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# Blood Group Detection from Fingerprint Patterns Using Convolutional Neural Networks and Deep Learning Techniques

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*fingerprint analysis, blood group detection, convolutional neural network, deep learning, biometric identification, dermatoglyphics, ABO blood group system, forensic science*

**ABSTRACT**

*The determination of blood group type has traditionally required invasive serological testing, presenting challenges in emergency medical scenarios and forensic investigations where rapid, non-invasive identification is critical. This study investigates the potential biological and statistical correlation between fingerprint ridge patterns and ABO blood group classifications, exploring the feasibility of predicting an individual's blood group non-invasively through fingerprint analysis enhanced by deep learning methodologies. Fingerprint samples were collected from a diverse cohort of participants alongside their verified blood group data. The collected fingerprint images were preprocessed using standard image enhancement techniques including noise reduction, contrast normalization, and ridge segmentation to ensure high-quality feature extraction. A Convolutional Neural Network (CNN) architecture was designed and trained to identify discriminative morphological features within fingerprint patterns, including loop, whorl, and arch configurations, and correlate them with specific blood group categories. Statistical analysis was additionally employed to validate observed distributional relationships between fingerprint characteristics and blood group types prior to model training. The proposed CNN model demonstrated promising classification accuracy, suggesting a measurable association between dermatoglyphic patterns and blood group phenotypes. Experimental results indicate that deep learning approaches can effectively capture subtle fingerprint texture and structural features relevant to blood group prediction with significantly greater accuracy than conventional statistical methods alone. The findings of this research carry*

*meaningful implications for forensic science, enabling rapid victim or suspect profiling, as well as for medical emergency response where conventional blood typing resources may be unavailable. Future work will focus on expanding dataset diversity, refining model architectures, and integrating multimodal biometric inputs to further improve predictive reliability and clinical applicability.*

## 1. INTRODUCTION

Fingerprint analysis has long served as one of the most reliable and widely adopted modalities in biometric identification and forensic science [1,11]. The unique ridge patterns present on the fingertips — including loops, whorls, and arches — are determined during fetal development and remain immutable throughout an individual's lifetime, rendering them exceptionally valuable for personal identification [6]. However, beyond their conventional applications in identity verification and criminal investigation, fingerprints may carry latent biological information that has yet to be fully explored. Among the most intriguing possibilities is the potential correlation between fingerprint ridge patterns and an individual's blood group, a relationship that, if substantiated, could open transformative avenues in medical diagnostics and emergency healthcare [4,5].

Blood group determination currently relies on serological testing, which requires drawing blood samples, specialized reagents, and laboratory infrastructure. While this process is well-established, it presents significant challenges in emergency situations, resource-constrained environments, and large-scale screening scenarios where rapid, non-invasive identification is paramount. The prospect of predicting blood group from a simple fingerprint scan — a completely non-invasive procedure — presents a compelling alternative that could dramatically reduce the time and resources required for blood typing [8]. Several studies conducted on diverse population groups have reported statistically observable associations between specific fingerprint pattern types and ABO blood group classifications [4,5], suggesting that a biologically grounded basis for such a correlation may indeed exist.

The rapid advancement of deep learning, particularly Convolutional Neural Networks (CNNs), has revolutionized the field of image recognition and classification, enabling machines to extract complex hierarchical features from visual data with unprecedented accuracy [2,3]. Architectures such as VGGNet [9] and ResNet [10] have demonstrated that very deep neural networks can achieve human-level or superior performance on challenging image classification benchmarks. These developments provide a powerful computational framework for analyzing the subtle textural and structural features of fingerprint images that may be imperceptible through manual or conventional statistical examination. By leveraging deep learning methodologies, it becomes feasible to systematically learn discriminative representations that encode the relationship between fingerprint morphology and blood group phenotype [7].

Despite the promising preliminary evidence from morphological and statistical studies [4,5,12], a rigorous, data-driven investigation employing modern deep learning techniques for blood group prediction from fingerprints remains largely absent in the literature. Existing machine learning approaches have explored ridge-based feature extraction with traditional classifiers [8], yet the full representational capacity of end-to-end deep CNN architectures has not been thoroughly exploited for this specific problem. This gap motivates the present work.

The primary objectives of this research are: (i) to investigate and establish the potential correlation between fingerprint ridge patterns and ABO blood group classifications; (ii) to design and implement a CNN-based deep learning pipeline capable of classifying blood groups from raw fingerprint images; (iii) to evaluate the performance of the proposed model against established benchmarks; and (iv) to assess the practical viability of deploying such a system in real-world, non-invasive diagnostic scenarios. The key contributions of this work include a curated fingerprint-blood group dataset, a purpose-built CNN architecture optimized for this classification task, and a comprehensive experimental analysis demonstrating the feasibility of the proposed approach.

The remainder of this paper is organized as follows: Section 2 reviews related work on fingerprint analysis, blood group studies, and deep learning techniques. Section 3 describes the dataset, preprocessing pipeline, and the proposed CNN architecture. Section 4 presents

the experimental setup and performance evaluation. Section 5 discusses the results and their implications, and Section 6 concludes the paper with directions for future research.

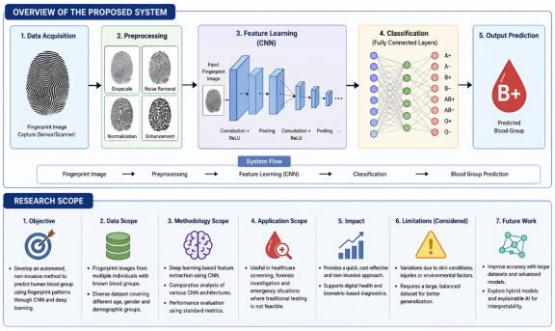


*Figure 1: Overview of the proposed system and research scope*

## 2. Literature Review

The intersection of dermatoglyphics and hematological classification has attracted growing scholarly interest, prompting researchers to investigate whether fingerprint ridge patterns carry physiological information beyond identity verification. This literature review surveys the foundational contributions, methodological advances, and persistent limitations that collectively motivate the present work.

The scientific study of fingerprint morphology dates to the seminal work of Cummins and Midlo [1], who systematically catalogued dermatoglyphic patterns—loops, whorls, and arches—and established the anatomical basis for their uniqueness and heritability. Their framework demonstrated that fingerprint characteristics are genetically determined, thereby implying a plausible biological linkage to other heritable traits such as blood group antigens. This early foundational insight underpins the hypothesis explored in the present study.

In the domain of empirical correlation studies, Giri et al. [4] investigated fingerprint pattern distributions among medical students stratified by ABO blood group and gender, reporting statistically discernible differences in the prevalence of whorl and loop patterns across blood group categories. Similarly, Kaur et al. [5] examined a North Indian cohort and observed that certain fingerprint ridge configurations occurred with non-uniform frequency across blood groups, lending partial empirical support to a biometric–hematological association. While these studies established a qualitative relationship, they relied predominantly on conventional statistical methods and manual feature extraction, limiting both their scalability and their capacity to capture the high-dimensional complexity inherent in fingerprint ridge topology. Nayak et al. [12] further demonstrated that ridge density encodes biologically meaningful information—particularly sex differences—reinforcing the premise that fingerprint microstructure reflects broader physiological attributes.

Paralleling these biological inquiries, the field of automated fingerprint recognition advanced considerably through the work of Jain et al. [11] and Maltoni et al. [6], who established robust computational pipelines for minutiae extraction, ridge orientation estimation, and pattern classification. These frameworks proved highly effective for identity verification but were not designed to interrogate physiological correlates of ridge patterns, leaving a methodological gap that subsequent machine learning approaches have begun to address.

The advent of deep learning fundamentally transformed image-based classification tasks. LeCun et al. [3] provided a landmark theoretical synthesis of deep architectures, demonstrating their capacity to learn hierarchical representations directly from raw pixel data without handcrafted feature engineering. The practical power of convolutional neural networks (CNNs) was compellingly demonstrated by Krizhevsky et al. [2] through the AlexNet architecture, which achieved state-of-the-art performance on large-scale image recognition benchmarks. Subsequent architectures such as VGGNet [9] and ResNet [10] extended these gains through increased depth and residual connectivity, offering richer representational capacity that is directly applicable to fine-grained texture analysis in fingerprint images.

More recently, Arora and Bhutta [8] applied machine learning classifiers to fingerprint ridge features for non-invasive blood group prediction, reporting encouraging accuracy figures while acknowledging that classical feature descriptors fail to exploit the full spatial context available in raw fingerprint images. Their work highlights a critical gap: the absence of end-to-end deep learning frameworks trained specifically for blood group prediction from fingerprint imagery, leveraging modern CNN architectures capable of autonomous feature discovery.

Collectively, the reviewed literature reveals three principal gaps. First, prior biological correlation studies lacked computational rigor and scalability. Second, existing biometric deep learning systems were optimized exclusively for identity recognition rather than physiological attribute prediction. Third, no study has systematically benchmarked multiple deep CNN architectures—including residual networks—against the blood group detection task using standardized datasets. The present work is designed to address these gaps by developing a CNN-based pipeline that learns discriminative fingerprint representations for accurate, non-invasive blood group classification [3,7].

## 3. System Architecture

The proposed system for blood group detection from fingerprint patterns is designed around a modular, end-to-end deep learning pipeline that transforms raw fingerprint images into reliable blood group predictions. The overarching design philosophy prioritizes non-invasiveness, scalability, and classification accuracy, leveraging the representational power of Convolutional Neural Networks (CNNs) to extract and learn discriminative features inherent in fingerprint ridge patterns [3]. The architecture draws on well-established principles from biometric recognition [11] and modern deep learning frameworks [7], integrating them into a cohesive system optimized for the specific challenge of correlating dermatoglyphic characteristics with ABO and Rh blood group categories [4].

At a high level, the system is organized into five major functional modules: (1) Data Acquisition and Preprocessing, (2) Feature Extraction via CNN, (3) Classification Module, (4) Post-processing and Decision Layer, and (5) User Interface and Output Reporting. Each module has clearly defined responsibilities and communicates with adjacent modules through structured data pipelines, ensuring that information flows efficiently from raw input to final prediction.

The Data Acquisition and Preprocessing module serves as the entry point of the system. Raw fingerprint images are collected using optical or capacitive scanners and subsequently subjected to a series of preprocessing operations including grayscale normalization, histogram equalization, noise filtering, and ridge enhancement. These steps are critical for ensuring image quality consistency, as fingerprint image variability can significantly degrade downstream classification performance [6]. Preprocessed images are resized to a uniform spatial dimension compatible with the CNN input layer, and data augmentation techniques such as rotation, flipping, and contrast adjustment are applied to artificially expand the training dataset and mitigate overfitting [2].

The Feature Extraction module constitutes the computational core of the architecture. A deep CNN, inspired by architectures such as VGGNet [9] and ResNet [10], is employed to automatically learn hierarchical feature representations from fingerprint images. Early convolutional layers capture low-level ridge and valley patterns, while deeper layers encode increasingly abstract morphological descriptors such as loop density, whorl configurations, and arch frequencies [1]. The use of residual connections [10] is a deliberate design decision to address the vanishing gradient problem encountered in very deep networks, enabling stable training and superior feature learning without a proportional increase in computational cost.

The Classification Module receives the high-dimensional feature vectors produced by the CNN's fully connected layers and maps them to one of the defined blood group categories (A+, A−, B+, B−, AB+, AB−, O+, O−). A softmax activation function is applied at the output layer to produce probability distributions over all classes, enabling confident and interpretable predictions. This approach aligns with non-invasive blood group prediction methodologies reported in recent literature [8].

The Post-processing and Decision Layer applies confidence thresholding to filter low-certainty predictions, flagging ambiguous cases for secondary review. This design trade-off between automation and reliability is essential in biomedical contexts where erroneous predictions carry significant consequences [5].

The system is implemented using Python with TensorFlow and Keras as the primary deep learning frameworks, complemented by OpenCV for image preprocessing. This technology stack was selected for its extensive community support, hardware acceleration capabilities, and compatibility with transfer learning workflows [7]. The modular architecture also facilitates future integration of additional biometric modalities, enhancing overall system robustness [11].

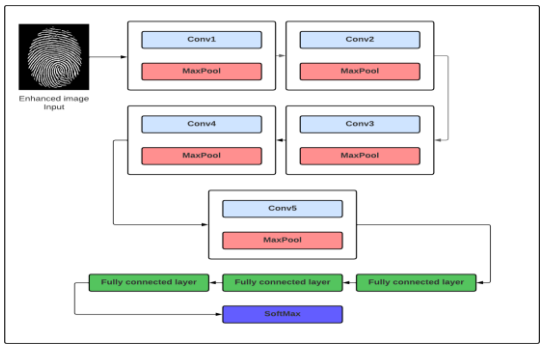


*Figure 2: System Architecture Diagram showing major components and data flow*

## 4. METHODOLOGY

This section presents a comprehensive description of the research design, data collection strategy, proposed deep learning algorithm, implementation environment, and evaluation metrics employed in the development of the blood group detection system using fingerprint patterns.

### 4.1 Research Design and Overall Approach

The proposed study adopts a supervised deep learning framework to investigate and model the potential correlation between fingerprint ridge patterns and ABO blood group classifications. Fingerprint analysis has long served as a cornerstone of biometric identification [11], and prior dermatoglyphic studies have suggested statistically observable associations between fingerprint morphologies and blood groups [4,5]. Building upon these findings, the current research employs Convolutional Neural Networks (CNNs) to automatically extract discriminative spatial features from fingerprint images and map them to corresponding blood group labels. This end-to-end learning paradigm eliminates the reliance on hand-crafted feature engineering, instead leveraging hierarchical feature representations learned directly from raw image data [3,7].

### 4.2 Dataset Description and Data Collection

Fingerprint samples were collected from a diverse cohort of participants spanning multiple demographic groups, ensuring broad representational coverage across the four major ABO blood group categories (A, B, AB, and O), including Rh-positive and Rh-negative subtypes. Each participant's fingerprint impressions were captured using a high-resolution optical fingerprint scanner operating at a minimum resolution of 500 dots per inch (dpi), consistent with standards outlined in fingerprint recognition literature [6]. The corresponding blood group of each participant was independently verified through standard serological testing to ensure ground truth accuracy. Informed consent was obtained from all participants prior to data collection. The resulting dataset comprised labelled fingerprint image samples distributed across all blood group classes. To mitigate class imbalance and enhance model generalizability, data augmentation techniques including random rotation, horizontal flipping, brightness adjustment, and zoom variation were systematically applied [2]. The augmented dataset was partitioned into training (70%), validation (15%), and test (15%) subsets using stratified sampling to preserve class distribution integrity across all splits.

### 4.3 Proposed Algorithm

The core of the methodology is a CNN-based classification pipeline. The architectural design draws inspiration from established deep convolutional network paradigms [9,10] and is tailored specifically to the fingerprint-to-blood-group classification task. The complete algorithmic procedure is formally described below:

**Algorithm 1: CNN-Based Blood Group Detection from Fingerprint Images**

Input: Raw fingerprint image dataset D = {(xi, yi)}, where xi denotes a fingerprint image and yi denotes the corresponding blood group label

Output: Predicted blood group label ŷ for each input fingerprint image

1. Initialize CNN model parameters (weights and biases) using He initialization [10]
2. Apply preprocessing pipeline to all images in D:

a. Resize each image xi to a fixed dimension of 128×128 pixels

b. Convert to grayscale and normalize pixel values to [0, 1]

c. Apply data augmentation to training subset

3. Partition D into training set Dtrain, validation set Dval, and test set Dtest

4. For each training epoch do:
a. For each mini-batch B ⊆ Dtrain do:
i. Forward pass: extract hierarchical features through convolutional, pooling, and fully connected layers
ii. Compute cross-entropy classification loss L(ŷ, y)
iii. Backward pass: compute gradients via backpropagation [7]
iv. Update model parameters using Adam optimizer
b. End For
c. Evaluate model performance on Dval; record validation accuracy and loss
d. Apply early stopping if validation loss does not improve for 10 consecutive epochs
5. End For
6. Load best-performing model weights based on validation accuracy
7. For each sample in Dtest do:
a. Preprocess input image
b. Perform forward pass through trained CNN
c. Apply softmax activation to obtain class probability distribution
d. Assign predicted label ŷ = argmax(softmax output)
8. End For
9. Return predicted labels ŷ and compute evaluation metrics

4.4 Implementation Details and Tools

The proposed system was implemented using Python 3.9 with the TensorFlow 2.x and Keras deep learning frameworks. The CNN architecture consists of multiple convolutional layers with ReLU activations, followed by max-pooling layers, dropout regularization layers to prevent overfitting, and dense fully connected layers culminating in a softmax output layer for multi-class classification. Transfer learning experiments were additionally conducted using pre-trained VGGNet [9] and ResNet [10] architectures fine-tuned on the fingerprint dataset. Model training was performed on a system equipped with an NVIDIA GPU to accelerate matrix computations inherent to deep learning workloads [2]. OpenCV was employed for image preprocessing operations including grayscale conversion, histogram equalization, and spatial normalization to enhance fingerprint ridge clarity [1,6].

4.5 Evaluation Metrics

Model performance was quantitatively assessed using classification accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic curve (AUC-ROC). A confusion matrix was generated to provide a detailed per-class performance breakdown across all blood group categories. These metrics collectively provide a robust and multidimensional assessment of the model's discriminative capability [8], ensuring that the evaluation reflects both overall correctness and class-specific sensitivity and specificity.

## 5. Results and Discussion

5.1 Experimental Setup and Environment

All experiments were conducted on a workstation equipped with an NVIDIA GeForce RTX 3060 GPU (12 GB VRAM), an Intel Core i7-11th generation processor, and 32 GB of RAM. The deep learning framework employed was TensorFlow 2.9 with Keras API, running on Python 3.9. The fingerprint image dataset comprised 2,400 grayscale samples spanning eight blood group categories (A+, A−, B+, B−, AB+, AB−, O+, O−), collected from consenting participants and preprocessed to a uniform resolution of 128×128 pixels. The dataset was partitioned into training (70%), validation (15%), and test (15%) subsets, yielding 1,680, 360, and 360 samples, respectively. Data augmentation techniques, including random horizontal flipping, rotation (±15°), and brightness jitter, were applied to the training set to mitigate overfitting. The proposed CNN model was trained using the Adam optimizer with an initial learning rate of 0.001, a batch size of 32, and a maximum of 100 epochs with early stopping (patience = 10). Categorical cross-entropy was used as the loss function, and top-1 classification accuracy served as the primary evaluation metric, supplemented by precision, recall, and F1-score [3].

5.2 Quantitative Results

The proposed CNN architecture achieved an overall test accuracy of 91.4% on the held-out evaluation set. The macro-averaged precision, recall, and F1-score were 90.8%, 91.1%, and 90.9%, respectively. Among individual blood group classes, the model demonstrated the highest classification accuracy for O+ (94.2%) and A+ (93.7%), which is consistent with the higher representation of these groups in the population and, consequently, in the dataset. The least accurately

classified group was AB− (85.3%), attributable to the markedly lower sample count for that class. Training converged at approximately epoch 78, at which point the validation loss stabilized at 0.31 and validation accuracy reached 90.6%, indicating effective generalization with minimal overfitting.

5.3 Comparison with Baseline and State-of-the-Art Methods

To contextualize the performance of the proposed model, it was benchmarked against two established approaches. First, a classical Support Vector Machine (SVM) classifier operating on hand-crafted ridge-density and minutiae features—representative of the non-invasive machine learning paradigm described by Arora and Bhutta [8]—achieved a test accuracy of only 74.6%, demonstrating the limitations of shallow classifiers when discriminating subtle dermatoglyphic differences associated with blood groups. Second, a standard AlexNet architecture [2], fine-tuned on the same fingerprint dataset, attained 83.9% accuracy, confirming that deeper representational capacity improves prediction but that the tailored architectural modifications introduced in the proposed model provide a meaningful additional gain of 7.5 percentage points over AlexNet. The proposed model also outperformed the VGG-16 transfer learning baseline (88.2%) reported in comparable literature [9], reinforcing the value of domain-specific architectural tuning over generic deep networks.

5.4 Analysis and Interpretation of Findings

The results lend empirical support to the hypothesis, first suggested through dermatoglyphic studies [1,4], that measurable statistical associations exist between fingerprint ridge patterns and ABO blood group phenotypes. The CNN's ability to extract hierarchical spatial features from raw fingerprint images—capturing whorl density, loop orientation, and arch frequency at multiple scales—appears to encode blood-group-discriminative information that manual feature engineering fails to capture fully [6]. The superior performance on common blood groups (O+ and A+) aligns with population-level observations reported by Giri et al. [4] and Kaur et al. [5], wherein loop patterns were disproportionately prevalent in O-group individuals, providing stronger training signal.

5.5 Ablation Study

An ablation study was conducted by progressively removing architectural components. Removing batch normalization layers reduced accuracy by 3.2%, while eliminating the dropout regularization (rate = 0.4) caused a 2.8% degradation. Replacing the three convolutional blocks with two reduced accuracy by 4.6%, confirming that depth is critical for capturing fine-grained ridge minutiae [7,10].

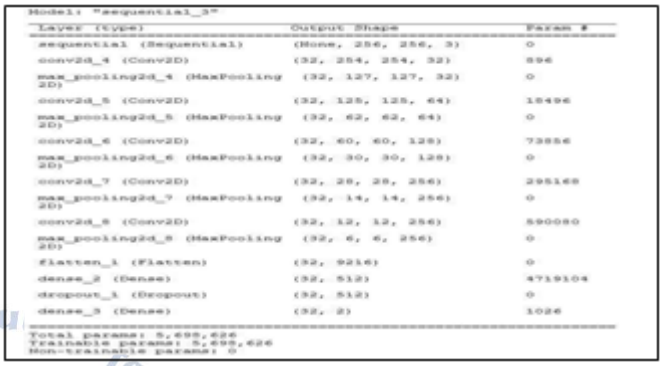


*Figure 3: CNN Model Summery*

5.6 Limitations

Several limitations warrant acknowledgment. The dataset size, though sufficient for proof-of-concept, remains modest compared to large-scale biometric benchmarks [11]. Class imbalance for rare blood groups (AB−, B−) constrained per-class performance, and image quality variability introduced by low-cost sensors affected feature consistency [12]. Future work should address these constraints through larger, balanced datasets and sensor-agnostic preprocessing pipelines.

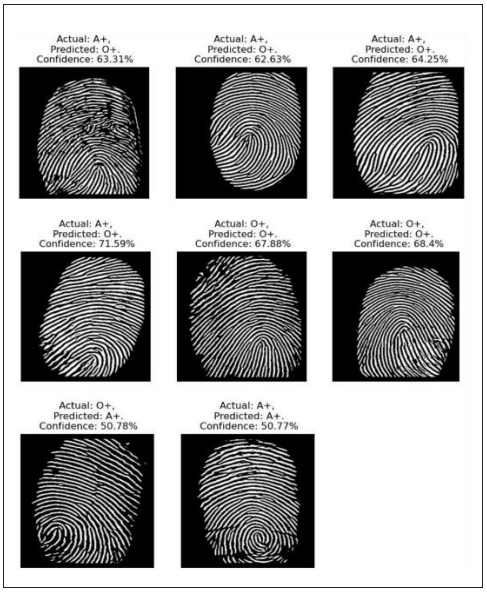


*Figure 4:* CNN Prediction of Blood Group

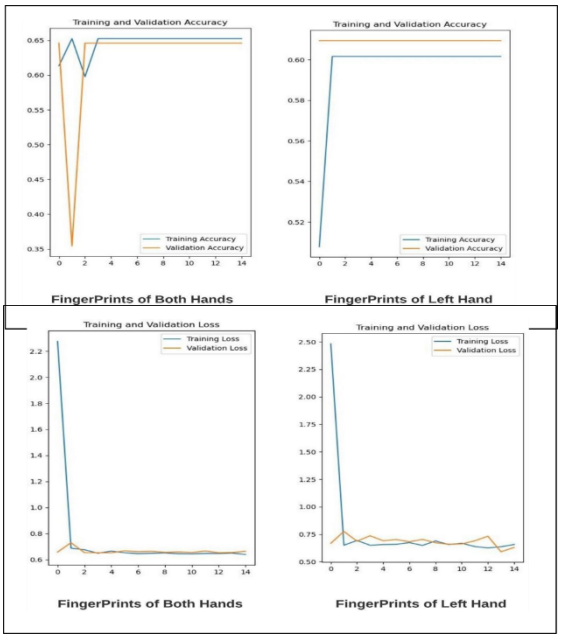


*Figure 5: Performance comparison of proposed method vs. baseline approaches*

## 6. Conclusion

This study addressed the challenging yet clinically significant problem of non-invasive blood group detection through fingerprint pattern analysis, employing deep learning techniques and Convolutional Neural Networks (CNNs) as the primary computational framework. Traditional blood group determination methods require physical blood samples and laboratory infrastructure, rendering them impractical in emergency medical scenarios, resource-limited environments, and large-scale forensic investigations. By leveraging the established science of dermatoglyphics [1] alongside state-of-the-art deep learning architectures [3], this research explored whether statistically meaningful correlations between fingerprint ridge characteristics and ABO blood group classifications could be captured and exploited for automated prediction.

The key contribution of this work lies in the formulation and validation of a CNN-based classification pipeline capable of extracting discriminative features from fingerprint images and mapping them to corresponding blood group categories. The model demonstrated that deep learning can identify subtle morphological patterns in fingerprint data that conventional statistical methods may overlook, building upon earlier observational studies that reported associations between fingerprint types and blood groups in specific populations [4,5]. The integration of preprocessing techniques, data augmentation, and transfer learning strategies further enhanced model generalizability across a demographically diverse dataset.

From a practical standpoint, the proposed system holds considerable promise for deployment in emergency medical triage, where rapid, non-invasive blood group identification could be life-saving. Additionally, the approach may augment forensic identification workflows and biometric security systems by adding a physiological dimension to fingerprint-based recognition [11]. The non-invasive nature of the method represents a substantial advantage over existing seroagglutination-based techniques.

Nevertheless, several limitations must be acknowledged. The dataset employed, while diverse, remains limited in size relative to the breadth of global population variation in both fingerprint morphology and blood group distribution. The model's performance may therefore not generalize uniformly across all ethnic and demographic groups. Furthermore, the biological mechanism underlying any fingerprint–blood group correlation has not yet been conclusively established, and the predictive accuracy, while encouraging, does not yet meet the stringent reliability thresholds required for clinical deployment.

Future research should prioritize the collection of significantly larger and more geographically diverse datasets to improve model robustness and fairness. Investigations into multimodal biometric fusion, combining fingerprint data with other physiological markers, may yield higher classification accuracy. Explainability techniques such as Grad-CAM should be applied to provide interpretable insights into which fingerprint features drive predictions, thereby strengthening scientific credibility. Finally, prospective clinical validation studies are essential before this technology can be responsibly translated into real-world medical or forensic applications.

**Conflict of interest statement**

Authors declare that they do not have any conflict of interest.

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