

Deep Learning Models for Non-Invasive Blood Group Detection Using Fingerprint Images

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Abstract: In the context of medical diagnosis, the identification of human blood groups plays a significant role. To perform the identification of human blood groups, usually invasive identification methods are used. However, due to the limitations of the invasive methods of blood group identification, the use of fingerprint-based identification of human blood groups gained significance recently. In this paper, an accurate comparison of the recently developed deep learning models of fingerprint-based blood group identification techniques is provided. Five CNN-based models, such as ConvNeXt-Tiny, ConvNeXt-Small, EfficientNetV2-S, RepVGG-B3g4, and MobileViT-V2 models for the identification of human blood groups, are implemented. The results obtained in the experiment, considering the accuracy of the models, have proved the EfficientNetV2-S model to have the highest accuracy of 98.84%, followed by the ConvNeXt-Small, ConvNeXt-Tiny, MobileViT-V2, and RepVGG-B3g4 models with accuracies of 97.66%, 97.21%, 97.08%, and 96.98%, respectively.

Index Terms: Blood Group Detection, Fingerprint Analysis, Deep Learning, Convolutional Neural Networks, EfficientNetV2-S, Comparative Study, Non-Invasive Diagnosis

1. Introduction

A highly important medical investigation requisite for blood transfusions, transplantation, emergencies, and trauma cases is the identification of blood groups. Proper identification of the blood group is a must to avert transfusion reactions. Ordinary procedures for the identification of blood group entail the implementation of a process called serological testing,

which consists of sample collection, chemical reagent application, equipment, and trained professionals. Even though these procedures for identification are effective, they entail invasion and are not very effective for emergencies and areas devoid of basic amenities [1]. To surmount the limitations associated with these methods, non-invasive blood group detection methods have started to receive research interest. Fingerprints can be classified as an anthropometric trait that is attuned to genetic influences. They tend to remain unchanged throughout the course of an individual's lifetime. Previous research has suggested the statistical relationship that can be achieved between fingerprint features on blood group classification, thus suggesting the feasibility of fingerprint-based blood group detection methods [2,10]. Recent developments in machine learning and deep learning have greatly enhanced the efficiency of biometric recognition techniques. Previously, researchers have used the strong potential of Convolutional Neural Networks (CNNs) to obtain discriminative features from images of fingerprints instead of considering feature engineering techniques. Researchers have employed CNN-based models such as MobileNetV2 and ResNet50 to detect the blood group through the fingerprint recognition method in their previous work, achieving promising results [3,4,5]. However, the limitation is the evaluation of models, along with the lack of a comprehensive evaluation of the current models available. However, with the development of deeper learning models such as Efficient Net, ConvNeXt, Rep VGG, etc., better efficiency has been reported in classification processes compared to traditional images. The utilization of these in non-invasive blood group detection remains an unexplored territory.

Comparing deep learning models becomes more difficult than it appears. In most studies comparing deep learning models, differences between the models, datasets, pre-processing procedures, and training configurations are considered; therefore, the success of a model over another could be a result of something else rather than the model architecture itself.

This paper aims to resolve this issue by controlling all experimental conditions such as using the same data, applying the same pre-processing techniques, training configuration, and evaluation metrics for the models. This experiment involves four recently proposed models, namely ConvNeXt, EfficientNetV2, RepVGG, and MobileViT, alongside two baseline models, ResNet50, and MobileNetV2. It is important to note that including baseline models in the comparison is necessary because new models will not have anything to compare themselves against otherwise. It is not the purpose of this paper to present any novel models. The idea was to construct a benchmark where comparisons would be valid. This proved to be a valuable exercise in itself in an area in which previous researches could not be easily compared. The conclusions drawn here indicate the position of each of these models in terms of generalization ability and computation costs.

2. Related Works

The use of non-invasive blood group determination based on fingerprint images was investigated with various approaches in image processing, machine learning, and deep learning algorithms. Past research mainly tried to establish a relationship between fingerprint patterns and blood group determination [12,13,14,15]. In dermatoglyphic analysis, fingerprint patterns such as loops, whorls, and arches were found to have different occurrences in different blood groups.

Literature followed by incorporating image processing techniques for better image quality and discriminative features. Techniques like image normalization, ridge information, and texture were commonly used for accurate classification performance [6,7]. Machine learning algorithms like k-Nearest Neighbor and Support Vector Machine have also been incorporated to fingerprint features for moderate accuracy and sensitivity to features and data size [9]. However, with the advancement in deep learning technology, Convolutional Neural Networks have dominated fingerprint-based blood group detection systems. They can learn the required feature set from fingerprint images in a hierarchical manner without the requirement for feature extraction methods. For example, the lightweight structure of MobileNetV2 was used for its computational benefits in real-time applications [3,4]. Larger models like ResNet50 had better performance due to residual learning but demanded more computation, hence limiting their usage in low-resource environments [5]. The recent works bear out the limitations of the existing approaches, the most important being the evaluation on a handful of models, class imbalance issues, and a unified experiment comparison not offered [3,4,5]. Modern deep learning architectures such as Efficient Net, ConvNeXt, Rep VGG, and hybrid CNN–Transformer models have recently shown superior performance in general image classification tasks. Their effectiveness in the task of fingerprint-based blood group detection has not been investigated thoroughly. It therefore motivates the present work, which will perform a systematic comparison of classical and modern deep learning architectures under a unified experimental framework to find an optimal model for non-invasive blood group detection.

3. Relationship Between Blood Group and Fingerprint Patterns

The similarities between fingerprints and blood groups lie in the fact that they are both genetically determined characteristics. However, despite such similarities, there is no evidence of an interaction between them. There is no biological link that can explain such a relationship.

The patterns on fingerprints are formed when the fetus is in the womb and remain unchanged throughout its whole life. They consist of three main types: loops, whorls, and arches. These classifications have long been proven. The process

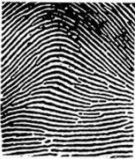
of blood group transmission occurs completely independently of these patterns as they do not depend on one another at all genetically. Antigens define a person's blood group.

Some studies show that one type of fingerprint pattern can be predominant among one group, while the others occur in lower frequency. The type of fingerprint that appears mostly often in people of various blood types is the loop one. Whorls are less frequent than loops but more common than arches. Arch patterns can be considered rare among most of the known populations. The results are inconsistent, but even more importantly, no one provided any biological reasons behind their association.

It is more reasonable to explain the findings based on data peculiarities and insufficient sample size rather than to postulate an existing biological correlation, which cannot be backed up with data at hand, as both of the considered characteristics are affected by distinct parameters and are not interconnected in their changeability.

In this experiment, fingerprints are employed as a source of training and validation data for artificial neural networks. Our objective was to test whether machine learning algorithms could find certain associations within the dataset corresponding to specific blood group designations, rather than to prove any biological correlation.

Table 1. Frequency Distribution of Fingerprints among Blood Groups

Fingerprint pattern	Blood Group Related	Reason for Relation
 Loops	O+,O-,A+,A-	Loops are common pattern Identified in the O and A groups
 Whorls	B+,B-,AB+,AB-	Whorls are moderately common and are often linked to genetic makers seen in B and AB blood groups.Rh factor distribution aligns with these findings.
 Arches	AB+,AB-,B+,B-	Arches are rare , similar to the lower prevalence of AB and B blood groups in most Populations.rarity extends across Rh+ and Rh-.

4. Data Collection & Preprocessing

4.1. Dataset Description

In this experiment, the dataset includes fingerprint images for eight classes of blood groups: A+, A-, B+, B-, AB+, AB-, O+, and O-. The fingerprint images were obtained using common fingerprint acquisition devices. This ensured adequate ridge-valley detail. Fingerprints have been selected as the biometric feature as they are unique, permanent, and can be non-invasive [6,7]. Fingerprints are unique patterns that can be. Each of the images was checked and labelled manually depending on their respective blood grouping categories. The data was structured in a class-wise directory naming system for training supervised deep learning.

4.2. Data Splitting Strategy

The dataset was divided into training, validation, and test sets using a stratified splitting approach to maintain class distribution consistency across all subsets. This ensures that each blood group category is proportionally represented during training and evaluation, thereby reducing bias due to class imbalance.

The splitting process was performed at the image level, as subject-level identifiers were not available within the dataset. As a result, it is possible that multiple fingerprint samples originating from the same individual may exist across different subsets. This introduces a potential risk of data leakage, where the model may partially benefit from previously seen patterns.

This limitation is acknowledged, and the results of this study should be interpreted within this context. Future work will focus on constructing subject-level separated datasets to ensure a more rigorous evaluation of model generalization.

4.3. Image Preprocessing

In order to have uniformity in the data and facilitate the feature extraction process, the following preprocessing operations were performed:

In order to ensure uniformity in the dataset and facilitate effective feature extraction, a series of preprocessing operations was applied. All fingerprint images were resized to a fixed resolution compatible with the input requirements of the deep learning architectures. Pixel intensity values were normalized to improve numerical stability and convergence during training. Additionally, grayscale fingerprint images were converted into RGB format to meet the input constraints of pre-trained convolutional neural networks.

The preprocessing pipeline was intentionally designed to be minimal in order to preserve the intrinsic ridge–valley structures of fingerprint patterns, which are critical for classification. No aggressive transformations such as excessive filtering, smoothing, or geometric distortion were applied, as these could alter discriminative fingerprint features.

However, the impact of preprocessing operations on fingerprint feature preservation was not quantitatively analyzed in this study. This is acknowledged as a limitation, and future work will investigate the effect of different preprocessing techniques on model performance and feature retention.

1. Image Resizing

All fingerprint images have been resized to a constant resolution suitable for the input of EfficientNetV2-S and ConvNeXt.

2. Normalization

Pixel intensities were normalized to ensure that the model converged better during training.

3. Color Space Support

The images were converted to RGB color format to maintain the texture features. Preprocessing is a significant step for fingerprint images and may be affected by illumination, noise, and contrast, which might deteriorate fingerprint image classification accuracy [8, 9]. The inherently grayscale fingerprint images were converted to RGB format to satisfy the input requirements of pre-trained convolutional neural network architectures. This conversion does not introduce additional information, as all three channels contain identical intensity values, but ensures compatibility with models originally trained on RGB image datasets.

4.4. Data Augmentation

For improved generalization and prevention of overfitting, only the training set had data augmentation:

- Horizontal flip
- Random Change in Brightness and Contrast
- Geometric changes

Data augmentation helps in making the data more diverse, and that, in turn, has proved beneficial for improving the robustness of biometric and medical image classification using deep learning [10,11].

4.5. Class Imbalance Handling

Class for handling class imbalance, class-weighted loss functions were used. This is intended to make sure that classes with minority blood group distributions make an equal input into the learning process, thereby eliminating the dominance of certain classes.

5. Proposed Methodology

5.1. System Overview

This proposed system uses the unified approach that deep learning can offer on the non-invasive blood group detection process through fingerprint images, as can be best explained with the flowchart in Fig.1. This process includes the acquisition, preprocessing, data augmentation, feature extraction, and classifying the fingerprint images. The framework is designed to ensure a fair and consistent comparison by maintaining identical experimental conditions across all evaluated models.

In all tests, there is a common data set used, preprocessing techniques employed, training process, and evaluation process. For all tests, it is only the backbone of the neural networks that is varied.

A. Deep Learning Models

Five contemporary architecture deep learning paradigms have been used as interchangeable backbones in the presented scheme:

ConvNeXt-Tiny: A lightweight contemporary CNN following the principles of the transformer model.

ConvNeXt-Small: This is another variant of the ConvNeXt model that is deeper for improved features.

EfficientNetV2-S: A compound-scaled CNN model that strikes a perfect balance between the speed of training and its accuracy.

RepVGG-B3g4: A VGG-based approach for efficient inference through structural re-parameterization.

MobileViT-V2: A hybrid CNN-Transformer model that uses both localized convolutional information and global contextual information. Both models automatically extract features from fingerprint images and then undergo fully connected layers and a Softmax classifier that predicts one of the eight blood group classes.

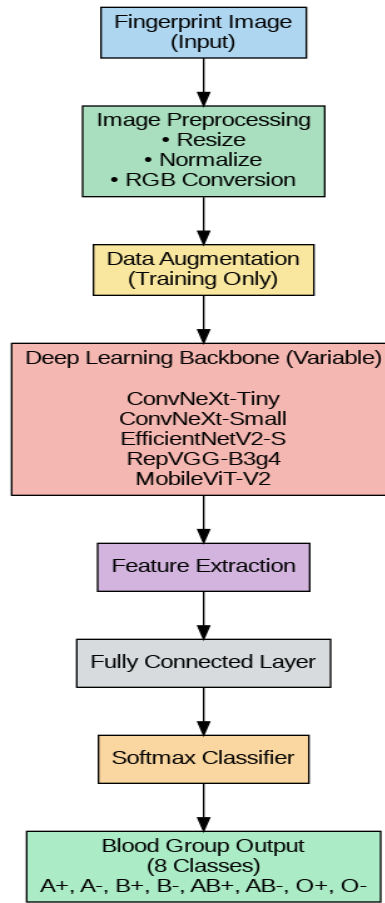


Fig. 1. Unified Architecture for Fingerprint-Based Blood Group Detection

The final Classification layer utilizes the Softmax function to convert the output logits into class probabilities

$$P(y=i) = \frac{e^{z_i}}{\sum_{j=1}^C e^{z_j}} \quad (1)$$

Where:

- $P(y=i)$ is the predicted probability of class i
- z_i is the output logit for class i
- C is the total number of classes (eight blood groups)
- e is the exponential function

5.2. Training Strategy

All models are trained on the same training dataset to maintain consistency. The validation data is used only for monitoring convergence and tuning Hyperparameters. Because the classes are imbalanced among blood group categories, class-weighted loss functions are utilized such that the minority classes contribute equally in training. The process of applying a data augmentation operation occurs solely in the training dataset, which is done in order to improve generalization, as well as prevent overfitting.

5.3. Evaluation Metrics

Initially, the general metrics used are measures like accuracy, precision, recall, or the F1 score. Here, the test model accuracy metric is used as the main metric for the comparative analysis among the proposed models. This is because the comparative study depends on the generalization ability possessed by the model on the unseen fingerprint images. All the results are generated on the same data.

$$\text{Precision} = \frac{TP}{TP + FP} \quad (2)$$

where:

- TP (True Positives): correctly predicted samples
- FP (False Positives): incorrectly predicted as positive

$$\text{Recall} = \frac{TP}{TP + FN} \quad (3)$$

where:

- FN (False Negatives): actual positive samples incorrectly predicted as negative

$$F1 = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (4)$$

where:

- F1-score represents the harmonic mean of precision and recall

5.4. Training Configuration

All the backbone models were trained with the same set of hyperparameters. The optimizer, learning rate, batch size, and number of epochs were set to be the same for all experiments. Mixed precision training was also enabled to reduce the computational cost of training on the GPU. This is shown in Table 2.

Table 2. Dataset Split Distribution

Blood Group	Training	Validation	Test	Total
A+	954	205	204	1363
A-	1679	360	359	2398
AB+	1185	254	254	1693
AB-	1281	274	275	1830
B+	1088	233	233	1554
B-	1266	271	272	1809
O+	1410	302	303	2015
O-	1192	256	255	1703
Total	10055	2155	2155	14365

All backbone models were trained using a consistent set of hyperparameters to ensure a fair and controlled comparison under identical experimental conditions. The optimizer, learning rate, batch size, and number of epochs were kept the same across all architectures to eliminate variability arising from training configurations.

However, it is acknowledged that different architectures may benefit from architecture-specific hyperparameter tuning. The use of identical hyperparameters may therefore not reflect the optimal performance of each individual model. This limitation is accepted in order to maintain experimental consistency and comparability across models.

The model is trained using categorical cross-entropy loss function:

$$L = - \sum_{i=1}^C y_i \log(\hat{y}_i) \quad (5)$$

where:

- L is the loss value
- y_i is the ground truth label (one-hot encoded)
- $\hat{y}_i$ is the predicted probability for class i
- C is the total number of classes

The number of training epochs was set to 25 based on empirical observations during experimentation. It was observed that the models achieved stable performance within this range without significant fluctuations in training behavior. However, a formal convergence analysis was not conducted, and the selected number of epochs may not represent the optimal training duration for all architectures. This limitation is acknowledged, and future work will explore extended training and convergence validation to further improve model performance.

5.5. Computational Performance

For the assessment of the feasibility of the proposed system, the computational power of the system has been analyzed in terms of training speed and inference time. For all experiments, the GPU environment has been used to ensure equal hardware settings. The training time has been measured for all epochs, and the inference time has been measured per fingerprint image with a batch size of one. The results give an indication of the real-time feasibility of the proposed system. The hardware details and results are presented in Table 3.

Table 3. Training Configuration

Parameter	Value
Optimizer	AdamW
Initial Learning Rate	1×10^{-4}
Weight Decay	1×10^{-4}
Batch Size	32
Number of Epochs	25
Loss Function	Cross-Entropy Loss
Precision Mode	Mixed Precision (AMP)
Scheduler	ReduceLROnPlateau

Table 4. Hardware and Computational Performance

Parameter	Value
Hardware Platform	Google Colab (Google Compute Engine)
GPU Type	NVIDIA Tesla T4
GPU Memory	~15 GB VRAM
Total Training Time	31 minutes 5 seconds
Average Time per Epoch	1 minute 26 seconds
Number of Epochs	25
Average Inference Time	35.91 ms
Throughput	27.84 images/second
Test Samples	2,155

The reported training time corresponds to execution in a GPU-accelerated environment using mixed precision training on a Tesla T4 GPU. The measurements include the complete training process over 25 epochs under the specified hardware configuration. It is important to note that training time may vary depending on system specifications, dataset loading overhead, and implementation details. The reported values are intended to provide a relative estimate of computational performance rather than an absolute benchmark.

6. Result and Discussion

It is basically a presentation of the experimental results obtained using the proposed fingerprint-based blood group detection and does the detailing of a comparative analysis for the evaluated deep learning models. The experiments have

been replicated using exactly the same data split, standard preprocessing pipeline, and protocol of evaluation to take Care of fairness and reproducibility.

6.1. Quantitative Performance Analysis

Therefore, test accuracy is the primary metric considered to evaluate the performance of the proposed models, as it reflects the generalization capability of the models on unseen fingerprint images. The test accuracy achieved by each model is summarized in Table 5.

Table 5. Comparison of test accuracy for proposed models

Model	Test Accuracy (%)
EfficientNetV2-S	98.84
ConvNeXt-Small	97.66
ConvNeXt-Tiny	97.21
RepVGG-B3g4	96.98
MobileViT-V2	97.08

EfficientNetV2-S achieved the highest test accuracy of 98.84% among the evaluated models. ConvNeXt-Small and ConvNeXt-Tiny exhibited comparable performance, while MobileViT-V2 also demonstrated competitive results despite its hybrid architecture. RepVGG-B3g4 showed relatively lower accuracy, which may be attributed to architectural trade-offs between computational efficiency and feature representation capacity.

The observed differences in performance across the models are relatively small. Since statistical significance testing was not conducted, these results should be interpreted as empirical observations within the given experimental setup. All models were evaluated using the same dataset and identical training conditions, ensuring a fair comparison. However, the marginal differences in accuracy are not sufficient to establish definitive superiority of one architecture over another.

Table 6. Per-Class Performance Metrics of EfficientNetV2-S

Class	Precision	Recall	F1-Score	Samples	ROC-AUC	PR-AUC
A+	0.9803	0.9755	0.9779	204	0.9991	0.9947
A-	0.9834	0.9889	0.9861	359	0.9997	0.9985
AB+	0.9767	0.9921	0.9844	254	0.9991	0.9948
AB-	0.9782	0.9782	0.9782	275	0.9995	0.9961
B+	0.9827	0.9742	0.9784	233	0.9994	0.9962
B-	0.9963	0.9926	0.9945	272	1.0000	1.0000
O+	0.9899	0.9736	0.9817	303	0.9996	0.9975
O-	0.9612	0.9725	0.9669	255	0.9992	0.9950

Table 6 presents the per-class evaluation metrics of the EfficientNetV2-S model. The results indicate consistently high performance across all classes, with most F1-scores exceeding 0.97. The B- class achieves the highest performance, while relatively lower performance is observed for the O- class, indicating minor classification challenges. The ROC-AUC and PR-AUC values are close to 1.0 for all classes, demonstrating strong class separability and robustness of the model.

Table 7. Overall Performance Metrics

Metric	Value
Accuracy	0.9814
Macro Precision	0.98
Macro Recall	0.98
Macro F1-Score	0.98

The overall test accuracy achieved is 98.84%, with macro-average precision, recall, and F1-score values all approximately equal to 0.98, indicating balanced model performance across all classes.

Table 8. Comparison with Baseline CNN Models under Same Dataset

Model	Test Accuracy (%)
ResNet50	97.12
MobileNetV2	97.91
EfficientNetV2-S (Proposed)	98.84

To further validate the effectiveness of the evaluated architectures, additional experiments were conducted using widely adopted baseline models, namely ResNet50 and MobileNetV2. These models were selected due to their established performance in image classification tasks and their frequent use in prior fingerprint-based studies. All baseline models

were trained and evaluated under the same dataset, preprocessing pipeline, and training configuration to ensure a fair comparison.

As shown in Table 8, EfficientNetV2-S achieves higher accuracy compared to both ResNet50 and MobileNetV2, indicating its strong performance within the defined experimental framework. However, it is important to note that the baseline comparison in this study is limited to selected architectures, and more recent models such as transformer-based or hybrid architectures could be explored in future work for a more comprehensive evaluation.

6.2. Training Performance of the Best Model

For the learning behavior analysis of the best performing model, the training and validation accuracy and loss curves of EfficientNetV2-S are shown in Fig. 2.

Fig. 2(a). reflects a good feature learning as indicated by a steady increase in both training and validation accuracy. Fig. 2(b): Loss plots have consistently decreasing losses, stability of the convergence, and the absence of signs of overfitting. From these observations, we are again confident that discriminable fingerprint features are learned effectively and efficiently by the proposed CNN model called “EfficientNetV2-S.”

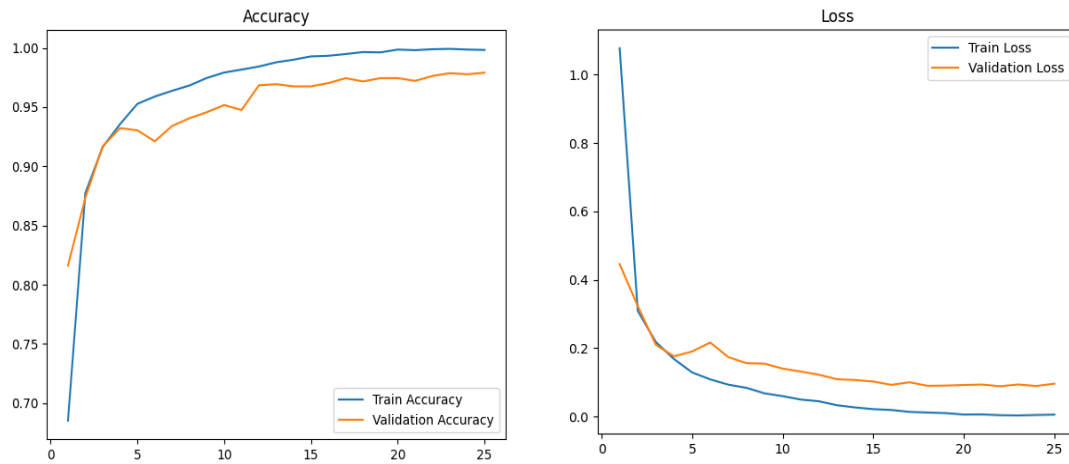


Fig. 2. Training performance of EfficientNetV2-S: (a) training and validation accuracy, and (b) training and validation loss.

6.3. Confusion Matrix Analysis

The confusion matrix provides a clear display of the actual number of classification predictions for each of the eight blood types. It is evident that there is a strong diagonal dominance, which indicates that there is a high level of correct predictions for each class. For example, there were a high number of correct predictions for each class, and the number of incorrect predictions was low and mostly between the similar blood types. These numbers form the basis of the robustness and high discriminative power of the proposed EfficientNetV2-S model.

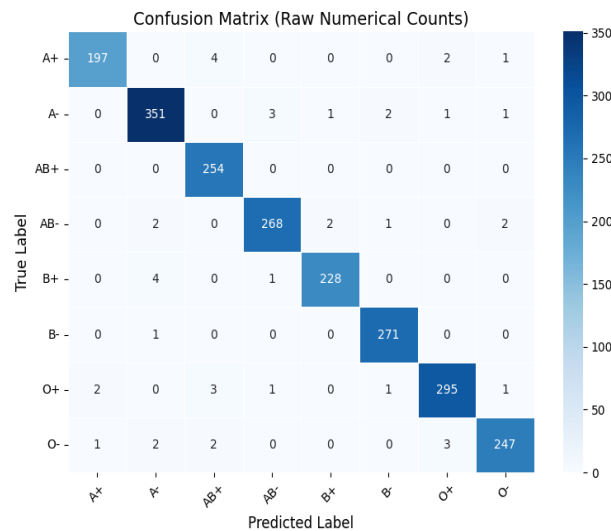


Fig. 3. Confusion matrix of EfficientNetV2-S for eight blood group classes.

Table 9. Error Characteristics Derived from Confusion Matrix

Class	Recall	F1-Score	Error Observation
A+	0.9755	0.9779	Minor misclassification with similar classes
A-	0.9889	0.9861	High classification accuracy, minimal errors
AB+	0.9921	0.9844	Very strong recall, negligible confusion
AB-	0.9782	0.9782	Balanced performance across predictions
B+	0.9742	0.9784	Slight confusion with neighboring classes
B-	0.9926	0.9945	Near-perfect classification performance
O+	0.9736	0.9817	Minor misclassification observed
O-	0.9725	0.9669	Lowest F1-score, relatively higher confusion

The confusion matrix exhibits strong diagonal dominance, confirming that most samples are correctly classified across all blood group categories. This observation is consistent with the high precision and recall values obtained for all classes. However, a detailed examination reveals that classes such as O- and B+ show relatively lower recall and F1-scores, indicating minor misclassification. These errors may be attributed to similarities in fingerprint ridge structures or overlapping feature representations learned by the model.

In contrast, classes such as B- and AB+ demonstrate near-perfect classification with minimal off-diagonal errors, indicating that the model effectively captures discriminative features for these categories. The overall distribution of errors is limited and does not show any significant bias toward a particular class, suggesting that the model maintains balanced performance across all classes.

6.4. Visualization of Comparative Accuracy

For visual comparison of the performance of all the evaluated models, an accuracy comparison graph is presented in Fig. 4. The bar chart clearly underlines the superiority of EfficientNetV2-S among other architectures while illustrating close margins in the performance of ConvNeXt and MobileViT variants.

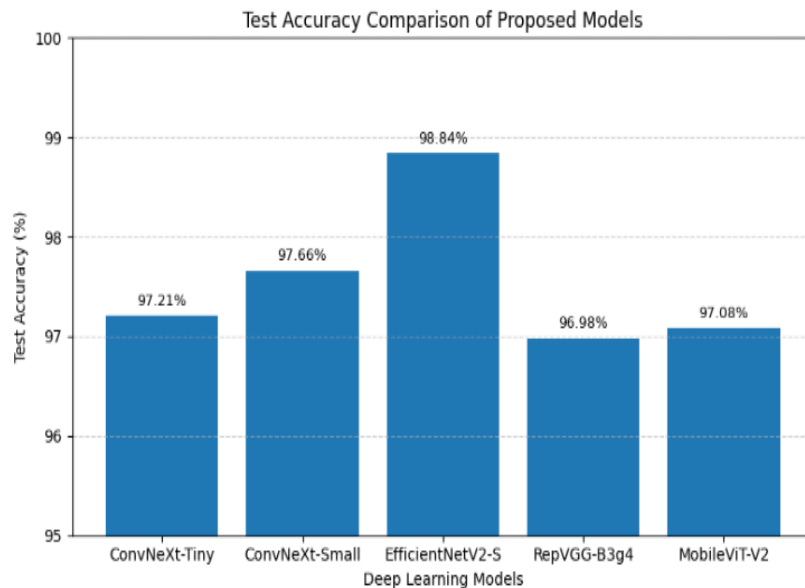


Fig. 4. Comparison of test accuracy of proposed deep learning models.

7. Conclusion

In the paper, a comparative study on the state-of-the-art in deep learning architecture for non-invasive blood group recognition through fingerprint image-based techniques is presented. In conducting the study, a unified experimental configuration was used to evaluate the various deep learning architecture models. The models, namely, ConvNeXt-Tiny, ConvNeXt-Small, EfficientNetV2-S, RepVGG-B3g4, and MobileViT-V2, were employed to test their effectiveness in blood group classification techniques. From the experimental findings based on test accuracy measures of performance, it is evident that EfficientNetV2-S yielded an optimal classification performance with an accuracy of 98.84%. Notably, this performance was higher than that of the other evaluated architectures. ConvNeXt-based architectures also demonstrated strong performance, while MobileViT-V2 provided a favorable trade-off between computational efficiency

and classification accuracy. These results demonstrate improved classification performance under the given experimental setup. From the findings of the study, the significance of selecting the backbone architecture is emphasized in the context of supporting computational analysis in fingerprint-based classification tasks. Furthermore, statistical significance analysis was not performed in this study, and future work will focus on incorporating rigorous statistical validation to strengthen comparative conclusions. The findings highlight the importance of a unified evaluation framework for analyzing deep learning architectures under consistent experimental conditions. However, this work does not propose a novel model architecture and remains focused on comparative evaluation. Additionally, more recent architectures, including transformer-based models, can be explored in future work to further enhance the analysis. Future research will also focus on extending the dataset and improving evaluation methodologies for more robust performance assessment.

All the Declarations and Statements

Author Contributions Statement

Rajendra Prasad Banavathu: Conceptualisation, Methodology, Supervision, Project Administration, Validation, and Manuscript Review. Proposed the research idea, designed the overall research framework, supervised the project execution, validated the methodology, and reviewed the manuscript.

James Stephen Meka: Investigation, Literature Review, Writing – Original Draft Preparation, and Technical Guidance. Contributed to the literature survey, assisted in drafting the manuscript, and provided technical guidance throughout the study.

K. Venkateswara Rao: Data Curation, Software Implementation, Experimental Design, and Validation. Managed dataset preparation, preprocessing, software implementation, and contributed to the experimental design and validation process.

B. Raja Rao: Formal Analysis, Visualization, Statistical Analysis, and Performance Evaluation. Performed comparative analysis of experimental results, prepared tables and figures, and evaluated the performance of all deep learning models.

Yaswanth Kumar Peddagamalla: Software Development, Model Training, Experimental Validation, Writing – Review and Editing, Visualization, and Documentation. Implemented the deep learning models, conducted model training and evaluation, analyzed the results, prepared visualizations, and contributed to manuscript editing and documentation.

All authors have read and agreed to the published version of the manuscript.

Conflict of Interest Statement

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this manuscript.

Funding Declaration

This research received no external funding.

Data Availability Statement

The dataset used in this study is publicly available. The fingerprint image dataset was obtained from the Roboflow Universe repository and is available at:

<https://universe.roboflow.com/ahsan-khan-iw5ip/blood-group-detection-kmolp/dataset/1/images>

The dataset was accessed on 01 August 2025.

The experimental results generated during this study are available from the corresponding author upon reasonable request.

Ethical Declarations

This study does not involve human participants, animals, clinical trials, or patient-specific information. The research was conducted using a publicly available fingerprint image dataset that contains no personally identifiable information. Therefore, ethical approval and informed consent were not required for this study.

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Declaration of Generative AI in Scholarly Writing

During the preparation of this manuscript, the authors used generative artificial intelligence (AI) tools solely to improve the language, grammar, readability, and overall presentation of the manuscript. No AI tools were used to generate the research methodology, experimental design, data analysis, results, conclusions, or scientific interpretations. All scientific content, experimental work, analyses, and conclusions were independently developed, verified, and approved by the

authors. The authors take full responsibility for the accuracy, originality, and integrity of the contents of this manuscript. (arXiv)

Abbreviations

This manuscript uses the following abbreviations:

Abbreviation	Full Form
AI	Artificial Intelligence
CNN	Convolutional Neural Network
DL	Deep Learning
ML	Machine Learning
RGB	Red, Green, Blue
GPU	Graphics Processing Unit
AMP	Automatic Mixed Precision
ROC	Receiver Operating Characteristic
AUC	Area Under the Curve
PR	Precision–Recall
TP	True Positive
FP	False Positive
FN	False Negative
CNN	Convolutional Neural Network
AdamW	Adaptive Moment Estimation with Weight Decay

Appendix A/B/C..., with appendix title

The experiments were conducted using Google Colab on an NVIDIA Tesla T4 GPU with approximately 15 GB of GPU memory. All deep learning models were trained using identical hyperparameters to ensure a fair and consistent comparison. The optimizer used was AdamW with an initial learning rate of 1×10^{-4} and a weight decay of 1×10^{-4} . The batch size was set to 32, and each model was trained for 25 epochs using the Cross-Entropy Loss function. Mixed Precision (AMP) training was enabled to improve computational efficiency, and the ReduceLROnPlateau scheduler was employed to adjust the learning rate during training.

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