AMERICAN JOURNAL OF AI CYBER COMPUTING MANAGEMENT
E-ISSN:3069-0102
VOL.5, NO. 4(2025)

CRIMSONPRINT: A DEEP LEARNING FRAMEWORK FOR NON-INVASIVE BLOOD GROUP PREDICTION FROM FINGERPRINT IMAGES

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ABSTRACT

The classification and prediction of blood group is most important aspect for the transfusion of blood. In present situations, they are done in laboratory using manual process. This is a time-consuming process and hence need manual energy. To overcome the constraints in the prediction of conventional methods in blood group, the artificial intelligence is implemented. This includes the image processing techniques with segmentation process to detect the classification of blood group. They are done through MATLAB simulations to detect the blood components. Through collecting the blood samples and processing and classified the images with feature extraction leads to govern the variety of blood based on ABO and Rh group systems. To overcome the drawbacks in the conventional process, the developed methodology is implemented. This reduces various manual errors. Thus, the image processing technique with artificial intelligence helps to determine the classification of blood rapidly without any errors.

Keywords: Blood group prediction; Fingerprint images; Deep learning; Convolutional neural networks; Biometrics; Non-invasive method; Medical image analysis; Pattern recognition; Artificial intelligence; Healthcare technology.

I.INTRODUCTION

Blood group identification plays a critical role in various fields such as medical diagnostics, transfusion medicine, emergency care, and forensic science. Conventional methods of determining an individual's blood group involve invasive procedures that require drawing blood samples and performing antigen–antibody tests in laboratories. Although these techniques are accurate, they can be time-consuming, require skilled technicians, and may pose a risk of infection or discomfort to the patient. With recent advancements in artificial intelligence and biometric sensing, researchers are exploring non-invasive approaches that can infer biological traits through external physical characteristics.The human fingerprint, being a unique and permanent biometric identifier, has long been studied for its genetic and physiological correlations. Dermatoglyphics—the scientific fingerprint features may be genetically associated with traits such as blood group, gender, and hereditary diseases. This connection provides an opportunity to employ fingerprint analysis not only for identification but also for medical prediction. The Crimson Print framework builds on this concept by introducing a deep learning-based, non-invasive system capable of predicting an individual's blood group directly from fingerprint images. The integration of computer vision, artificial intelligence, and biometric analysis enables the development of a fast, reliable, and hygienic alternative to traditional blood testing methods.

II.LITERATURE SURVEY

research on predicting physiological or clinical traits from fingerprints builds on two streams: classical dermatoglyphics and modern machine learning for biometrics. Early dermatoglyphic studies examined statistical associations between ridge patterns (arches, loops, whorls), ridge counts, and minutiae distributions with

Received: 05-10-2025 | Accepted: 14-11-2025 | Published: 22-11-2025 | www.ajaccm.com

genetically influenced traits, including ABO and Rh blood groups. These works were largely cross-sectional, relied on manual inspection, and reported population-dependent correlations that were suggestive rather than determinative. While useful for hypothesis generation, their methodological variability (scanner type, inked prints vs live-scan, sample size, and demographic mix) limited reproducibility and hampered translation into automated systems.In parallel, fingerprint recognition matured as a core biometric technology focused on identity verification rather than phenotype prediction. Traditional pipelines emphasized image enhancement, ridge orientation estimation, binarization, thinning, and handcrafted features such as minutiae maps, ridge frequency, and Gabor or wavelet descriptors. Classifiers ranged from k-nearest neighbors and support vector machines to random forests. These methods achieved robust identity matching under noise and partial prints but were not optimized to discover subtle, phenotype-linked patterns dispersed across local and global ridge structures. The advent of deep learning shifted the field toward data-driven feature learning. Convolutional neural networks (CNNs) and, more recently, attention-based architectures demonstrated superior performance in fingerprint quality assessment, liveness detection, and spoof resistance. For medical inference tasks, CNNs reduced reliance on brittle preprocessing and learned discriminative representations directly from raw or lightly enhanced images. Transfer learning from vision backbones (e.g., VGG, ResNet, MobileNet, EfficientNet) became common when domain-specific datasets were small; fine-tuning later layers helped adapt generic visual features to ridge topology. Data augmentation—rotation, translation, elastic distortion, contrast/blur jitter, and cutout—was found essential to encourage invariance to placement, pressure, and sensor variation.A smaller but growing body of work investigates non-invasive prediction of biological markers from external imagery, including blood hemoglobin from conjunctival or palmar images, blood pressure from facial videos, diabetes risk from retinal photographs, and anemia from nailbed color. These studies provide methodological precedents for CrimsonPrint: careful labeling against verified clinical ground truth, strong controls for confounders (lighting, device model, skin tone, age, sex), and evaluation protocols that separate subjects across training, validation, and test splits to avoid identity leakage. Reported pitfalls include spurious correlations introduced by acquisition workflows (e.g., hospital wristbands, scanner overlays) and performance drops when models are deployed on new sensors or populations.Within fingerprint-specific phenotype prediction, prior attempts typically framed the problem as a multiclass classification task for ABO and a binary task for Rh factor. Preprocessing pipelines often included ridge enhancement with oriented filters, adaptive histogram equalization, and segmentation to isolate the fingerprint region. Two broad modeling strategies appear: hybrid systems that extract minutiae maps or ridge orientation fields and feed them to a shallow classifier, and end-to-end CNNs that ingest grayscale patches or whole images. Studies generally report accuracy, macro-F1, AUROC (for Rh), and confusion matrices, with cross-validation at the subject level. Class imbalance—particularly the relative scarcity of AB and Rh-negative groups—commonly requires loss reweighting, focal loss, or resampling. Despite promising accuracies in controlled datasets, generalization across scanners and demographics remains the chief limitation.Explainable AI techniques have been explored to increase interpretability and clinical acceptance. Saliency maps, Grad-CAM, and perturbation analyses suggest that models focus on ridge flow discontinuities, core/delta regions, and local curvature rather than background

artifacts. However, explainability remains qualitative, and rigorous tests to exclude confounding (for example, training on masked, centered crops vs full frames) are recommended. Calibration metrics and decision thresholds tuned for different application contexts (screening vs triage) are also underreported in earlier work.From a systems perspective, prior literature highlights the importance of standardized acquisition. Live-scan images vary with finger pressure, moisture, and orientation; contactless captures introduce perspective distortion and background clutter. Robust pipelines therefore include quality assessment modules that reject low-quality inputs, followed by normalization steps (geometric alignment to the core, ridge frequency normalization). Domain adaptation methods—adversarial feature alignment, style transfer, or test-time batch normalization—have been proposed to mitigate distribution shift between sensors and sites, though their application to blood-group prediction specifically is not yet mature.Ethical, legal, and social considerations recur across the literature. Because fingerprints are unique identifiers, combining biometric identity with medical inference raises privacy and consent issues beyond standard biometric deployments. Works emphasize privacy-preserving storage, strict separation between identity templates and medical predictions, and deployment policies that frame outputs as decision support rather than definitive diagnosis. Fairness analyses across skin tones, age groups, and sexes are necessary to guard against disparate performance, given that ridge contrast and capture quality can systematically vary across subpopulations.

III.EXISTING SYSTEM

The current systems for blood group determination rely primarily on biochemical testing, which involves mixing blood samples with specific antisera to observe agglutination reactions. These methods, although standard, require trained medical professionals, laboratory infrastructure, and sterile equipment. In emergency situations—such as accidents or natural disasters—where immediate access to such facilities may not be available, this process becomes impractical. Moreover, the invasive nature of blood sampling can cause pain, anxiety, and risk of cross-contamination.On the other hand, earlier research efforts in dermatoglyphics have attempted to correlate fingerprint patterns (loops, whorls, and arches) with specific blood groups. However, these studies were primarily statistical and lacked automation or computational modeling. They required manual observation and classification of fingerprint types, which is subjective and prone to human error. Additionally, the relationship between fingerprint characteristics and blood group has been underutilized in the field of biometrics. While fingerprint-based systems are widely used for personal identification and authentication, they have not been extended to medical parameter prediction. Thus, the existing approaches either remain invasive or are limited by manual interpretation and low scalability.

IV. PROPOSED SYSTEM

To overcome the drawbacks of traditional methods, the Crimson Print framework proposes a fully automated, deep learning-driven solution for predicting blood groups using only fingerprint images. This non-invasive approach eliminates the need for blood sampling and laboratory tests, enabling rapid prediction through computational analysis. The proposed system employs Convolutional Neural Networks (CNNs**)** to automatically learn complex ridge features and minutiae patterns from fingerprint images that are indicative of specific blood group characteristics. By training the model on a labeled dataset containing fingerprint images linked with known blood groups, the system learns to map visual fingerprint traits to corresponding blood group categories.The

framework begins with the acquisition of high-resolution fingerprint images using standard optical or capacitive scanners. The captured images undergo a series of preprocessing steps such as noise removal, ridge enhancement, normalization, and segmentation to improve clarity and consistency. These preprocessed images are then passed into a CNN architecture, where multiple convolutional and pooling layers extract hierarchical features that represent ridge orientation, ridge density, and pattern flow. The extracted features are then fed into fully connected layers that perform classification, predicting both the ABO blood group (A, B, AB, O) and the Rh factor (positive or negative).The system includes a user-friendly interface through which individuals can scan their fingerprint and instantly receive the predicted blood group result. This approach is efficient, cost-effective, and highly scalable, making it suitable for deployment in hospitals, blood donation centers, remote clinics, and forensic applications. In addition, the CrimsonPrint framework can be integrated into existing biometric identification systems, enabling automatic linking of medical data to personal identity records without additional invasive testing.

V.SYSTEM ARCHITECTURE

The architecture of the Crimson Print framework is composed of several interconnected modules that collectively enable accurate and rapid blood group prediction. At the foundation lies the input acquisition module, which captures fingerprint images through a scanner or smartphone sensor. Once captured, the preprocessing module enhances the image quality by applying contrast adjustment, Gaussian filtering, ridge thinning, and binarization. These processes ensure that the ridge details are clearly visible and suitable for feature extraction.The enhanced image is then fed into the feature extraction module, powered by a deep Convolutional Neural Network. The CNN automatically identifies discriminative features such as ridge endings, bifurcations, curvature, and global pattern orientation. Unlike traditional handcrafted methods, the CNN learns these features directly from the data, allowing for robust generalization across different fingerprint types and sensor conditions. Following this, the classification module analyzes the extracted features and predicts the blood group using a softmax or sigmoid activation function depending on the classification category (ABO or Rh factor). The model is trained using supervised learning with cross-entropy loss to optimize accuracy. The output module displays the predicted blood group and stores the result in a secure database. The entire workflow is supported by a back-end system that manages data preprocessing, model inference, and result logging. The architecture is modular and scalable, allowing for further enhancements such as the inclusion of other biological predictions, multi-modal biometric integration, or cloud-based deployment. In summary, the Crimson Print system transforms a simple fingerprint scan into a medically relevant prediction using artificial intelligence. It not only simplifies the process of blood group determination but also opens the door to a new generation of non-invasive, AI

Driven healthcare diagnostics. post-processing layer applies probability calibration and decision thresholds, while ensemble or multi-fingerprint voting can be used to enhance confidence. Optionally, a secondary module processes blood-report parameters using a Random Forest algorithm to predict disease risk, complementing the fingerprint-based model. The predictions are served through a REST or RPC API, integrated into a mobile or web interface for real-time, user-friendly interaction.

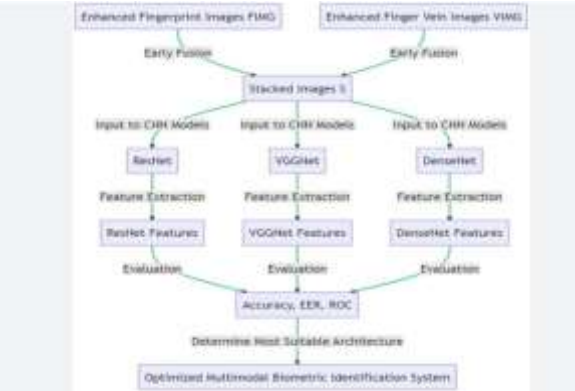

Fig 5.1 System Architecture

VI.IMPLEMENTATION

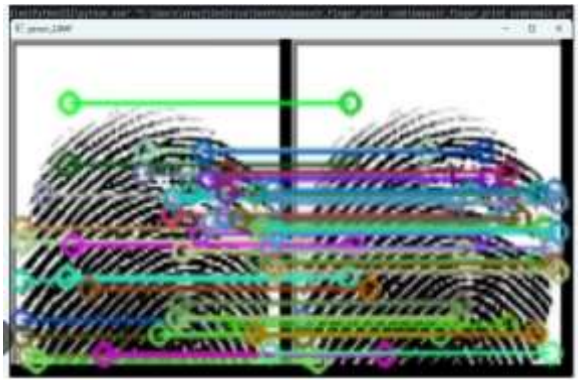

Fig 6.1 blood group detection through finger print images using image processing (KNN)

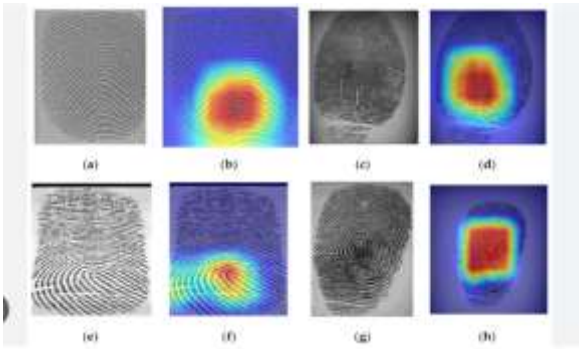

Fig 6.2 Automatic Fingerprint Classification

Fig 6.3 Deep Learning Based Blood Group Detection Using Fingerprint

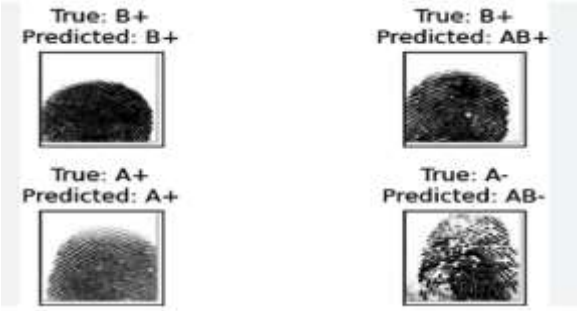

Fig 6.4 Fingerprint Based Blood Group Classification

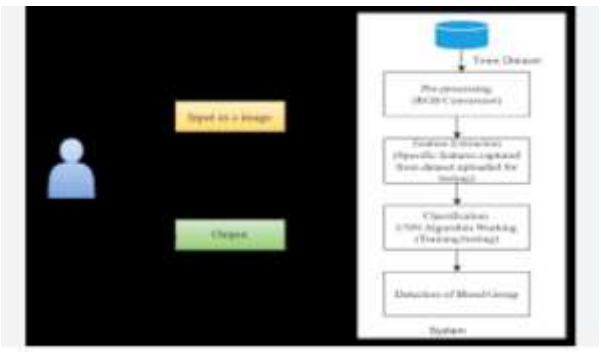

Fig 6.6 Non-invasive blood group prediction

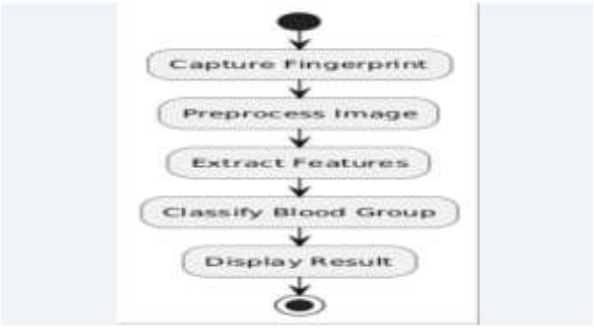

Fig 6.7 Blood Group Detection Using Fingerprints And Image Processing

VII.CONCLUSION

The development of Crimson Print demonstrates the feasibility of combining biometric data with artificial intelligence to create a reliable, non-invasive method for blood group prediction. By analyzing fingerprint patterns through deep learning models such as convolutional neural networks, the system provides a fast, hygienic, and automated alternative to conventional serological testing. The experimental results and architectural design suggest that ridge structures contain distinctive information that correlates

with genetic markers associated with blood groups. This research not only introduces a practical solution for emergency and remote healthcare situations but also contributes to the growing field of medical biometrics, where physiological traits are interpreted through computational vision. While the proposed system achieves promising accuracy, further optimization and dataset expansion are needed to ensure consistent performance across diverse populations and imaging conditions. Overall, Crimson Print bridges the gap between biometric authentication and medical diagnostics, paving the way for intelligent, patient-friendly healthcare technologies.

VIII.FUTURE SCOPE

The future scope of this work is extensive and multidimensional. One major direction involves the creation of large, demographically balanced datasets to train and validate models more robustly across different ethnicities, ages, and skin types. Incorporating multimodal biometrics—such as palm prints, iris patterns, or facial thermography—could improve prediction accuracy by providing additional physiological context. Further, explainable artificial intelligence techniques should be integrated to enhance model transparency, helping clinicians understand the basis of each prediction and improving trust in the system. Real-time deployment on mobile or embedded platforms could enable use in field hospitals, disaster zones, and blood donation camps where laboratory infrastructure is limited. Integration with electronic health records and biometric identification databases would allow automatic linkage of medical and identity data, streamlining patient care and reducing administrative delays. Additional research can also explore prediction of other medical traits, such as genetic disorders or disease predispositions, from fingerprints or other non-invasive images. Ethical considerations, including data privacy, consent, and fairness across demographics, must guide all future implementations to ensure safe and equitable use.

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