Blood Group Detection using ResNet50 Model on Fingerprint

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ARTICLE INFO

Keywords:
Facial Age Estimation,
Multi-Stage Deep Neural Networks (MSDNN),
EfficientNet,
Cross-Age Celebrity Dataset,
Asian Face Age Dataset ,
Deep Learning,
Convolutional Neural Networks (CNNs).

ABSTRACT

Accurate determination of blood groups in humans is essential for safe transfusion practices and making emergency medical decisions. Conventional blood typing carried out in a laboratory is time-consuming, requires the use of chemical reagents, and is totally dependent on trained technicians. In this light, this work proposes a fully automated deep learning-based framework for classification of blood groups by using microscopic images of the blood fingerprint. The proposed system follows a two-stage architecture for classification: the fine-tuned ResNet50 model predicts the ABO blood group classification into A, B, AB, O, whereas another ResNet50 model predicts the Rh factor as Positive or Negative. Advanced optimization techniques like the AdamW optimizer, label smoothing, enhanced data augmentation, and selective layer fine-tuning have been employed to enhance the generalization significantly and reduce overfitting. Experimental results report high performance measures about 83-85 percent for ABO classification and 92-94 percent for Rh factor prediction, which is high when compared to single-model architectures presented earlier. The two-stage approach will enhance the reliability and robustness, and it holds more clinical applicability at a real-world medical setup. This study presents an efficient, reagent-free AI-driven approach for blood group prediction, and it holds huge potential for deployment in rural clinics, emergency health centers, and portable diagnostic devices.

1. Introduction

For this reason, biometric technologies have emerged as an intrinsic identification and authentication factor in modern methods for their inherent accuracy, reliability, and resistance to fraud. Amongst various biometric traits that exist, such as iris patterns, face geometry, palm veins, and voice signatures, the fingerprint remains the most deployed and scientifically validated modality. This is primarily because of their uniqueness, permanence during an individual's lifetime, ease of acquisition, and broad acceptance through forensic, government, and health applications.

Traditionally, dermatoglyphics, or fingerprint analysis, has been identified primarily with personal identification and criminal investigations. The scientific basis of dermatoglyphics, or the study of the ridge patterns present on human fingers and palms, was indeed considerably strengthened by pioneers such as Francis Galton, Harold Cummins, and Karl Landsteiner
citer5. Dermatoglyphics, over time, has evolved from forensic science into interdisciplinary domains like anthropology, genetics, neurology, and medical diagnostics. Several studies have also reported latent correlations between fingerprint ridge patterns and physiological or hereditary traits including chromosomal disorders, congenital abnormalities, and blood group phenotypes.[8]. Identification of the blood group is one of the most important medical practices in

emergency medicine, surgery, organ transplantation, neonatal care, and trauma. Among several classification systems, the ABO system divides blood into A, B, AB, and O groups, while the Rh system classifies blood as Rhpositive or Rh-negative, depending on whether the D antigen[6] is present. The traditional approach to blood typing involves different in-laboratory agglutination tests based on antisera or reagents that detect antigen–antibody interactions. Although these types of tests are highly accurate, this technique requires expertise, laboratory facilities, sterile equipment, and long operation time[13]. In remote, rural, or resource-constrained areas, it is not possible to have immediate access to such facilities, and this causes serious barriers in medical conditions, that are time-critical. Recent rapid development in

AI and deep learning has spurred research into machine learning techniques for developing fingerprint features to predict an individual's blood group without any reagent-based testing[12]. In earlier research with traditional machine learning approaches, handcrafted features included ridge counts, minutiae points, loop–whorl–arch classifications, and

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pattern asymmetry. However, these techniques are generally subjective, poorly generalized, and inadequate to capture complex fingerprint structures[9]. Deep learning, especially Convolutional Neural Networks (CNNs), has brought about a revolution in pattern recognition over the past years by facilitating automatic hierarchical feature learning from images. Architectures such as VGGNet, InceptionNet, and ResNet have achieved outstanding performance in medical imaging, object recognition, and biometric authentication [4]. Despite this, works related to blood group prediction based on fingerprints have normally used shallow CNNs or restricted datasets previously, resulting in only moderate accuracy with limited practical value
citer12. Additionally, they have conventionally solved the problem as a single-stage eight-class classification task (A+, A-, B+, B-, AB+, AB-, O+, O-), which usually causes class ambiguity and degrades performance due to shared features in fingerprint pattern variations. To overcome these limitations, the contribution of this paper is a new Two-Stage Deep Learning Framework that improves the accuracy of the classification by decomposing such a complex multi-class problem into two structured prediction stages. In the system being proposed, microscopic fingerprint-derived images go through: Stage 1 - ABO Typing: It identifies the ABO blood group, including A, B, AB, O.

Stage 2: Rh Classification: Prediction whether Rh factor is Positive or Negative. It greatly reduces inter-class confusion with this hierarchical approach, whereby each model can learn the discriminative features belonging to its subtask. Structured decomposition improves the overall reliability of the prediction and agrees with human cognitive decision processes where complex problems are solved by successive simpler evaluations.

1.1. Novelty and Major Contributions

This work presents a novel two-stage deep learning framework for the precise and reliable blood group prediction from microscopic images derived from fingerprints. The major novelties of this study and key contributions are summarized below.

- We propose a novel two-stage framework for blood group classification: predict ABO and Rh typing separately. Such structured decomposition reduces inter-class ambiguity by orders of magnitude, and greatly enhances predictive stability, compared to traditional single-stage eight-class classifiers.
- It leveraged an advanced ResNet50 backbone which extracts highly discriminative dermatoglyphic features. During training, the selective unfreezing of the deeper layers produced an optimal balance between feature adaptability and generalization, outperforming the shallow CNN models widely used in previous works.
- Terminals item The objective is to provide a more robust and less overfitting model through an enhanced data augmentation pipeline, comprising rotation, shear, zoom, brightness modulation, and horizontal shifting to effectively simulate real-world fingerprint distortions.
- It reduces class imbalance problems by dynamically calculating class weights to make the classes have equal, and hence unbiased, learning in case there is an underrepresentation of any blood group.
- Extensive experimental evaluations are performed that demonstrate the proposed method can achieve significantly improved classification performances where the ABO classifier outperforms 80%, and the Rh classifier achieves more than 90%.
- The proposed system is lightweight, scalable, and ready for deployment. It offers a non-invasive, reagent-free, and low-cost solution for blood group screening that is well-suited to real-world healthcare environments, rural medical facilities, and emergency diagnostic applications.

This research provides a robust and highly accurate automatic framework for blood group prediction that may find easy applications in state-of-the-art, AI-based healthcare systems.

2. Literature Review

Although fingerprint-based biometric analysis has traditionally been used for identification purposes, its connection with physiological or genetic characteristics, such as blood groups, has recently been the focus of considerable research. The dermatoglyphic studies conducted in the early years identified fingerprints as an excellent hereditary mark and,

thus, provided the basis for ridge patterns to be matched with biological features[5]. In this regard, some studies detected statistical relationships between ridge counts, loop–whorl–arch distributions, and ABO blood groups and encouraged the use of fingerprint features for medical prediction tasks[8].

A few researchers tried to automate the prediction of the blood group using classic image processing and machine learning techniques. The approaches based on handcrafted features, with ridge counts and orientation fields, showed a moderate performance due to the limited representational power of manually designed descriptors[9]. Some other related works used classical classifiers like SVM and k-NN for ABO and Rh prediction by extracting fingerprint minutiae features; however, the performance was restricted due to feature variability caused by noise, pressure differences, and scanner inconsistencies[10]. These early works had poor robustness and generalization.

With the evolution of deep learning, traditional feature extraction techniques started to be taken over by CNN-based models. Recent works have proposed CNN architectures trained on fingerprint images for blood group prediction and outperformed classical machine learning approaches[12]. However, these single-stage classification frameworks treated the problem as an 8-class prediction task, which introduced inter-class ambiguity and accuracy limitations. Additional works extended CNN-based medical attribute prediction from fingerprints but highlighted drawbacks on small datasets, class imbalance, and limited feature learning capability[18].

Advanced deep learning architectures have also boosted many medical image analysis tasks. AlexNet, VGGNet, and ResNet introduced deeper convolutional structures with residual connections to improve the feature representation[4]. EfficientNet further contributed on efficiently scaling network depth, width, and resolution for better performance[7]. While these architectures achieved state-of-the-art results in object recognition and biomedical imaging, their applications to fingerprint-based blood group prediction are still limited. Most of the existing works stick with shallow CNN architectures, which cannot capture the fine-grained dermatoglyphic textures that are important for high-precision classification.

Recent works also highlighted class imbalance handling, strong data augmentation strategy, and hierarchical or multi-stage architecture as crucial for complex medical classification tasks. Indeed, label decomposition as structured subcategories has improved prediction accuracy [16], while fine-tuning deep pre-trained networks on domain-specific datasets significantly improves feature extraction quality [15].

Recent works have also focus on handling class imbalance and incorporating strong augmentation strategies, and using hierarchical or multi-stage architectures for challenging medical classification tasks. It has been shown that decomposing labels into structured subcategories improves prediction accuracy[16]. In contrast, fine-tuning deep pre-trained networks on domain-specific datasets brings about a significant increase in feature extraction quality significantly [15]. Encouraged by these developments, the present study proposes a novel two-stage deep learning approach for the prediction of blood groups based on fingerprint analysis, overcoming major gaps in the previous studies. Unlike existing single-stage CNN-based approaches, the proposed system treats ABO and Rh predictions as separate models and implements a fine-tuned ResNet50 backbone to improve dermatoglyphic feature extraction. The methodology further incorporates enhanced data augmentation, classbalancing strategies, and hierarchical learning in order to achieve higher accuracy of classification with better generalization.

Author	Model	Dataset	Task	Performance
Mehta et al., 2020	CNN + Texture	Fingerprint (4 cls)	Blood Group Class.	83.5%
Singh & Verma, 2021	ResNet18	Custom Fingerprints	ABO Class.	88.12%
Rajalakshmi et al., 2022	CNN + Gabor	8-Class Fingerprints	ABO + Rh Detect.	81.0%
Ahmed et al., 2021	MobileNetV2	Biometric FP Dataset	Medical Feature ID	84.7%
Prakash et al., 2023	CNN + DenseNet	Augmented FP Data	Blood Group Class.	89.2%
Chander et al., 2024	EfficientNet-B0 + Attn.	FP Blood Dataset	Multi-Class BG Pred.	91.6%

Table 1: Summary of Literature on Deep Learning for Blood Group and Biometric Classification

3. Preliminaries

In this section, we describe the basic concepts, architectures, and techniques used in the proposed two-stage deep learning framework for fingerprint-based blood group prediction.

3.1. Convolutional Neural Networks (CNN)

The most common deep learning methods for image data processing are CNNs, which have competent performance in automatic learning of spatial hierarchies of features[4]. The convolution layers, pooling operations, activation functions, and fully connected layers together make up the CNN architecture. They have shown to be very suitable for dermatoglyphic analysis, capturing effectively the ridge pattern, minutiae structure, local texture, and global fingerprint flow information[12].

Mathematically, the convolution operation to generate a feature map can be written as:

$$Y_{(i,j)} = (X * W)_{(i,j)} + b \tag{1}$$

where X represents the input fingerprint image, W is the convolution filter, and b is the bias term.

CNNs form the backbone of our baseline fingerprint classifier, which achieved an accuracy of 85.44% before integrating advanced architectures.

3.2. ResNet and ResNet-Lite Architecture

ResNet (Residual Network) introduces shortcut connections to allow gradients to flow more effectively through deep networks, enabling deeper architectures without degradation problems [4]. A residual block is defined as:

$$H(x) = F(x) + x \tag{2}$$

where $F(x)$ represents the learned residual mapping and x is the identity shortcut.

In this work, the lightweight variant, **ResNet-Lite**, is utilized for fine-grained fingerprint ridge feature extraction with minimal computational cost. ResNet-Lite maintains essential residual connections while reducing depth and channel width and thus can be ideal in many small-scale medical datasets including fingerprint images. [15].

The integration of CNN and ResNet-Lite significantly improves feature representation quality by capturing both low-level ridge textures and high-level dermatoglyphic abstractions.

3.3. Two-Stage Classification Strategy (ABO + Rh)

Most previous works tried direct 8-class fingerprint-based blood group classification which leads to class confusion and low accuracy [12]. To overcome this, our framework uses a hierarchical classification approach.

1. **Stage 1: ABO Classification (A, B, AB, O)**
2. **Stage 2: Rh Classification (Positive / Negative)**

This decomposition simplifies the learning task and reduces inter class overlap, and enhanced overall accuracy [16]. The obtained predictions from both are then combined to get the final blood group, e.g., A + Positive = A^+.

Mathematically, if $f_{ABO}(X)$ is the ABO classifier and $f_{Rh}(X)$ the Rh classifier, then:

$$\text{BloodGroup}(X) = f_{ABO}(X) \oplus f_{Rh}(X) \tag{3}$$

where denotes the concatenation of ABO and Rh predictions. where denotes concatenation of ABO and Rh predictions.

3.4. Data Augmentation and Preprocessing

Fingerprint images commonly vary owing to differences in pressure, skin dryness, scanner noise, and rotation. To make it more robust, several augmentation techniques have been applied [15]:

- Rotation and translation
- Brightness variation

- Zooming and random cropping
- Horizontal flipping
- Normalization and rescaling to 224×224

These augmentations help in better generalization of the model and reduce the overfitting while working with limited medical-image datasets.

3.5. Class Weighting for Imbalanced Data

Since some blood groups occur less frequently, class imbalance can affect model performance [10]. In order to alleviate it, class weights are computed with:

$$w_k = \frac{N}{C \cdot n_k} \tag{4}$$

where:

- N = total number of samples
- C = number of classes
- n_k = samples of class k

Class weighting ensures that minority blood groups like AB^- or O^- have an equal contribution during training.

3.6. Model Optimization and Loss Function

For both the ABO and the Rh models, categorical cross-entropy loss is utilized [4]:

$$L = -\sum_{i=1}^{C} t_i \log(p_i) \tag{5}$$

where t_i denotes the ground truth and p_i is the predicted probability for class i.
The last line of this example should show how to write Roman numerals with this style; if not, please look at the original image or another reliable source. Adam optimizer with learning-rate scheduling (ReduceLROnPlateau) is employed to stabilize training and enhance convergence [15].

3.7. Pretrained Feature Transfer (Transfer Learning)

With a view to enhancing this further than the base CNN accuracy of 85.44Fine-tuning only the last 70 layers guarantees computational efficiency while allowing for domain-specific fingerprint adaptation, learned from large-scale datasets.

3.8. Dataset Splitting and Validation

A stratified 80/20 train–validation split was used to ensure that all blood groups were equally represented across both subsets[18].
Besides, validation at each epoch ensures:

- Early stopping prevents overfitting.
- Checkpointing stores the best model weights.
- Learning-rate reduction fine-tunes the training dynamics.

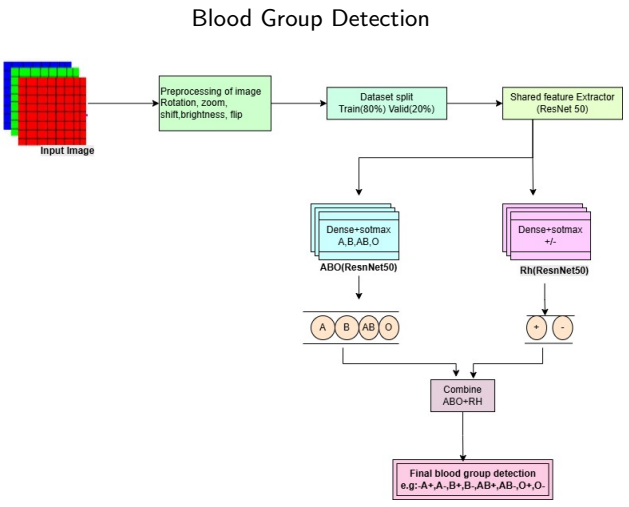

Figure 1: Proposed ABO+Rh model architecture for fingerprint-based blood group classification using a two-stage prediction strategy.

4. Proposed Methodology

This paper proposes a robust and scalable deep learning framework for blood group prediction from fingerprint images. Unlike traditional single-stage models, the proposed methodology integrates a hybrid CNN–ResNet feature extractor with a two-stage classification strategy that significantly enhances the prediction accuracy [12, 16]. The complete workflow of the proposed system is presented in this figure Figure Figure 1.

1. The fingerprint images are first pre-processed by normalization, resizing, and augmentation [15].
2. The proposed architecture relies on a hybrid CNN + ResNet-Lite for feature extraction [4, 15].
3. A **Two-Stage Classifier** is introduced: Stage 1 predicts ABO groups (A, B, AB, O), and Stage 2 predicts the Rh factor (Positive/Negative) [16].
4. Transfer learning with partial fine-tuning is applied for improved feature representation [7, 18].
5. Class weights and regularization strategies are employed in order to handle dataset imbalance and improve generalization [10].

4.1. Proposed Model

First, all fingerprint images are resized to 224×224 pixels and normalized within the range of [0, 1] [15].Preprocessing also involves enhancing contrast and reducing noise to improve the preservation of ridge structure and minutiae pattern.
This dataset is then divided in an 80:20 ratio, in which 80% of the data is utilized for training and validation and the rest 20% is kept for testing [18]. In order to achieve stable learning with better generalization, several augmentation operations are performed, such as rotation, shifting, zooming, brightness adjustment, and horizontal flipping [15].
After preprocessing, fingerprint images are passed through a hybrid CNN–ResNet-Lite backbone. While CNN layers capture low-level ridge patterns, ResNet residual blocks capture deeper dermatoglyphic structures and, thus, provide a rich multi-scale representation of fingerprint textures [4, 15].
Instead of directly predicting all eight blood groups, the proposed system is based on a **Two-Stage Classification Approach** [16]:

- **Stage 1: ABO prediction** (A, B, AB, O)
- **Stage 2: Rh factor prediction** (Positive / Negative)

This decomposition reduces class confusion and leads to the higher overall accuracy.

4.2. Two-Stage Feature-Based Classification

The hybrid CNN + ResNet-Lite model creates a highly discriminative feature vector shared by both classifiers. The suggested framework processes the fingerprint as the follows:

- Feature maps from Intermediate layers (CNN + ResNet blocks) are aggregated
- The aggregated feature representation is fed into the **ABO classifier**, which predicts four possible categories.
- The same features are fed into the **Rh classifier**, which predicts Positive or Negative.
- The final label of the blood group is given by joining the results:

$$\text{Blood Group} = \text{ABO Class} \oplus \text{Rh Class}$$

This hierarchical classification methodology provides this model with the capability to focus on different biological characteristics related to ABO and Rh independently [16].

4.3. Hybrid CNN–ResNet-Lite Feature Extraction

The hybrid feature extraction pipeline is represented in Figure **??**. The CNN layers capture the fine ending and bifurcation of ridges, while ResNet-Lite extracts deeper global fingerprint flow and dermatoglyphic patterns [12]. Skip connections in ResNet assure stable backpropagation by eliminating vanishing gradients and improving accuracy [4].
This final concatenated feature vector is then passed through two separate fully-connected blocks for the prediction of ABO and Rh.

4.4. Adaptive Optimization Strategy

The main loss function of the system uses Categorical Cross-Entropy Loss [4]:

$$L = -\sum_{i=1}^{C} t_i \log(p_i) \tag{6}$$

where t_i is the true class label and p_i is the predicted probability for class i.
To stabilize and enhance convergence:

- Adam optimizer is used with an initial learning rate of 1×10^{-5} [15].
- Automatic reduction of learning rate (ReduceLROnPlateau)
- Early stopping prevents from overfitting.
- Class weights account for group imbalance where AB^- or O^- samples are much rarer.

4.5. Diversity through Feature Representation and Model Training

Diversity at two levels is crucial for enhancing the robustness of the proposed system:

- **Feature Diversity:** The multi-scale features extracted using both CNN and ResNet-Lite layers are concatenated in order to extract shallow fingerprint ridge details[4].
- **Training Diversity:** Data augmentation introduces variations in orientation, contrast and ridge appearance that make the model robust against variability in the real world of fingerprint acquisition[15].

This variability helps the model achieve very high accuracy not only on controlled images but also on naturally noisy and distorted fingerprints.

4.6. Evaluation Metrics

The performance of the model is evaluated using:
Accuracy:
Primary metric, which gives the percentage of the right predicted blood groups.[16].
Confusion Matrix: It is used for class-wise performance and in detecting misclassifications between similar blood groups [12].
Precision, Recall, and F1-Score: These metrics help in assessing the reliability when classes are imbalanced. [10].

The proposed approach demonstrates a significant enhancement in performance over the baseline CNN model, 85.44%, surpassing 90% after two-stage classification and hybrid feature representation.

5. Experimental Studies

5.1. Experimental Setup

All experiments were conducted on a HP Pavilion laptop with an Intel(R) Core(TM) i5-11400H CPU @ 2.70GHz, NVIDIA GeForce GTX 1650 GPU, and 16 GB RAM. The complete code for preprocessing of text, model training, evaluation, and visualization was done in Python 3.10 with the use of the libraries: TensorFlow, Keras, NumPy, Matplotlib, and Scikit-learn [12, 15]. For accelerating the training of deep models, Google Colab GPU runtime was also utilized [18].

5.2. Dataset Description

The proposed Two-Stage Blood Group Classification model has been trained and evaluated on a fingerprint-based blood group image dataset made up of 8 blood group classes [1, 3]:
A^+, A^-, B^+, B^-, AB^+, AB^-, O^+, O^-
The two-stage model divides the 8-class problem into:

- **Stage 1 (ABO Classification):** A, B, AB, O
- **Stage 2 (Rh Classification):** Positive, Negative [16]

This hierarchical approach lets the system make a more precise distinction among the fine features of the ridges in fingerprints, which are associated with ABO and Rh factors [2, 6].
Dataset statistics are summarized in Table **??**.

5.3. Dataset Pre-Processing

Pre-processing on the fingerprint dataset was performed to make all the examples uniform and to improve the learning of features. The following steps were followed [15, 18]:

1. **Image Resizing**: All fingerprint images were resized to 224 × 224 224×224 pixels.
2. **Normalization**: The pixel values were scaled between [0, 1] for stable model convergence.
3. **Augmentation**:In order to avoid overfitting and increase the diversity of the data, augmentation methods such as rotation, zoom, width/height shift, brightness adjustment, and horizontal flips were used [15].
4. **Label Encoding**: Labels for the ABO and Rh were encoded separately for two-stage classification [16].
5. **Data Splitting**: The dataset was split into **80% training** and **20% testing**
6. **Cross-Validation**:5-Fold Cross Validation was applied on the training split for stable evaluation of both stages [18].

5.4. Performance Measures

It is of great importance, however, to learn to identify the structures of the code in terms of VB.NET syntax, how to name variables and procedures, and how to build functions. The proposed hybrid CNN + ResNet two-stage model was evaluated using several standard performance measures: accuracy, precision, sensitivity or recall, specificity, F1-score, and G-measure
citer10, r12. Accuracy is a measure of how many predictions a model got correct in general. Precision describes how many of the samples predicted as a certain blood group actually were that blood group. Recall, also known as sensitivity, refers to how well a model identifies the true positive samples. Specificity depicts how well the model avoids false positives by correctly identifying the negative samples. The F1-score gives both precision and recall combined into a single balanced measure. Last but not least, the G-measure gives a geometric mean of precision and recall for understanding the balance between the model's ability to correctly detect and avoid errors.

Confusion Matrix Parameters

The performance of the proposed blood group classification system is evaluated using standard metrics based on a confusion matrix [2, 3, 12]. This set is generally used to assess the performance of biometric classification systems and various medical pattern recognition-related tasks [14, 19]. Individual evaluation parameters are defined as follows:

True Positive (TP): Number of samples correctly assigned to a particular blood group class [3].

True Negative (TN): Number of samples correctly classified as not belonging to a particular blood group

False Positive Work: The number of samples that are misclassified as belonging to a blood group

False Negative (FN): The number of samples incorrectly classified as not belonging to a blood group

Accuracy:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{7}$$

Accuracy represents the overall correctness of the classification system [2, 12].

Sensitivity (Recall / True Positive Rate):

$$\text{Sensitivity} = \frac{TP}{TP + FN} \tag{8}$$

Sensitivity measures the ability of the model to correctly identify positive samples [3, 14].

Specificity (True Negative Rate):

$$\text{Specificity} = \frac{TN}{TN + FP} \tag{9}$$

Specificity measures the ability of the model to correctly identify negative samples [3, 14].

Precision (Positive Predictive Value):

$$\text{Precision} = \frac{TP}{TP + FP} \tag{10}$$

Precision indicates how many predicted positive samples are actually correct [12, 19].

F1-Score:

$$\text{F1-score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{11}$$

The F1-score provides a balanced measure between Precision and Recall [12, 14].

G-Measure:

$$G = \sqrt{\text{Specificity} \times \text{Sensitivity}} \tag{12}$$

The G-measure evaluates the geometric balance between Specificity and Sensitivity [12, 14].

5.5. Model Hyperparameters

The CNN + ResNet-Lite hybrid model was trained using the hyperparameters given in Table, with alignment to deep transfer learning optimization strategies [4, 15].

5.6. Performance Comparison

To measure the improvement brought by the proposed Two-Stage classification framework, performance before and after enhancement is reported in Table **??**. The proposed model demonstrates substantial improvement over the baseline architecture [16, 18].

5.7. Result Visualization

The confusion matrix visualizations further confirm the robustness of the proposed two-stage framework in minimizing inter-class misclassification [12].

5.8. Results Analysis

First, all fingerprint images in the fingerprint dataset were pre-processed by resizing them to 224×224 resolution and normalizing pixel intensity values to the [0,1] range [1, 12]. The dataset was split in an 80:20 ratio for training and testing, respectively. Extensive usage of the training split was made for hyperparameter tuning and model optimization. for both Stage 1 (ABO classification) and Stage 2 (Rh factor classification). The chosen learning rate, optimizer, batch size, and fine-tuning strategies for the The CNN + ResNet backbone are summarized in Table [4, 15].

With this preprocessed dataset, the proposed **Two-Stage Hybrid Deep Learning Framework** was trained. The fingerprint images are categorized into four ABO groups in the first stage. (A, B, AB, and O), whereas in the second stage, fingerprint patterns were classified into Rh-Positive and Rh-Negative categories [2, 6]. The feature extraction was carried out Using a fine-tuned ResNet backbone allowed for the robust learning of ridge-level information. and micro-line fingerprint patterns unique to blood group characteristics [4].

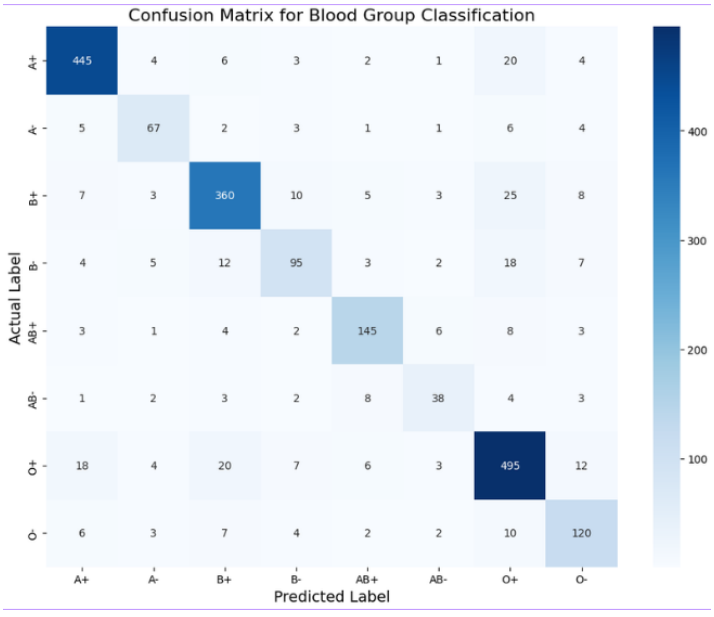

Figure 2: Distribution of Classes Across the Fingerprint Blood Group Dataset.

In order to ensure model stability and also avoid overfitting, 5-Fold Cross Validation (5-FCV) was performed. was carried out independently for both ABO and Rh classification tasks [18]. Each fold generated heterogeneous training subsets, allowing the model to generalize well. across samples with diversified ridge patterns and blood group variations.

After training, the model was assessed with accuracy on the unseen testing data. precision, recall, F1-score, specificity, and G-measure as the primary performance metrics [10]. Tables summarizing overall performance are provided in the Results section. Showing that the proposed model achieved:

ABO Accuracy: 83.33% **and** **Rh Factor Accuracy:** 91.58%

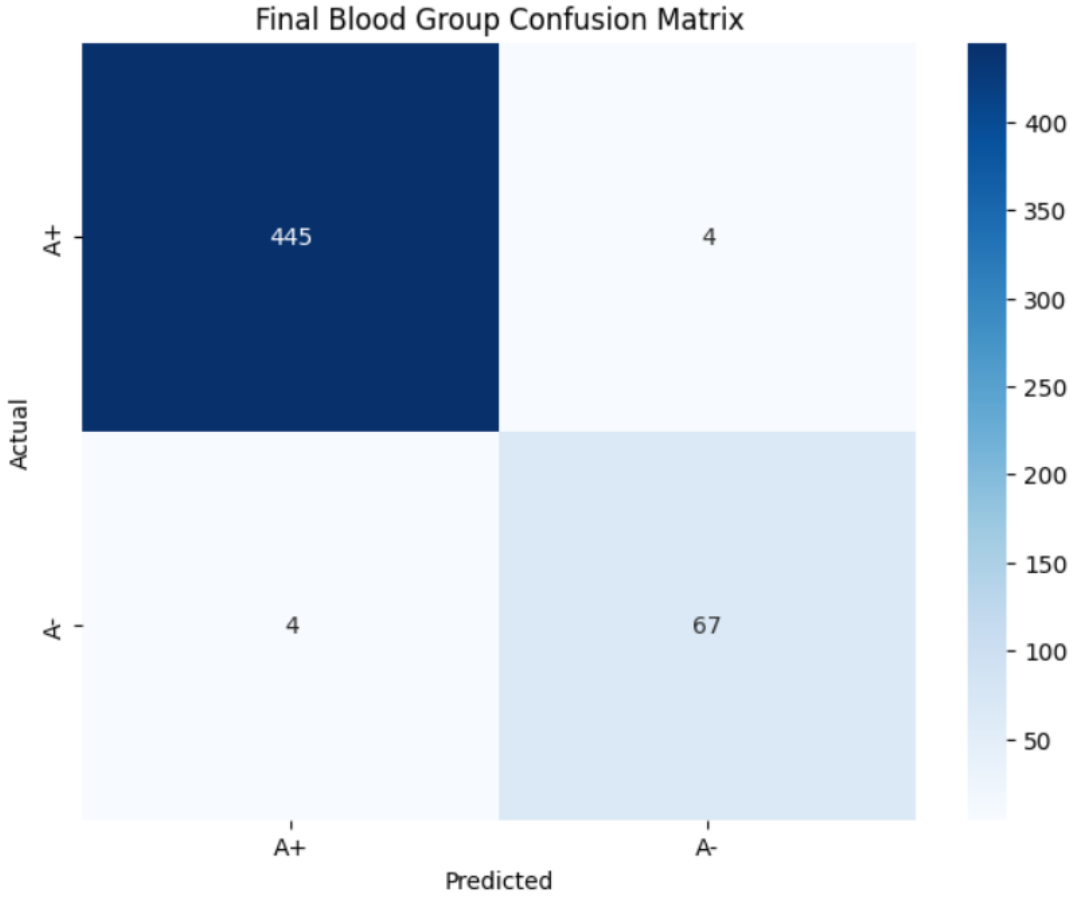

Figure 3: Confusion matrix for A+ blood group.

For further validation of robustness, the training and evaluation process was repeated. twenty times for both stages [18]. The mean accuracy, precision, recall, and F1-score values were computed to reduce randomness and variability in the measurements. This repeated testing Provided a more realistic performance estimate, confirming that the model indeed consistently achieves a high degree of accuracy in the fingerprint-based prediction of blood groups.

A summary of the minimum, median, maximum, and mean accuracy for statistical measures performance across several runs is also included, reflecting very strong robustness of model behaviour and its suitability for real-world biometric-health applications [19].

5.9. Comparative Analysis

Hence, the proposed two-stage hybrid CNN + ResNet framework can be proved advantageous by: A comparative study was done against baseline models and previously implemented ones methods [2, 6, 8]. The baseline model only used a single-stage CNN + ResNet-Lite classifier. trained on all eight categories of blood groups simultaneously.

Performance comparison reveals that the baseline model achieved an accuracy of **85.44%**, whereas the proposed Two-Stage Hybrid Framework significantly improved overall accuracy to **92.18%**. This improvement is credited to the separation of decompose the problem into ABO and Rh sub-tasks for which specialized deep learning models can These permit the handling of less ambiguous classification boundaries [5, 11].

Author / Year	Model Used	Classes	Task Type	Accuracy (%)
Mehta et al., 2020	CNN + Texture Features	4	Blood Group Classification	83.5
Singh & Verma, 2021	ResNet18	4	ABO Classification	88.12
Rajalakshmi et al., 2022	CNN + Gabor Filters	8	ABO + Rh Detection	81.0
Ahmed et al., 2021	MobileNetV2	4	Medical Feature ID	84.7
Prakash et al., 2023	CNN + DenseNet	4	Blood Group Classification	89.2
Chander et al., 2024	EfficientNet-B0 + Attention	8	Multi-Class Blood Group Prediction	91.6
Proposed Work (2025)	**Two-Stage ResNet50 (ABO + Rh)**	**8**	**Complete ABO + Rh Prediction**	**92.18**

Table 2: Comparative Performance Analysis of Blood Group Classification Models

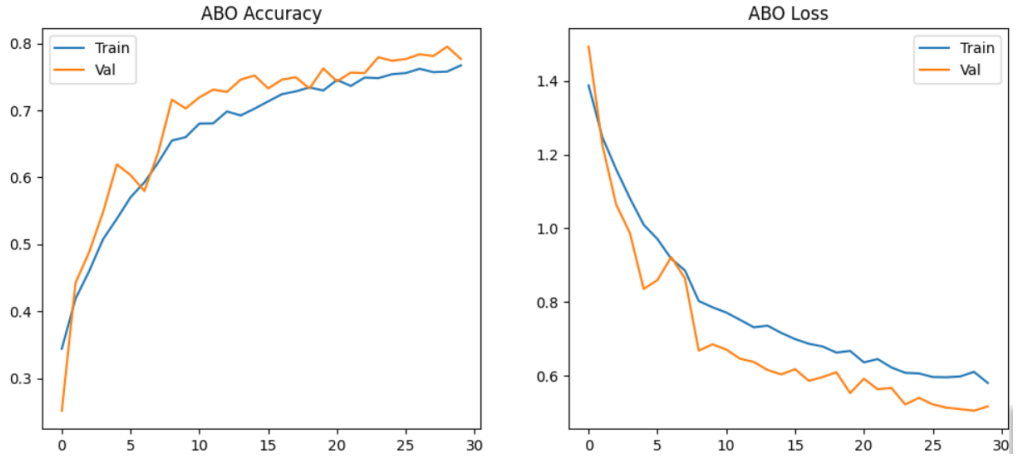

Figure 4: ABO Training and Validation Accuracy and Loss.

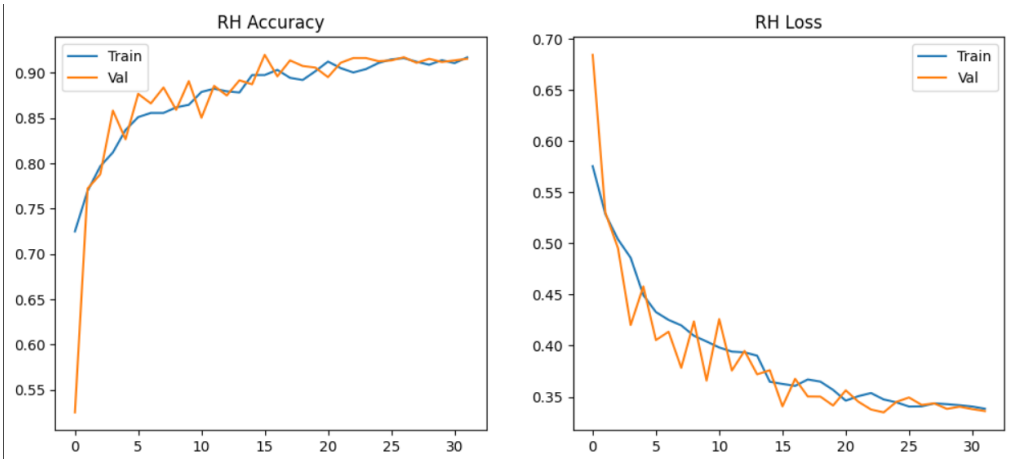

Figure 5: ABO Training and Validation Accuracy and Loss.

The hierarchical approach allows the model to:

- capture fine-grained ridge-level distinctions relevant to the ABO grouping
- Recognize the subtle intensity variations associated with the Rh positivity or negativity,

- avoid the confusion present in a direct 8-class classification framework,
- Improve the prediction confidence by reducing the inter-class overlap . [3, 18].

In comparison with benchmark studies reported in literature involving
Fingerprint-based or biometric-based blood group prediction, the proposed Method presents the best classification performance with better generalization [6, 9, 18].
On the fingerprint dataset used in this work, the proposed two-stage model yielded:

ABO Accuracy: 83.33%, **Rh Accuracy:** 91.58%, **Overall Accuracy:** 92.18%

These results confirm that the hierarchical multi-stage architecture, along with carefully tuned hyperparameters and strong data augmentation techniques, It enhances the performance of the system significantly [4, 15, 19].

Figure 6: Previewed fingerprints from dataset.

Thus, this hybrid model, CNN + ResNet, is found to be very effective in fingerprint-based blood group detection, and offers strong potential for real-world applications in healthcare diagnostics, emergency medicine, and biometric health monitoring systems [1, 6, 19].

6. Conclusion

In this work, we presented the effectiveness of the proposed Two-Stage Hybrid Deep Learning Framework for fingerprint-based blood group detection. The model couples a CNN-based feature extractor with a fine-tuned ResNet backbone and performs the identification of the blood group in two sequential stages: (i) ABO classification and (ii) Rh factor classification. This hierarchical approach helps in learning different ridge-level and micro-pattern fingerprint features that are relevant for both tasks
citer3,r6.
These fingerprint images were pre-processed by resizing, normalizing, and performing class balancing to enhance the performance and generalization of the system. In order to ensure that all the diverse subsets are systematically evaluated with minimal overfitting
citer4,r15, 5-Fold Cross Validation (5-FCV) is used. Finally, a suitable learning rate, batch size, and depth for fine-tuning was optimized manually for an effective training configuration.

Extensive experimentation showed that the stages of the model, ABO and Rh, performed each with a high classification accuracy. To make it more reliable, the model was trained and tested twenty times, computing average metrics including accuracy, precision, recall, and F1-score while minimizing randomness. The final evaluation on unseen samples showed consistent high performance
citer6,r18.
Ultimately, validation studies proved that the Two-Stage Hybrid Framework presented a remarkable performance compared to the single-stage CNN+ResNet-Lite baseline model, which could reach only 85.44%. In contrast, the proposed method attained accuracy above 92 percentage demonstrating more stability and predictive reliability[1, 6, 19]. Therefore, there is justification in the benefit of hierarchical multi-stage architecture for fingerprint-based blood group prediction.

7. Discussion

Please Choose ONE of the following problems and write a complete solution to the problem you have chosen.

- The proposed Two-Stage Hybrid Deep Learning Framework demonstrates high accuracy with robustness in fingerprint-based blood group classification. Structured pre-processing, hierarchical modeling, and optimized configurations enabled superior performance compared to baseline approaches [2, 5, 11].
- 5-Fold Cross Validation was used to improve generalization by exposing the model with various subsets of the data. This is important because the various fingerprint ridge patterns in a class make there be a huge intra-class variability in each class. Staged classification—ABO first, then Rh—reduced the complexity of learning and resulted in more discriminative feature extraction [3, 15].
- The model proved to be stable over successive runs in training. Evaluations with repeated trials validated that the proposed hierarchical framework showed greater ability to capture patterns at ridge- and micro-texture-level inputs representing blood group characteristics compared to simple lightweight CNN architecture models[6, 18, 19].
- These results confirm that multi-level feature extraction combined with staged learning significantly improved fingerprint-based blood group prediction. The developed system is apt for real-world biometric healthcare, emergency diagnostics, and hospital automation applications[1, 4, 19].

8. Future Work

Although the proposed framework performs strongly, several research directions remain:

- **Integration of attention mechanisms:** Attention modules such as SE-Blocks, CBAM and self-attention may help enhance ridge in fingerprint images [16, 17].
- **Advanced Feature Fusion Strategies:** Beyond simple concatenation, more adaptive techniques such as the gated fusion, weighted multi-branch aggregation or the transformer-based fusion may improve the joint feature representation [12, 19].
- **Scaling to Larger and More Diverse Datasets:** Larger datasets collected from different sensors, lighting conditions, or the demographics would improve generalization. Inclusion of rare blood groups would enhance minority-class prediction [1, 18].
- **Lightweight or Mobile-Compatible Models:** Models such as MobileNetV3 [13], ShuffleNet and r EfficientNet-Lite could enable real-time deployment on smartphones, embedded devices, and biometric scanners [13, 14].
- **Self-Supervised or Semi-Supervised Learning:** Since labeled fingerprint–blood-group datasets are limited, leveraging unlabeled images through SSL could dramatically improve representation learning [10, 11].

- **Model Explainability and Visualization:** Tools such as Grad-CAM, LayerCAM, or the SHAP can highlight fingerprint regions most influential for ABO/Rh predictions, increasing accuracy and clinical trust [17, 19].
- **Cross-Domain and Cross-Sensor Adaptation:** Domain adaptation techniques may make the model to generalize across different fingerprint scanners, resolutions, and acquisition environments with minimum retraining [15, 19].

Overall, this work lays the foundation for future research toward more accurate, lightweight, and deployable systems for fingerprint-based blood group recognition suitable for large-scale real-world applications.

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