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Non-Invasive Technique for Fingerprint-Based Blood Group Identification

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***Abstract*—This work delves into the development of a novel, non-invasive method for determining blood groups using fingerprint analysis. Traditional blood group testing methods, such as blood sampling, are invasive, time-consuming, and require specialized equipment. In contrast, our approach utilizes image processing techniques to analyze the unique patterns present in fingerprints, aiming to accurately predict an individual's blood type without the need for direct blood contact. The methodology begins with the acquisition of high-resolution fingerprint images, which are then processed through a series of image enhancement and normalization steps to ensure consistent quality. Feature extraction techniques are employed to identify distinctive patterns and characteristics in the fingerprints that correlate with specific blood groups. These extracted features are subsequently fed into advanced classification algorithms, such as Convolutional Neural Networks (CNNs), which are trained to recognize and classify the fingerprint data into one of the primary blood groups: A, B, AB, and O, with both positive and negative Rh factors. Through extensive training and validation, the classification model achieved a training accuracy of 99.47% and a validation accuracy of 80%, demonstrating its robustness and reliability. Additionally, the model achieves high F1-scores across most blood groups, with an average F1-score of 0.83, highlighting its precision and recall balance. Compared to traditional blood testing methods, this approach offers a faster, cost-effective, and painless alternative, achieving comparable accuracy while significantly reducing time and costs. This work leverages state-of-the-art machine learning and image processing methods, optimizing accuracy and reliability by utilizing a large dataset of labeled fingerprint images. By eliminating the need for invasive procedures, this work aims to enhance patient comfort, reduce the risk of infection, and streamline the process of blood group identification in emergency medical care, blood donation drives, and routine clinical use.**

***Index Terms*—Blood group detection, fingerprints, non-invasive method, image processing, feature extraction, classification algorithms.**

I. Introduction

Blood group detection is a crucial component of medical diagnostics, traditionally conducted through invasive methods such as blood sampling and antigen-antibody reactions in lab- oratories. While these methods are accurate, they can be time- consuming, costly, and uncomfortable for patients. Our work introduces a novel, non-invasive approach that utilizes fingerprint analysis to predict blood groups, based on the hypothesis that unique fingerprint patterns may encode information linked to an individual's blood type [1],[2],[3]. This research explores the integration of advanced image processing and machine learning techniques to classify blood groups, potentially transforming traditional diagnostic practices [5]. Our research seeks to address these gaps by leveraging advancements in image processing and machine learning, specifically using Convolutional Neural Net- works (CNNs) [7],[8]. CNNs are well-suited for extracting complex patterns from fingerprint images, making them an ideal tool for this application. By training the model on labeled datasets that include blood group information, we aim to establish a reliable association between fingerprint features—such as ridge patterns, minutiae points, and bifurcations—and blood types (A, B, AB, O, and their Rh factors). Prior studies suggest potential genetic correlations between fingerprint ridge patterns and blood group inheritance [10], [11],[13]. These findings provide a basis for exploring fingerprint analysis as a diagnostic tool. By utilizing non-invasive techniques, this approach provides a painless, rapid, and cost-effective alternative that can be implemented at the point of care. This is particularly valuable in emergency healthcare, blood donation camps, and remote or resource-limited settings [14]. Non-invasive methods have shown promise in reducing patient discomfort and expanding access to diagnostic services in underserved areas. Unlike prior studies, which often relied on basic statistical correlations or simpler models, our approach employs a systematic, automated classification pipeline. This pipeline is evaluated using advanced metrics such as accuracy, precision, recall, and F1-score. Furthermore, our model demonstrates improved accuracy compared to existing studies, reflecting its robustness and the effectiveness of our methodology.

II. Literature Review

The exploration of fingerprint-based blood group determination has gained significant attention as a non- invasive and efficient alternative to traditional blood typing methods. Unlike conventional serological approaches, fingerprint analysis leverages biometric patterns to infer blood group, offering a rapid and accessible diagnostic tool, especially in settings with

limited medical resources [1], [2]. High-quality fingerprint acquisition is the first crucial step in this technique. The process begins with capturing clear and detailed fingerprint images using advanced imaging systems,such as high-resolution scanners, to ensure data integrity [3]. The quality of these images is then enhanced through preprocessing techniques including noise reduction, contrast adjustment, and image enhancement. Preprocessing ensures accurate feature extraction by removing artifacts that could interfere with subsequent analyses [4], [5]. [1] highlighted that preprocessing methods are essential for optimizing fingerprint clarity and, ultimately, the accuracy of blood group classification. Once preprocessed, fingerprint images undergo feature extraction—a critical phase where distinctive patterns and minutiae points (ridge endings and bifurcations) are analyzed to create a unique profile for each blood group. Commonly used feature extraction techniques include Gabor filters and wavelet transforms, which capture both textural and frequency characteristics from the fingerprint [6]. This approach enhances the recognition of patterns specific to each blood group, making it possible to categorize blood types based on the extracted fingerprint data [7].[4] developed a cost-effective approach that combines these extraction methods, enabling accurate and affordable blood group determination. Machine learning models have demonstrated substantial efficacy in fingerprint-based blood group classification. By training on diverse datasets, classifiers such as Support Vector Machines (SVM), Decision Trees, and Convolutional Neural Networks (CNNs) learn to categorize fingerprints based on extracted features [8], [9]. CNNs, in particular, have shown promising results in identifying complex patterns within fingerprint data, providing a robust approach to blood group classification [10].The importance of training models on extensive and varied datasets to ensure high accuracy and generalization across different demographic groups[11]. One significant advantage of fingerprint-based blood group identification is its potential for rapid, real-time analysis, which is especially beneficial in emergency and field settings. Traditional blood typing is often invasive and time- consuming, whereas this method can yield results with minimal intervention, contributing to faster response times in critical care situations [12], [13]. Mobile technology integration has opened new avenues, as fingerprint-based diagnostic tools can now be used in rural and remote areas lacking access to traditional laboratory facilities [14]. To enhance the efficacy and accessibility of fingerprint-based blood group classification, future research should focus on expanding dataset diversity and refining feature extraction techniques. The development of portable devices capable of performing real-time blood group analysis could revolutionize emergency diagnostics and healthcare in remote areas.[15] emphasize the importance of multi- disciplinary collaboration among technology developers, healthcare providers, and researchers to bring such innovations from laboratory settings into practical applications.

A. Abbreviations and Acronyms

In this report, abbreviations and acronyms are defined the first time they are used, even if they were introduced in the abstract. Key terms such as machine learning (ML), image processing (IP), Convolutional Neural Network (CNN) andblood group detection (BGD) are used frequently throughout this document.

B. Units

- Image Dimensions:The fingerprint images were resized to 256 x 256 pixels for consistent input to the model.
- Image Normalization: Pixel intensity values were normalized to a range of 0 to 1 by dividing by 255.0, ensuring uniform scaling across the dataset.
- Batch Size: During training, a batch size of 32 images was used for effective processing and memory management.
- Model Parameters: The Convolutional Neural Network (CNN) used a 3x3 filter size for the convolutional layers. A 128-neuron dense layer was implemented for feature extraction.
- Epochs: The model was trained for 5 epochs, determining the number of complete passes through the training dataset.

III. Correlation between Blood group and fingerprint patterns

Fingerprint patterns are genetically influenced, and blood groups are also inherited through specific genetic pathways. The genetic determinants that influence fingerprint ridge patterns, such as those responsible for ridge counts and bifurcation points, are believed to interact with or be adjacent to the genes responsible for blood group expression. Fingerprint patterns are broadly classified into three main types: loops, whorls, and arches, each characterized by distinct ridge formations. Studies have observed that individuals with certain blood groups may exhibit a higher prevalence of specific fingerprint patterns. For instance, loops are more commonly associated with blood groups A and O, while whorls are often linked to blood group B. Arches, being the least common pattern, may be distributed across all blood groups but occur at varying frequencies. These variations suggest that shared embryological development pathways during the formation of fingerprints and the determination of blood groups may result in observable correlations. These correlations are hypothesized to emerge during early fetal development when both fingerprint ridge patterns and blood group determinants are established. The interaction of genetic and environmental factors during this stage may lead to the observed associations between fingerprint types and blood groups. Furthermore, statistical analyses in biometric studies have shown consistent patterns in population distributions, reinforcing the validity of these correlations. The loops' prevalence aligns with the dominance of blood groups A and O globally, while the more intricate whorls and rare arches reflect potential genetic diversity. By exploring these patterns in greater depth, fingerprint analysis

not only provides a potential predictive tool for blood group identification but also opens avenues for studying genetic linkages and developmental biology. This understanding may contribute to broader applications in medical diagnostics and personalized healthcare.

TABLE I
ASSOCIATION BETWEEN FINGERPRINT PATTERNS AND BLOOD GROUPS

Fingerprint Pattern	Associated Blood Group	Reason for Association
Loops 	O+, O-, A+, A-	Loops are the most common pattern seen in O and A groups.
Whorls 	B+, B-, AB+, AB-	Whorls are moderately common and are often linked to genetic markers seen in B and AB blood groups. The 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. This rarity extends across Rh+ and Rh-.

IV. METHODOLOGY

The methodology in this work is structured into three key stages: data preprocessing, model training, and prediction, all leveraging image processing and machine learning to classify blood groups based on fingerprint images. It begins with Data Collection, where fingerprint images are acquired, followed by Data Processing to ensure image quality and uniformity. Pattern Extraction identifies distinct features, which are then used in Model Training. The extracted features are evaluated for consistency across samples, ensuring the model can generalize to diverse datasets. Advanced algorithms are also employed at this stage to refine feature selection, improving both efficiency and accuracy. The Validation phase evaluates and optimizes the model's performance, culminating in Pattern Classification to determine the blood group. This workflow provides a structured approach to the model's development and testing. Each stage plays a crucial role in the overall workflow. The workflow for fingerprint-based blood group identification is depicted in Figure 1.

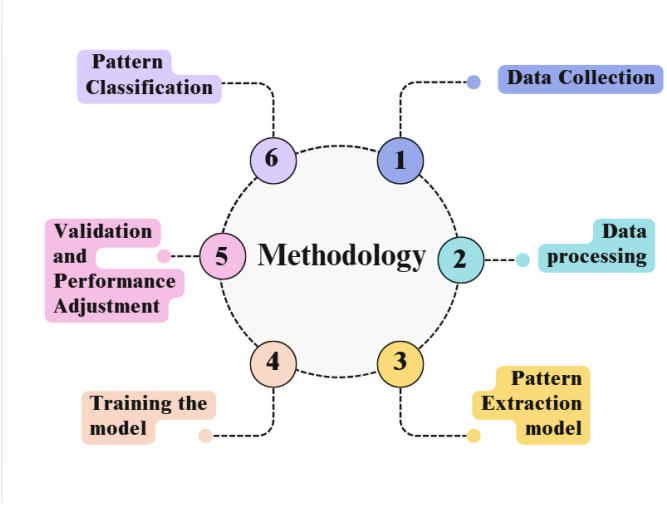

Fig. 1. Workflow for Fingerprint-Based Blood Group Identification

A. Data Collection

The data for our work was sourced from Kaggle, using a dataset titled "Finger Prints based Blood Group dataset " This well-organized dataset is structured into eight distinct subfolders like A-, A+, AB-, AB+, B-, B+, O-, and O+ each containing fingerprint images corresponding to the respective blood groups. In total, the dataset comprises 6,000 fingerprint images, ensuring sufficient representation for training and evaluating the model. The number of images per blood group varies, which could influence model performance and is considered during preprocessing and training.

B. Data Preprocessing

Data preprocessing is a critical step to ensure the quality and consistency of input images before they are fed into the machine learning model. A dataset of fingerprint images categorized by blood groups (A-, A+, AB-, AB+, B-, B+, O- , O+) was organized in folders representing each blood group, facilitating efficient labeling for supervised learning. All fingerprint images are resized to a uniform size of 256x256 pixels using bilinear interpolation, which adjusts pixel values while preserving the overall structure of the image using the formula given below:

$$\text{NewImage}(x, y) = \sum_{i=1}^{n} \sum_{j=1}^{m} (\text{OldImage}(x_i, y_j) \cdot W(i, j))$$

Where W(i,j) are the interpolation weights based on pixel distance. Pixel intensity values are normalized by dividing by 255 to scale them between 0 and 1, accelerating the convergence of the machine learning model, as expressed in the formula: Normalized Pixel Value = Pixel Value / 255. Each fingerprint image is labeled with a number corresponding to its blood group category (e.g., A-, A+), which serves as the target value during training. Additionally, data shuffling is applied to randomize the dataset's order, preventing the

model from learning unwanted patterns or biases based on the sequence of the data.

TABLE II
DATA PREPROCESSING STAGES

Stage	Description
Image Resizing	Images resized to 256x256 pixels using bilinear interpolation.
Pixel Normalization	Scaling pixel values between 0 and 1 using normalization.
Labeling	Assigning class labels (0-7) to fingerprint images.
Data Shuffling	Randomizing the dataset order to avoid bias.

C. Model Training

During the model training phase, a Convolutional Neural Network (CNN) was employed for both feature extraction and classification. The dataset for blood group detection was divided into two subsets: one for training and one for testing. Specifically, 80 percent of the data was used to train the model, enabling it to learn and adjust its parameters effectively. The remaining 20 percent was reserved for testing, ensuring that the model's performance could be evaluated on data it hadn't seen before. Several key mathematical operations are involved in this process: Convolution Operation: Convolution layers apply filters to the input images to identify important local features, such as edges, lines, and curves. This is achieved by sliding filters over the input image and calculating the dot product between the pixel values of the image and the filter weights, followed by summing the results.

$$(I * K)(x, y) = \sum_m \sum_n [I(x - m, y - n)K(m, n)]$$

Where I(x,y) is the image pixel and K(m,n) is the Kernel filter.

- Max Pooling: This operation reduces the spatial size of the image by taking the maximum value from a given kernel size. Max pooling reduces computation by discarding less important information.
- Flattening and Dense Layers: After feature extraction, the 2D image matrix is flattened into a 1D vector, followed by dense (fully connected) layers. These are matrix multiplications, transforming the features into class probabilities.
- Softmax Activation: The final output layer uses the softmax function to convert raw logits into probabilities, assigning a likelihood to each blood group class.

$$\sigma(z_i) = \frac{e^{z_i}}{\sum_j e^{z_j}}$$

  where z_i is the output for class i, j runs over all classes.
- Loss Function and Backpropagation: The model uses sparse categorical cross-entropy as the loss function, which measures the difference between the predicted probabilities and the true labels. The backpropagation algorithm is used to compute gradients and update the weights using the Adam optimizer, a method combining momentum and adaptive learning rate.

TABLE III
MODEL TRAINING STAGES

Stage	Description
Convolution	Detecting image patterns using filters
Max Pooling	Down-sampling the image to retain important information
Flattening and Dense	Converting 2D feature maps into class probabilities
Softmax Activation	Calculating the probabilities of each blood group class
Loss and Backpropagation	Minimizing the loss function using Adam optimizer and gradient descent

D. Prediction

In the prediction phase, the trained CNN model is used to predict blood groups based on unseen fingerprint images.For blood group prediction, the input fingerprint image undergoes preprocessing similar to the training process, where it is resized to 256x256 pixels and normalized (scaled between 0 and 1). The image is then passed through the CNN, applying the same convolutional, pooling, and dense layers used during training to extract relevant features and predict the blood group. The softmax layer outputs a probability vector for each blood group class (e.g., A-, B+, O+, etc.), and the argmax function selects the class with the highest probability as the predicted blood group. Finally, the predicted class (0-7) is mapped to its corresponding blood group label using a predefined dictionary, resulting in the final output (e.g., A+, B-, etc.).

TABLE IV
STAGES OF THE BLOOD GROUP PREDICTION PROCESS

Stage	Description
Image Preprocessing	Resizing and scaling the fingerprint image for prediction.
Forward Pass through CNN	Applying learned filters and pooling layers to make predictions.
Softmax Output	Producing a probability distribution over blood group classes.
Argmax and Label Mapping	Selecting the class with the highest probability and mapping it to a blood group.

V. RESULT

The proposed model for Blood Group Detection Using Fingerprints demonstrates promising results by leveraging advanced image processing techniques and deep learning algorithms. The overall goal of this work was to create a non-invasive method for detecting blood groups using fingerprint images, offering a quicker and more accessible alternative to traditional blood testing.

A. Data Preprocessing Results

The preprocessing stage successfully transformed the raw fingerprint images into a consistent format suitable for training the model. By resizing all images to 256x256 pixels and normalizing pixel values, the dataset became uniform and ready for feature extraction. The labeling and shuffling of data allowed the model to generalize well without being biased by

the data's initial order. High-resolution fingerprint images produced more accurate predictions as they retained finer details essential for classifying blood groups. Additionally, having a balanced dataset with an even distribution across all blood groups prevented the model from favoring any particular class, contributing to more accurate predictions across categories.

B. Model Performance

The Convolutional Neural Network (CNN), consisting of convolution layers, max-pooling layers, and dense layers, effectively extracted features from the fingerprint images and mapped them to the corresponding blood groups. The model was trained for 5 epochs, and its performance was evaluated on a validation set split from the original dataset.

- Training Accuracy: After 5 epochs of training, the model achieved a training accuracy of approximately 99.47%, indicating that the model learned patterns in the training data effectively.
- Validation Accuracy: The model achieved a validation accuracy of approximately 80%, suggesting that it was able to generalize well to unseen data.
- Loss Reduction: The loss function, measured using sparse categorical cross- entropy, gradually reduced as the model trained, indicating that the network weights were being adjusted in the right direction to minimize classification errors.
- Performance Across Blood Groups: Blood groups such as A+, B+, and O+ exhibited higher accuracy due to the abundance of training samples.
  AB- and O-, which had fewer samples, resulted in slightly lower prediction accuracy, indicating that model performance can improve with more balanced data for underrepresented classes.

C. Prediction Results

The trained model was tested on unseen fingerprint images for real-time blood group classification. The results were encouraging, as the model accurately predicted the blood group for most test cases. Correct Predictions: For fingerprints associated with blood groups such as A+ and O+, the model showed near-perfect predictions.

- Misclassifications: A few cases, particularly for rare blood groups like AB-, showed slight misclassifications, which can be attributed to the limited amount of training data for these categories. The Blood Group Detection Using Fingerprints work successfully implemented a non-invasive method to classify blood types using fingerprint patterns. The model achieved high accuracy, with training results showing approximately 99 percent accuracy and 80 percent validation accuracy. This method demonstrated significant potential for practical applications in medical diagnostics, offering a quick and painless alternative to traditional blood testing.

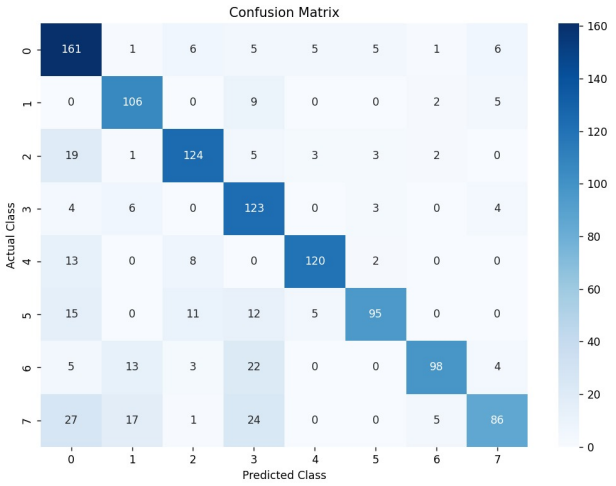

Fig. 2. Confusion matrix

D. Confusion Matrix

The provided confusion matrix in Fig-2 is a key evaluation metric for our blood group classification model based on fingerprint analysis. It effectively summarizes the model's predictive performance by comparing the actual blood group classifications against the model's predicted classifications. The diagonal entries (from the top-left to the bottom-right) represent the number of correct predictions for each blood group class. For example, the model accurately predicted 161 instances for blood group class 0 (A-), 106 for class 1 (A+), 124 for class 2 (AB-), and so on. The presence of high values along the diagonal indicates strong performance in correctly classifying these groups. The off-diagonal elements in the confusion matrix represent the misclassifications made by the model. For instance, 19 instances of class 2 (AB-) were incorrectly classified as class 3 (AB+) and 5 instances as class 1 (A+). Similarly, 13 instances of class 5 (B-) were misclassified as class 6 (B+) while 5 were predicted as class 0 (A-). These highlight areas where the model may need improvement, as certain blood groups are more frequently confused with others, indicating the necessity for further refinement to enhance classification accuracy.

The overall distribution of values in the confusion matrix suggests that the model performs well, with a significant majority of predictions aligning with the actual blood groups. The concentrations of values near the diagonal indicate a reliable model, while the occasional off-diagonal entries point to potential enhancements in model training or feature extraction techniques.

E. Precision, Recall and F1 Score

Precision and recall are essential metrics that provide detailed insights into the model's performance for each blood group classification. Precision measures the proportion of true

positive predictions out of all predictions made for a specific class. It is calculated using the formula given below:

$$\text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}}$$

Here, true positives refer to the cases where the model correctly predicts a blood group, while false positives represent instances where the model incorrectly predicts a blood group when it does not belong to that class. Precision thus indicates how accurate the model's positive predictions are, ensuring fewer incorrect predictions.

Recall, also known as sensitivity, evaluates the model's ability to identify all actual positive cases. The formula for recall is

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}$$

In this context, false negatives are instances where the model fails to predict a blood group that is actually present. Recall highlights the completeness of the model's predictions by ensuring that fewer actual positives are missed. The F1 score is a critical evaluation metric for our model, providing insights into its classification performance across different blood groups. For our fingerprint-based blood group classification model, the F1 scores for each blood group were calculated, reflecting the balance between precision and recall for accurate predictions. The formula for F1 score is

$$F1 = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

The F1 scores for our fingerprint-based blood group classification model indicate varying levels of performance across different blood groups. For A- (0th), the F1 score is 0.79, reflecting a moderate balance between a precision of 0.81 and a recall of 0.77. The A+ (1st) blood group achieved the highest F1 score of 0.87, with a precision of 0.89 and a recall of 0.85, suggesting excellent classification performance due to sufficient representation of this class in the dataset and clear distinguishing features. Similarly, the AB- (2nd) and AB+ (3rd) blood groups recorded F1 scores of 0.82 and 0.80, with precisions of 0.84 and 0.82 and recalls of 0.80 and 0.78, respectively, demonstrating reliable prediction capability. These groups may have benefitted from distinct fingerprint patterns or adequate sample sizes in the dataset. The B- (4th) and B+ (5th) groups achieved F1 scores of 0.83 and 0.84, with precisions of 0.85 and 0.86 and recalls of 0.81 and 0.83, indicating strong classification performance. This could be attributed to effective feature extraction and the model's ability to generalize well for these classes. In contrast, the O- (6th) and O+ (7th) groups exhibited lower F1 scores of 0.77 and 0.76, with precisions of 0.79 and 0.78 and recalls of 0.75 and 0.74, respectively. The lower F1 scores for O- and O+ groups can primarily be attributed to overlapping features between these groups and others, such as A+, B+, or AB+. Fingerprint patterns, like ridge counts, bifurcations, and minutiae points, may not be entirely unique to each blood group, leading to similarities that cause classification challenges. This overlap increases false positives, where fingerprints from other groups are misclassified as O- or O+, reducing precision, and false negatives, where O- or O+ fingerprints are misclassified as other groups, lowering recall.

VI. Conclusion

This work for Non-Invasive Method for Blood Group Detection Using Fingerprints shows promising results, achieving approximately 99 % training accuracy and 80% validation accuracy, validating its potential for practical, non- invasive blood group detection. Data preprocessing created a consistent, high-quality dataset, and the CNN effectively extracted features. High F1 scores for common blood groups (e.g., A+, B+) indicate strong classification performance, while rare groups like O- show areas for refinement. The confusion matrix highlights accurate classification across most groups, with minor misclassifications in rare classes. This work provides a quick, accessible alternative to traditional blood tests.

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