International Journal of
INTELLIGENT SYSTEMS AND APPLICATIONS IN ENGINEERING
ISSN:2147-6799 www.ijisae.org Original Research Paper

A Novel Approach for ABO Blood Group Prediction using Fingerprint through Optimized Convolutional Neural Network

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Submitted: 10/11/2021 Accepted : 30/01/2022

Abstract: The fingerprints of humans hold many potentials and having plenty of unique characteristics. It is one of the primary diagnostic tools used from accent's era because of their distinctive identity. It opens a lot of possibilities for human science research, by analyzing fingerprints, some researchers have tried to predict an individual's gender or age. In the 20th century, fingerprint identification and analysis have become commonplace also it has evolved into a crucial component of forensic at crime scenes. Similarly, like a fingerprint, the blood group is also unique for each individual. This study focuses on ABO and Rh systems, which are among the most prominent blood grouping methods. This paper proposed an optimized Convolutional Neural Network (CNN) which is designed as an extension of an AlexNet, that correlates the fingerprint patterns or different features of the fingerprint with the blood group of an individual. Researchers have only attempted to connect fingerprint patterns with blood types prior to this proposed method. The result and performance of proposed CNN framework is compared with three different CNN variations like LeNet-5, ZFNet, and AlexNet. The design of proposed CNN used for the prediction of the blood group having noticeable performance with 95.27 % accuracy rate.

Keywords: *Fingerprint classification, CNN, Deep learning, Neural Network, ABO blood group*

1. Introduction

In 1926, Dr. Harold Cummins introduced a study of fingerprint patterns, but it is even now it is used earlier than several hundred years ago. For almost a century, fingerprints have been utilized as a form of personal identification. Because of its uniqueness and persistence, it is currently widely used in biometric authentication. Although fingerprints may be classified into four fundamental categories: arch, tented arch, loop which is categorized as left loop and right loop and whorl, shown in Fig. 1. Furthermore, fingerprint made of ridges and valleys like minutia patterns. Ridge ends and ridge bifurcations are the two main minutia characteristics considered in fingerprint recognition. Other characteristics are used as well. Automatic fingerprint identification systems are divided into three categories based on the characteristics involved in fingerprint recognition: minutiae-based, image-based, and ridge feature-based approaches [1]. The Galton's details consist of more than 100 interleaved ridge and valley patterns on a single rolled fingerprint. For various identification purposes, fingerprints can be used due to their unchangeability during a person's lifetime and their uniqueness [2]. These days, Automatic Fingerprint Identification System (AFIS) and Automatic Fingerprint Recognition System (AFRS) as expressed by [2] are exceptionally mainstream because of their lower variability and simpler openness than different techniques, for example, mark and hand math. The Henry Fauld in 1880 was the first to experimentally prove that fingerprints are singular and unique. In the sixteenth century, methods for matching fingerprints were discovered. The work of Herschel [3] played an important role in the development of current fingerprinting identification. Sir Francis Galton [4] directed wide-ranging studies and ordered the essential shapes of fingerprints, as shown in fig. 1, such as loops, whorls, and arches.

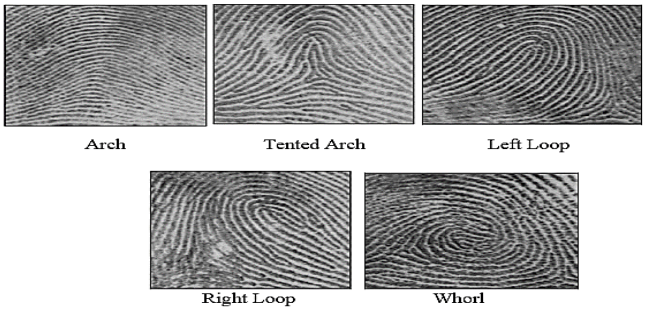

Fig 1. Basic Fingerprint Patterns

There is a broad scale of these characteristics in distinct local ridges. In many cases, these fingerprint patterns depend largely on the impression quality or processes of sample collection and condition of the fingerprint, and they are rarely observed. Fig. 2 demonstrates two of the most prominent features of local ridges: 1) ridge endings and 2) ridge bifurcations. As the name implies, a ridge ending is a hasty end of a ridge. Ridge bifurcations are points at which ridges diverge or fork into new branches. Known collectively as minutiae [5], these features make up the minutiae.
A person's blood group is another feature of their body that remains unchanged all their lives. Karl Landsteiner was the first to discover blood group structures back in 1900. There are currently 19 major blood groups. These groups are characterized by variations in the distribution of various races of humans. Among the blood groups that are relevant clinically are the ABO and Rhesus. By the presence of corresponding antigens in plasma, the "ABO" system can be further divided into A, B, AB, and O [6]. A study of dermatoglyphics and its importance in detecting diseases with genetic bases, such as high blood pressure, arthritis, and type-2

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diabetes

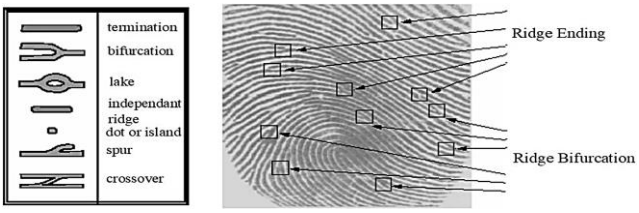

Fig 2. Different Minutiae Patterns

The distribution of finger-print patterns and blood groups were also found to be associated. Gowda and [6] reported a high frequency of loops with moderate whorls and low arches among individuals of the A, B, and O blood groups. According to [7], blood group "O" tends to have more loops and less whorls than blood group "A". In their study, they found more whorls and loops in Rh positive individuals rather than Rh negative. [8] found high frequency loops were found in blood group A. The Machine learning and Deep learning is becoming increasingly widely held in all sectors with the objective of enhancing revenue and shrinking costs; organizations may automate and improve their operations to do tough tasks fast by using machine learning techniques. It is proposed that research be conducted to develop a system that can detect the association between blood type and fingerprint patterns, which may be used to predict an individual's blood type. In addition to loops, whorls, arches, and composites, fingerprints typically have more than 100 intertwined ridges and valleys, which allows to design Deep Neural Networks and Convolutional Neural Networks (CNNs) to predict blood group based on unique characteristics of individuals. In real time, all 10 fingerprints will be collected of 392 subjects which include 268 male, 124 female having aged between 18-58 years at Bharati Vidyapeeth College of Engineering, Navi Mumbai, Maharashtra, India. by using DX HFDU06 - Fingerprint Scanner with 500 DPI.

The key objective of this paper is to design optimized CNN prediction model to predict the blood groups based on the fingerprints. Initially, the dimension of the input database is mitigated using statistical analysis through chi-square measure. Then, the dataset is divided into a two separate data chunks called as training set and testing set which are used to test prediction model. Then, designed available different classifier such as LeNet-5, ZFNet, and AlexNet and test the prediction accuracy using Confusion matrix, precision, recall, and F1 score are performance measures. After initial design and test of available classification models, proposed CNN prediction model for prediction of the blood group was designed. The design of such Multilayer Deep There are eleven 11x11, five 5x5, three 3x3 convolutional networks, max pooling, dropouts, data augmentation, and ReLU activations along with SGDs that support momentum. which is proposed.

The primary contributions in this paper are:

- An analysis of fingerprint patterns and blood group distribution is performed using statistical methods, such as chi-square.
- The LeNet-5, ZFNet, and AlexNet CNN models are designed to classify the blood group using fingerprint as input dataset based on the multiclass neural network.
- Design proposed optimized CNN model to predict blood group of an individual, Filter visualization during convolution layer and compare the performance of it with previous models.

In this paper, proposed an optimized CNN model for prediction of blood group based on fingerprint images. There are four sections to this study. The literature review is presented in Section 2. The material and methodology section 3 illustrate dataset description, statistical analysis, and design of proposed CNN model. Section 4 describe the result discussion and observation. Further it included conclusion and references.

2. Literature Review

According to Azhagiri R, et al. [7], 150 participants were selected from different locations at random, with 75 males and 75 females included in the study. According to the findings, the left thumb print had a total of 60 loops (40%) in both genders, followed by whorls (40%) and mixed patterns (17%). There were 16 arches detected in a low number of instances in the left thumb print. Most of the subjects in their study belonged to the blood group "O", followed by the blood groups "B", "A", and "AB". The blood groups O and AB were rarer, while they were more common with O blood groups. Loops are more common in blood groups O and B than blood groups A and AB.

According to Rastogi P, et al [8], the distribution of blood groups, genders, and fingerprints are associated. Majority of the study subjects belonged to blood group O, followed by blood groups B, A and AB. The study found that 96 percent of participants were Rh positive, while only 4 percent were Rh negative. In individuals with blood group A, B, AB, and O, the fingerprint distribution pattern was the same, with a high frequency of loops, a moderate number of whorls, and a low number of arches. According to the study conducted by Bharadwaj et al. [6], the findings were similar in blood group O positive and negative except in whorls from blood group O negative.

A study conducted by Bhradwaja et al [9] in 2000-2001 evaluated 300 medical students with ABO blood groups varying in Rajasthan. According to the researchers, people with blood group A accumulate more loops, whereas those with blood group AB accumulate more whorls. According to our findings, blood groups A and AB have higher levels of loops, whereas blood groups A and B have higher levels of whorls. Moreover, the study highlights those whorls are more common among blood group O and arches are common among blood group A.

A method proposed by Ferris [10], which uses image processing to determine an individual's blood type. It can be used in emergency situations when the blood type can be ascertained in a rapid amount of time (2 minutes). A new approach to commercial solutions, providing added value. A plate test is used to determine the blood type. This test involves blood samples from donors and serum samples for blood type determination. A CCD camera captures blood/serum mixtures that are analyzed using IMAQ Vision software from National Instruments.

As explained by Berlitz et al. [11], gold surfaces are coated with protein A to immobilize antibodies to blood group antigens A and B, enabling the detection of all four large blood groups including A, B, AB, and O with just two measurements. Several experiments were conducted on human erythrocytes and the presence of Rh-D, Rh-C, Rh-C, Rh-E and Rh-E antigens on these cells proved to be successful. Blood of type Kk and kk could be distinguished reliably with the Kell blood grouping system.

The blood group identification method requires actual blood sample, which tested on pathological lab by specialist against the agglutination and check how individuals blood react to it and then blood type identified. Consequently, there is a higher likelihood of human errors in this framework. Agglutination can only be used to determine blood type by specialists. Blood groups are typically distinguished by the plate and the tube tests [12]. It is a

standardized analog procedure with human observation for both. Due to the current technology, it would be in present digital world, it is inefficient to conduct such a basic yet vital medical treatment in a purely analogue setting. Several techniques are also offered, such as microplate tests and gel centrifugation [13-14].

Table 1 summarizes the many approaches used to identify blood groups, both conventional and unconventional methods using diodes and sensors as well as other electrical components. The fingerprint pattern analysis has only been studied by a few researchers to predict blood type with low accuracy because they collect samples using traditional paper and ink, which does not have high accuracy. There are various image (fingerprint) computing approaches available in today's digitization era that investigate a larger number of features from a fingerprint image, thus it is increasing the accuracy of the prediction process.

Table 1. Blood group prediction is done in a variety of ways [14]

Sr. No	Name	Samples	Method
1	Conventional Estimate	Blood samples	Through the use of antibodies and chemical reactions
2	Spectrophotometric	Image of a blood test plate	Processing of images
3	Mapping of Nucleotide Variants	DNA was taken from the outside world.	DNA microarray mapping of single nucleotide variants (SNVs)
4	IMAQ Concept	Photographs of slide tests	Techniques of image processing
5	Techniques of Machine Vision	Image or video of blood samples	Image processing through MATLAB
6	QCM Biosensors	Blood samples taken from real people	Quartz crystal microbalance sensors
7	ABI PRISMR 3100 genetic analyzer	DNA samples	SNPs analyses
8	The use of a light-emitting diode	As an example, use your finger.	Gene series, protein presence, and antigen structure all have a role.
9	Changeable-color paper	Blood samples taken from real people	Antibodies against antigens and proteins
10	Analysis of fingerprints	Fingerprints on paper with ink	Observation of fingerprint patterns

As per the literature, there are many alternatives to determine blood in a group, with some offering advantages and others offering disadvantages. Most traditional methods involve taking a Within 3 to 5 minutes, a blood sample is taken and analyzed against various antibodies to establish a person's blood type, although this might be challenging for small children and those who are afraid of blood. It is possible to fingerprint may be used to rapidly and reliably identify blood types which explores many unique patterns that may enhance the fingerprint's potential.

2.1. Motivation

The fingerprint pattern and blood group of an individual are remained same during its lifetime. The fingerprint is also used as primary means to identify individual uniquely. It is also one of the key diagnostic tools used from accent's era because of their distinctive identity. There are number of researchers tried to identify blood using fingerprint analysis, but few of them only correlate the different basic patterns of fingerprint to blood group. The data collection method used by most of researchers are traditional like pen and paper, it plays important role in accuracy and performance. Other tried image processing and electronic method, but it more time consuming than traditional method and having issues with accuracy as well.

3. Material and Methodology

In this section, the proposed methodology presented for classification of blood group using a fingerprint image from different class. The first step in this study is to describe the datasets used. In the next section, explain the process of feature extraction, which incorporates transfer learning theory. Finally, describe the classification techniques applied and the steps of their training.

3.1. Dataset Description

In real time, all 10 fingerprints will be collected of 392 subjects which include 268 male, 124 female having aged between 18-58 years at Bharati Vidyapeeth College of Engineering, Navi Mumbai, Maharashtra, India. by using DX HFDU06 - Fingerprint Scanner with 500 DPI. Depending on what the sensor resolution and finger placement are, a good fingerprint has 25 to 80 minutiae. In false minutiae, the finger is improperly placed on the scanner sensor, causing the ridges to break. It is difficult to extract details from fingerprints obtained from very dry fingers or fingers with thick scars or scratches. The fingerprint is defined in this step by the retrieved minutiae features for subsequent matching by creating feature vector having 3920 images. In this study, there were 1.21 males for every female. Majority of the subjects (33.68%) the blood group A was the extremely general in this study, followed by blood groups B and O, B (27.56%), O (25.52%) and AB (13.27%). Rh-positive cases constitute 87.2 percent of cases. There was a significant impact across finger patterns with whorl registering the highest frequency at 52.78%; followed by loop (38.82%) but with both right (13.29%) and left (25.53) loops, as well as arches (8.49%).

3.2. Statistical analysis

The ratio of males to females is more than 1.2:1 in this study, with the number of males being more than twice that of females. The Distribution of Samples according to sex and blood groups shown in Table 2. The most cases (33.77%) had blood group A. The next most common blood groups were blood groups O, B, and AB (28.17 %, 24.72 %, and 13.38 %). It was determined that the relationship between sex and blood group is statistically significant as $p < 0.05$ by Chi Square tests.

The distribution of samples according to ABO and Rh blood groups shown in Table 3, based on the results of the study, 91% of the cases were Rh + ve, 33.67 had blood group A. A blood group O, a blood group B, and a blood group AB account for 27.55 percent, 25.51%, and 13.26% respectively. The majority of Rh-positive cases (4.08%) belonged to blood group A. The distribution of cases according to ABO and Rh blood types is statistically highly significant as $p < 0.001$ when considering chi square. During the initial investigation, a similar statistical approach is used to perform statistical analysis of the feature vector dataset. The study performs the link between blood group and fingerprint-based identification on patterns only like a whorl, loop, etc.

Table 2: Distribution of Samples according to sex and blood groups (n = 392).

	A	B	AB	O	Total
Male % within sex	33.58	26.87	13.06	26.49	100
Female % within sex	33.877	22.58	13.71	29.84	100
Total count % within sex	33.77	24.72	13.38	28.17	100
Statistics	**$Chi^2 = 6.78$**			**$P < 0.05$**	

Table 3: Distribution of Samples according to ABO and Rh blood groups (n = 392).

Blood group	Rh + ve	Rh-ve	Total
A	29.59	4.08	33.67
B	24.49	1.02	25.51
AB	11.22	2.04	13.26
O	26.53	1.02	27.55
Statistics	**Chi2 = 11.64**		**P<0.005**

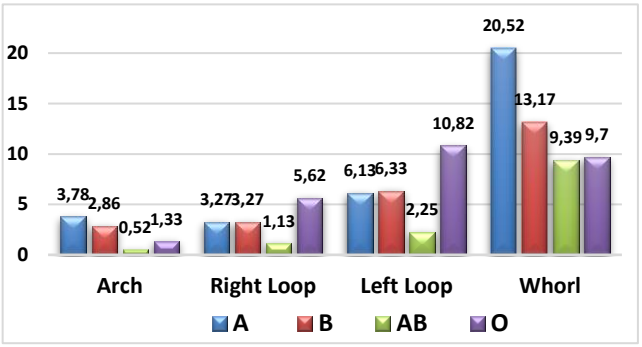

Fig 3: Distribution of fingerprint patterns and blood group

The statistical analysis of blood group vs fingerprint patterns shown in Table 4, indicates that the most common pattern among the samples is whorl which is 52.78% and the least is arch which is only 8.49%. Also, the distribution of A blood group during samples is most common which is around 33.70% and AB is the least, is 13.29% within total collected samples. The distributions of primary fingerprint patterns shown in Fig 3. This difference was statistically significant by using chi square test as $p < 0.05$.

Table 4: Distributions of primary fingerprint patterns in all fingers of both hands (n =3920).

	A	B	AB	O	Total
Arch	3.78%	2.86%	0.52%	1.33%	8.49%
Right loop	3.27%	3.27%	1.13%	5.62%	13.29%
Left loop	6.13%	6.33%	2.25%	10.82%	25.53%
Whorl	20.52%	13.17%	9.39%	9.70%	52.78%
Statistics	**Chi2 = 15.14**			**P < 0.05**	

3.3. Design of CNN architectures

A) AlexNet-CNN

There are eight layers to the AlexNet-CNN, including five convolutional layers and three fully linked layers [15]. However, this does not differentiate AlexNet from other convolutional neural networks; these are some of the novel aspects of AlexNet such as a) ReLU Nonlinearity, b) Multiple GPUs and C) Overlapping Pooling. Instead of using the tanh function, AlexNet-CNN uses Rectified Linear Units (ReLU). Using ReLU, CNNs were trained six times faster than those trained with Tanh, achieving a 25% error rate. A part of AlexNet's neurons is placed on one GPU while the other part is on yet another GPU to allow for multi-GPU training [16]. In addition to training a larger model, this also decreases the amount of training time. In general, traditional networks pool the outputs of adjacent neurons in a non-overlapping way. Dropout is the approach utilized to reduce overfitting in this case. A certain probability of turning off neurons (e.g., 50 percent) is involved in this method. Therefore, each neuron develops more resilient characteristics as it receives a different set of parameters with each cycle, which can be used with the other random neurons.

B) Lenet-5-CNN

Yann LeCun and colleagues first proposed the LeNET-5 model in 1998 [17]. In total, the network has 5 layers, all of which can be learned, hence the name Lenet-5. The convolution layers are made up of three sets, and the average pooling algorithm is used to calculate them. An additional two fully connected layers are then added to the convolutional and average pooling layers [18]. Following that, a Softmax classifier sorts the images according to their classification. Fig 4 illustrates the Lanet-5 CNN design.

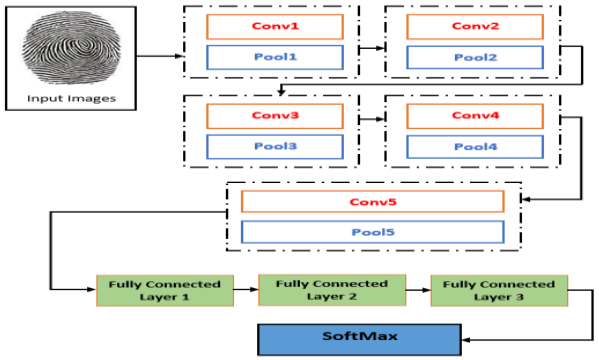

Fig 4. Lenet-5-CNN architecture design

C) ZFNet -CNN

ZFNet, which is a modified version of AlexNet [19] shown in Fig. 5, provides a higher level of accuracy than AlexNet in general. ZF Net used 7x7 filters and AlexNet used 11x11 filters, which differed in major ways between the two approaches. According to researchers, small filter sizes can help us retain much of the pixel information earlier convolution layers lost due to larger filters. Consequently, the layers become more complex as they become deeper. The ReLU are used for activation, just as they were with the previous network. Moreover, the network is trained using a batch stochastic gradient descent algorithm.

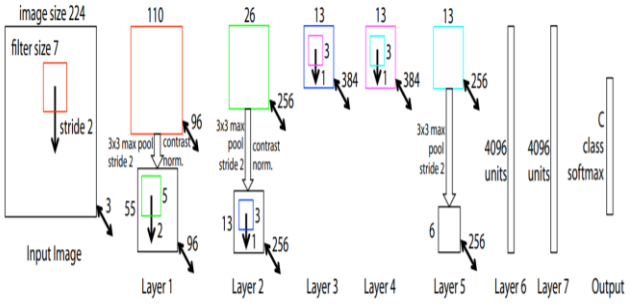

Fig 5. ZFNet -CNN design [19]

3.4. Design of proposed CNN architecture

The CNN model in 1998 and which Known as feedforward neural networks, CNNs are good at processing images and natural language. Popularly CNN is applied very effectively for prediction using 225 X 225 2D images dataset. The CNN model enforce local perception and weight sharing can significantly minimize the number of parameters for enhancing model learning efficiency. The CNN Model Framework Diagram shown in Fig 6 divided in two parts 1) Data Pre-processing which intended to prepare Feature vector, includes Feature selection, Feature weighting and Normalization 2) Design of CNN model for blood group prediction

using Feature vector prepared during first stage.

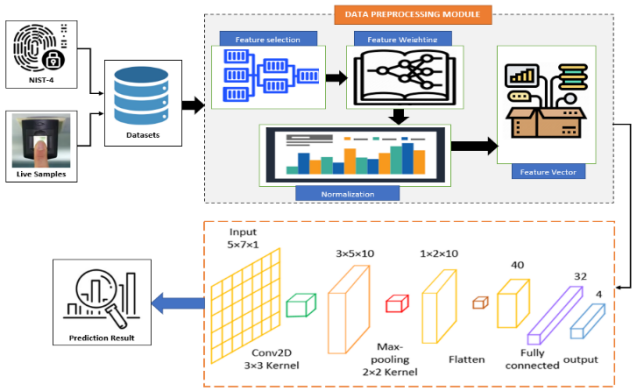

Fig 6. CNN Model Framework Diagram.

Algorithm: Blood Group Prediction using CNN

Input: labeled fingerprint data set as $T = \{x_i, y_i\}_{i=0}^{L}$
Input: CNN ← T % get extracted feature vectors from CNN using raw dataset
Output: $\tilde{T} = \{F^1, F^2, F^3, \ldots\ldots, F^k\}$ % the extracted feature vectors
Output: Blood group prediction function $\boldsymbol{PCNN}$

for $i = 1$ **,** k **do**
  D^i ← F^i calculate the distance vector between any of two points in extracted feature
  for $j = 1$ **,** i **do**
    $v_j \leftarrow vectorize(j, w)$
    $appned\ v_j\ to\ F^i$
    $appned\ F^i\ to\ \tilde{T}$
    normalize $\tilde{T}$
  end for
end for
$\tilde{T}_{train}, \tilde{T}_{test} \leftarrow split\ feature\ vector\ set\ to\ train\ and\ test$
PCNN ← $l_t(\tilde{T}_{train})$ reduce the feature dimension eq. 1
PCNN ← $hidden\ (Relu(x))$
PCNN ← $FConv\ (y_i)$ apply SoftMax function eq. 3
PCNN ← $\emptyset(w)$ add the error function eq. 4
M ← PCNN($\tilde{T}_{train}, \tilde{T}_{test}$)
for $i = 1$ **,** N **do**
  $score \leftarrow evaluate(i, \tilde{T}_{test}, \text{PCNN})$
  $\emptyset(w) \leftarrow update$
end for
returns $score$

A) Data Pre-processing

This model combines both feature extraction and classification from fingerprint images. Based on the effectiveness of the features, fingerprint images are automatically analysed during the learning phase. After scoring the input images on corners, lines, and edges in the first layer, high-level features are extracted. These are then used as features in the classification layer. A pooling layer is applied after the convolutional layer in order to reduce the size of these filtered images while preserving the information found in the convolutional layers. Therefore, the pooling layers are both feature reduction tools as well as directly affecting final accuracy and performance. These revealed features can be presented to the classification phase for activations, and they can be used to indicate a class. When images reach phase 8 of the fully connected layer, they are converted into four one-dimensional vectors. The class that receives the highest score using SoftMax activation will be determined as the winner.

B) Design of Optimized CNN model

The CNN's two most important layers are the convolution layer and the pooling layer. There are numerous convolution kernels in each convolution layer, and the formula for computing them is Eq (1). The data's features are obtained after the convolution layer's convolution operation; however, the extracted feature dimensions are relatively big, thus a pooling layer is added after the convolution layer to minimize the feature dimension and the network's training cost.

$$l_t = \tanh(x_t * k_t + b_t) \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

where l_t is the convolution output value, tanh is the activation function, x_t is the input vector, k_t is the convolution kernel weight, and b_t is the convolution kernel bias. The rest of hidden layers designed using ReLU as an activation function. While the Relu function is an effective activation function for addressing the challenges of gradient gradient-based learning, the problem will endure if the input vectors contain negative values [20], as seen below:

$$Relu(x) = \begin{cases} 0, & (x \le 0) \\ x, & (x > 0) \end{cases} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (2)$$

Secondly, the pooling layer get input as feature maps from the convolutional layer, here feature dimensions will be reduced, and computation will be accelerated by pooling them. The proposed max - pooling function for this study is shown below. The output of the final layer will be the input of a fully connected layer, which will aid with classification tasks, after numerous convolutional layers and pooling layers have been computed. The final prediction value will be based on an individual's blood group probability. Due to the proposed task being multiclass classification, the activation function of SoftMax would be used to calculate the output of the fully connected layer. To avoid overfitting in the fully connected layer, the proposed model also employs dropout strategy and sets 0.25 as its value. The resulting prediction value will be compared, and its average error will be computed. In order to improve the accuracy of any model, the error must be minimized, which requires the design and optimization of a loss function in the following two steps:
Initially, compute the outcome of the SoftMax function in the fully connected layer, which is described by the equation below. (3):

$$y_i = \frac{w^{a_i}}{\sum_{k=1}^{n} w^{a_k}}, i = 4 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3)$$

Where i shows the classification number, w is the complete or fully connected layer's output, n is the number of a, and w is a natural logarithm, whereas Eq. (4) will be used to derive the error function.

$$\emptyset(w) = -\sum_{i=0}^{n}\sum_{k=0}^{l} t_{ik} \log(y_{ik}) \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4)$$

Where n denotes the number of samples and l denotes the number of fully connected layer outputs. t_{ik} is the likelihood that sample k belongs to class i, y_{ik} denotes the likelihood that models predict sample k belongs to class I, and W denotes the filter weight coefficient.
In order minimize the loss, backpropagation algorithm is most used

to minimize it, which is based on gradient descent [21]. In [22], ADAM was proposed to be used to compute the optimization and updating the parameter W using the Equation defined in using Eq. (5):

$$W^* = W - \eta . \frac{\partial \emptyset(W)}{\partial W} \dots\dots\dots\dots \quad \dots\dots\dots\dots \quad \dots\dots\dots\dots . (5)$$

The learning rate is determined by examining the value of W^* after it has been updated each time a gradient descent step η has been computed which is set to be 0.0001 during training of proposed model

4. Result Discussion and Observations

To predict an individual's blood group, the proposed system uses various types of approaches. The image-based CNN approach is implemented, where all collected image samples are labeled with the blood group. The previous methods introduced in literature, used manual methods of fingerprint sample collection like ink and paper or they traditional method it requires actual blood samples for blood group identification.

At the next level, proposed CNN is designed as a multiclass prediction model for the prediction of blood groups. Similarly, the design of CNN is initiated with Conv2D input layer designed with 32 neurons whereas as an activation function Rectifier (ReLU) was used. The second Conv2D layer is made up of 64 neurons that employ the same activation function as the input layer. Finally, the fully connected layer designed with 32 neurons. Also, the average pooling layers are used with 0.25 dropout. The proposed model is trained using 50 epochs and uses Adam as an optimizer and SoftMax as an activation function, while categorical cross-entropy is utilized as a loss function. The proposed and other CNN models tested on local machine having intel i7 processor, 16 GB RAM with windows 10 operating system having 2GB GEFORCE NVidia 940 mx graphics. The Lenet-5, ZFNet and AlexNet CNN algorithms compared with proposed optimized CNN algorithm, Table 5 shows the comparative statistics of these algorithm with proposed CNN model.

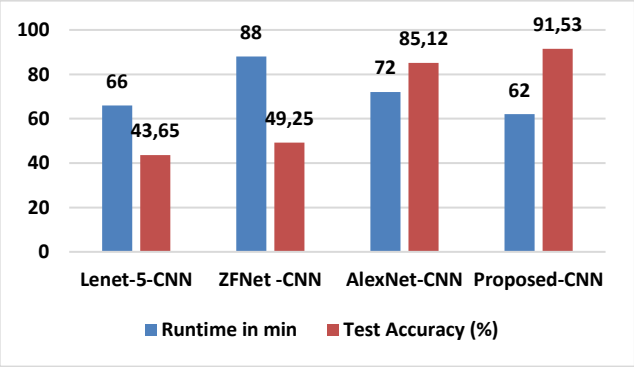

Fig 7: Model loss and accuracy graph of proposed- CNN model

The all models are tested with 50 epochs. The Lenet-5 having low accuracy with 43.65% and require 66 min to execute, whereas AlexNet produce 85.12% accuracy and 72 min require to execute the model. The proposed model shows significant improvement in prediction with 91.53% accuracy and take 62 min to execute. Fig. 7 shows comparison of all models listed in Table 5 with time require to execute vs test accuracy.

Table 5: The comparative statistics of these algorithm with proposed CNN model.

Classifiers	No. of Epochs	Runtime in min	Validation Accuracy (%)	Validation Loss (%)	Test Accuracy (%)
Lenet-5-CNN	50	66	39.54	54.83	43.65
ZFNet -CNN	50	88	38.21	55.23	49.25
AlexNet-CNN	50	72	82.35	50.57	85.12
Proposed -CNN	50	62	90.43	39.92	91.53

The model loss and accuracy graphs for AlexNet-CNN are shown in Fig. 8 and Fig. 9., here the AlexNet require 72 min to execute model and produce 85.12% test accuracy with 82.35% validation accuracy and 50.57% validation loss. The test accuracy of proposed CNN is 91.53% whereas 90.43% validation accuracy and 39.92 is validation loss respectively.

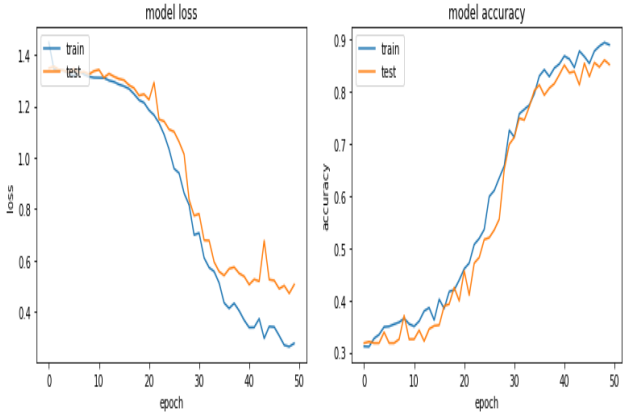

Fig 8: Model loss and accuracy graph of AlexNet-CNN

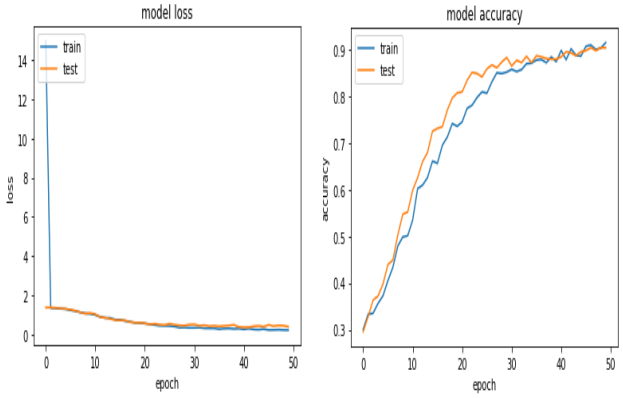

Fig 9: Model loss and accuracy graph of proposed- CNN model

The accuracy of the classifier, on the other hand, is the number of facts from our model that it uses to determine if the model is relevant or not. Recall refers to a model's ability to detect all the data points of concentration in a dataset, or its overnight delivery the ability to find all acceptable instances in a dataset. They combined as an F1 score to the performance in order to get the best combination of accuracy and recall. The F1 is the concordant mean of recall and accuracy, considering both measures. These values are derived using the following equations: Eq. (6), Eq. (7), and Eq. (8):

$$precision = \frac{true\ positives\ (TP)}{true\ positives\ (TP) + false\ positive\ (FP)} \dots 6)$$

$$recall = \frac{true\ positives\ (TP)}{true\ positives\ (TP) + false\ negative(FN)} \ldots\ldots (7)$$

$$F1 = 2 * \frac{precision * recall}{precision + recall} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (8)$$

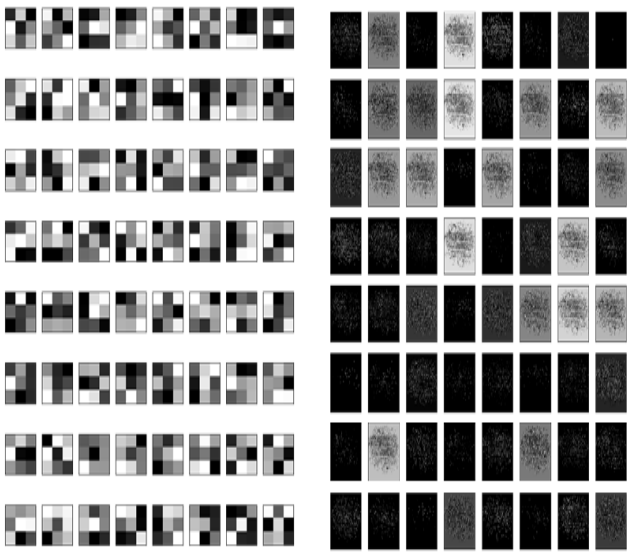

Fig 10: For examining the training and validation process, use the suggested CNN's filter and feature map visualization.

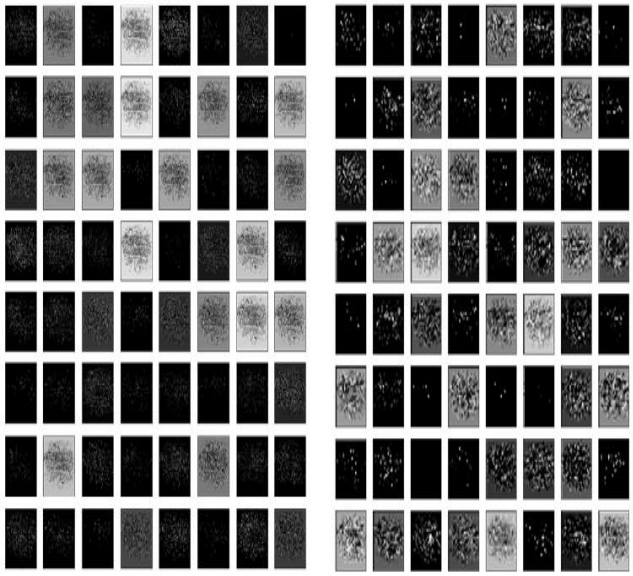

Fig 11: Filter visualization of proposed framework

The Stochastic Gradient Descent technique was used to train all of these CNNs. Table 6 compares the proposed CNN to different CNN models based on performance metrics such as Precision, Recall, and F1-Score. The precision and recall and F1-score are computed for both yes and no class. The proposed model having higher 90 % precision for kind of classes.

The visualized filters and feature maps of the proposed architecture are shown in Fig. 10 and Fig. 11. Filters used to input image and feature maps generated by preceding layers might result in feature maps that show how the model internally encodes an input at a certain location in the model [23]. The training and validation graphs in the study show how modified architectures gain better representations than other designs [24].

Table 6: Precision, Recall and F1-Score of different classifiers

Classifiers	Precision (Class Yes)	Recall (Class Yes)	F1-Score (Class Yes)	Precision (Class No)	Recall (Class No)	F1-Score (Class No)
Lenet-5-CNN	0.72	0.76	0.75	0.73	0.79	0.71
ZFNet -CNN	0.78	0.81	0.74	0.77	0.77	0.74
AlexNet-CNN	0.83	0.85	0.84	0.82	0.84	0.87
Proposed-CNN	0.90	0.91	0.91	0.90	0.95	0.93

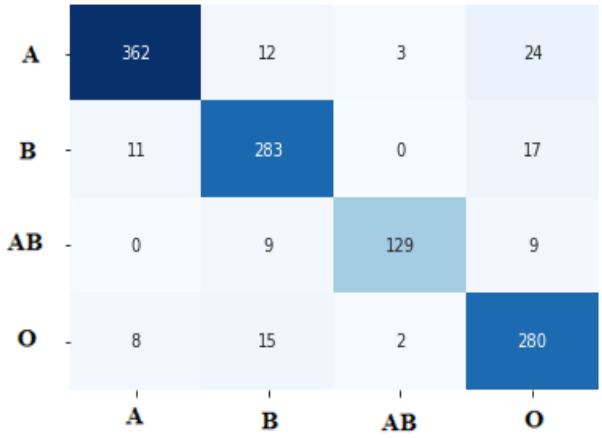

Fig 12: Confusion Matrix of proposed- CNN prediction models

A model that is evaluated by metrics that measure the generalization ability of the model is required to be able to assess its generalization performance. As evaluation metrics, Accuracy, Precision, Recall, and F1-Score are also used together with this confusion matrix to determine the performance of this proposed model [25].

Table 7: Accuracy computation using confusion matrix

Class	No. of Records	Training / Test set	Correctly classified no. of instances		Incorrectly classified no. of instances		Accuracy
			TP	TN	FP	FN	
A	3920	2756/1164	362	744	39	19	95.01%
B	3920	2756/1164	283	817	28	36	94.50%
AB	**3920**	**2756/1164**	129	1012	18	05	98.02%
O	3920	2756/1164	280	809	25	50	93.55%

The Fig. 12 show the confusion matrix of proposed classification model. Table 7 describe the computation of accuracy of model using confusion matrix, here the prediction accuracy is computed form each blood group independently through values extracted from confusion matrix as true positive (TP), true negative (TN), false positive (FP) and false negative [26-27].

Table 8: Precision, Recall and F1-Score of each blood group computed using confusion matrix

Class	Precision	Recall	F1-score
A	0.90	0.95	0.93
B	0.91	0.89	0.90
AB	0.88	0.96	0.92
O	0.92	0.85	0.88

The average accuracy computed using confusion matrix is 95.27%. The blood group A having 33.67 % of samples produces 95.01 % accuracy, similar blood B, AB and O having 25.51%, 13.26%, 27.55% of total samples produces 94.50%, 98.02%, and 93.55% accuracy respectively. Table 8 summary of the comparative performance using precision, Recall and F1-Score of each blood group. The blood group O having higher high in precision with 92%. followed by blood group AB with lower 88% precision.

5. Conclusion

Fingerprints are an effective way of identifying people because of their immense potential. A novel minutiae-based approach is proposed to identify blood groups. Additionally, fingertip patterns of individuals have multiple minutiae, it is very much feasible to exact maximum minutia from fingerprints if it must be taken with a digital equipment. Blood group identification is becoming a more appealing option because to recent advancements in fingerprint detecting and image processing technology and advances in the accuracy and speed of recent algorithms to identifying approaches that have been used having accuracy with 95.27 %. Furthermore, similar studies help to predict individual diseases at a young age. Analyzing and classifying communities according to age, blood group, fingerprint patterns, and lifestyle disorders can all be used to assist prepare for future pandemics, such as COVID-19, in which mankind will be plagued by lifestyle-related diseases like type 2 diabetes and hypertension.

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