Fingerprint Based Blood Group Identification Using Histogram of Gradients HOG Feature Extraction with Machine Learning Models

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ABSTRACT

Identifying blood groups plays crucial role in medical diagnosis, blood transfusions and emergency healthcare. The usual ways to determine blood typification style it rely on serologic tests. To perform these tests, we need medical experts to collect blood samples and to testing blood sample they need reagents, and have access to a laboratory. Usually, they take time, more money and they use the patient's blood in more quantity. To address this, this study examines a new, non-invasive approach to detect blood groups using fingerprint analysis. Both fingerprints and blood groups come from our genes. So, the patterns in fingerprints like loops, whorls, and arches might link to blood group traits. The new system involves extracting fingerprint features using a Histogram of oriented gradients (HOG), which is a widely used feature descriptor for pattern recognition. These extracted features are then classified using the support vector machine (SVM) and random forest (RF) to predict blood groups. The study evaluates the performance of the model using accuracy, precision, recall, F1 score and confusion matrices. The HOG-SVM achieves high accuracy of 90.69% and HOG-RF model achieves accuracy of 87.36%. In contrast to prior statistical or manual correlation studies, our method applies a fully-automatic machine learning-based pipeline, obtains an accuracy of 90% irrespective of blood samples and laboratory testing. The study results that HOG-SVM performs high classification accuracy compared to HOG-Random Forest.

KEYWORDS: Histogram of Oriented Gradients (HOG), Fingerprint Feature Extraction, Support Vector Machine (SVM), Blood Group Prediction, Random Forest, Biometric-Based Diagnosis.

1. INTRODUCTION

Determining a patient's blood group is essential for the healthcare system, especially when it comes to diagnosis, blood donation, and other emergencies. Old methods of blood typing take advantage of serological techniques that involve blood samples using reagents, and having lab facilities. While these approaches are predominant and efficient, they do have restrictions like invasive techniques, time delays, and a need for experts. Such limitations are extremely problematic when immediate action is required, such as rapid blood typing for critical procedures [1][3][9][37]. Serological approaches are invasive, slow and not appropriate in low resource or emergency conditions. An accurate, rapid, convenient and noninvasive portable method is urgently needed. New developments in biometric systems and AI techniques have enabled the detection of blood groups without any prior patient information. Research has proved that fingerprint scan contains distinct features which are sufficient for classifying the individual's blood group [6][7][8]. Machine learning and deep learning algorithms have been successfully implemented for feature extraction from fingerprints and determining blood groups [11][13][21][10]. Furthermore, the use of image processing methods through MATLAB and Python allows the implementation of this amendment in practice [16]][22][12][14]. This study presents a new, non-invasive blood group detection device using fingerprint scanning technology. Following the differential biochemical and physiological features of fingerprints, this method has the ability to detect blood groups without drawing blood samples. The device can be deployed quickly in emergency medical facilities, blood donation facilities, and in outreach medical services, offering a cost-cutting, efficient, and transportable means of blood typing compared to traditional methods [18][20][2][5]. This approach can provide a quick, cost effective and accessible alternative for conventional blood tests, potentially in favor of emergency medical services, blood donation centers and external health care settings. This makes medical testing more efficient [4][17][19]. This method renders invasive techniques unnecessary, thus leading to better patient access and lower reliability on laboratory systems [15][32][36]. Through the fusion of high-level background checks with diagnostic tools, this method is considered a major step toward healthcare technology. It can absolutely transform blood group evaluation by giving an expedited and efficient tool that can be easily used by healthcare professionals, especially in the case of emergency and resource limitations.

2. LITERATURE SURVEY

There has been growing trend and interest in using biometrics in healthcare diagnostics and there have been performed several studies to correlate fingerprint patterns with some biological markers such as blood groups. This section provides a literature review in three main themes: studies that focused on statistical relationships between fingerprint and blood group patterns, improvement on fingerprint recognition via feature extraction, and attempts in automating blood typing with image processing. A review of such methods is the starting point of the present work and will realize the position of our contributions as discussed in the next section.

2.1. Fingerprint–Blood Group Correlation Studies-

Many studies had highlighted a possible link between fingerprint patterns and blood groups. D. Roy, et al. [23], explained about the development of a system that is correlating fingerprints of a person with his gender and blood group. For reducing the noise fingerprints will be collected, studied and analyzed statistically. They identified the blood group that having the whorls structure in A+ and AB+ blood group, loop structure predominates in O blood group and arches are high in B blood group. This study opens a field that lead to various developments in this domain. H. O. Smail, et al. [24], addressed the possible link between the fingerprint patterns and some types of blood groups and each human finger has a unique fingerprint pattern. They said that it is possible to predict the blood group of a person based on their fingerprint patterns. D. Deopa, et al. [25], reported that number of whorls was maximum in A & AB positive followed by loops for O & B blood type. Arches were minimum in all the blood groups. There is an individual's distribution of fingerprint patterns may be related to his blood group. B. Desai, et al. [26], identified the most common fingerprint pattern to be the loop and least the arch. Blood Groups- B and O often presented a loop and arch. Similarly, B+ and O+ have high number of whorls. The minimum arches available are found in blood group AB. Blood group B and O possessed significantly more loops than blood group A and AB.

2.2. Feature Extraction for Fingerprint Recognition-

Pradeep N.R, et al. [27], introduced a new HOG based finger print recognition system. They describe a tripartite contribution- first is to guarantee that the process of fingerprint detection is robust. Second is it can effectively deal with noisy data. Third is that the results that prove that the extractor of the HOG characteristic and the recognition of fingerprint perform recognition at an accuracy rate which is about 100% in medium. V.

Kumar, et al. [28], implemented various fingerprint recognition techniques using HOG, Gabor filters and DCT for better biometric identification That HOG-based methods yield the best results, achieving the lowest error rate on average.

2.3. Automated Blood group classification Using Image Processing-

D. Jayaram, et al. [29], developed an effective approach to indicate the agglutination and certainly the blood group of the patient. They employed an image processing method in which agglutination is automatically detected and the blood type of the patient is identified very quickly. This is useful in a case of emergency. K. Lahari, et al. [30], explained about the deep learning as a non-invasive, quick, and reliable substitute in comparison to traditional blood group tests which may be more applicable to fields like emergency healthcare and medical diagnostics. H. Krishna, et al. [31], addressed about the fingerprint pattern is unalterable and it remains the same until death of an individual. Each human's finger print featured is unique. So no two humans have exactly the same pattern and the probability of two people having the same minutiae pattern is almost virtually impossible. Even among genetically identical twins have different finger print patterns. The ridge pattern is unique and does not alter after birth of the person. R. V. Rashmi, et al. [33], illustrated about the the possibility of applying fingerprint patterns as the trustworthy biometric marker for blood typing. In this study, a user's friendly interface and automated features are developed, makes it a useful tool to address the problem. fingerprint diagnostics have the potential to solve the specific drawbacks of classical methods, i.e. invasiveness and human error reliability. S. K. P. M. Sekkeena Khan, et al. [34], developed a system that holds great promise for applied use in such things as emergency response, rural health care. It provides rapid blood group estimates through a direct image upload, economizing on costs and infrastructure. With the requirement of being light weight and being secure, scalable. M. Prasad, et al. [35], presented a non-invasive image processing technique for blood group determination using image processing. While interaction between theoretical development and detection model has been done, the present work aims to provide a non-estimative way to develop a real-world, image-based device for blood group estimation. The main in this study is to provide suggestions for data recording, signal and feature extraction, and image processing, which are feasible to realize precise non-invasive detection of blood groups.

2.4. Limitations in Prior Work

Although previous studies have demonstrated the potential correlations between fingerprint patterns and blood groups, they exhibit several key limitations. The prior studies done by the some researchers like by Roy et al. [23], Smail et al. [24], and Deopa et al. [25] have been used manual statistical analysis. This makes them biased hard to scale up, and not good for real-time use. These studies didn't use computer models or automatic sorting methods. Other work observed for fingerprint recognition using things like HOG or Gabor filters [27], [28], but only for checking identity, not for medical uses like guessing blood groups. Some image-based blood typing methods [29] still needed to take blood samples so they weren't non-invasive. Many of these studies also lacked big datasets full performance measures, or real-world use cases such as comprehensive performance metrics, or practical deployment scenarios—limiting their generalizability and clinical utility.

Traditional blood typing is invasive and time consuming, and cannot be performed without lab infrastructure and trained staff, thus, it is not practicable for emergency use. This study presents an innovative and non-invasive automated approach by means of fingerprint images and machine learning (HOG + SVM/RF) for accurately predicting of blood groups.

3. METHODOLOGY

This method uses machine learning techniques for blood group classification from fingerprints using a generalized feature extraction approach and various classifiers. It has a systematic approach where the process starts with data collection and preprocessing of the fingerprint images.

To ensure consistency across all samples, median filtering was applied for noise reduction. The fingerprint images are resized to a fixed size of 128 × 128 pixels and, converted to greyscale. In this way, features were extracted from the images to represent essential ridge patterns, and they were stored with corresponding blood group labels. Dataset used in this research is taken from Kaggle, which is a well-established platform that offers a wide range of dataset for the machine learning program. In this model 5-fold cross-validation of SVM model was applied to evaluate the robustness and extension of model over the different subsets of data. The mean value over the five folds was also applied as an indication for the stability of model. In particular, the high-resolution dataset contains high resolution, which acts as the primary input in this proposed machine learning models. The dataset contains 8000+ fingerprint samples. In this research considered maximum of 2400 samples, ensuring variability in as patterns, orientation and

quality. For Feature selection HOG is the best method than SIFT and LBP. LBP is quick but noise-sensitive, whereas SIFT is strong but computationally demanding. HOG is perfect for spotting patterns like whorls and loops hence it is the best option due to its balance of accuracy, resilience, and efficiency.

The processed features are used to train two classifiers- one is Support Vector Machine (SVM) with hyperparameters like a linear kernel and regularization parameter ©, and other is Random Forest (RF) with hyperparameters including multiple decision trees and the Gini impurity criterion.

3.1 Flow Diagram:

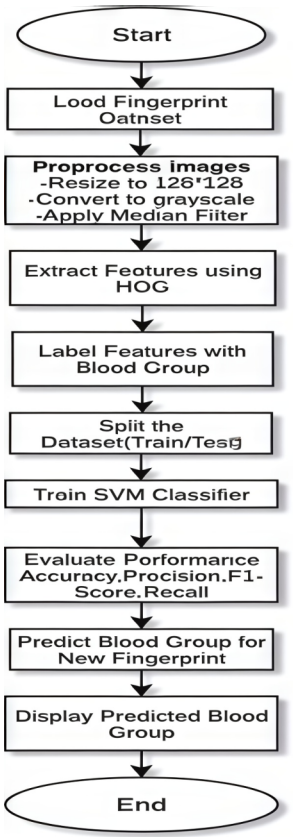


Figure 1: Flow chart of the proposed model

The algorithm classifies blood groups that use fingerprint images through a structured machine learning approach. The algorithm includes the following steps:

- Preprocessing, where images are shaped, converted into grayscale.
- Stores the features and calculates the total number of samples.
- The dataset is Splitted into training data and testing data helps for balanced learning.
- Training the model with the right classifier on the features.
- Evaluating the model using accuracy, precision, recall, and F1 score
- At the end, we test a new fingerprint image.
- The likely blood group shows up.

This method offers an effective way to classify blood groups.

4. ENVIRONMENTAL SETUP

The fingerprint-based blood group classification system was developed in this study. The system is configured with a 2.5 GHz processor, 8 GB of RAM and 120 GB SSD. The implementation was performed using Python, which was used for imaging, feature extraction and machine learning model training. The system can be performed on Windows, Linux or MacOS, requiring an active python 3.8+ layout with the required addition installed. This model is designed to be available on various data units such as desktop machines, laptops and cloud-based servers. It supports testing and classification of new fingerprint images, which is suitable for forensic and medical applications.

5. RESULTS

In order to assess the effectiveness of fingerprint -based blood group classification, two machine learning models were used: Histograms of oriented gradients (HOG) with support Vector machine (SVM) and HOG with Random Forest (RF).

5.1 Comparison of Evaluation Metrics of the two models -

The model was evaluated on a dataset with 1600, 2000, 2400 sample sizes, and their classification performance was analyzed using accuracy, confusion matrix, precision, recall, F1score.

5.1.1 Accuracy of HOG - SVM and HOG – Random Forest -

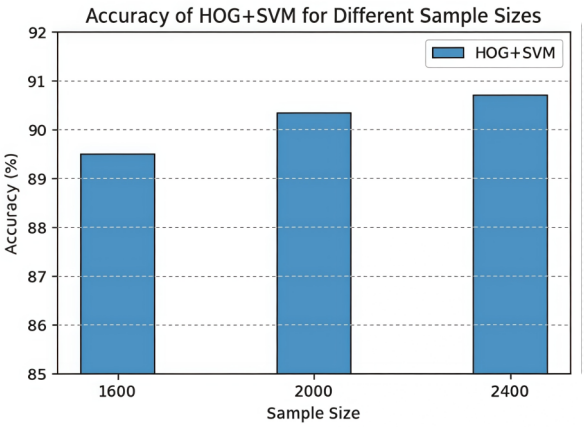


Figure 2a: Bar graph of HOG+SVM model accuracy For different sample sizes

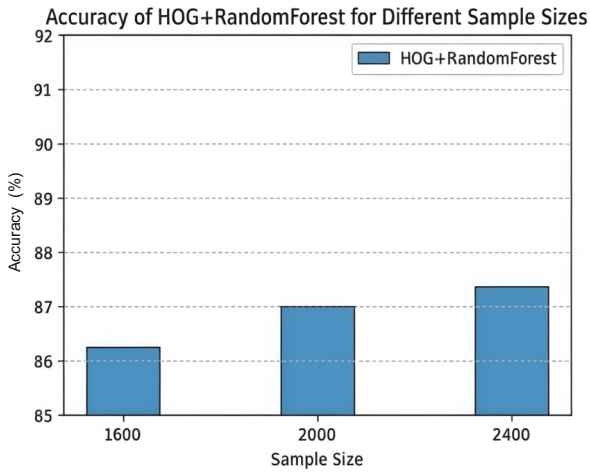


Figure 2b: Bar graph of HOG +Random Forest For different sample sizes

Figure 2a and Figure 2b represents the Hog + SVM performs better than Hog + Random Forest in continuous all data set sizes. Hog + SVM at 1600, 2000 and 2400 samples, the model accuracy is 89.5%, 90.33%and 90.69%receive, while random forests model accuracy is 86.25%, 87.0%and 87.36%. Both models improve with large datasets, but SVM is better for HOG facilities when it comes to accuracy.

Comparison of two models Accuracy-

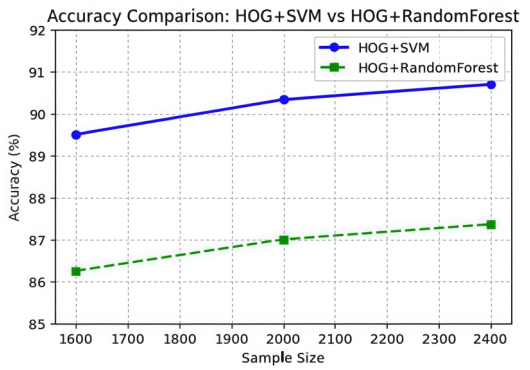


Figure 2c: Line chart of the two model's accuracy

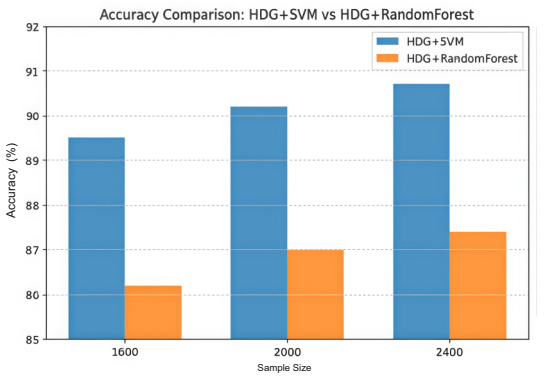


Figure 2d : Bar graph of the two model's accuracy

The Figure 2c and Figure 2d explains the graph that compares the accuracy of two models HOG-SVM and HOG-Random Forest in separate sample sizes.

- X-axis (sample size): It represents the number of sample sizes (1600, 2000, 2400).
- Y-axis (accuracy %): It represents the accuracy of the model as a percentage.
- Blue Solid Line (Hog and SVM): The accuracy indicates that accuracy is improved from 89.38% to 90.69% as sample size increases.
- Red Dash Line (Hog and Random Forest) is also improved, but lowers from 86.25% to 87.36%.
- General trend: Both models are improved with large test sizes, but Hog + SVM continuously improves HOG + Random Forest.
- Statistical calculation(p-value):

A paired t-test was performed in this study to check the significance of the accuracy of the HOG + SVM versus HOG + Random Forest on the three different sizes of datasets (1600, 2000, 2400). The average result was statistically better the p-value was 0.04 in performance, HOG + SVM was performing better than HOG+ Random Forest consistently over classification accuracy.

5.1.2 Evaluation Metrics for HOG+SVM and HOG + Random Forest (Per Sample Size)

5.1.2.1 Metrics for 1600 Sample-

The Below are the metrics for the sample size of 1600-

```
Total samples: 1600
Feature vector size: 8100
Test Set Accuracy: 89.38%

Classification Report:
              precision    recall  f1-score   support

          A+       0.89      0.95      0.92        60
          A-       0.92      0.90      0.91        60
         AB+       0.96      0.87      0.91        60
         AB-       0.85      0.93      0.89        60
          B+       0.92      0.98      0.95        60
          B-       0.98      0.88      0.93        60
          O+       0.84      0.87      0.85        60
          O-       0.81      0.77      0.79        60

    accuracy                           0.89       480
   macro avg       0.90      0.89      0.89       480
weighted avg       0.90      0.89      0.89       480
```

Figure 3: Classification Report for HOG+Svm

```
Total samples: 1600
Feature vector size: 8100
Test Set Accuracy: 86.25%

Classification Report:
              precision    recall  f1-score   support

          A+       0.91      0.97      0.94        60
          A-       0.84      0.87      0.85        60
         AB+       0.88      0.88      0.88        60
         AB-       0.84      0.80      0.82        60
          B+       0.89      0.92      0.90        60
          B-       0.90      0.88      0.89        60
          O+       0.83      0.80      0.81        60
          O-       0.81      0.78      0.80        60

    accuracy                           0.86       480
   macro avg       0.86      0.86      0.86       480
weighted avg       0.86      0.86      0.86       480
```

Figure 4: Classification Report for HOG+Random Forest

Figure 3 showcases the Hog + Svm model which achieves 89.38% accuracy, which shows strong classification performance, especially for B- and A + blood groups, while the O- blood group class is the most difficult to classify. Large precision and recall average indicate a balanced model. Figure 4 represents the Hog + random forest model receiving 86.25% accuracy, with + the best performance and o- is the most challenging. The accuracy and recall are slightly lower, indicating a slightly weak performance.

(Rows represent actual blood groups, columns represent predicted classes.)

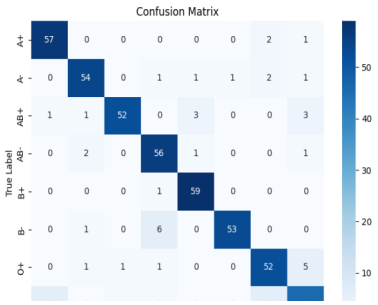


Figure 5: Confusion Matrix for HOG+Svm

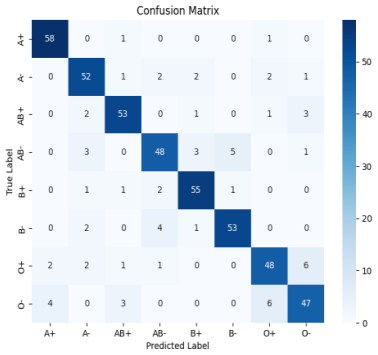


Figure 6: Confusion Matrix for HOG+Random Forest

Figure 5 represents HOG + SVM has Higher accuracy, fewer misclassifications, especially for B+, AB-, and O+. O- misclassified as O+ (6 cases). Figure 6 represents HOG + Random Forest: More errors, especially in AB- (48/60) and O- (47/60). Struggles to separate AB- and B-. Several key misclassifications were observed during model evaluation. Some O- samples were mistakenly identified as A+ or O+, which might be because their fingerprint patterns are quite alike and the Rh factor doesn't make a big visual difference. Confusion between O+ and O-, probably due to the same reason—those subtle differences are tough for the feature extraction method to catch. AB- was occasionally labeled as AB+ or even B+, possibly because their features overlap or there weren't enough unique examples of AB- in the training data.

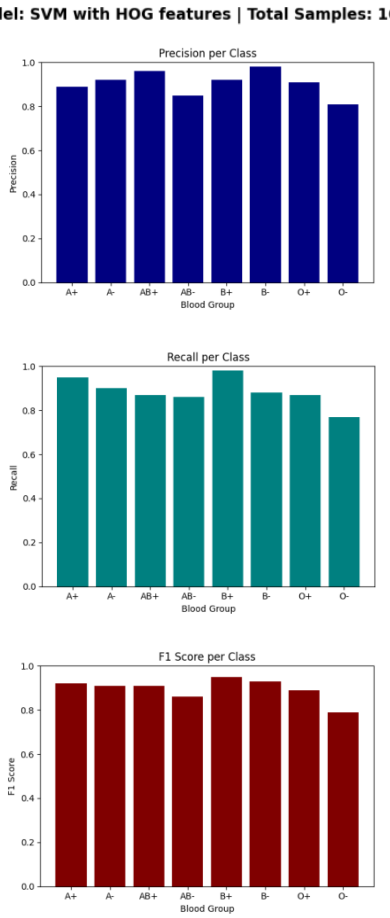
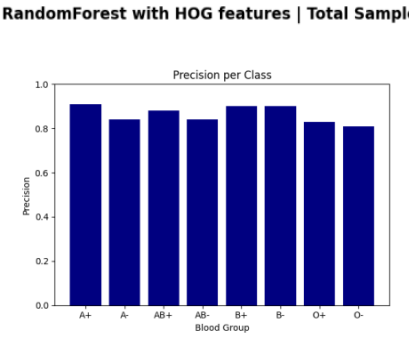


Figure 7: Performance Metrics for Blood Group classification of svm and hog

Figure 7 presents Precision, recall and F1 score for different classifications of the blood group. Each chart imagines the performance of the model in different classes, indicating better predictions with high values. The results suggest that some blood groups (eg B and A+) have strong performance, while others (eg o-) remember relatively rarely.



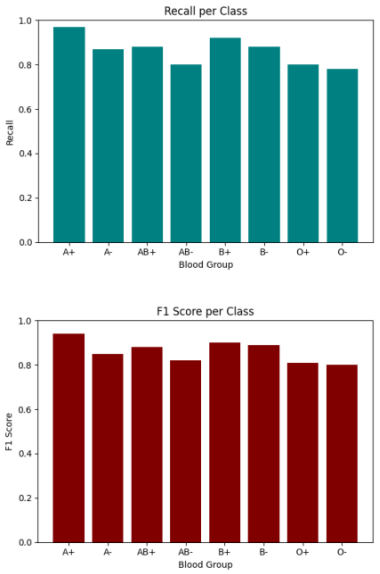


Figure 8: Performance Metrics for Blood Group classification of RandomForest and Hog

Figure 8 presents Precision, recall and F1 score charts for different classifications of the blood group. Each chart imagines the performance of the model in different classes, indicating better predictions with high values.

5.1.2.2 Metrics for 2000 Sample

Total samples: 2000
Feature vector size: 8100
Test Set Accuracy: 90.33%

Classification Report:

	precision	recall	f1-score	support
A+	0.92	0.96	0.94	75
A-	0.87	0.88	0.87	75
AB+	0.95	0.95	0.95	75
AB-	0.85	0.85	0.85	75
B+	0.92	0.96	0.94	75
B-	0.96	0.97	0.97	75
O+	0.89	0.89	0.89	75
O-	0.85	0.76	0.80	75
accuracy			0.90	600
macro avg	0.90	0.90	0.90	600
weighted avg	0.90	0.90	0.90	600

Figure 9: Classification Report for HOG+Svm

Total samples: 2000
Feature vector size: 8100
Test Set Accuracy: 87.00%

Classification Report:

	precision	recall	f1-score	support
A+	0.89	0.96	0.92	75
A-	0.84	0.77	0.81	75
AB+	0.90	0.95	0.92	75
AB-	0.82	0.84	0.83	75
B+	0.89	0.95	0.92	75
B-	0.91	0.93	0.92	75
O+	0.87	0.81	0.84	75
O-	0.84	0.75	0.79	75
accuracy			0.87	600
macro avg	0.87	0.87	0.87	600
weighted avg	0.87	0.87	0.87	600

Figure 10: Classification Report for HOG+Random Forest

Figure 9 showcases the Hog + Svm model which achieves 90.33% accuracy, which shows strong classification performance, especially for AB+ and A + blood groups, while the O-class is the most difficult to classify. Large precision and recall average indicate a balanced model. Figure 10 represents the Hog + random forest model receiving 87% accuracy, with B- the best performance and AB- is the most challenging.

(Rows represent actual blood groups, columns represent predicted classes.)

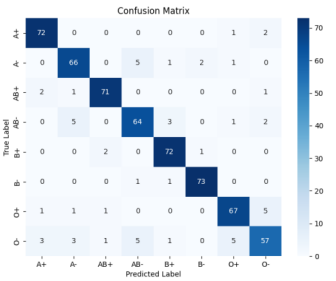


Figure 11: Confusion Matrix for HOG+Svm

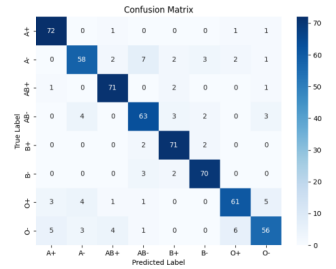
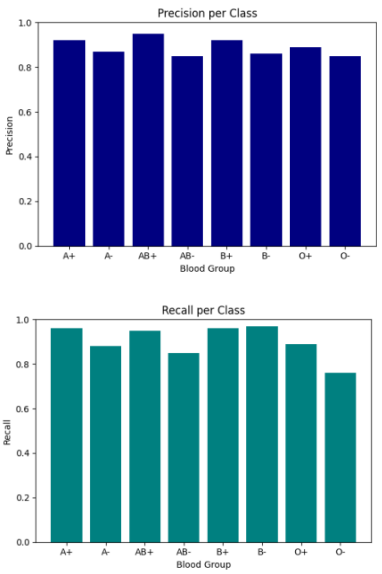


Figure 12: Confusion Matrix for HOG+Random Forest

Figure 11 represents HOG + SVM with High accuracy with fewer misclassifications, especially for B+, AB-, and O+. However, O- is misclassified as O+ in 5 cases. Figure 12 represents HOG + Random Forest has more misclassifications, especially in A- in 8 cases and O- in 4 cases, showing challenges in differentiating A- and O-. O- samples were sometimes confused for B+, AB+, or O+ due to the similarities in their fingerprint patterns and the difficulty in separating the Rh factor from visual textures. Similarly, O+ was occasionally mistaken for O-, indicating that the model was unable to identify subtle differences between these closely related groups.

Model: Svm with HOG features | Total Samples: 2000



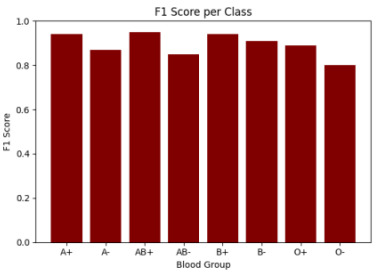


Figure13: Performance Metrics for Blood Group classification of Svm and HOG

Figure 13 represents the bar chart representing the Precision, Recall and F1 score for classification using SVM models with HOG features. The model performs well for B- and A+, shows high recalls and accuracy, while O-has the lowest recall. Overall, the results suggest strong classification performance with certain variations in blood groups.

Model: RandomForest with HOG features | Total Samples: 2000

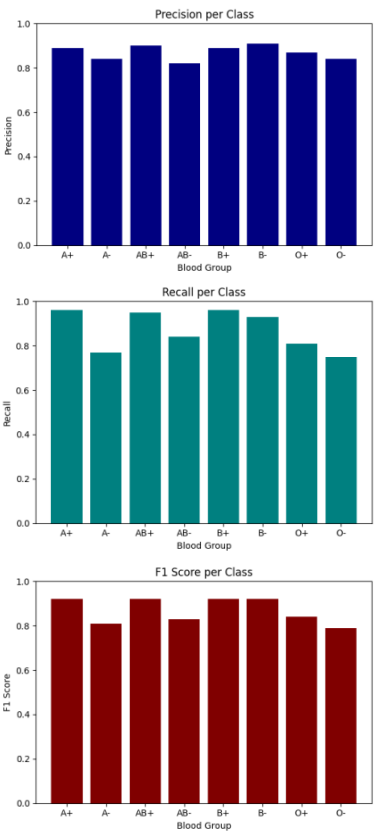


Figure 14: Performance Metrics for Blood Group classification of RandomForest and HOG

Figure 14 presents the bar charts representing the Precision, Recall, and F1 Score for classification using the Random Forest model with HOG features. The model works well for B- and A+, shows high recall and precision, while O- and A- has lower recall.

5.1.2.3 Metrics for 2400 Sample

```
Total samples: 2400
Feature vector size: 8100
Test Set Accuracy: 90.69%

Classification Report:
              precision    recall  f1-score   support

          A+       0.96      0.96      0.96        90
          A-       0.84      0.89      0.86        90
         AB+       0.84      0.94      0.89        90
         AB-       0.92      0.88      0.90        90
          B+       0.94      0.91      0.93        90
          B-       0.92      0.98      0.95        90
          O+       0.92      0.87      0.89        90
          O-       0.94      0.83      0.88        90

    accuracy                           0.91       720
   macro avg       0.91      0.91      0.91       720
weighted avg       0.91      0.91      0.91       720
```

Figure 15: Classification Report for HOG+Svm

```
Total samples: 2400
Feature vector size: 8100
Test Set Accuracy: 87.36%

Classification Report:
              precision    recall  f1-score   support

          A+       0.93      0.93      0.93        90
          A-       0.82      0.79      0.80        90
         AB+       0.83      0.94      0.89        90
         AB-       0.91      0.88      0.89        90
          B+       0.92      0.87      0.89        90
          B-       0.85      0.96      0.90        90
          O+       0.86      0.88      0.87        90
          O-       0.88      0.74      0.81        90

    accuracy                           0.87       720
   macro avg       0.88      0.87      0.87       720
weighted avg       0.88      0.87      0.87       720
```

Figure 16: Classification Report for HOG+Random Forest

Figure 16 represents the Hog + Svm model which achieves 90.69% accuracy, which shows strong classification performance, especially for B+ and A+ blood groups, while the A- class is the most difficult to classify. Figure 17 represents the Hog + random forest model receiving 87.36% accuracy, with A+ the best performance and O- is the most challenging. The overall performance of the SVM model is superior, with better precision and recall across most classes.

(Rows represent actual blood groups, columns represent predicted classes.)

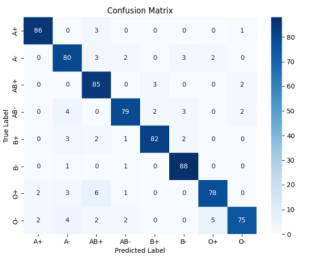


Figure 17: Confusion Matrix for HOG+Svm

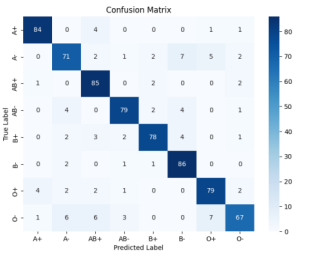


Figure 18: Confusion Matrix for HOG+Random Forest

Figure 17 represents the HOG + SVM of High accuracy with fewer misclassifications, especially for B+ and AB-. However, O- is misclassified as O+ in 5 cases. Figure 18 represents HOG + Random Forest: More misclassifications, especially in A- (9 cases) and O- (7 cases). Some O- samples were incorrectly labeled as B+, AB+, or O+, likely because their fingerprint patterns look similar, and it's not easy for the model to pick up on the Rh factor just from image features. O+ and O- also got mixed up at times, due to slight differences.

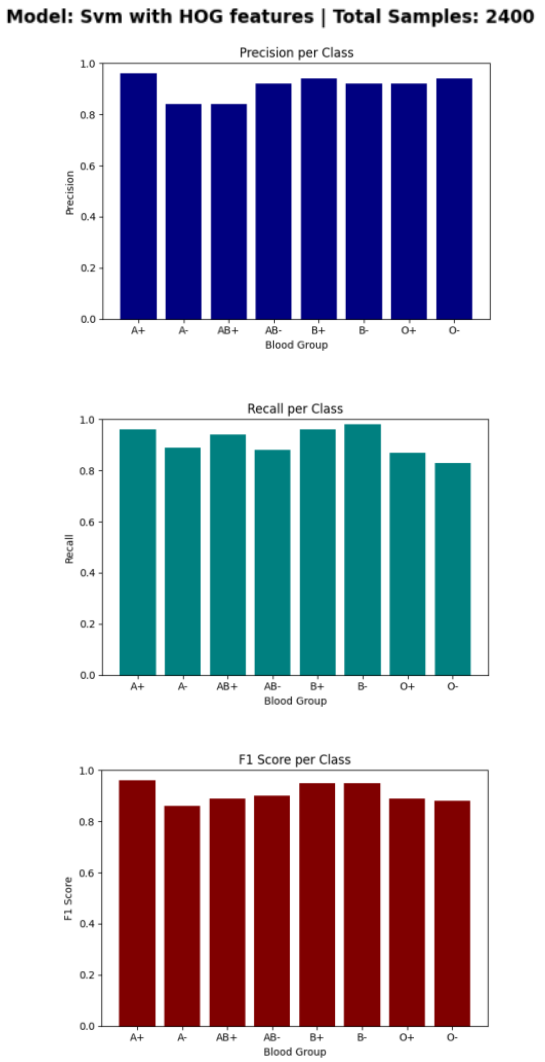


Figure 19: Performance Metrics for Blood Group classification of Svm and HOG

Figure 19 represents the bar graphs and explains the Precision, Recall, and F1 Score for blood group classification using the SVM model with HOG features on 2400 samples. The model shows strong performance, especially for A+, B+, and B-, while O- and A- exhibit slightly lower recall.

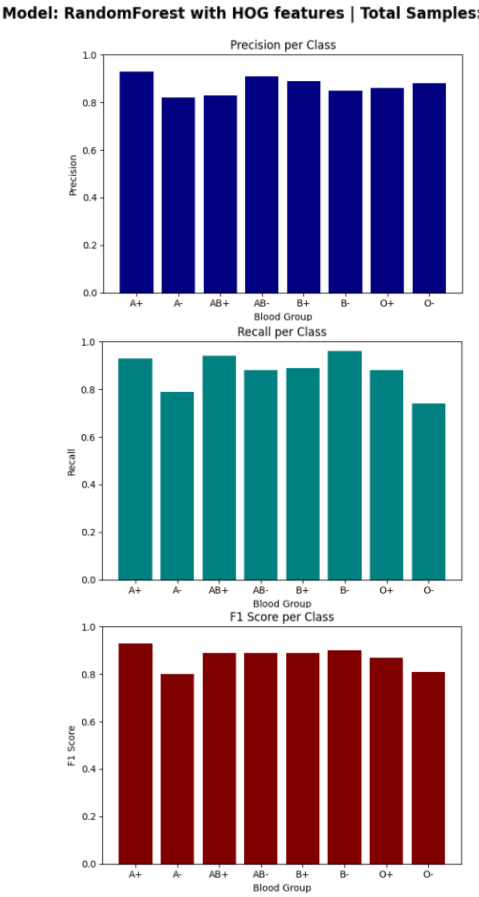


Figure20: Performance Metrics for Blood Group classification of Random Forest and HOG

Figure 20 represents the bar graphs and explains the Precision, Recall, and F1 Score for blood group classification using the Random Forest model with HOG features on 2400 samples. The model shows high precision and recall for A+, AB-, and B-, while A- and O- show slightly lower recall.

The study evaluates fingerprint -based blood group classification using HOG + SVM and HOG random forests in three test sizes (1600, 2000 and 2400). Model performance metrics as accuracy, accurate, recall, F1 score and confusion matrix were analyzed.

- Hog + SVM continuously performs better than hog + random forest, and increases accuracy with increased accuracy size.
- Hog + SVM receives 89.38% to 90.69% accuracy, while HOG + Random Forest receives 86.25% to 87.36% accuracy, indicating that SVM is a stronger classifier for HOG features of fingerprint.
- Hog + SVM specifically shows high precision, recall and F1 score for A + blood groups.

5.2 Prediction of Blood Groups Using New Fingerprint Images -

The following are the prediction of the blood groups using new data

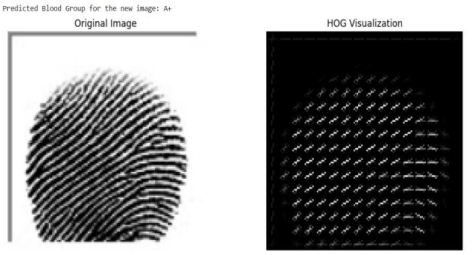


Figure 21: Prediction of A+ Blood Group

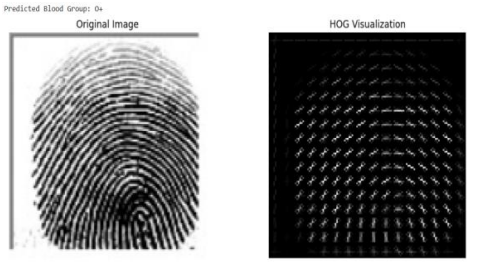


Figure 22: Prediction of O+ Blood Group

Figure 21 explains the prediction of A+ blood group person fingerprint having High ridge density, frequent arch patterns, sharp ridge endings, and bifurcations.

Figure 22 explains the prediction of O+ blood group person fingerprint having Dominance of whorl patterns, thicker ridge structure with lower ridge density and frequent presence of double loops.

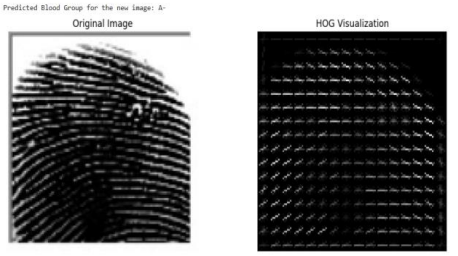


Figure 23: Prediction of A- Blood Group

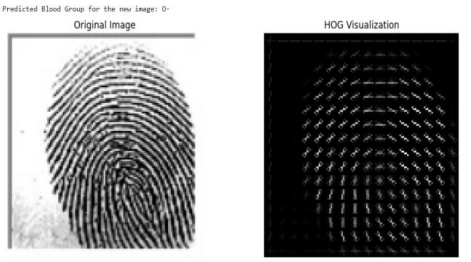


Figure 24: Prediction of O- Blood Group

Figure 23 explains the prediction of A- blood group person fingerprint having High ridge density, frequent arch patterns, sharp ridge endings, and bifurcations.

Figure 24 explains the prediction of O- blood group person fingerprint having Dominance of whorl patterns, thicker ridge structure with lower ridge density and frequent presence of double loops.

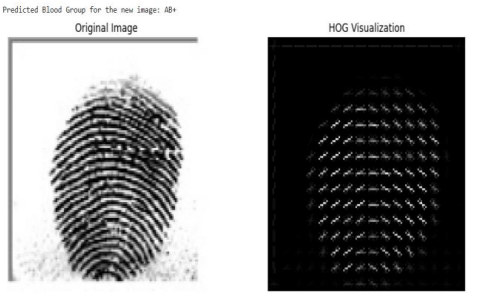


Figure 25: Prediction of AB+ Blood Group

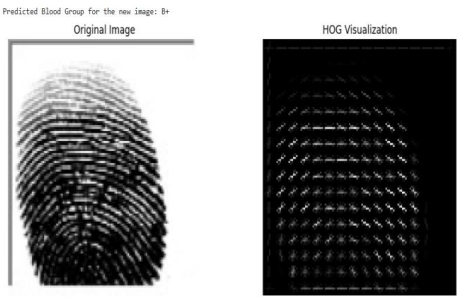


Figure 26: Prediction of B+ Blood Group

Figure 25 explains the prediction of AB+ blood group person fingerprint having a mix of loops and whorls, complex ridge structures with multiple bifurcations.

Figure 26 explains the prediction of B+ blood group person fingerprint having more loop patterns (radial), Moderate ridge density and slightly wider ridges compared to A-group.

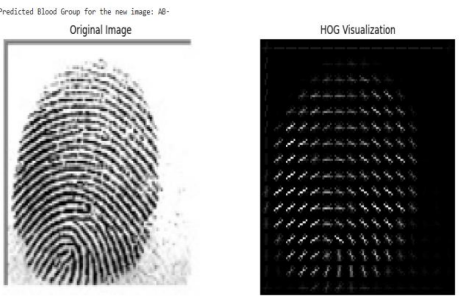


Figure 27: Prediction of AB- Blood Group

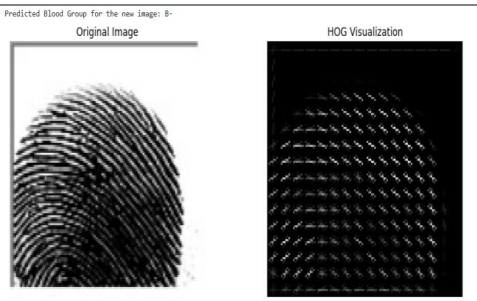


Figure 28: Prediction of B- Blood Group

Figure 27 explains the prediction of AB- blood group person fingerprint having a mix of loops and whorls, complex ridge structures with multiple bifurcations.
Figure 28 explains the prediction of B- blood group person fingerprint having more loop patterns, Moderate ridge density and slightly wider ridges compared to A-group.

6. DISCUSSION AND FINDINGS

The proposed fingerprint-based blood group detection system shows a viable, fast and non-invasive alternative for traditional blood sample methods. This study highlights its ability to revolutionize therapy diagnosis, especially in emergency and resource limit settings. In this study, adapted this technology to blood group detection and developed a simple fingerprint-based system that permits an immediate, non-invasive determination of blood group within about a minute. The HOG-SVM model exhibited a good performance in classification accuracy and may serve as a reliable screening tool, in particular as a screening method in emergency or non-rich conditions. However, there were limitations that must be taken into account. First, the image quality of fingerprint has a great impact on the extraction and classification result. It is also possible for variations in skin conditions (example dryness, moisture, dirt, scars, or worn ridge patterns) to add noise and accuracy especially in non-controlled field environments. Second, the dataset underpinning the analysis may have demographic biases of its own (e.g., due to over/under-representation of different age groups, ethnicities or regions). This could hinder the general uptake of the model to new populations. Overcoming these challenges will be crucial to the real-world adoption and clinical adoption.

7. CONCLUSION AND FUTURE WORK

This study examines a non-invasive approach to identify blood groups using fingerprint analysis and machine learning. This study uses a HOG feature extraction with SVM and Random Forest classifiers. This study demonstrates that HOG-SVM continuously performs better than HOG-RF, and gets high accuracy, accuracy, recall and F1 score in three test sizes. This study also addresses a correlation between fingerprint patterns like loops, whorls, archs and blood groups, which strengthen the feasibility of this method. The proposed method for the fingerprint-based blood group classification provides a fast, cost -effective and available alternative for traditional serological tests, making it valuable for emergency medical services, blood donation centers and distance health services.

The future work is to increase fingerprint-based blood group classification by integrating automated facilities like implementing a real-time embedded system using IoT-based fingerprint sensors will be developed for live blood group detection. This approach will contribute to biometric authentication, forensic science and health diagnostics, making the classification of the blood group more efficient, accurate and widely accessible. With further progress, this technique can revolutionize medical diagnosis, plays an important role in forensic sciences and global health services.

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