResNetV2 used 299×299 pixels, as specified by Szegedy et al. (2017), suitable for hierarchical feature extraction and adopted in medical image studies such as cancer detection (Gao et al., 2020). MobileNetV2 employed 224×224 pixels, aligning with its lightweight efficiency (Sandler et al., 2018), validated in biomedical research (Howard et al., 2017; Montalbo, 2021). This preprocessing ensured compatibility and fairness in comparative evaluation.

3.5 Evaluation Metrics

To evaluate the predictive performance of AlexNet, MobileNetV2, and InceptionResNetV2, standard metrics were employed. Accuracy measured overall correctness, while Precision assessed correctly identified sickled cells among positive predictions. Recall quantified correctly detected actual sickled cells, and the F1-score, the harmonic mean of Precision and Recall, offered a balanced evaluation. Collectively, these metrics ensured a comprehensive assessment beyond simple accuracy.

Table 1: Hyperparameter Configuration of the Models

Comparison of training hyperparameters used for AlexNet, MobileNetV2, and InceptionResNetV2, including input size, optimizer, loss function, batch size, epochs, and regularization details.

Parameter	AlexNet	MobileNetV2	InceptionResNetV2
Input Size	227 × 227 × 3	224 × 224 × 3	299 × 299 × 3
Optimizer	Adam (lr = 1e-5)	Adam (default lr = 0.001) (likely)	Adam (lr = 0.0001)
Loss Function	categorical_crossentropy	categorical_crossentropy	binary_crossentropy
Batch Size	32	32	32 (standard in your code)
Epochs (Max)	30–50 (EarlyStopping used)	100 (EarlyStopping used)	20 (EarlyStopping used)
Callbacks	EarlyStopping (patience=5), educeLROnPlateau	EarlyStopping (patience=3)	EarlyStopping (patience=3)
Regularization	L2 (0.0001), Dropout (0.5)	Dropout (default layers in MobileNetV2)	BatchNorm + Dropout (built-in)
Augmentation	Rotation, Zoom (0.3), Flip, Brightness	Rotation, Flip, Zoom	Resizing + Normalization
Trainable Params	~4.54 M	~2.2 M (MobileNetV2 lightweight)	~55 M (InceptionResNetV2 very deep)
Validation Split	25%	20% (from flow_from_directory split)	20% (defined in your code)

a. lr – Learning rate used during model optimization. b. Epoch – A complete training cycle over the entire dataset. c. Dropout and regularization techniques were used to prevent overfitting. d. Validation Split – The percentage of data reserved for model validation during training.

Table 2 presents the hyperparameter configuration of AlexNet, MobileNetV2, and InceptionResNetV2. While AlexNet required a larger input size (227×227), consistent with its original design, MobileNetV2 and InceptionResNetV2 used 224×224 and 299×299, respectively. The Adam optimizer with tuned learning rates ensured fair comparison across models. These settings provided a standardized experimental framework.

4. RESULTS AND DISCUSSION

The comparative evaluation of AlexNet, InceptionResNetV2, and MobileNetV2 revealed significant performance differences across the models (Figures 2–4). AlexNet achieved a test accuracy of 76.26% but showed poor generalization, as reflected in the divergence between training and validation curves. While the training accuracy remained relatively stable, the validation accuracy dropped after the third epoch, accompanied by a sharp rise in validation loss, indicating overfitting.

In contrast, MobileNetV2 demonstrated a marked improvement, achieving 93% accuracy with consistent training and validation performance. The loss curves confirmed efficient convergence, with validation loss stabilizing after the initial epochs. This highlights MobileNetV2's strength as a lightweight yet reliable architecture for medical image classification.

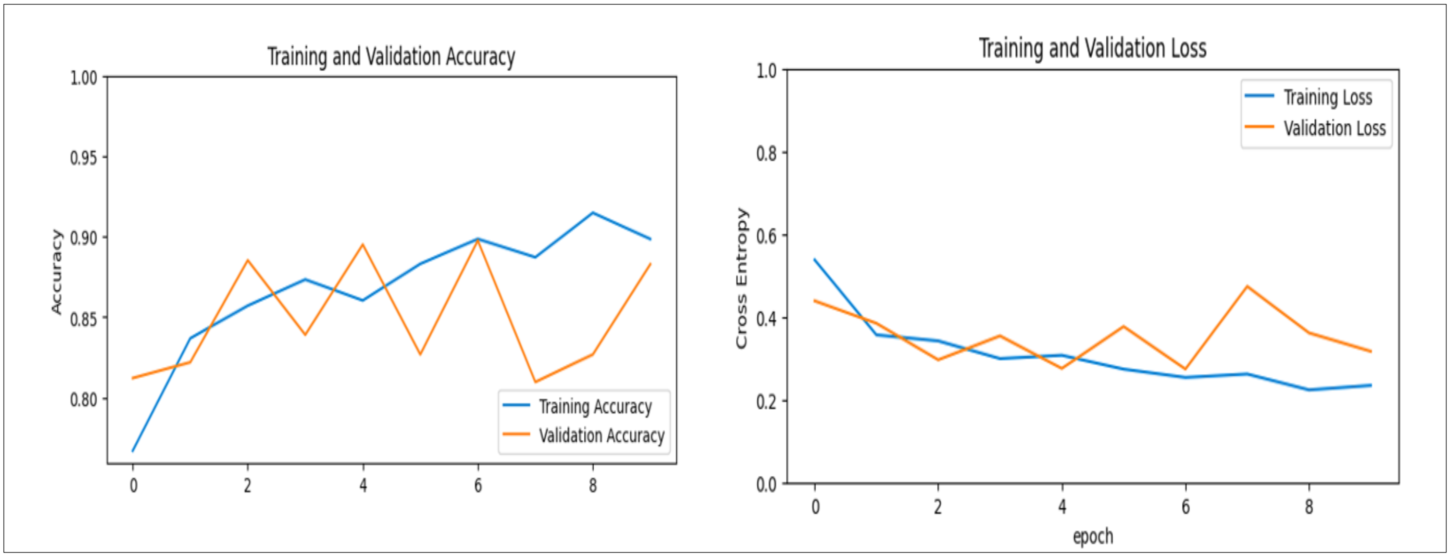


Fig. 2. Training and validation performance curves of the InceptionResNetV2 model showing loss and accuracy trends across epochs.

a. Loss – Error metric representing deviation between predictions and true labels.

b. Accuracy – Percentage of correctly classified samples.

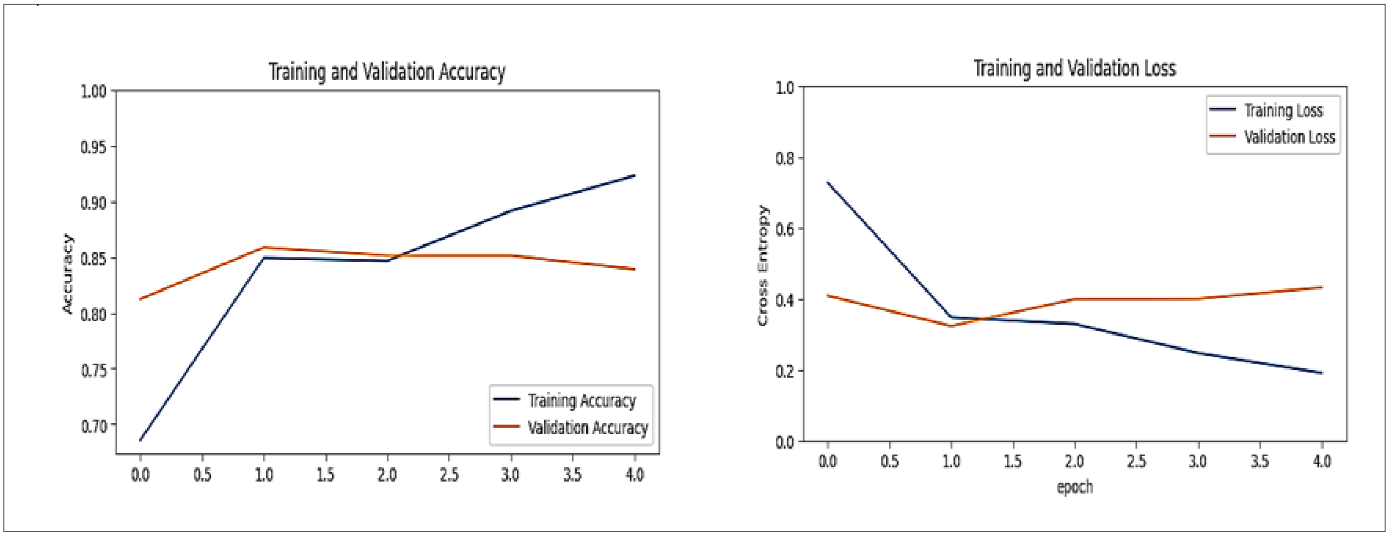


Fig. 3. Training and validation curves of the MobileNetV2 model demonstrating accuracy, stability, and convergence performance.

a. Validation curve indicates the stability of the training process

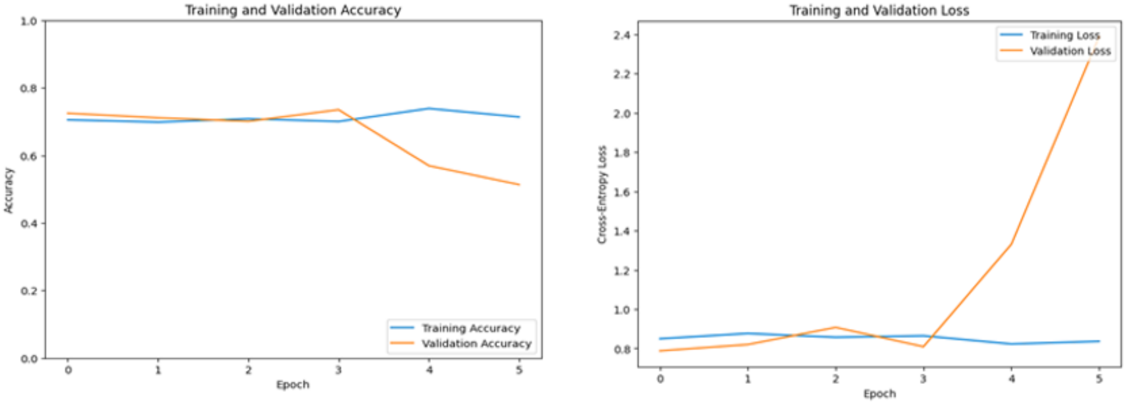


Fig. 4. Training and validation accuracy and loss curves of the AlexNet model indicating overfitting and poor generalization trends.

a. Overfitting is reflected by divergence between training and validation loss.

The best results were obtained with InceptionResNetV2, which reached 94% accuracy. Both training and validation accuracy curves showed steady improvement across epochs, and the loss values declined consistently, suggesting better learning stability and generalization compared to AlexNet and MobileNetV2.

Figures (5-7) represent confusion matrices of AlexNet. Misclassified many normal samples, indicating weaker generalization. MobileNetV2 improved balance with fewer misclassifications, while InceptionResNetV2 delivered the most.

Consistent predictions. Overall, deeper architectures enhanced reliability and accuracy, highlighting their effectiveness for sickle cell detection compared to AlexNet.

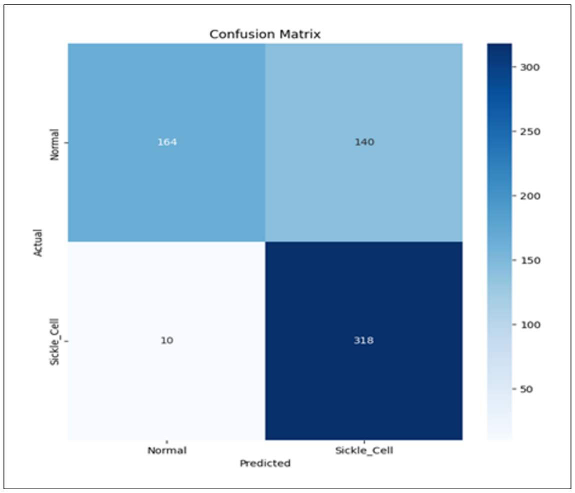


Fig. 5. Confusion matrix for AlexNet showing classification outcomes for normal and sickle cell classes

a. Higher false negatives indicate weaker generalization capability.

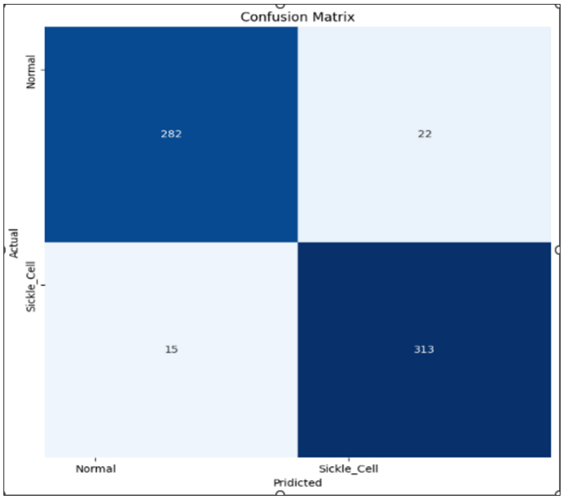


Fig. 6. Confusion matrix illustrating InceptionResNetV2's superior classification balance and minimal misclassification rate.

a. Balanced precision and recall demonstrate strong robustness across both classes.

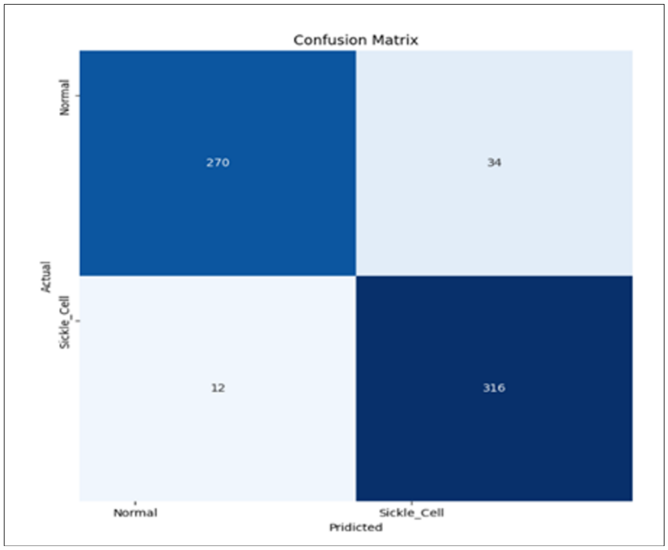


Fig. 7. Confusion matrix of MobileNetV2 showing reliable classification with few misclassified samples.

a. Indicates effective feature extraction with high class-wise consistency.

Table 2 presents the Comparison between MobileNetV2, InceptionResNetV2, and AlexNet Models' performance. The comparative analysis of AlexNet, MobileNetV2, and InceptionResNetV2 highlights the progressive improvement in detecting sickle cell and normal samples. AlexNet achieved an overall testing accuracy of 76%, with relatively high recall for sickle cell cases (97%) but poor recall for normal samples (54%), indicating a strong bias towards identifying abnormal cells while misclassifying many normal instances. It's low F1-Scores for both classes (81% for sickle cell, 69% for normal) further confirm weak generalization.

Table 2. Comparison Between Three Models

Performance comparison of AlexNet, MobileNetV2, and InceptionResNetV2 on the test dataset based on accuracy, precision, recall, and F1-score.

Pre-Trained Model	Sickle Cell F1- Score	Sickle Cell Recall	Sickle Cell Precision	Normal F1-Score	Normal Recall	Normal Precision	Testing Accuracy
MobileNetV2	93%	96%	90%	92%	89%	96%	93%
InceptionResNetV2	94%	95%	93%	94%	93%	95%	94%
AlexNet	81%	97%	69%	69%	54%	94%	76%

a Accuracy – The percentage of correctly predicted samples. b Precision – The ratio of true positive predictions to all predicted positives. c Recall – The ratio of correctly identified positive samples to all actual positives. d F1-score – The harmonic mean of precision and recall.

MobileNetV2 improved performance considerably, achieving 93% accuracy with balanced results across both classes. It attained 93% F1-score for sickle cell detection and 92% for normal cells, with recall rates of 96% and 89%, respectively. This demonstrates its capability as a lightweight yet robust architecture, offering consistent precision and recall across categories.

InceptionResNetV2 outperformed both models, reaching 94% testing accuracy with nearly uniform precision, recall, and F1-scores around 93–95% for both classes. This balanced performance indicates superior generalization and stability, making it highly suitable for clinical applications where misclassification of either class can have critical consequences.

4. CONCLUSION

This research involves the comparison of three deep learning architectures, AlexNet, MobileNetV2, and InceptionResNetV2, for the automated detection of sickle cell disease (SCD) from blood smear images. The results show that AlexNet was able to classify the images correctly with a moderate accuracy of 76%, but was unable to generalize well, especially in the case of differentiating normal red blood cells. In contrast to AlexNet, both MobileNetV2 and InceptionResNetV2 performed better to a great extent, resulting in the correctness of their classifications at 92.7% and 94.1% respectively. In fact, the precision, recall, and F1 scores achieved by both models were at the same level for all the classes, which shows that they can be trusted in diagnostic applications.

The results demonstrate that deeper and more sophisticated convolutional architectures, particularly InceptionResNetV2, are more capable of dealing with complicated medical imaging tasks like the detection of SCD. AlexNet experienced difficulties with class imbalance and generalization, and the excellent performance of MobileNetV2 and InceptionResNetV2 is a testament to the fact that modern architectures play a crucial role in diagnostic accuracy and clinical reliability. In addition, the invariability of InceptionResNetV2's class-wise performance metrics at a high level is an indication of its potential use in computer-aided diagnostic (CAD) systems.

In the next study, it would be beneficial to collect more data that covers different samples from various medical centers so as to enhance the generalization of the model and its applicability in the clinical setting. Also, the adoption of explainable AI (XAI) approaches would help in clarifying and thus gaining the trust of doctors by giving them a visual representation of the decision regions on the images. Furthermore, the optimization of lightweight models like MobileNetV2 for mobile or edge deployment can facilitate point-of-care screening in deprived areas. Last but not least, investigating the potential of hybrid frameworks that integrate deep learning features with clinical and laboratory data to not only enhance diagnostic precision but also to be compatible with real-world healthcare workflows is an exciting avenue of research.

REFERENCES

1. Adegun AA, Viriri S. Deep learning-based system for automatic detection of sickle cell disease from blood smear images. *Diagnostics*. 2021;11(6):1035. doi:10.3390/diagnostics11061035
2. Adepoju OE, Akinola SO, Omisore OM. Hemoglobin electrophoresis in the diagnosis of sickle cell disease: Methods and applications. *Afr J Lab Med*. 2021;10(1):123–130. doi:10.4102/ajlm.v10i1.1287
3. Anwar SM, Majid M, Qayyum A, Awais M, Alnowami M, Khan MK. Medical image analysis using convolutional neural networks: A review. *J Med Syst*. 2018;42(11):226. doi:10.1007/s10916-018-1088-1
4. Becking LGB. Geobiology. *Geochem Perspect*. 2022;11(1):1–168. doi:10.7185/geochempersp.11.1
5. Bukhari SUK, Qureshi HN, Aftab M, Lee BD, Lee YJ. An inception-based CNN with residual connections for breast cancer histopathological classification. *Cancers*. 2020;12(10):2790. doi:10.3390/cancers12102790
6. Centers for Disease Control and Prevention. About sickle cell disease. *U.S. Department of Health & Human Services*. 2025 Feb 21. Available from: https://www.cdc.gov/sickle-cell/about/index.html
7. Chollet F. *Deep learning with Python*. 2nd ed. Manning Publications; 2018.
8. Chowdhury MEH, Rahman T, Khandakar A, Al-Madeed S, Zughaier SM, Doi SA, Mahmud S, Reaz MBI. An early warning tool for predicting the mortality risk of COVID-19 patients using machine learning. *Comput Biol Med*. 2020;127:104066. doi:10.1016/j.compbiomed.2020.104066
9. Das R, Pal M, Acharya UR. Automated detection of morphological changes in red blood cells using deep learning techniques. *Biomed Signal Process Control*. 2020;62:102115. doi:10.1016/j.bspc.2020.102115
10. Das R, Pal M, Acharya UR. Automated detection of sickle cells in microscopic images using deep convolutional neural networks. *Comput Biol Med*. 2022;145:105419. doi:10.1016/j.compbiomed.2022.105419
11. Elendu C. Understanding sickle cell disease: Causes, symptoms, and pathophysiology. *Natl Cent Biotechnol Inf (NCBI)*. 2023. Available from: https://pmc.ncbi.nlm.nih.gov/articles/PMC10519513/
12. Esteva A, Robicquet A, Ramsundar B, Kuleshov V, DePristo M, Chou K, et al. A guide to deep learning in healthcare. *Nat Med*. 2019;25(1):24–29. doi:10.1038/s41591-018-0316-z
13. Gao X, Li W, Loomes M, Wang L. A fused deep learning architecture for lung cancer histopathology image classification. *Med Image Anal*. 2020;60:101622. doi:10.1016/j.media.2019.101622
14. Geraldine M. Haemoglobin electrophoresis in diagnosing sickle cell disease: A clinical approach. *J Hematol*. 2001;7(3):145–150. Available from: https://pmc.ncbi.nlm.nih.gov/articles/PMC3453643/
15. Goodfellow I, Bengio Y, Courville A. *Deep learning*. MIT Press; 2016.
16. Hassan MS. A perspective on the genesis, diagnostics, and management of sickle cell disease. *J Med Genet Genomics*. 2024;5(2):110–120. Available from: https://jmhg.springeropen.com/articles/10.1186/s43042-024-00623-1
17. Howard AG, Zhu M, Chen B, Kalenichenko D, Wang W, Weyand T, et al. MobileNets: Efficient convolutional neural networks for mobile vision applications. *arXiv Preprint*. 2017. arXiv:1704.04861. Available from: https://arxiv.org/abs/1704.04861
18. Hussain Z, Gimenez F, Yi D, Rubin D. Differential data augmentation techniques for medical imaging classification tasks. *Artif Intell Med*. 2018;90:62–70. doi:10.1016/j.artmed.2018.07.006
19. Jain S, Singh AP, Kumar A, Saluja R, Nema R. Stem cells research prospects towards precision medicine. *Bratisl Lek Listy*. 2022;123(11):795–805. doi:10.4149/bll_2022_128
20. Kingma DP, Ba J. Adam: A method for stochastic optimization. *Int Conf Learn Represent (ICLR)*. 2015. Available from: https://arxiv.org/abs/1412.6980
21. Krizhevsky A, Sutskever I, Hinton GE. ImageNet classification with deep convolutional neural networks. *Adv Neural Inf Process Syst*. 2012;25:1097–1105. doi:10.1145/3065386
22. LeCun Y, Bengio Y, Hinton G. Deep learning. *Nature*. 2015;521(7553):436–444. doi:10.1038/nature14539
23. Litjens G, Kooi T, Bejnordi BE, Setio AAA, Ciompi F, Ghafoorian M, et al. A survey on deep learning in medical image analysis. *Med Image Anal*. 2017;42:60–88. doi:10.1016/j.media.2017.07.005
24. MedlinePlus Genetics. Sickle cell disease. *U.S. Natl Libr Med*. 2024 Mar 14. Available from: https://medlineplus.gov/genetics/condition/sickle-cell-disease/

25. Montalbo FJP. Deep learning using a convolutional neural network for the classification of COVID-19 lung X-ray images. *Int J Adv Trends Comput Sci Eng*. 2021;10(1):1–6. doi:10.30534/ijatcse/2021/011012021
26. Nair V, Hinton GE. Rectified linear units improve restricted Boltzmann machines. *Proc 27th Int Conf Mach Learn*. 2010;807–814.
27. Olugbara OO, Abayomi-Alli A, Adegun AA. Image acquisition techniques for sickle cell disease diagnosis using brightfield microscopy and EDoF algorithms. *J Med Imaging Health Inform*. 2020;10(6):1231–1240. doi:10.1166/jmihi.2020.3061
28. Oyelade ON, Akinola SO, Olugbara OO. Transfer learning with deep convolutional neural networks for automatic detection of sickle cell disease. *J Appl Sci Eng Technol*. 2022;26(4):98–106. doi:10.9734/jaset/2022/v26i430343
29. Pan SJ, Yang Q. A survey on transfer learning. *IEEE Trans Knowl Data Eng*. 2010;22(10):1345–1359. doi:10.1109/TKDE.2009.191
30. Rajaraman S, Antani SK, Poostchi M, Silamut K, Hossain MA, Maude RJ, et al. Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images. *PeerJ*. 2018;6:e4568. doi:10.7717/peerj.4568
31. Sandler M, Howard A, Zhu M, Zhmoginov A, Chen LC. MobileNetV2: Inverted residuals and linear bottlenecks. *Proc IEEE Conf Comput Vis Pattern Recognit (CVPR)*. 2018;4510–4520. doi:10.1109/CVPR.2018.00474
32. Shen D, Wu G, Suk HI. Deep learning in medical image analysis. *Annu Rev Biomed Eng*. 2017;19:221–248. doi:10.1146/annurev-bioeng-071516-044442

Creative Commons (CC) License

About the Corresponding Author

Mr. Abhishek Tiwari, PhD Research Scholar in IT and Computer Science. At Dr.C.V. Raman University, Bilaspur, Chhattisgarh, His research focuses on comparing deep learning architectures like AlexNet, MobileNetV2, and InceptionResNetV2 for predicting sickle cell disease using medical imaging. He has more than 4 years of teaching experience in Computer Science and IT.