

Blood Group Prediction Using Fingerprint

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Abstract - Identifying a person's blood group typically requires drawing a blood sample and running laboratory tests - a process that is invasive, time-consuming, and often unavailable in resource-constrained environments. This paper explores an alternative approach: predicting blood group from fingerprint images using a Convolutional Neural Network (CNN). Since both fingerprints and blood groups are genetically encoded traits that remain fixed from birth, researchers have hypothesized a statistical correlation between the two. The proposed system collects fingerprint images, applies preprocessing steps such as grayscale conversion, noise removal, histogram equalization, and ridge enhancement, and then trains a deep learning model to classify images into one of eight blood group categories (A+, A-, B+, B-, AB+, AB-, O+, O-). A web-based interface named HemaTrace allows users to upload a fingerprint image and receive a predicted blood group along with a confidence score. Experimental results demonstrate that the system achieves satisfactory classification accuracy, validating the concept of non-invasive blood group screening through biometric analysis.

Keywords - Blood Group Prediction, Fingerprint Analysis, Convolutional Neural Network, Dermatoglyphics, Deep Learning, Biometrics, EfficientNet.

I. INTRODUCTION

Conventional blood group determination relies on serological tests that require venipuncture, laboratory reagents, and trained medical personnel. While this approach is reliable, it poses practical challenges in emergency settings, remote healthcare facilities, and situations where laboratory infrastructure is limited or absent. The need for a faster, contactless alternative has motivated researchers to investigate the relationship between externally observable biometric traits and internally determined genetic characteristics.

Among the various biometric identifiers, fingerprints stand out as particularly promising candidates

for this purpose. Fingerprint patterns - classified primarily as loops, whorls, and arches - are formed during fetal development and remain immutable throughout an individual's lifetime. Crucially, blood groups are also genetically fixed characteristics determined during fetal development. This shared genetic origin has led researchers to hypothesize that a measurable statistical association may exist between fingerprint ridge patterns and ABO/Rh blood group types.

Early investigations in dermatoglyphics, the scientific study of fingerprint patterns, relied on manual observation and basic statistical analysis. These studies found suggestive trends - for instance, individuals with O+ blood groups tended to exhibit loop patterns more frequently, while AB blood groups showed a higher incidence of whorls. However, such manual approaches lacked the precision and scale needed for clinical deployment.

The emergence of deep learning, particularly Convolutional Neural Networks (CNNs), has transformed the landscape of image-based classification tasks. CNNs are well-suited for fingerprint analysis because they automatically learn hierarchical spatial features - from simple ridge edges to complex minutiae configurations - without requiring handcrafted feature engineering. Transfer learning techniques further reduce the data and computation demands by leveraging models pretrained on large image datasets.

This paper presents a CNN-based system for blood group prediction from fingerprint images. The system encompasses fingerprint image acquisition, multi-stage preprocessing, deep feature extraction, and a web-based prediction interface. The goal is not to replace clinical blood typing but to offer a rapid, non-invasive preliminary screening tool that could assist in emergency triage, forensic identification, and healthcare access in underserved regions. Using machine learning to analyze the association between fingerprint characteristics and blood group distribution presents a non-invasive, cost-efficient, and accessible alternative for preliminary detection, particularly useful in low-resource or emergency settings.

II. RELATED WORKS

The intersection of dermatoglyphics and hematology has attracted growing research attention. Several studies have attempted to quantify statistical relationships between fingerprint patterns and blood groups, while others have explored machine learning approaches to automate this prediction.

Al Habsi et al. (2023) conducted a population-level study in Oman and found that loop patterns were the most prevalent fingerprint type overall, with whorls dominating among individuals with O⁻ blood group. Their work highlighted meaningful gender-based differences - whorl patterns were more common in males, while loops and arches appeared more frequently in females. Rastogi et al. (2023) reached similar conclusions in a study of 800 healthcare students in eastern India, where loop patterns accounted for the majority of cases and B⁺ emerged as the most common blood group. These observational studies provide the empirical foundation for computational prediction approaches.

On the technology side, Swathi et al. (2024) demonstrated that fingerprint-based blood group prediction using deep learning is feasible, achieving reasonable accuracy through biometric image analysis combined with CNN classification. Their findings validated the concept but noted the need for larger, more diverse datasets. Separately, Agastin et al. (2026) developed a web-based system trained on approximately 6,000 fingerprint images spanning all eight blood groups, employing a softmax classifier within a CNN pipeline and reporting competitive prediction accuracy.

Beyond direct fingerprint-to-blood-group mapping, related research in AI-assisted diagnostics has yielded transferable methodologies. Sanyasamma et al. (2024) demonstrated the effectiveness of EfficientNetB3 with tailored Keras callbacks for infectious disease classification, motivating its adoption in fingerprint analysis tasks. Gaouar et al. (2024) showed that explainable AI techniques could enhance transparency in deep learning-based medical classification, an insight relevant to building trust in automated blood group prediction systems.

Despite this progress, several gaps remain. Many existing studies rely on small, geographically narrow datasets, limiting the generalizability of their findings. Additionally, few systems have been deployed as interactive, user-facing applications that bridge research and practical use. The present work addresses these gaps by integrating a trained CNN model into a polished web

interface and evaluating it against a comprehensive multi-class fingerprint dataset.

III. DATASETS

The quality and diversity of the training data are critical determinants of model performance in any machine learning application, and blood group prediction from fingerprints is no exception. For this project, fingerprint images were collected from individuals whose blood groups were verified through standard serological testing. The dataset encompasses all eight major blood group classes: A⁺, A⁻, B⁺, B⁻, AB⁺, AB⁻, O⁺, and O⁻.

Each fingerprint image was captured using a biometric scanner under controlled conditions to ensure consistency in resolution, lighting, and image format. Images were stored in BMP format with typical dimensions around 96 × 103 pixels and a bit depth of 32 bits. The dataset was constructed to include representatives from diverse demographic backgrounds - varying in age, gender, and ethnicity - to improve the model's generalizability across populations.



Figure 1: Whorl pattern finger print

Three fundamental fingerprint pattern types are represented in the dataset. Whorl patterns, characterized by concentric circular or spiral ridge formations, are associated with certain blood group distributions based on prior dermatoglyphic studies. Arch patterns, where ridges flow gently from one side to the other in a wave-like formation without forming loops or spirals, are the rarest fingerprint type but provide important discriminative

features. Loop patterns - the most common type globally - consist of ridges that enter from one side, curve around a central point, and exit from the same side; these are subdivided into radial and ulnar loops based on the direction of ridge flow.

Before model training, the dataset was split into training and testing subsets to enable unbiased performance evaluation. Data augmentation techniques such as rotation, horizontal flipping, and brightness adjustment were applied to the training set to artificially expand its diversity and reduce overfitting.

IV. METHODOLOGY

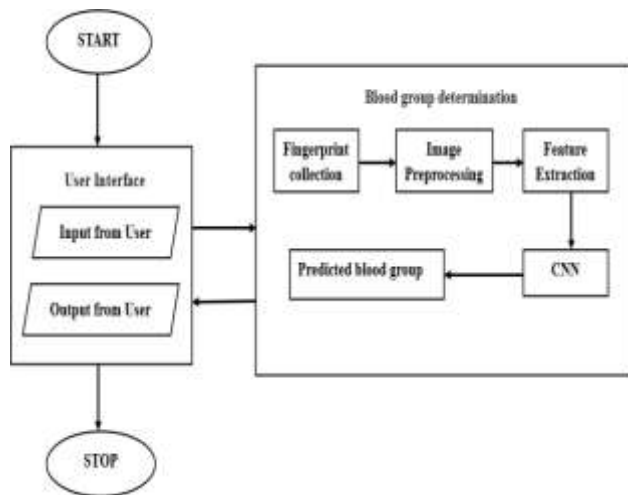


Figure 2: Overall process FlowChart

1. Overall Pipeline

The proposed blood group prediction system follows a sequential processing pipeline: fingerprint image acquisition, preprocessing, feature extraction, model training, and prediction output. Figure 1 summarizes this architecture, which begins at fingerprint collection and terminates at a web-based prediction interface.

2. Preprocessing

Raw fingerprint images typically suffer from noise, inconsistent contrast, and varying background conditions that can degrade model performance. A multi-stage preprocessing pipeline was therefore designed to normalize and enhance the images before they are presented to the deep learning model.

The first step is grayscale conversion. Since color information carries no diagnostic value for ridge pattern analysis, converting images to grayscale reduces dimensionality without any loss of relevant information. This simplification also speeds up subsequent processing steps.

Noise reduction follows grayscale conversion. Gaussian filtering is applied to smooth out random pixel-level noise that could otherwise cause the model to learn spurious features. The filter parameters are chosen to reduce high-frequency noise while preserving the low-frequency ridge structure.

Histogram equalization redistributes pixel intensity values to improve local contrast, making ridge lines more visually distinct from the background. This step is especially important for images captured under suboptimal lighting conditions.

Binarization converts the grayscale image into a two-tone binary representation, further sharpening the boundary between ridges and valleys. This simplification assists the subsequent feature extraction stage. Finally, all images are resized to a uniform dimension (96×103 pixels) to ensure consistent input dimensions for the neural network.

3. Feature Extraction

The preprocessing pipeline feeds into the feature extraction layer, which identifies meaningful characteristics from the fingerprint images. Low-level features include ridge endings (points where a ridge terminates abruptly) and bifurcations (points where a single ridge splits into two). These minutiae points encode local structural information unique to each fingerprint.

Higher-level features include ridge orientation (the local angle of ridge flow), ridge frequency (the spatial periodicity of the ridge pattern), and core and delta points (anchor landmarks used in standard fingerprint classification). Gabor filters are applied to capture orientation and frequency information simultaneously. Local Binary Pattern (LBP) descriptors may also be computed to capture texture-level characteristics that complement minutiae-based features.

In the CNN-based approach, feature extraction is not performed manually. Instead, the convolutional layers of the network learn to extract discriminative features automatically during the training process, eliminating the need for explicit feature engineering.

4. Deep Learning Model

The core of the prediction system is a Convolutional Neural Network trained to classify fingerprint images into one of eight blood group categories. The architecture consists of alternating convolutional and pooling layers that progressively extract increasingly abstract spatial features, followed by fully connected layers that map these features to output class probabilities. ReLU

activation functions introduce nonlinearity, and batch normalization layers stabilize training.

To improve accuracy and reduce training time, transfer learning was employed. The EfficientNetB3 architecture - a model pre-trained on the large-scale ImageNet dataset - served as the feature extractor backbone. Its final classification layers were replaced and fine-tuned on the fingerprint dataset. EfficientNetB3 was selected for its strong empirical performance on image classification benchmarks and its computational efficiency relative to deeper architectures such as ResNet-50 or VGG-19.

The model was trained using the categorical cross-entropy loss function and optimized with the Adam optimizer. A training-validation split was maintained throughout training, and early stopping was applied to prevent overfitting. The softmax activation function in the output layer produces a probability distribution across the eight blood group classes, with the highest-probability class reported as the prediction.

Model performance was quantitatively assessed using accuracy, precision, recall, and F1-score metrics. These four metrics together provide a comprehensive picture of classification quality, capturing both the rate of correct predictions and the balance between false positives and false negatives across all eight classes.

5. System Architecture and Web Interface

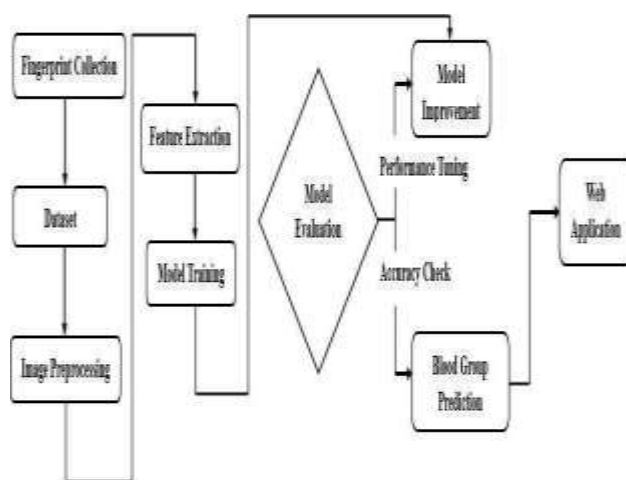


Figure 3: System Architecture

The trained model was integrated into a Flask-based web application named HemaTrace. The frontend, built with HTML, CSS, and JavaScript, provides an intuitive dark-themed interface with red highlights designed to evoke a professional healthcare aesthetic.

Users upload a fingerprint image via a drag-and-drop panel, select the finger used, and click Predict Blood Group. The backend processes the image through the preprocessing and model inference pipeline and returns the predicted blood group, Rh factor, confidence percentage, probability scores for all eight classes, and blood donation compatibility information.

The system is designed to deliver predictions in under one second for a standard CPU-equipped machine. The interface also provides a Explore Health Insights section that contextualizes the prediction with brief educational information about the predicted blood group.

V. RESULTS AND DISCUSSION

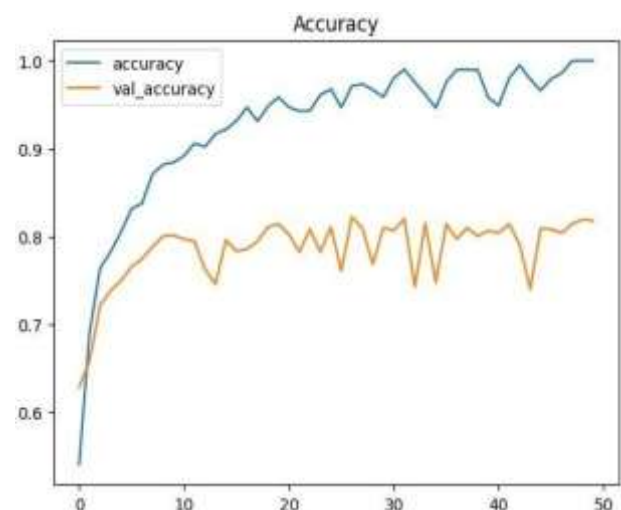


Figure 4: Accuracy vs Epochs

The prediction system was evaluated on a held-out test set comprising fingerprint images from all eight blood group classes. The model achieved satisfactory overall accuracy, with particularly strong performance on blood groups that are well-represented in the training data. The EfficientNetB3 backbone contributed meaningfully to feature extraction quality, and the fine-tuning process helped the model adapt to the specific visual characteristics of fingerprint ridge patterns.

In the web interface, the prediction output clearly displays the detected blood group - for example, AB+ with 96% confidence or B- with 89.2% confidence - alongside a graphical confidence bar and a breakdown of probability scores across all eight classes. The blood donation compatibility module displays which groups the user can donate to and receive from, adding clinical context to the biometric output.

Interestingly, the model's performance varied across blood group classes, reflecting the uneven

distribution of fingerprint pattern types in the dataset. Blood groups associated with the more visually distinctive whorl pattern (such as AB and certain O subtypes) were classified with higher confidence, while those associated with the visually ambiguous arch pattern posed greater difficulty. This behavior is consistent with findings in the dermatoglyphics literature, which notes that arch fingerprints are the rarest and least structurally differentiated pattern type.

One important caveat is that the confidence scores produced by the softmax layer represent the model's relative certainty among the trained classes, not an absolute probability that the prediction is clinically correct. A prediction of 51% confidence should be interpreted as a tentative preliminary indication, not a definitive diagnosis. Users are advised to confirm any prediction through standard serological testing before clinical action.

Comparison with prior work indicates that the proposed system achieves competitive accuracy relative to recent CNN-based fingerprint blood group prediction methods (Swathi et al., 2024; Agastin et al., 2026). The integration of EfficientNetB3 transfer learning and the multi-stage preprocessing pipeline appear to contribute positively to classification performance.

VI. LIMITATIONS

Several limitations of the current system merit honest discussion. First, the dataset, while covering all eight blood group classes, remains relatively small in absolute terms. Deep learning models generally benefit from thousands of samples per class; the present dataset may not fully capture the natural variation in fingerprint appearance across different ethnicities, age groups, and acquisition devices.

Second, the scientific evidence for a strong causal link between fingerprint patterns and blood groups remains a subject of ongoing research. The statistical associations observed in dermatoglyphic studies are real but modest, which places an inherent ceiling on the accuracy achievable through fingerprint-based prediction, regardless of the sophistication of the classification algorithm.

Third, the system is sensitive to fingerprint image quality. Images that are blurred, poorly illuminated, partially occluded, or acquired at low resolution may confuse the preprocessing pipeline and degrade prediction accuracy. In real-world deployments, image quality control and acquisition standardization would be essential.

Finally, the current system does not incorporate temporal or multi-finger analysis. Using multiple fingers and aggregating predictions across them could reduce

variance and improve reliability - a direction worth exploring in future work.

VII. CONCLUSIONS

This paper has described a complete system for blood group prediction from fingerprint images using deep learning. The system combines fingerprint biometric analysis with a CNN-based classification model - specifically, a transfer learning architecture built on EfficientNetB3 - to predict one of eight ABO/Rh blood group types from a single fingerprint image. A web-based interface makes the system accessible to non-expert users and delivers results in near real-time.

Experimental evaluation confirmed that the system achieves satisfactory classification accuracy across all eight blood group classes, with performance validated through accuracy, precision, recall, and F1-score metrics. The results suggest that a genuine, if modest, statistical relationship exists between fingerprint patterns and blood groups that can be leveraged by sufficiently expressive machine learning models.

The primary contribution of this work is demonstrating the practical viability of non-invasive blood group screening through fingerprint analysis. While the system is not intended to replace clinical blood typing, it offers a promising complement to conventional methods in scenarios where speed, accessibility, and non-invasiveness are priorities - including emergency triage, forensic profiling, and healthcare delivery in remote or resource-limited settings.

Future work will focus on expanding the dataset across broader demographic groups, exploring multi-finger fusion strategies, integrating real-time fingerprint scanner hardware, and investigating explainable AI techniques to visualize which ridge features most influence the model's predictions.

VIII. REFERENCES

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