

Blood Group Identification from Fingerprint Images Using Deep Learning and Fingerprint Sensor Integration

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Abstract:

This study investigates an exploratory approach to classifying four positive blood-group labels—A+, B+, AB+, and O+—from fingerprint images using deep learning and a Mantra MFS100 fingerprint sensor. A canonical fingerprint dataset containing approximately 6000 images was used for model development. The selected four-class model reportedly achieved 87.89% accuracy (370/421) on the canonical test set. In a separate exploratory MFS100 evaluation, 78 images were grouped into 26 timestamp-defined capture bursts; the reported image-level accuracy was 46.15% (36/78), with strong prediction bias toward O+. Available metadata do not establish biological donor independence between groups. Three consecutive left-thumb scans are aggregated by averaging class probabilities, although an accuracy improvement from this strategy has not been established. The system is a research prototype and is not a substitute for clinical blood typing.

Keywords — blood-group classification, fingerprint biometrics, deep learning, convolutional neural network, Mantra MFS100, domain shift.

I. INTRODUCTION

Blood-group identification is essential in transfusion medicine and healthcare. ABO and Rh

blood groups are conventionally determined using blood samples and serological procedures. These established clinical methods must not be replaced by an unvalidated computational prediction.

Compact biometric sensors and deep-learning methods motivate investigation of whether fingerprint images contain features associated with recorded blood-group labels. Fingerprints contain ridge structures, but useful predictive information for blood-group classification must be demonstrated empirically and independently.

This study investigates a four-class fingerprint-image classification pipeline and its integration with a Mantra MFS100 sensor. The focus is the difference between performance on a canonical source dataset and performance under a separate sensor-acquisition domain. The work does not establish clinical validity.

II. LITERATURE SURVEY

Traditional fingerprint systems use minutiae, ridge orientation, ridge frequency, and local texture descriptors. Their performance can be affected by pressure, displacement, image quality, and sensor characteristics. Deep convolutional neural networks learn hierarchical image representations and are widely used in visual classification [1], [4].

Fingerprint recognition and blood-group classification are different tasks. A recognition system verifies or identifies an individual, whereas this study investigates classification against blood-group labels. Recognition performance alone does not demonstrate that blood groups can be inferred from fingerprints.

Data augmentation can expose classifiers to synthetic spatial, intensity, and quality variations. However, performance on synthetic perturbations does not establish generalization to a real independent sensor. Cross-sensor fingerprint research emphasizes that sensor differences can alter image appearance and matching performance [3].

Several recent studies have examined fingerprint-based blood-group prediction. Eenaja et al. [9] compared multiple CNN models, including ResNet50, MobileNet, and VGG16, although the datasets used for comparison differed. Dharani Sai et al. [10] applied a CNN with preprocessing and augmentation to ABO classification, but the Rh factor was not included and the dataset size was

unclear. Vijay Kumar and Vineela [11] used MobileNetV2 for fingerprint and blood-image analysis and reported fingerprint accuracy of around 90%, with possible overfitting. Sreekanth et al. [12] combined VGG19, DenseNet201, and ResNet50 in an ensemble, but used a small dataset of about 800 images and computationally heavy models.

Other studies rely on conventional feature extraction or remain at the proposal stage. Srinivasa Rao et al. [13] used HOG features with SVM and Random Forest classifiers on a limited dataset. Mondal et al. [14] applied the discrete wavelet transform (DWT) and a binary transform to a dataset of 60 images covering only Rh-positive groups, with low accuracy and no deep learning. Nihar et al. [15] proposed Gabor filters and CNN architectures but reported low accuracy (about 62%) and an incomplete implementation. Susmitha et al. [16] discussed CNN and minutiae-based feature extraction without experimental results, Padole et al. [17] reviewed machine-learning and CNN approaches without an experimental implementation, and Pallapu et al. [18] proposed a deep learning architecture, the Crimson Print framework, without quantitative results or dataset details.

General fingerprint-recognition surveys cover acquisition, preprocessing, enhancement, and matching techniques [19], [20], and rule-based fingerprint classification using minutiae distribution has also been studied [21]. However, these works address identification and classification rather than blood-group prediction. The limitations observed across the literature, namely small datasets, limited class coverage, missing experimental evidence, and the absence of independent validation, motivate the careful evaluation protocol adopted in this study.

III. COMPARISON WITH EXISTING APPROACHES

TABLE 1:
COMPARISON OF APPROACHES

Approach	Input/features	Strength	Limitation
Conventional blood typing	Blood sample and reagents	Established clinical method	Requires laboratory procedure
Traditional fingerprint recognition	Minutiae/ridge descriptors	Interpretable features	Sensitive to quality and sensor changes
Generic CNN	Fingerprint image	Learns hierarchical representations	May overfit source-domain characteristics
CNN with augmentation	Image plus simulated shifts	Tests selected perturbations	Does not prove external generalization
Proposed prototype	MFS100, CNN, 3-scan aggregation	Integrated acquisition workflow	Clinical validity unestablished

The table summarizes methodological differences and does not claim superiority over conventional blood typing.

IV. PROPOSED SYSTEM

The workflow consists of fingerprint acquisition, preprocessing, CNN-based classification, probability generation, and multi-scan aggregation: sensor → image acquisition → preprocessing → CNN → class probabilities → three-scan aggregation → experimental output.

The application averages probability vectors from three consecutive left-thumb captures before selecting a final class. The output must be identified as an experimental prediction, not a medically verified blood group. The overall architecture is shown in Fig. 1.

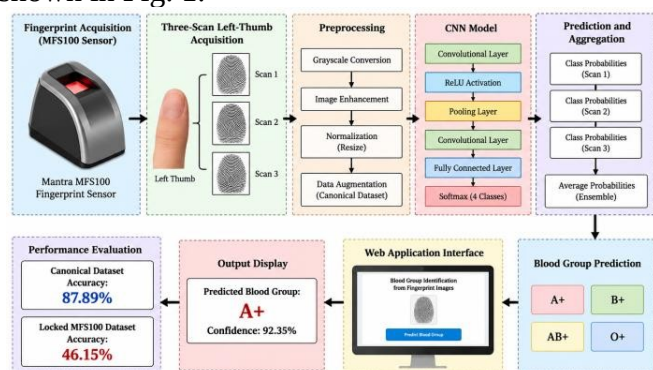


Fig. 1. Proposed workflow for fingerprint-based blood-group prediction using three-scan acquisition, CNN classification, and probability aggregation.

V. DATASET AND PREPROCESSING

A. Canonical Dataset

The canonical dataset contains approximately 6000 fingerprint images and is used for model development and source-domain evaluation. The target classes are A+, B+, AB+, and O+. Training data optimize model parameters, validation data support model development and checkpoint selection, and the test partition is reserved for source-domain evaluation. Exact class counts, participant-identity availability, and partitioning must be documented. If reliable participant identifiers are unavailable, the evaluation must not be described as participant-independent.

B. MFS100 Dataset

The MFS100 evaluation described in this paper contains 78 images. Timestamp analysis using a 5000-ms window yielded 26 capture groups, each label-pure with respect to recorded labels. Label purity does not establish biological donor identity, nor does the available metadata establish that different groups represent different individuals. The MFS100 data are therefore treated as an exploratory dependent holdout.

MFS100 images were not used for training, fine-tuning, checkpoint selection, hyperparameter tuning, or augmentation-policy design. Random image-level splitting is leakage-prone when correlated captures may be distributed across partitions.

C. Preprocessing

Fingerprint images are resized and normalized to the selected model's input representation. Synthetic spatial, intensity, and quality perturbations are generated only from the canonical domain. Reproducibility requires reporting original and input dimensions, channel conversion, interpolation, normalization, and augmentation parameters.

VI. DEEP LEARNING MODEL

A CNN processes each preprocessed fingerprint image and produces scores for A+, B+, AB+, and O+. The scores are converted into class probabilities, and the class with the maximum

probability is selected. Earlier experiments investigated frozen CNN representations and transfer-learning strategies.

The exact architecture and checkpoint behind the reported results must be identified. The final paper should state architecture/version, input dimensions, initialization or pretrained weights, trainable layers, classification head, loss function, optimizer, learning rate, batch size, training duration, and checkpoint-selection rule. Do not identify Model A as ResNet-50 unless the checkpoint records confirm this.

VII. CANONICAL-ONLY ROBUSTNESS TRAINING

Robustness experiments were conducted within the canonical domain using synthetic perturbations intended to emulate spatial changes, intensity variation, image-quality degradation, and combinations of these effects. No MFS100 images or labels were used to design these transformations. Synthetic out-of-distribution performance is reported separately from MFS100 performance because simulated shifts do not establish generalization to a physical sensor. The final report should clarify the random seeds and whether results represent a single run or an aggregate.

VIII. EXPERIMENTAL PROTOCOL AND LEAKAGE CONTROL

A timestamp-based investigation grouped 78 MFS100 images into 26 capture bursts using a 5000-ms window. Within-group similarity was reported to exceed between-group similarity in evaluated image representations. These observations suggest that correlated capture bursts can inflate image-level performance if related images occur across partitions.

The grouping does not prove that images within a group came from one donor or that separate groups came from independent donors. The MFS100 evaluation should therefore not be presented as a confirmed participant-independent test. The final experimental report should identify the checkpoint, evaluation script, split definition, random seeds, and metric-calculation procedure. Any repeatedly

inspected test set should be described as an exposed holdout.

IX. THREE-SCAN LEFT-THUMB ACQUISITION

The application captures three consecutive left-thumb images. For scan i , the classifier returns a probability vector $P_i = [p_{A+}, p_{AB+}, p_{B+}, p_{O+}]^T$, where $i \in \{1, 2, 3\}$. The final vector is:

$$P_{final} = (P_1 + P_2 + P_3)/3. \quad (1)$$

The final class is $\hat{c} = \arg \max_{c \in C} P_{final,c}$, where $C = \{A+, AB+, B+, O+\}$. This strategy is intended to aggregate multiple captures; its quantitative benefit must be measured by comparing single-scan and three-scan performance under the same evaluation protocol.

X. WEB APPLICATION

The web application guides the user through scanner initialization, three left-thumb captures, inference, and display of the aggregated research prediction. It may display per-scan predictions, probability scores, and the final class. Model-derived confidence must not be presented as clinically verified certainty.

The interface must state that fingerprint-based blood-group prediction has not been clinically validated and must not be used for healthcare, transfusion, or emergency decisions.

XI. RESULTS AND DISCUSSION

A. Reported Accuracy

TABLE I.
REPORTED ACCURACY ON CANONICAL AND MFS100 DATASETS

Evaluation	Model	Correct/total	Accuracy
Canonical test	Four-class Model A	370/421	87.89%
MFS100 evaluation	Four-class Model A	36/78	46.15%

The reported canonical result is 87.89% accuracy (370/421), while the reported MFS100 result is 46.15% (36/78). These figures are reproduced from the supplied manuscript and must be checked against the final evaluation logs, checkpoint, and protocol before submission.

B. Class-Wise MFS100 ResultsTABLE II.
REPORTED PER-CLASS RECALL ON MFS100

Class	Recall
A+	0.00%
AB+	0.00%
B+	12.50%
O+	100.00%

Approximately 92.31% of MFS100 predictions were assigned to O+, demonstrating substantial prediction bias. Recall was zero for A+ and AB+, while O+ recall was 100%. Overall accuracy alone therefore does not adequately describe model behavior.

The final results should also report balanced accuracy, macro F1-score, per-class precision, a confusion matrix, prediction counts by class, and a majority-class baseline, provided these are computed from the same predictions.

C. Cross-Sensor Generalization

The difference between canonical and MFS100 results indicates reduced performance under the evaluated acquisition conditions. Sensor characteristics, resolution, contrast, ridge appearance, and capture quality are plausible contributors, but the available results do not isolate the cause.

Because donor independence is not established, the MFS100 result should be interpreted as exploratory cross-sensor evidence rather than a definitive estimate of performance on independent participants.

D. Three-Scan Aggregation

The paper describes probability averaging across three scans, but the reported results do not establish that it improves accuracy. A controlled single-scan versus three-scan comparison is required before claiming an accuracy benefit.

XII. LIMITATIONS

- The MFS100 evaluation contains only 78 images in 26 timestamp-defined capture groups.
- Biological donor and finger independence could not be established from available MFS100 metadata.

- The model shows strong O+ prediction dominance and poor recall for A+ and AB+.
- The canonical and MFS100 datasets have different acquisition conditions.
- Blood-group label verification must be documented; self-reported labels are not equivalent to laboratory-confirmed serology.
- The experiments do not establish clinical validity or utility.
- The benefit of three-scan aggregation has not been established by a controlled comparison.

XIII. FUTURE WORK

Future work should prioritize a larger, independently collected dataset with multiple participants, multiple fingers per participant, multiple sessions, and multiple sensors. Blood-group labels should be verified using appropriate laboratory procedures, and explicit donor and finger identifiers should be retained.

Evaluation should use participant-level separation, balanced class representation, and a prespecified protocol. Report accuracy, balanced accuracy, macro F1-score, class-wise precision and recall, confusion matrices, and uncertainty estimates.

Further studies should compare single-scan and three-scan aggregation, examine preprocessing and resolution, evaluate alternative CNN architectures, calibrate probabilities, and investigate cross-sensor methods without target-data leakage.

XIV. CONCLUSION

This study investigated a CNN-based approach for classifying four positive blood-group labels from fingerprint images and integrating the pipeline with a Mantra MFS100 sensor. The reported model achieved 87.89% accuracy on the canonical test set, whereas the exploratory MFS100 evaluation achieved 46.15% accuracy and showed substantial O+ prediction bias, including zero reported recall for A+ and AB+. These results do not establish reliable cross-sensor generalization. Timestamp grouping highlights the risk of correlated captures, but the available metadata do not establish biological donor independence. The three-scan

workflow provides a practical acquisition procedure, although its accuracy benefit remains unverified.

A larger dataset with laboratory-verified labels, explicit participant identifiers, subject-independent evaluation, and sensor-diverse acquisition is required before stronger claims can be made. The system remains an exploratory research prototype and must not replace conventional laboratory blood typing.

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