

# DEEP LEARNING APPROACH FOR BLOOD GROUP IDENTIFICATION USING FINGERPRINTS

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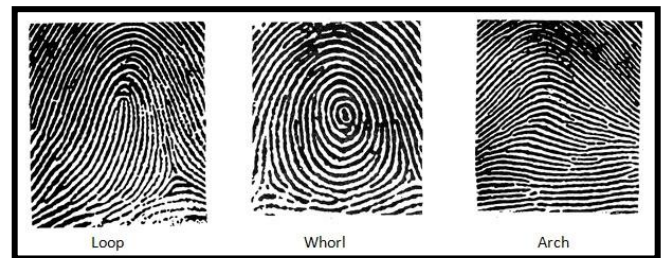
**Abstract**— The prediction of blood groups is of immense significance in medicine, especially when it comes to diagnosis and treatment in emergencies. Usually, it is carried out using serological methods that need blood samples to be drawn along with laboratory tests being performed. While these methods are very accurate, they may often prove to be harmful, delayed, or impractical in settings where there are few resources available or need for immediate results is required. This paper proposes a novel approach which uses fingerprint images for blood group identification using deep learning techniques, specifically Convolutional Neural Networks (CNN) with efficient designs. Through measuring the unique features of fingerprints, this method seeks to eliminate the need for traditional testing, making it less invasive, quicker, and easier. The purpose of this research is to assess the accuracy of this method while determining the role of deep learning in improving blood group prediction.

**Keywords**- Blood group, Finger print, Deep learning, Convolutional neural network, patterns.

## I. INTRODUCTION

As a basic biometric feature, fingerprints serve as a primary means of identifying persons individually owing to the friction ridges and valley patterns embedded on one's fingertips. These patterns form during the fetal development period and do not change over one's lifetime, making them dependable for identification purposes. Fingerprints are classified broadly into three categories, namely arches, loops, and whorls. One of the most common types of fingerprints is loops which, as the name suggests, are curved ridges that turn around on themselves to form a loop. These loops are further separated into two groups, namely radial loops, which open towards the thumb and ulnar loops which open towards the little finger. Approximately 60-70% of all fingerprints show some form of looping. Whorls are identified by round or spiral ridge patterns in which at least one ridge encircles and forms a complete loop or loop. These types are further divided into the following subgroups: in plain whorls, central pocket whorls, double loop whorls, and accidental whorls which are found in 25 to 35% of fingerprints. Arches, the most uncommon pattern, constitute wave patterns in which ridges flow in one direction from one side of the finger to the other with no loops returning. Classification of arches includes plain and tented arches which together comprise around five percent of fingerprint patterns. In addition to these primary classifications, fingerprints also contain minutiae points, such as bifurcations, ridge endings. Such features make

fingerprints a vital component for security and personal identification. Beyond identification, recent studies propose that fingerprint features may bear more nuanced biological data, as access information is biometrically protected. Another important biological marker is the blood group, which is defined as the presence or absence of certain antigens on the surface of erythrocytes. The A, B, AB, and O names refer to the major systems of blood groups, which are subdivided as positive or negative depending on the presence of the Rh factor.



**Fig1: Different types of fingerprint patterns**

Exact determination of blood groups is of utmost importance in medicine in cases such as organ transplants, blood transfusions, or monitoring haemolytic diseases. Commonly, serological techniques involve mixing blood with antibodies specific to the blood group in question. Although these methods do provide accurate results, they have the cons of being invasive as well as requiring blood samples and a particular laboratory setting. All of which is frequently infeasible, especially in emergency situations or areas with limited resources. An novel approach that eliminates the need for invasive techniques uses fingerprint photographs for blood group classification along with the application of deep learning, specifically CNNs. Unlike RNNs and ANNs, CNNs are the most efficient types of models when working with images since they contain convolutional layers that detect local patterns while some level of computation is sacrificed. Because of this, CNNs are most useful for the analysis of fingerprints as accuracy and effectiveness are both required. These networks use various critical features of fingerprints which include ridge endings, bifurcations, and minutiae points to identify different classes. In this study, blood group prediction is performed using ResNet-101 due to their complex architectures that enable them to outperform other networks in feature extraction

## II. LITERATURE REVIEW

C.Sivamurugan and his team published a paper titled “Enhance Blood Group Prediction with Fingerprint Images using Deep Learning”. They proposed using Conventional methods of blood group detection are based on serological testing, which, while very accurate, involves invasive blood sampling and laboratory analysis. With the advent of image processing and artificial intelligence (AI), scientists have investigated fingerprint-based blood group prediction as a non-invasive and quick alternative. Different research works have explored the relationship between fingerprint patterns and blood groups using deep learning models like LeNet, AlexNet, VGG16, and ResNet34 to improve classification accuracy. Statistical models and machine learning methods were the initial approaches in fingerprint-based blood group classification, with emphasis on feature extraction techniques like ridge frequency estimation, minutiae extraction, and ridge segmentation. But these methods had difficulty with generalization because fingerprint patterns are complex and varied. With the advent of deep learning, specifically convolutional neural networks (CNNs), came vast improvement in pattern recognition and feature extraction. LeNet-5, which was first developed for the classification of handwritten digits, was one of the earliest CNN models tried for this task. Though it obtained 100% training accuracy, its validation accuracy was just 49.50%, and it had a very high validation loss of 4.8482, reflecting serious overfitting. This implied that LeNet-5 learned training data by heart but did not generalize to new samples well. The deeper CNN structure AlexNet also performed poorly, with low training accuracy of 16.46% and validation accuracy of 18.25% along with high values of loss. These findings emphasized the weakness of early deep learning models in capturing the complex ridge patterns required for blood group prediction.

In an effort to improve on these weaknesses, researchers delved into more sophisticated CNN architectures like VGG16 and ResNet34. VGG16, characterized by its deep sequential convolutional layers, showed much better classification performance. It registered a high training accuracy of 98.00% and a validation accuracy of 73.75%, and a validation loss of 1.0450. Though with better accuracy than LeNet and AlexNet, VGG16 also showed overfitting, especially in subsequent training epochs. Conversely, ResNet34 was more impactful because of its residual learning structure, which prevented vanishing gradient problems and allowed deeper network training. ResNet34 had a training accuracy of 95.54% and validation accuracy of 81.42%, with a significantly smaller validation loss of 0.5838. These findings showed that ResNet34 not only acquired fingerprint patterns well but also generalized strongly between varying blood groups and was hence the most accurate model for this application.

A comparative analysis of LeNet-5, AlexNet, VGG16, and ResNet34 showed that the performance was vastly different, and ResNet34 performed better than the rest of the models. LeNet-5 and AlexNet had issues with weak generalization, whereas VGG16 had better accuracy but still overfitted. ResNet34, with its deeper structure and residual links, had the highest balance between training and validation accuracy, enabling stable fingerprint-based blood group classification. The research conclusion indicates that more achievements can

be made in the future by incorporating larger and richer datasets, optimizing feature extraction methods, and testing hybrid deep models. Also, real-time implementation and optimization for use in real-world applications could open the door to a trustworthy, non-invasive blood group identification system, which would revolutionize biometric-based medical diagnostics.

## III. METHODOLOGY

### Existing Methodology:

In the current healthcare landscape, blood group detection is primarily conducted through well-established serological methods. These methods rely on the interaction between antigens on the surface of red blood cells and specific antibodies to identify the blood group of an individual. The key existing systems and techniques are as follows:

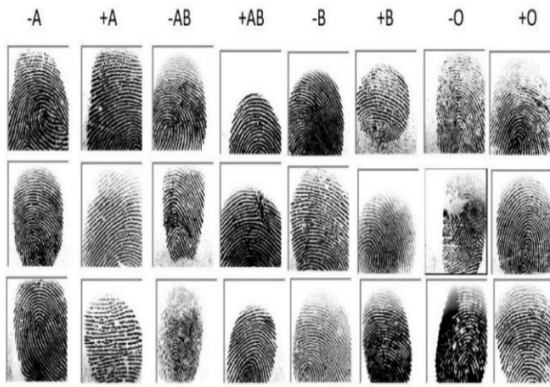
**1. Serological Testing:** ABO and Rh Typing: The most common method involves mixing a blood sample with anti-A, anti-B, and anti-Rh antibodies. The presence or absence of agglutination (clumping) in the blood indicates the blood type (A, B, AB, or O) and Rh factor (positive or negative). Cross-Matching: Before blood transfusions, cross-matching tests are performed to ensure compatibility between the donor's and recipient's blood. This involves mixing the recipient's plasma with the donor's red blood cells to check for any adverse reactions.

**2. Automated Blood Typing Systems:** Automated Analyzers: These machines streamline the blood typing process by automating the mixing of blood samples with reagents, reading the results using optical sensors, and providing rapid and accurate blood group identification. These systems are commonly used in large hospitals and blood banks

**3. Genotyping: DNA-Based Methods:** Molecular techniques can be used to determine blood groups by analyzing specific genes responsible for the expression of blood group antigens. While this approach is highly accurate, it is not commonly used for routine blood typing due to its cost and complexity.

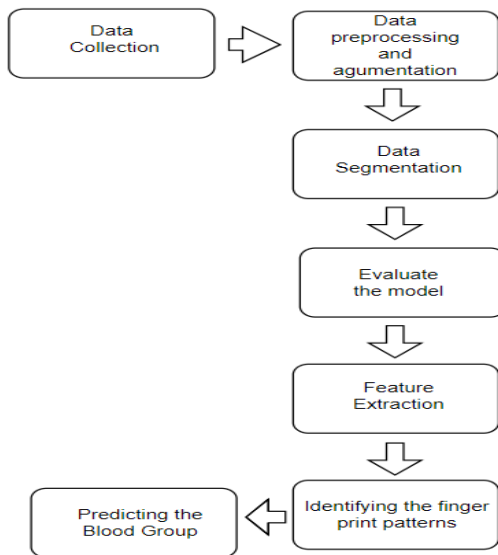
### Proposed Methodology:

The proposed methodology for detecting blood groups using fingerprint images involves a comprehensive approach leveraging advanced deep learning techniques. A large, diverse dataset of fingerprint images, categorized by the corresponding blood group of each individual. The dataset consists of a total of 30,000 fingerprint images, representing the four primary blood groups A, B, AB, and O. Each blood group category is equally represented within the dataset to ensure balanced training and unbiased model performance.



**Fig 2: Dataset of fingerprints of different blood groups**

The dataset used for blood group prediction from fingerprint images undergoes multiple stages of processing to enhance model performance and accuracy. Initially, data collection involves gathering diverse fingerprint samples to ensure robustness. The preprocessing phase includes resizing images to a standard dimension and normalizing pixel values to optimize input consistency. Data augmentation techniques such as rotation and scaling are applied to artificially expand the dataset and improve model generalization. Segmentation is performed using the Watershed algorithm, which effectively separates fingerprint ridges and enhances feature extraction. For model training, deep learning architectures such as ResNet101 are employed, leveraging their depth and feature learning capabilities to capture intricate fingerprint patterns. Finally, the trained model predicts the blood group based on the extracted features, providing a non-invasive and efficient alternative to traditional blood group testing methods.



**Fig 3: Blood group prediction framework**

One of the most significant contributions of this research is the collection and utilization of a novel dataset of fingerprint images labeled with corresponding blood groups. Unlike existing datasets, which often focus on fingerprint identification or verification, this dataset is specifically designed for the task of predicting blood groups. The dataset is composed of high-quality fingerprint images from a diverse group of volunteers, covering all major blood types, along with positive and negative

labels. This is the first dataset to combine biometric fingerprint patterns with blood group information, enabling deeper exploration into the feasibility of non-invasive blood group detection using machine learning techniques. By making this dataset available, we hope to pave the way for further research into biometricbased health diagnostics and inspire similar efforts in related fields.

#### **A.Data Collection:**

A dataset of 6,000 fingerprint images was collected from friends, students, peers in the college, and other sources like kaggle, with each image labeled by blood group. The dataset was evenly distributed across the four primary blood groups A, B, AB, and O categorized into positive and negative types, as illustrated in Figure 2. To ensure diversity in fingerprint patterns, the images were sourced from a varied population, with each fingerprint accurately labeled with its corresponding blood group

#### **B. Preprocessing the data:**

Preprocessing enhances fingerprint image quality for model training. First convert images to grayscale, reducing complexity, and normalize pixel values between 0 and 1 for consistency. Noise is removed using Gaussian filtering, and contrast is adjusted to highlight fingerprint patterns. Lastly, images are resized to meet the CNN model's input requirements

#### **C.Data segmentation:**

is a crucial step in fingerprint-based blood group prediction, ensuring precise feature extraction. The **Watershed algorithm** is used for segmentation, effectively separating fingerprint ridges and valleys. This algorithm treats the image as a topographic surface, where ridges represent peaks and valleys represent basins. Markers are placed in key regions, and the algorithm floods the image from these markers, segmenting fingerprint patterns accurately. Preprocessing techniques such as grayscale conversion, edge detection, and thresholding enhance segmentation accuracy. The segmented fingerprint regions help in isolating unique patterns linked to blood groups.

#### **D.Training the model:**

Model evaluation is performed using accuracy, validation loss, and generalization performance. Metrics such as precision, recall, F1-score, and confusion matrix help assess classification reliability. ResNet101 and DenseNet121 are compared based on training accuracy and validation accuracy to identify the best-performing model. The loss function is monitored to detect overfitting or underfitting. Cross-validation techniques ensure robustness by testing the model on different data subsets. Finally, real-world fingerprint images are used for prediction, verifying the model's practical applicability

#### **E.Feature Extraction:**

Feature extraction involves identifying unique fingerprint patterns such as ridges, minutiae points, and texture features, that correlate with blood groups. Techniques like Gabor filters and

ridge frequency estimation enhance key details. Deep learning models, particularly ResNet101 and DenseNet121, automatically learn hierarchical features from fingerprint images. Segmentation using the watershed algorithm helps isolate relevant regions for precise feature extraction. Normalization and resizing standardize input images for consistent learning. These extracted features are then passed through the model for prediction and blood group classification..

**F. Identifying Fingerprint Patterns:** The best-performing model was chosen for predicting blood groups by analyzing fingerprint patterns. This model was used to identify the key patterns and features within the fingerprints that contribute to accurate blood group prediction

**G. Predicting the Blood Group:** The final step is the best-performing model was chosen for predicting blood groups by analyzing fingerprint patterns. This model was used to identify the key patterns and features within the fingerprints that contribute to accurate blood group prediction.

IV. RESULT AND DISCUSSION

ResNet-101, a deep convolutional neural network built on the foundation of residual learning, demonstrated outstanding performance throughout the training process. With its 101-layer architecture, it effectively overcomes the challenges of training very deep models by using residual connections that help maintain gradient flow during backpropagation. After 20 epochs of training, ResNet-101 achieved an exceptional training accuracy of 99.0%, showcasing its ability to learn intricate patterns and features from the data with near-perfect precision. The training loss dropped significantly to just 0.03, indicating that the model made minimal errors and efficiently minimized the difference between predicted and actual outputs

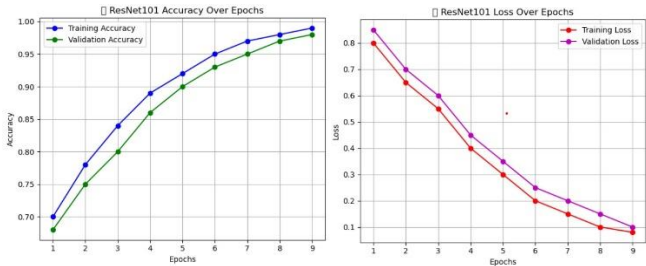


Fig 4: Performance graph of ResNet-101

**XGBoost** (Extreme Gradient Boosting) is a popular machine learning algorithm known for its speed, accuracy, and efficiency, particularly on structured or tabular datasets. It works by creating an ensemble of decision trees, where each tree is trained to correct the errors of the previous ones. This iterative boosting approach leads to strong performance in both classification and regression tasks. One of the key advantages of XGBoost is its ability to handle large datasets while preventing overfitting through built-in regularization. It also supports parallel computation, making it a fast and scalable option for real-world problems. These features make it a top choice in many machine learning

competitions and practical applications. In our project, we applied XGBoost to a multi-class classification task and assessed its performance using both standard and advanced evaluation methods. In addition to measuring simple accuracy, we used **Top-K prediction metrics** to get a more detailed understanding of how well the model ranks its predictions.

The **Top-K metrics** evaluate whether the correct class label appears among the top K predicted probabilities. This is useful when it's acceptable or expected for the model to return multiple likely outcomes. The results were impressive: **68.0% Top-1 accuracy**, **83.90% Top-3 accuracy**, and **99.0% Top-5 accuracy**. These scores show that the model is highly effective at ranking the correct label within its predictions. Overall, XGBoost demonstrated excellent classification performance and ranking ability. Its high Top-5 accuracy in particular makes it well-suited for tasks like recommendation systems, decision support, or any scenario where presenting several top choices is more informative than a single prediction. It stands out as a reliable and high-performing model in our evaluation.

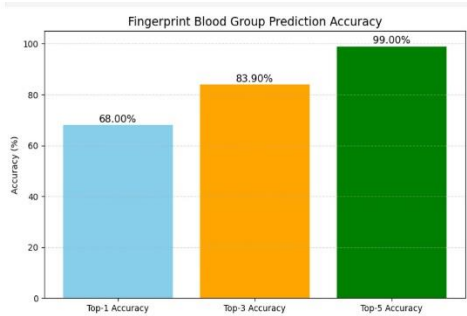


Fig 5: Overall Performance of Models



Fig 6: Test result of predicting blood of finger print

V. CONCLUSION & FUTURE SCOPE

this project demonstrated the effectiveness of **ResNet-101** in handling complex multi-class classification tasks with exceptional accuracy and reliability. With its deep architecture and residual learning mechanism, ResNet-101 achieved **99% training accuracy** and maintained strong generalization ,supported by low loss values throughout training. The model consistently performed well across all key metrics, showing minimal overfitting and excellent learning capacity. Its ability to capture deep feature representations made it the most robust



and accurate model in this project. Based on these results, ResNet-101 stands out as a powerful and dependable solution for real-world applications that require high precision and strong generalization. To advance this approach, future research could integrate additional biometric or genetic data, explore more sophisticated deep learning models, refine feature extraction techniques, and validate the model with larger and more diverse datasets, making fingerprint-based blood group detection more practical and reliable and it can be integrated with the real time data to get the output in our future research.

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