People's Democratic Republic of Algeria

Ministry of Higher Education and Scientific Research

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Faculty of new information and communication technologies

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Master Thesis

BLOOD GROUP PREDICTION USING DEEP LEARNING

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2022/2023

Acknowledgments

I want to express my sincere gratitude to my supervisor Leila Amrane for all of her helpful suggestions, help, and criticism throughout this project. Her knowledge, encouragement, and experience have had a big impact on the direction and scope of this research.

I also want to thank my friends and classmates for their helpful discussions, helpful advice, and assistance with the data collection and analysis. Their assistance was essential to the success of this project.

I am appreciative that volunteers gave me access to the fingerprint dataset for this study. Their kindness and assistance made it possible to conduct this research.

I want to thank my family and friends for their continuous encouragement and support throughout my academic journey. They have been a continual source of encouragement and inspiration because of their love, support, and compassion.

Finally, I would like to thank my university Kasdi Merbah, as well as the information and technology department, for their assistance in collecting my dataset, which was critical to the successful completion of this project.

Abstract

This study aims to investigate the potential correlation between fingerprints and blood groups, exploring the possibility of predicting an individual's blood group based on their fingerprint patterns. Fingerprint analysis has long been utilized in forensic science and biometric identification, but its association with blood groups remains relatively unexplored. The research involves collecting fingerprint samples from a diverse group of participants and analyzing them in conjunction with their known blood group data. Statistical analysis and deep learning techniques and Neural Networks “CNN” will be employed to identify any patterns or relationships between fingerprint characteristics and blood groups. The findings of this study could have significant implications in various fields, including forensic investigations, medical emergencies, and biometric identification

Key words: Fingerprint, Blood group, Deep learning, Neural Network, CNN

الملخص

تهدف هذه الدراسة إلى استكشاف الارتباط المحتمل بين بصمات الأصابع والزمر الدموية، واستكشاف إمكانية التنبؤ بزمرة الدم لفرد ما بناءً على أنماط بصمات أصابعه. لقد تم استخدام تحليل بصمات الأصابع في علم الجنائيات والتحقق البيومتري لفترة طويلة، ولكن ارتباطها بالزمر الدموية لا يزال غير مستكشف بشكل كبير. تتضمن البحث جمع عينات بصمات الأصابع من مجموعة متنوعة من المشاركين وتحليلها بالاشتراك مع بيانات زمر دمهم المعروفة. سيتم استخدام التحليل الإحصائي وتقنيات التعلم العميق والشبكات العصبية "CNNs" لتحديد أي أنماط أو علاقات بين خصائص بصمات الأصابع وزمر الدم. قد يكون لنتائج هذه الدراسة آثار كبيرة في مجالات متعددة، بما في ذلك التحقيقات الجنائية وحالات الطوارئ الطبية والتحقق البيومتري.

الكلمات المفتاحية: بصمات الأصابع، الزمر الدموية، التعلم العميق، الشبكات العصبية.

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General Introduction

I. Problem and research objectives

Fingerprints have long been recognized as a unique and distinguishing feature of individuals, extensively utilized for identification purposes in various domains, such as law enforcement and access control systems. The intricate patterns formed by ridges and furrows on fingertips have been shown to possess a high level of distinctiveness and permanence. However, the association between fingerprint patterns and specific physiological traits or genetic information remains an area of ongoing research.

Blood group classification, which is based on whether or not specific antigens are present on red blood cells, is crucial for many medical procedures, transfusion compatibility, and forensic investigations. These days, blood group identification is done in a laboratory setting using serological techniques. These tests are reliable, but they require particular equipment, knowledgeable personnel, and time for analysis. Investigating alternative methods that could predict blood types quickly and non-invasively would be very helpful in emergency situations and situations where prompt blood typing is required.

This study aims to investigate the feasibility of predicting an individual's blood group solely from their fingerprints. By examining a large dataset of fingerprint samples and corresponding blood group information, we will analyze the relationship between fingerprint patterns and blood group types. Leveraging statistical analysis and machine learning algorithms, we will explore potential correlations and patterns that may exist. If successful, this research could pave the way for the development of a non-invasive and rapid blood group prediction method, utilizing readily available fingerprint data.

Through this study, we aim to contribute to the growing body of knowledge on the potential relationship between fingerprints and blood groups. By exploring this uncharted territory, we hope to shed light on the feasibility of using fingerprints as a predictor of blood group, thereby opening up new possibilities for improved forensic investigations, emergency medical procedures, and biometric identification systems.

Stay tuned as we embark on this fascinating journey into exploring the intriguing relationship between blood group systems and fingerprint recognition technology.

II. Organization of the project

Chapter 1: Blood Group Systems and fingerprints:

This chapter provides an introduction to our project on predicting blood groups from fingerprints. We discuss the relevance of this research, basic concepts of blood groups, and the association between fingerprints and blood groups. We outline the project's objectives and methodology.

Chapter 2: Methodology and Deep Learning Approach:

In this chapter, we describe the data collection process, including fingerprint dataset diversity and preprocessing techniques. We present the four models used: VGG16, ResNet, AlexNet, and a custom CNN. We explain the training process.

Chapter 3: Implementation and results:

Here, we present the results of our trained models, including performance metrics such as accuracy, precision, recall. We analyze the strengths and limitations of each model in predicting blood groups from fingerprints.

Conclusion:

The conclusion summarizes our findings, contributions, and implications for biometric recognition and blood group prediction. We discuss limitations and suggest future research directions.

Chapter 01:

Blood Group Systems and Fingerprints

Chapter I Blood Group Systems and Fingerprints

1.1. Introduction

Biometric technology developments have recently revolutionized many industries, including healthcare, forensics, and personalized medicine. Among the various biometric modalities, fingerprints have become one of the most popular and trustworthy forms of identity verification. Fingerprints have proven to have distinctive patterns and ridge details that are challenging to mimic. As a result, fingerprint recognition technology has attracted a lot of interest and been widely adopted.

Simultaneously, blood groups play a crucial role in numerous aspects of healthcare, forensic investigations, and genetic research. Blood group systems, such as the ABO system and Rh factor, provide valuable information about an individual's blood type, allowing for appropriate medical treatments, blood transfusion compatibility, organ transplant matching, and forensic identification. Determining an individual's blood group accurately and efficiently is of paramount importance in these critical scenarios.

Chapter I provides the groundwork for this research by establishing a comprehensive overview of blood group systems and fingerprint recognition technology. The chapter begins by elucidating the significance of blood groups in various healthcare contexts, such as transfusion medicine, genetic research, and personalized medicine. We delve into the ABO system, Rh factor, and other important blood group systems, highlighting their role in determining an individual's blood type.

Furthermore, this chapter explores the unique characteristics of fingerprints, including ridge patterns, minutiae points, and ridge counts, which form the basis for fingerprint identification. An overview of fingerprint recognition techniques.

1.2. Blood Group Systems and Clinical Significance

1.2.1 Historical

Due to a lack of understanding of the blood group system, there were many deaths and a significant loss of life, which caused the world to suffer greatly. This persisted until 1900, when Karl Landsteiner at the University of Vienna figured out why some blood transfusions were successful while others were fatal. When Landsteiner combined serum from his employees with red blood cells, he saw that some of the serum agglutinated with the red blood cells of other people, which led him to the discovery of the ABO blood group system.

Following these investigations and observations, three distinct blood types—designated "A," "B," and "C"—were discovered. But the type "C" was later renamed as "O," which comes from the German word "ohne," which means "without" or "zero" (i.e., lacking any antigens) (Dariush & Marjan, 2013). The fourth blood type, which is the least common, was discovered after a year and given the name "AB." Karl Landsteiner received the Nobel Prize in Physiology or Medicine in 1930 [1] in appreciation of his contribution.

1.2.2 Definitions and concepts

The word "blood group" refers to the entire blood group system, which includes the RBC antigens unique to that system. These antigens are regulated by a number of genes that may be allelic or located close together on the same chromosome. The term "blood type" refers to a distinct antibody response pattern inside a certain system.

Antigens on the red blood cell membranes, specifically A, B, and Rh antigens, might cause immunological antibodies to be produced after blood transfusion or donation. This can lead to a variety of consequences, some of which may even be life-threatening, such as immune-mediated hemolysis. This demonstrates how important it is to do blood type tests in order to identify antigens and guarantee the safety of blood transfusions, eventually saving the lives of patients. According to the International Society of Blood Transfusion ISBT (International Society of Blood Transfusion, 2022), there are currently around 44 blood group systems with 345 identified antigens on human red blood cells.

Antibodies that are generated as a result of active immunization to non-self RBC antigens after exposure to human RBCs from another person or that arise "naturally" as a result of meeting antigens that are pervasive in the environment are defined as antigens. The red cell surface antigens that are present or absent because of hereditary variation determine a person's blood type. [2]

Anyone older than 6 months has clinically significant levels of anti-A and/or anti-B antibodies in their serum, making ABO the most important of the 44 systems for transfusion and transplantation. Blood group A contains an antibody against blood group B in serum, and vice versa, whereas blood group O lacks the A/B antigen but does contain both of their antibodies in serum.

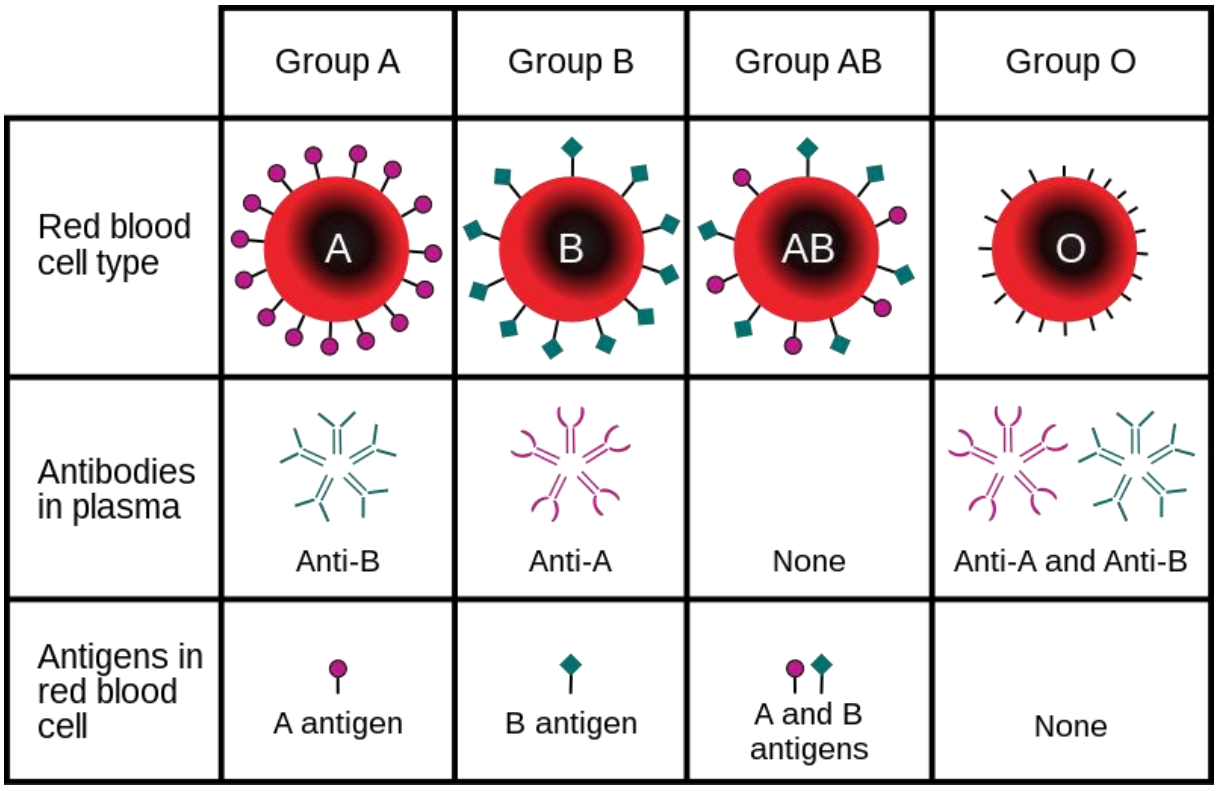

Figure I. 1: Microscopic characteristics of blood groups (wikipedia, s.d.)

1.3. Blood Group Testing Methods

1.3.1 Serological testing

In this technique, a glass slide or white porcelain support is partitioned into three sections. For each section, a drop of blood from the donor or recipient is mixed separately with anti-A, anti-B, and anti-D. By visually observing the agglutination or clumping of blood, the ABO and RhD (Rhesus D) blood types can be determined. This test is completed within 5-10 minutes and is cost-effective, requiring only a small amount of blood typing reagents. However, it is a less sensitive method and primarily serves as a preliminary blood group matching tool for obtaining initial results. The test cannot be conducted for weakly or rarely reactive antigens, making the interpretation of results difficult. Moreover, a low concentration of anti-A or anti-B antibodies may lead to false positive or false negative outcomes. While the slide test proves useful for outdoor blood typing, it may not provide the level of reliability required for completely safe transfusions [3].

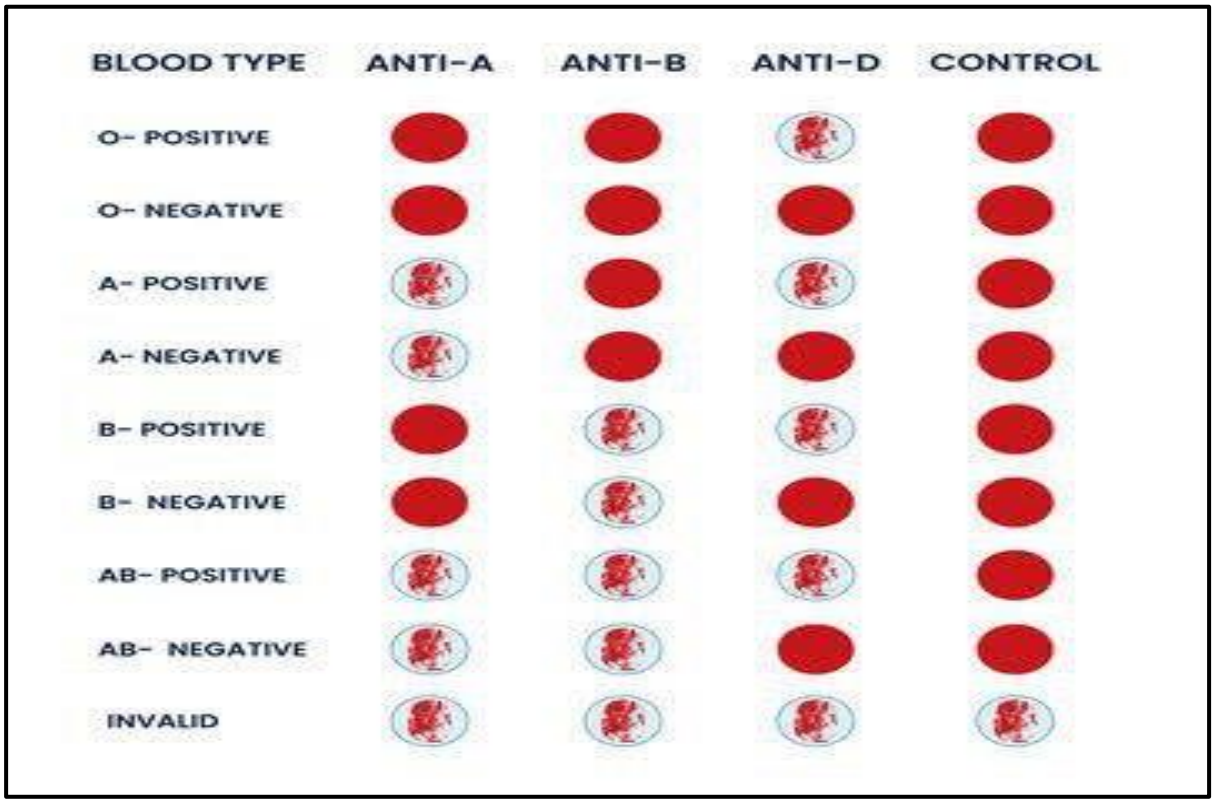

Figure I. 2: Slide Test (slideshare.net, s.d.).

1.3.2 Molecular Testing

Molecular testing methods involve the detection of specific genes and DNA sequences associated with blood group antigens. These methods are more advanced and precise than serological testing and can provide detailed information about the presence or absence of specific antigens. Polymerase chain reaction (PCR) and DNA sequencing techniques are commonly used in molecular testing for blood group determination.

Serological testing has long been used in the field of pre-transfusion compatibility testing. The availability of antibody reagents, however, falls short for a sizable portion of rare blood group antigens when it comes to satisfying the demands for rare blood requirements. Overcoming serology's limitations in this situation requires genotyping. Genotyping offers a more streamlined approach and makes it easier to identify uncommon blood group antigens thanks to its high throughput capacity.

As we have discussed earlier, various genetic tests such as PCR-RFLP, PCR-SSCP, DNA sequencing, and others are commonly employed for blood typing purposes. These tests serve the purpose of identifying rare blood types and investigating the inheritance patterns and frequencies of rare blood antigen genes. For instance, real-time fluorescent PCR proves to be effective in this regard. Additionally, Next-Generation Sequencing (NGS) holds promise in identifying rare blood types even without prior knowledge of specific antibodies [4].

Presently, there are a plethora of rapid and cost-effective genotyping kits available, boasting multiplex capacity and high-throughput capabilities. These advancements have made large-scale rare blood group genotyping more affordable and accessible than ever before [5].

1.3.3 Alternative Testing Methods:

Alternative blood group testing methods have emerged as non-invasive and convenient alternatives to traditional serological and molecular methods. These methods include saliva-based testing, urine-based testing, and fingerprint-based testing. They rely on the detection of blood group antigens or genetic markers in these alternative bodily fluids or samples. While these methods are still under development and evaluation, they hold the potential for rapid and non-invasive blood group determination.

1) Saliva-based Testing:

Saliva contains secretions from the oral mucosa, which may include blood group antigens. Saliva-based testing involves collecting saliva samples and analyzing them for the presence of specific blood group antigens or genetic markers associated with blood group determination. This method offers a non-invasive and easily accessible approach for blood group testing [6].

2) Urine-based Testing:

Urine has been investigated as a potential alternative sample for blood group determination. Some blood group antigens or their degradation products can be detected in urine. Urine-based testing involves collecting urine samples and analyzing them to determine the presence or absence of blood group antigens or genetic markers.

3) Fingerprint-based Testing:

This method is still under study and exploration, and it is what we will test it on our project. The idea about Fingerprint-based testing utilizes the unique ridge patterns and other features of fingerprints to predict blood group. Research has shown that certain blood group antigens or genetic markers can be detected in the sweat and oils present in fingerprints. By analyzing the fingerprint patterns and associated biological markers, it may be possible to predict an individual's blood group.

1.4. Fingerprints

1.4.1 What is a Fingerprint

On the surface of the fingertips, palms, and soles of the feet, there is a distinctive pattern of ridges and valleys known as a fingerprint. Tens of thousands of tiny ridges that make up the friction ridge skin's patterning create it. Fingerprints are created when a fetus is developing and, with the exception of minor changes brought on by wounds or skin conditions, remain largely unchanged throughout a person's lifetime.

The three major types of fingerprint ridges are whorls, loops, and arches. Often, ridges will enter an arch from one side and exit from the other without fully looping. Each ridge in a

loop exits from the same location and all curves or loops in the same direction. Whorls are circular or spiral-shaped structures with ribbed edges.

The uniqueness and individuality of fingerprints are the basis for their use in forensic science and biometric identification. The pattern of ridges and their characteristics, such as ridge endings, bifurcations, and ridge counts, are used to distinguish one fingerprint from another. Even identical twins have distinct fingerprints.

Fingerprint identification has been widely adopted for personal identification and forensic investigations due to its reliability, permanence, and ease of capture. Automated fingerprint recognition systems use algorithms to extract and compare the minutiae points or other features of a fingerprint for matching against a database of known prints.

With applications in law enforcement, access control, identity papers, and several other industries needing safe and precise personal identification, fingerprints are one of the most popular and commonly used biometric identifiers [7].

1.4.2 Fingerprint Types

1) Arches:

Arches are the simplest and least common type of fingerprint pattern, accounting for approximately 5% of all fingerprints. They are characterized by ridges that enter on one side of the finger and exit on the other side, forming a smooth and continuous arch-like pattern. Arches do not possess any delta (triangular ridge point) or core. There are two subtypes of arches: plain arches, which are gently sloping, and tented arches, which have a more pronounced upward thrust in the center.

Moreover, even within this type, we distinguish two primary or main subtypes of brackets, which are:

- Plain Arches:

Plain arches are characterized by a smooth, gently sloping ridge pattern that forms a consistent arch shape from one side of the finger to the other. They have ridges that enter on one side of the finger, rise in the center, and exit on the opposite side, creating a simple arch

without any significant upward or downward thrust. The ridges in a plain arch pattern do not make any significant twists or turns. The ridge flow is continuous and smooth, creating a plain and uniform appearance. Plain arches are the most common subtype of arches.

- Tented Arches:

Tented arches, also known as peaked arches, have a more pronounced upward thrust or spike in the center of the arch. Unlike plain arches that have a smooth and gently sloping ridge flow, tented arches exhibit a more pointed or tent-like formation at the top of the arch. The ridges in a tented arch pattern enter on one side of the finger, rise sharply in the center, and exit on the opposite side. The central spike or tent formation can be relatively sharp or more rounded, depending on the individual's fingerprint. Tented arches are less common than plain arches but still fall under the arch category.

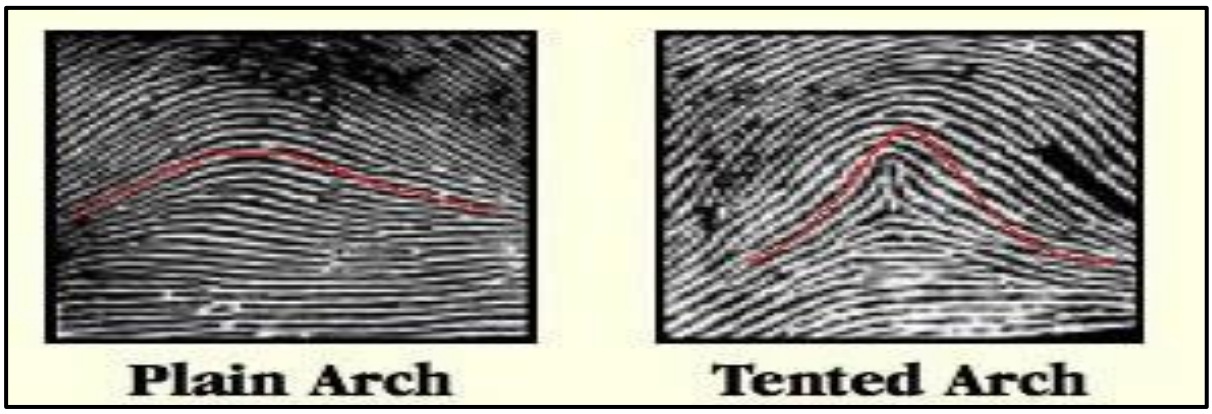

Figure I. 3: Plain arches vs Tented arches (bayometric, s.d.).

2) Loops:

Loops make up roughly 60-70% of all fingerprint patterns. They have ridges that enter the finger from one side, recurve, and exit on the same side. One or more ridges create a distinct loop shape in loop patterns. One delta and one or more cores are present in loops. Loops are classified into two types: radial loops with ridges that flow toward the thumb side of the hand and ulnar loops with ridges that flow toward the little finger side of the hand (S. Mahaboob, Sarma, & A. S. N., 2013) [8]. Moreover, even within this type, we distinguish two primary or main subtypes of brackets, which are:

- Radial Loups:

Radial loops, also known as outward loops or ulnar loops, are loop patterns where the ridges flow towards the thumb side of the hand. In a radial loop, the ridges enter on one side of the finger, recurve, and exit on the same side towards the thumb. The loop appears to radiate away from the center of the hand. Radial loops typically have a distinctive rounded or U-shaped appearance. The core of the loop, which is the innermost point of the recurve, is located on the same side as the entry of the ridges.

- Ulnar Loups:

Ulnar loops, also referred to as inward loops or radial loops are loop patterns where the ridges flow towards the little finger side of the hand. In an ulnar loop, the ridges enter on one side of the finger, recurve, and exit on the same side towards the little finger. The loop appears to curve towards the center of the hand. Ulnar loops have a similar rounded or U-shaped appearance as radial loops, but the flow of ridges is in the opposite direction. The core of the loop is located on the same side as the entry of the ridges.

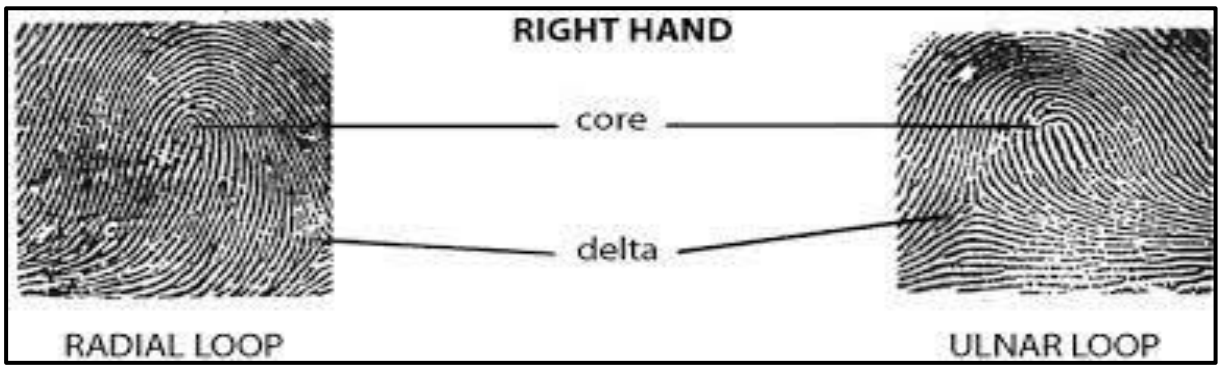

Figure I. 4: Radial loop vs Ulnar loop (casdschools.org, s.d.).

3) Whorls:

Whorls are the second most common fingerprint pattern, accounting for between 25 and 35% of all fingerprints. Ridges form circular or spiral patterns on them. Whorls have at least one ridge that completes a circuit, as well as two deltas and one or more cores. Plain whorls have a circular pattern with ridges that spiral around a central point; central pocket whorls have a whorl pattern with a core that looks like a central pocket; double loop whorls have two separate loop formations combined into a whorl; and accidental whorls have a combination of two or more patterns (e.g., a loop combined with a whorl).

There are four types of whorls: Plain Whorl, Central Pocket Whorl, Double Loop Whorl, and Accidental Whorl (S. Mahaboob, Sarma, & A. S. N., 2013), as shown in Figure 5.

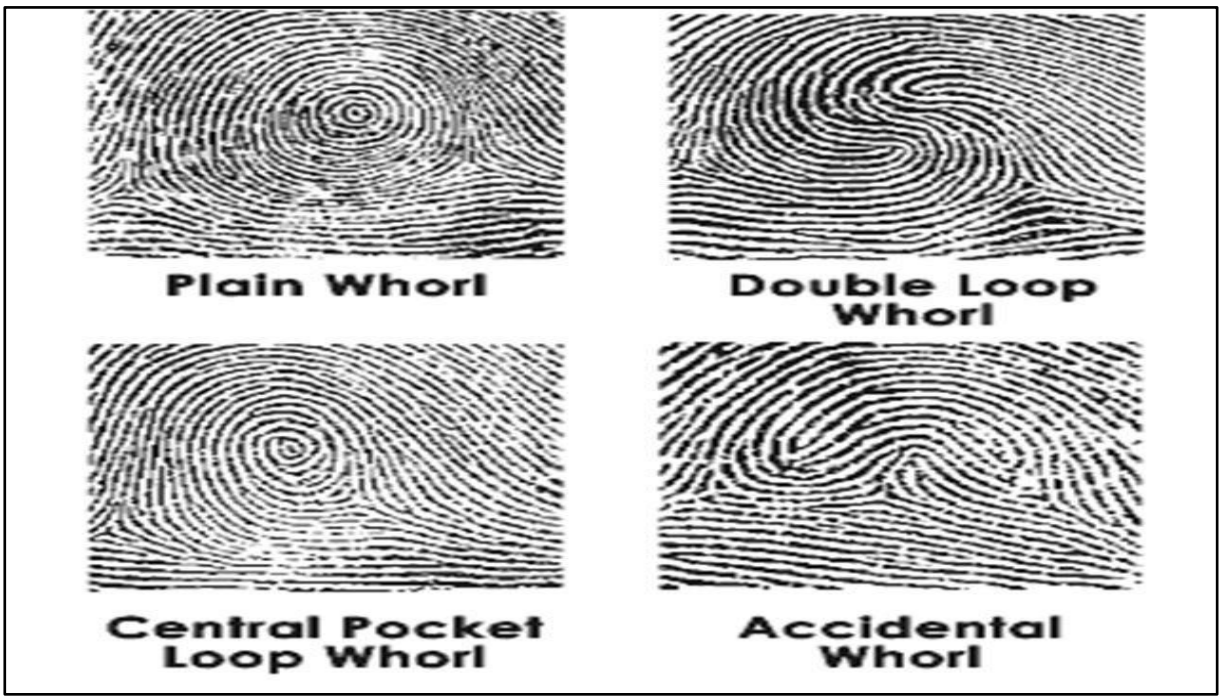

Figure I. 5: Whorls types (slideplayer, s.d.)

1.5. Related Works

This section explores the connection possible between ABO-Rh blood groups and fingerprint patterns. We seek to study the potential relationship between these distinctive biometric markers and blood group categorizations by comparing the results of several studies performed on various populations.

In a recent study [9] conducted on the Omani population, the aim was to investigate the potential association between fingerprint patterns and ABO-Rh blood groups. The researchers examined the frequency of blood groups (ABO and Rh) among the study participants and analyzed the prevalence of different fingerprint patterns in relation to these blood groups.

The results provided valuable insights into the potential correlation between fingerprint characteristics and blood group types.

Among the participants, the frequency of blood groups (ABO and Rh) was observed in the following order, from highest to lowest prevalence: O+ (54.0%), A+ (19.0%), B+ (18.0%), AB+ (4.5%), O- (2.5%), and A- and B- (1.0% each). Notably, none of the subjects in the study exhibited the AB- blood group, indicating its rarity within the Omani population.

Interesting results were obtained from the comparison of fingerprint patterns to blood groups. It was discovered that people with the AB+ and O- blood groups had whorl patterns more frequently than other patterns. The loop pattern, on the other hand, was discovered to be the most common among people with the A+, A, B+, B-, and O+ blood groups. According to these findings, there may be a connection between particular fingerprint patterns and particular blood group types among Omani people.

These findings contribute to the growing body of evidence regarding the potential connections between fingerprint characteristics and blood group prediction. While further research is needed to establish a definitive causal relationship and generalize the findings to larger populations, this study provides valuable insights into the association between fingerprint patterns and blood groups within the Omani population.

A study conducted by Bhradwaja et al **[10]** 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.

In this article **[11], t**he work titled "Association of Fingerprint Patterns with ABO Blood Groups" explores the potential association between fingerprint patterns and ABO blood groups. This study aims to investigate if specific fingerprint characteristics can be used to predict an individual's ABO blood group.

In this research, Kanchan, Prusty, and Krishan collected a dataset of 110 students fingerprint from a diverse population and recorded the corresponding ABO blood group

information. The study involved a meticulous analysis of fingerprint patterns, considering various ridge characteristics and their correlation with ABO blood groups.

By employing statistical analysis and pattern recognition techniques, the researchers aimed to identify potential associations between fingerprint patterns and ABO blood groups. The study sought to determine if specific fingerprint features, such as ridge count, ridge density, or pattern types, exhibit variations among different ABO blood groups.

The results of this research offered valuable insights regarding possible connections between fingerprint patterns and ABO blood groups. The research identified specific fingerprint traits that showed statistically significant variations between various ABO blood group types. These findings help us understand how fingerprints might be possible to use as a non-invasive way to determine someone's ABO blood group.

The research **[12]** titled "Study of Fingerprint Patterns in Relation to Gender and Blood Group" focuses on investigating the relationship between fingerprint patterns, gender, and blood groups. The study aims to explore potential associations and variations in fingerprint characteristics based on gender and blood group types.

In this study, they conducted a comprehensive analysis of 100 subjects (50 male and 50 female) having different ABO blood groups and belonging to different age groups. The research involved the careful examination and classification of fingerprint patterns, considering primary pattern types such as loops, whorls, and arches.

The primary objective of their work was to identify any discernible variations in fingerprint patterns based on gender and blood group types. The researchers employed statistical analysis techniques to assess the potential associations between specific fingerprint characteristics and gender, as well as different blood group categories.

The results of this study shed light on the relationship between blood type, gender, and fingerprint patterns. The study showed possible correlations between specific fingerprint traits and gender, showing differences in fingerprint patterns between male and female people. The study also looked into any possible connections between fingerprint patterns and various blood group categories.

A significant contribution in the field of predicting blood groups from fingerprints is the work **[13]** titled "A Novel Approach for ABO Blood Group Prediction using Fingerprint through Optimized Convolutional Neural Network". In this study, they proposed a novel approach that leverages a Convolutional Neural Network (CNN) for accurate blood group prediction based on fingerprint patterns.

This research addresses the need for a reliable and efficient method of predicting ABO blood groups, which have critical implications in medical procedures and transfusion compatibility. By employing a CNN-based approach, the study aimed to exploit the intricate patterns of fingerprints to identify potential correlations with ABO blood groups.

This study involved a dataset consist of fingerprint of 392 subjects (268 male and 124 female) and corresponding blood group data. The CNN architecture was optimized to effectively extract and analyze fingerprint features relevant to blood group prediction. The study encompassed several stages, including data preprocessing, training and fine-tuning of the CNN model.

The findings of this study **[13]** demonstrated promising results, indicating a correlation between fingerprint patterns and ABO blood groups. The CNN model achieved high accuracy in blood group prediction, highlighting the potential of fingerprints as a non-invasive and accessible means of determining ABO blood groups.

The study [14] titled "Relationship of Primary Fingerprint Patterns with Blood Groups and Gender: A Dermatoglyphic Study" focuses on exploring the relationship between primary fingerprint patterns, blood groups, and gender. This study utilizes Dermatoglyphic analysis to investigate potential correlations and variations in fingerprint patterns based on blood groups and gender.

In this research, they conducted a comprehensive Dermatoglyphic study using a fingerprint of 138 students. The study involved the careful examination and classification of primary fingerprint patterns, such as loops, whorls, and arches, in individuals with different blood group types and genders.

By employing statistical analysis methods (chi-square tests, analysis of variance (ANOVA)...etc.) and Dermatoglyphic techniques, the researchers aimed to identify any

significant associations or differences in primary fingerprint patterns based on blood group types and gender. The study sought to determine if certain fingerprint pattern types are more prevalent or distinctive among specific blood group categories and gender groups.

According to the findings of this study, gender or blood type have no effect on the distribution of fingerprint patterns. Because each fingerprint is unique, it is possible to identify people in gang-related crimes and many other forensic situations. In order to confirm the accuracy of the correlation between dactylographic pattern and sex and blood, many more studies with larger sample sizes are required.

1.1. Conclusion

In conclusion, Chapter 1 provides a comprehensive overview of the fundamental concepts related to our research on predicting blood groups from fingerprints using deep learning. We discussed the significance of blood groups in healthcare, forensic investigations, and personalized medicine. Knowledge of an individual's blood group plays a crucial role in medical treatments, blood transfusions, organ transplant compatibility, and forensic identification.

We explored the different types of fingerprint patterns, such as whorls, loops, and arches, along with their subtypes. These distinct patterns form the basis for fingerprint identification and personalization.

Chapter 1 also establishes the background information and context for our research project, laying the foundation for the subsequent chapters. In the upcoming chapters, we will delve into the methodologies, deep learning strategies, and data analysis techniques employed to investigate potential connections between fingerprint features and blood group prediction.

Chapter 02:

Methodology and Deep Learning Approach

Chapter II: Methodology and Deep Learning Approach.

2.1. Introduction

This chapter provides an in-depth exploration of the methodology and deep learning approach employed in this research project for predicting blood groups from fingerprints. This chapter outlines the research design, data collection, preprocessing techniques, deep learning model architecture, training and evaluation procedures, as well as ethical considerations and limitations encountered throughout the study.

Blood group prediction. It highlights the significance of fingerprint data in biometric research and emphasizes the potential of deep learning algorithms to extract relevant features for blood group determination.

Next, the data collection and preprocessing procedures are detailed, including the source of the fingerprint datasets used and the steps taken to ensure data quality and diversity even the material used. The preprocessing techniques applied to the fingerprint data, such as image enhancement and feature extraction, are described to optimize the input data for deep learning model training.

Subsequently, the deep learning model architecture specifically designed for blood group prediction from fingerprints is presented. The selected neural network architecture and its suitability for capturing fingerprint features are explained, establishing the foundation for accurate blood group inference.

Overall, Chapter 2 offers a comprehensive overview of the methodology and deep learning approach adopted to predict blood group from fingerprints. This chapter serves as a crucial foundation for the subsequent chapters, where the results, analysis, and implications of the blood group prediction model will be discussed.

2.2. Research Methodology

2.2.1. Deep Learning:

Deep learning is a powerful technique for removing important patterns and features from complex data. It has achieved astounding success in a variety of fields, such as computer vision and pattern recognition [15]. By utilizing deep learning algorithms, we can take advantage of neural networks' capability to automatically learn and represent complex relationships within fingerprint data.

Fingerprints have complex ridge patterns that make conventional methods of analysis difficult. Deep learning presents a promising method to efficiently capture and utilize the rich information contained in fingerprint images because of its capacity to learn hierarchical representations and capture complex features. We may find hidden correlations between fingerprint characteristics and blood groups by using a large dataset of fingerprint images to train a deep learning model.

2.2.2. Convolutional Neural Networks (CNNs):

CNNs are a specific kind of deep learning architecture that work particularly well for image analysis tasks. Because of their ability to automatically [16] learn hierarchical representations of visual data, they are especially well suited for fingerprint recognition.

In fingerprints, the ridge patterns and local structures show the possible relationships that can be efficiently captured by CNNs. The pooling layers in CNNs work to capture the spatial invariance of these patterns throughout the fingerprint image, while the convolutional layers are capable of learning local patterns, edges, and textures. CNNs are able to learn more intricate and abstract representations of fingerprint features by using a variety of convolutional and pooling layers.

Furthermore, CNNs have shown impressive performance in various image recognition tasks, including biometric recognition [17]. They have been successfully applied in fingerprint recognition systems, achieving high accuracy and robustness. By leveraging the capabilities of CNNs, we can leverage their ability to extract discriminative features from fingerprint images, aiding in the prediction of blood groups.

In summary, the rationale behind choosing deep learning and CNNs for blood group prediction from fingerprints lies in their ability to learn automatically intricate patterns and features from complex image data. By leveraging the power of deep learning and the specific architectural design of CNNs, we aim to enhance the accuracy and efficiency of blood group prediction, ultimately contributing to advancements in personalized medicine, forensic investigations, and healthcare practices.

1.5.1. Why Deep Learning & CNNs

1. Ability to Capture Complex Patterns: Deep learning algorithms, like CNNs, can automatically identify complex patterns and features from large amounts of complex data [18]. Fingerprints have distinctive ridge patterns and minute details that make conventional methods of analysis difficult to interpret. Precision and sturdiness in fingerprint analysis are made possible by deep learning models' superior ability to recognize and exploit these complex patterns.

2. End-to-End Learning: Deep learning frameworks enable end-to-end learning, in which the model picks up new information directly from the unprocessed input data without the need for manual feature extraction [16]. This is especially helpful for fingerprint analysis because it eliminates the need for labor-intensive, mistake-prone manual feature extraction techniques. CNNs can directly learn meaningful representations of fingerprint images from pixel-level data thanks to their hierarchical architecture.

3. Scalability and Adaptability: Deep learning models, including CNNs, are highly scalable and adaptable to large datasets. Fingerprint databases can contain millions of images, and deep learning techniques can efficiently process and analyze this vast amount of data. Furthermore, deep learning models can generalize well to unseen fingerprint images, enabling the prediction of blood groups for new individuals with high accuracy.

4. Robustness to Variations: Fingerprints can vary significantly due to factors such as image quality, skin condition, and pressure during capture. Deep learning models, trained on diverse and representative datasets, can learn to be robust to these variations. CNNs, in particular, have been shown to handle translation, rotation, and scale variations [19], making them well-suited for fingerprint analysis tasks.

5. Previous Success in Biometric Applications: Deep learning, including CNNs, has demonstrated exceptional performance in various biometric applications, including fingerprint recognition. CNN-based fingerprint recognition systems have achieved state-of-the-art accuracy and have been widely adopted in real-world scenarios. Leveraging this success, deep learning techniques offer a reliable and proven approach for blood group prediction from fingerprints [17].

2.3. Data Collection

2.3.1. Dataset collection:

In this study, fingerprints of the right and left thumbs were collected from 280 male and female individuals ranging in age from 18 to 60 years at the University of Kasdi Merbah, Faculty of Information and Communication, Ouargla, Algeria the volunteers were apparently healthy with no history of any genetic disorders. The participants explained the procedure and rolled fingerprints were taken for two fingers using the ZK9500 Fingerprint sensor as described in (Table 1) Thus, a total of 560 fingerprints were obtained that were analyzed using VeriFinger developed by Neuro technology (Figure II. 1). The fingerprint patterns were identified and classified as loops, whorls, and arches.

2.3.2. Material and devices:

1) ZK9500:

Table 1 : ZK9500 Information

Scanner Name	ZK9500 USB Fingerprint Scanner
Manufacturer	ZKTeco Co, Ltd.
Connection	USB 2.0
Supported OS	Microsoft Windows
Resolution	500 ppi
Image capture area (Platen size)	17 x 23 mm (0.7" x 0.9") - platen size 15 x 20 mm (0.6" x 0.8") - sensing area
Fingerprint image size	300 x 400 pixels
Sensor type	Optical, CMOS
Device size	76 x 53 x 19 mm (3.0" x 2.1" x 0.7")
Operating temperature	-20°C ~ +50°C (-4°F ~ +122°F)

Operating humidity	0% - 90%

2) VeriFinger:

VeriFinger is a software development kit (SDK) for fingerprint recognition and verification. It is being developed by Neurotechnology, a company that specializes in biometric technologies. Programmers can include fingerprint recognition functionality in their applications, systems, or devices with the help of the VeriFinger SDK. The key traits and competencies of VeriFinger include:

- **Fingerprint Recognition:** VeriFinger enables the recognition of fingerprints by capturing, processing, and analyzing fingerprint images.
- **Template Extraction and Matching:** VeriFinger can extract unique fingerprint templates from fingerprint images. These templates contain essential features and characteristics that are used for matching and verifying fingerprints.
- **Biometric Standards Compliance:** VeriFinger supports various international biometric standards.
- **Fingerprint Database Management:** VeriFinger includes features for managing large-scale fingerprint databases efficiently. It provides functions for adding, deleting, searching, and updating fingerprint records in the database.
- **Quality Assessment:** VeriFinger incorporates quality assessment tools to evaluate the quality of fingerprint images.
- **Platform Support:** VeriFinger SDK is available for various platforms, including Windows, Linux, macOS, Android, and iOS.

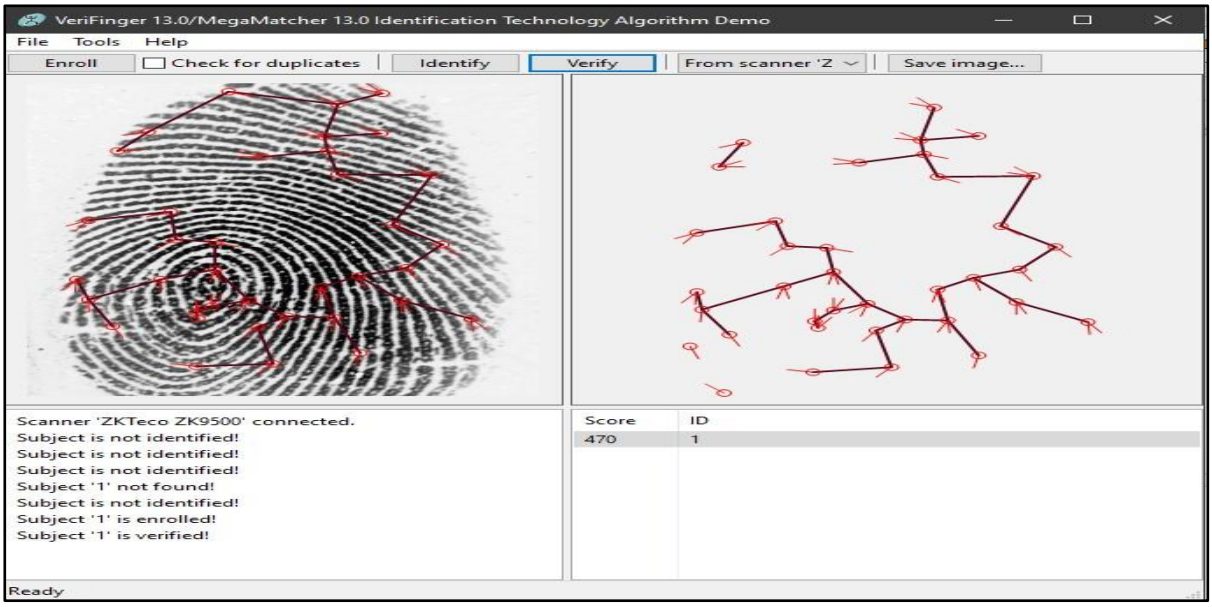

Figure II. 1: VeriFinger User Interface

2.3.3. Statistical analysis

Firstly, an analysis of the Rh factor distribution within each blood group was conducted. Out of the total fingerprint patterns in the O blood group, 120 (90%) exhibited a positive Rh factor, while 12 (10%) displayed a negative Rh factor. Similarly, in the B blood group, 33 (91%) fingerprint patterns had a positive Rh factor, whereas 3 (9%) showed a negative Rh factor. For the AB blood group, the majority of fingerprint patterns, 10 (91%), had a positive Rh factor, with only 1 (9%) pattern displaying a negative Rh factor. Lastly, in the A blood group, 67 (92%) fingerprint patterns had a positive Rh factor, while 6 (8%) exhibited a negative Rh factor. These findings provide valuable insights into the distribution of the Rh factor within each blood group, further enriching the understanding of the relationship between fingerprint patterns and blood group characteristics.

Table 2: Distribution of Samples according to ABO and Rh blood groups

	Rh+	**Rh-**	**Total**
O	47.6	4.8%	52.4
B	13%	1.2%	14.2
AB	4%	0.4%	4.4
A	26.6	2.4	29

A comprehensive statistical analysis was conducted on the dataset to examine the distribution of fingerprint patterns within different blood groups. The results revealed interesting patterns and variations across the blood groups. In the A blood group, 59% of the fingerprints exhibited loop patterns, indicating a higher prevalence compared to other patterns. Whorls accounted for 32% of the fingerprints in this group, while the remaining 9% displayed arch patterns. Similarly, loops were the most common fingerprint pattern in the B blood group, comprising 53% of the samples, followed by whorls at 33%. The remaining 14% were characterized by arch patterns. For the O blood group, loop patterns were again predominant, representing 54% of the fingerprints, while whorls accounted for 31%. Arch patterns constituted 15% of the fingerprint samples in this group. In contrast, the AB blood group exhibited a different distribution, with arch patterns being the most prevalent at 42%. Loops were found in 33% of the fingerprints, and whorls accounted for 25%. These findings were further visualized through a table (Table 2) and histogram (Figure II.2), providing a clear representation of the fingerprint pattern distribution across different blood groups.

Table 3: Distribution of Fingerprint patterns and Blood Group

	A+	**O+**	**AB**	**B+**
Loops	42	71	4	19
Whorls	23	42	3	12
Arch	6	19	4	5
Total	71	132	11	36

Figure II. 2: Distribution of Fingerprint Patterns and Blood Group

2.4. Data Preprocessing

2.4.1 Remove Duplicate

During the data cleaning process, the dataset was carefully examined to identify and remove duplicate fingerprint images. Duplicate images often arise due to multiple scans of the same finger or accidental repetitions. To detect duplicates, a hashing technique was employed, where each image was assigned a unique hash value based on its content. By comparing these hash values, duplicate images were identified and subsequently removed from the dataset. This step ensured that each fingerprint sample in the dataset was unique, avoiding any potential bias or redundancy in the analysis.

2.4.2 Quality Control and Removing Corrupted Images

To ensure the dataset's quality, a stringent quality control process was implemented. Each fingerprint image was visually inspected to detect any low-quality or unusable samples. Images with smudged patterns, insufficient contrast, or excessive noise were identified and removed from the dataset. This manual inspection helped to maintain a dataset of high-quality fingerprint images, reducing the potential for false predictions and ensuring the reliability of the blood group prediction system.

In addition, to maintain the quality and reliability of the dataset, special attention was given to identifying and handling corrupted or unreadable fingerprint images. Corrupted images can contain artifacts, distortions, or incomplete data, which could affect the accuracy of subsequent analysis. A thorough visual inspection was conducted to identify such images, and they were subsequently removed from the dataset. By excluding these corrupted or unreadable images, the integrity and usability of the remaining fingerprint dataset were preserved, ensuring the accuracy of the blood group prediction system.

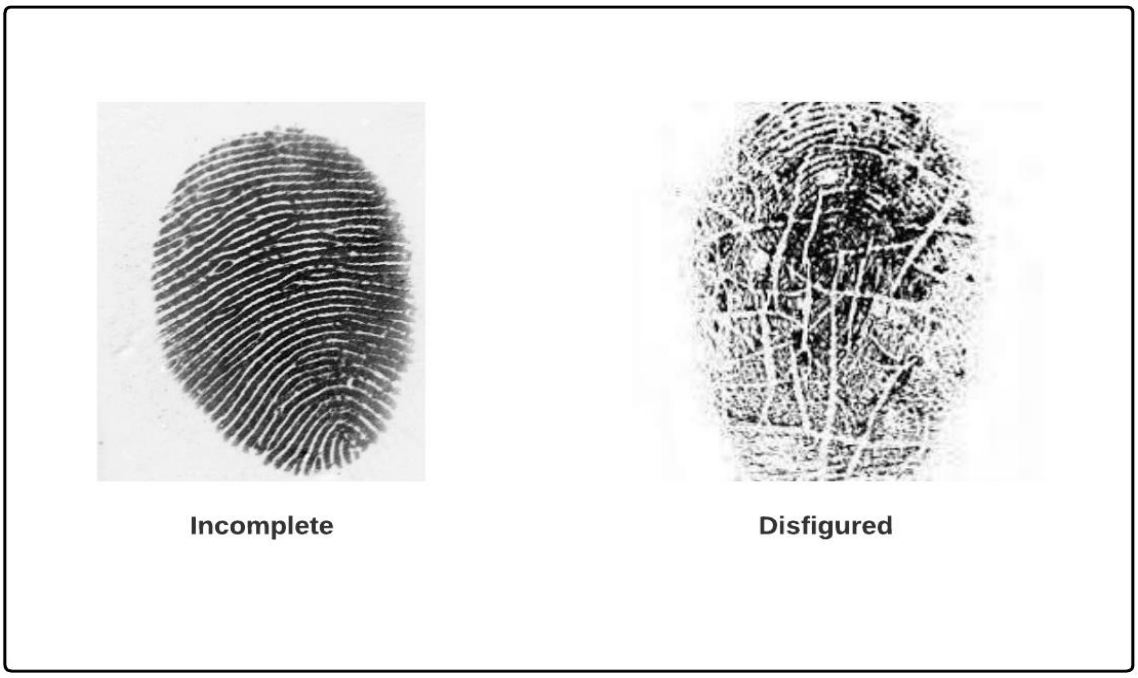

Figure II. 3: Example of unusable samples

2.4.3 Data Enhancing:

In the Preprocessing stage, we use "fingerprint-enhancer" program, based on the paper [20], was incorporated into the preprocessing stage to enhance the quality of the collected fingerprint images. This library, specifically designed for fingerprint image enhancement, employs a range of functions and algorithms to improve the clarity and visibility of ridge patterns. By applying these enhancements, the accuracy and reliability of fingerprint analysis were enhanced, reducing noise and artifacts in the images.

The use of the "fingerprint-enhancer" library played a crucial role in improving the quality of the fingerprint dataset for blood group prediction. The preprocessing step, which involved applying the library's functions and algorithms, resulted in enhanced ridge visibility and clearer fingerprint images. These enhancements ensured the accuracy and reliability of subsequent stages in the blood group prediction process.

By utilizing the "fingerprint-enhancer" program, the overall quality and usability of the fingerprint dataset were significantly improved. The enhanced fingerprint images served as the

input for subsequent stages, including feature extraction and deep learning model training, enabling more precise and reliable blood group prediction.

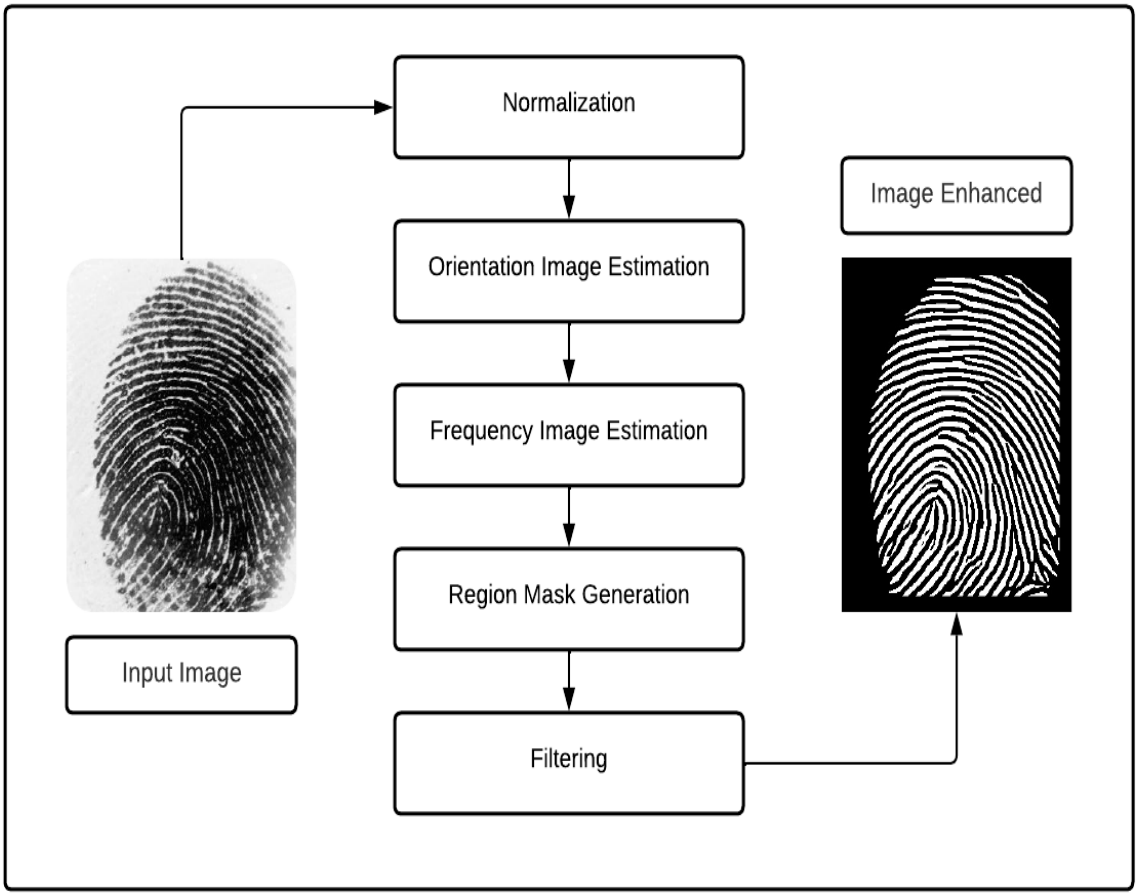

Figure II. 4: The Steps of Enhancing a fingerprint image

2.5. Deep Learning Model Architecture

To explore the performance of different deep learning models for blood group prediction from fingerprints, a comparative analysis was conducted using multiple CNN architectures. The objective was to assess the effectiveness and accuracy of various CNN models in capturing fingerprint patterns and predicting blood groups. Several well-established CNN architectures, including VGGNet, ResNet, and InceptionNet, were implemented and trained on the fingerprint dataset. Each CNN model offered unique characteristics, such as deeper or wider network structures, different types of skip connections, or specialized convolutional operations. By comparing the accuracy and performance of these CNN models, valuable insights could be gained into the suitability of different architectures for blood group prediction from fingerprints. This comparative analysis aimed to identify the most effective CNN model architecture that could deliver the highest prediction accuracy and guide future improvements in blood group inference from fingerprints.

2.5.1 Res-NET

The idea here is to use ResNet50 architecture for a classification task and leverage the pre-trained weights of the ResNet50 model, which has been trained on a large dataset (ImageNet) for general image recognition tasks, and adapt it to our problem "try to find a classification for fingerprints could help to predict blood group from it".

The architecture consists of the following components:

- Input Shape: It defines the shape of the input images, including the image size (height and width), the number of color channels, and the batch size.
- Preprocessing Layer: It applies necessary preprocessing operations to the input images, such as resizing and rescaling, to prepare them for feeding into the network. In this case, the images are rescaled by dividing the pixel values by 255 to bring them within the range of 0 to 1.
- Base Model (ResNet50): It is a pre-trained convolutional neural network architecture that has shown strong performance on various image recognition tasks. The ResNet50 model

is loaded with pre-trained weights from the ImageNet dataset. By setting "include_top=False", the final fully connected layers of the original ResNet50 model are excluded.

- Freezing the Base Model: The weights of the pre-trained ResNet50 model are frozen, preventing them from being updated during training. This is done to retain the knowledge learned from the ImageNet dataset and prevent overfitting on the new dataset.

- Additional Layers: After the base model, additional layers are added to adapt the features learned by ResNet50 for the classification task at hand. These layers include a global average pooling layer to reduce spatial dimensions, a dense layer with ReLU activation, a dropout layer for regularization, and a final dense layer with softmax activation to produce class probabilities.

- Compilation: The model is compiled by specifying the optimizer, the loss function, and the evaluation metrics. In this case, Adam optimizer, sparse categorical cross-entropy loss, and accuracy metric are used.

- Training: The model is trained on a training dataset with the specified parameters, including batch size, number of epochs, and validation data. The training process updates the trainable parameters of the fine-tuned layers while keeping the pre-trained weights fixed.

The diagram below depicts the architecture of the model:

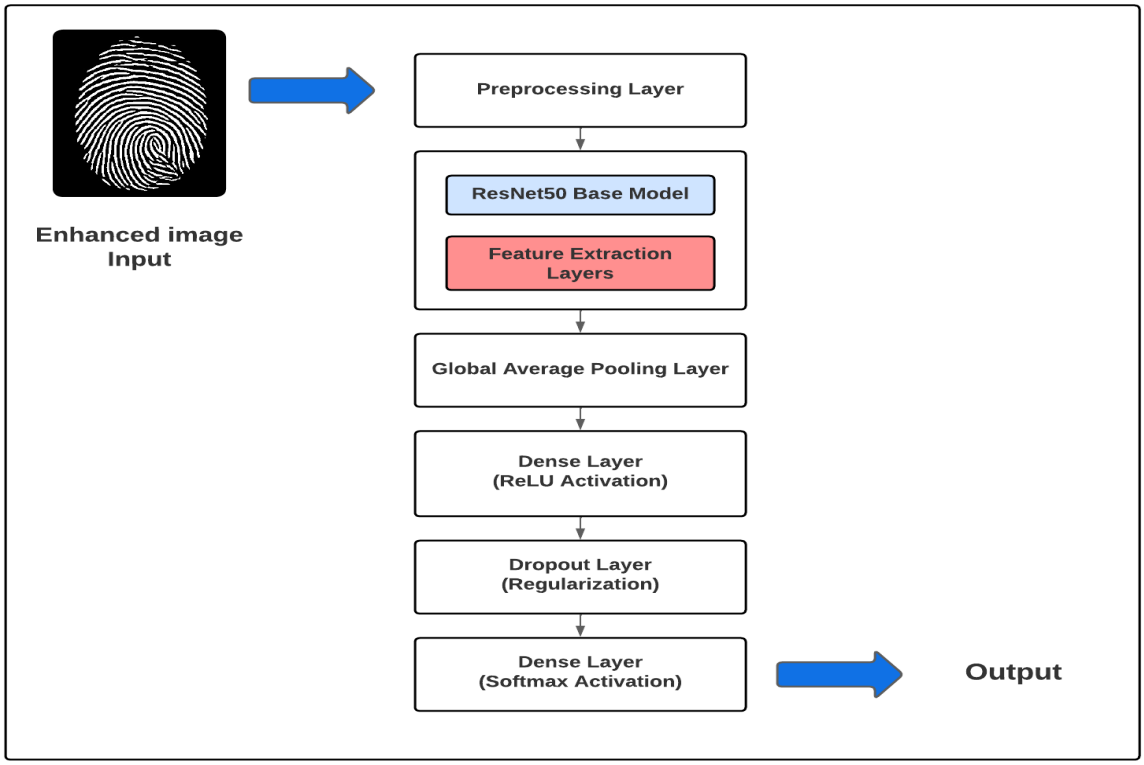

Figure II. 5: Res-Net architecture design

2.5.2 ALexNET

We attempt to utilize AlexNet since it is a well-known convolutional neural network (CNN) architecture that received recognition for defeating the competition for ImageNet Large-Scale Visual Recognition (ILSVRC) in 2012. A deep architecture with several convolutional and fully linked layers was also introduced. AlexNet stands out for its deep structure, huge filter sizes in convolutional layers, ReLU activation, overlapping pooling, data augmentation, and dropout regularization. The success of AlexNet revealed the potency of deep CNNs and encouraged the creation of later CNN models for computer vision tasks, making it a strategy that can be successful in solving our challenge.

The differences between AlexNet architecture and the normal CNN model (Lenet):

- Architecture Depth: In comparison to LeNet-5, AlexNet has a deeper architecture. As compared to LeNet-5, which has just seven layers and only two convolutional layers and three fully connected layers, AlexNet has eight layers, including five convolutional layers and three fully connected layers.

- Convolutional Layer Design: Compared to LeNet-5, AlexNet's convolutional layers are designed with bigger filter sizes. LeNet-5 employs lower filter sizes of 5x5 and 3x3 in its two convolutional layers while AlexNet uses 11x11 and 5x5 filters in its first and second convolutional layers, respectively.

- Activation Function: Both models use the ReLU activation function, but LeNet-5 uses sigmoid activation in its output layer, while AlexNet uses softmax activation in its final fully connected layer for multi-class classification.

- Pooling Layer: AlexNet employs overlapping pooling layers, which allow pooling regions to overlap, while LeNet-5 uses non-overlapping pooling layers with a fixed stride.

- Model Size: Due to its deeper architecture and larger number of parameters, AlexNet is generally a larger model compared to LeNet-5, requiring more computational resources for training and inference.

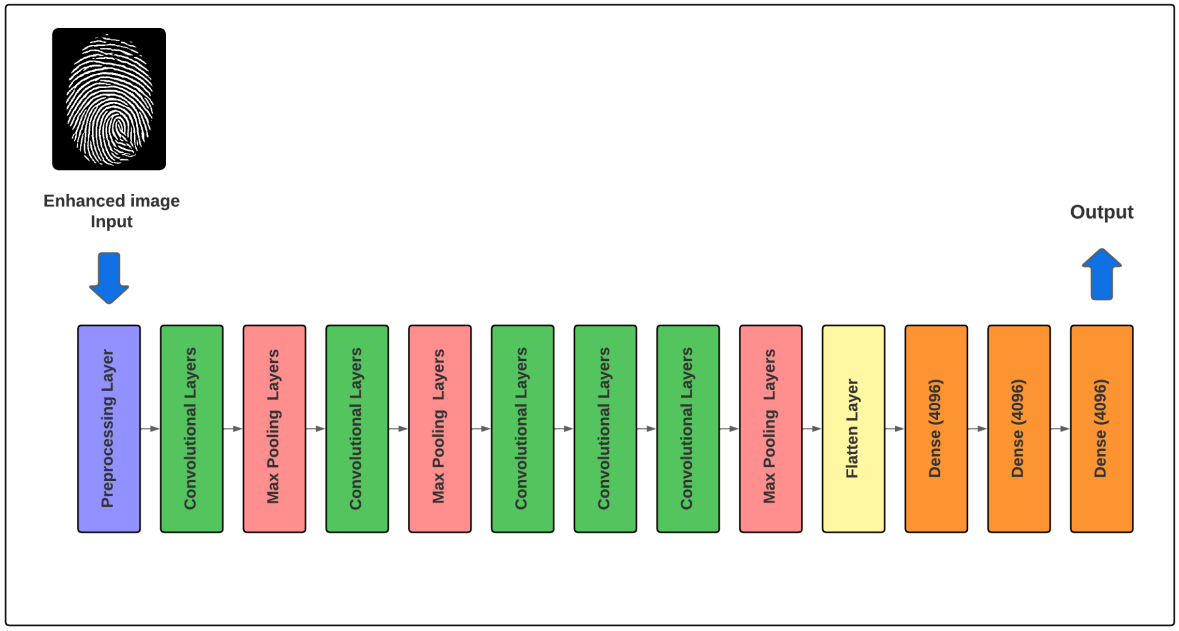

Figure II. 6: Alex-Net Model architecture design

2.5.3 VGG-16

The VGG16 architecture has shown impressive performance in image categorization tasks. It is renowned for its efficiency and simplicity in removing hierarchical characteristics from photos. The purpose of the VGG16 architecture is to apply the learned representations from a big dataset (ImageNet) to our particular problem, which is to predict blood type from fingerprints. Transfer learning allows us to take advantage of the detailed feature representations that the VGG16 model has previously acquired.

- Input Images: The model receives fingerprint images that capture unique patterns.
- Preprocessing: The images are resized to a specific size and pixel values are normalized.
- VGG16 Base: The VGG16 model serves as the base architecture for feature extraction. It consists of several convolutional layers followed by max pooling layers (Figure 2.7), which progressively learn and downsample the spatial features of the input images. The pre-trained weights of the VGG16 model, which were learned on the large-scale ImageNet dataset, capture general visual patterns that can be relevant for various image classification tasks.

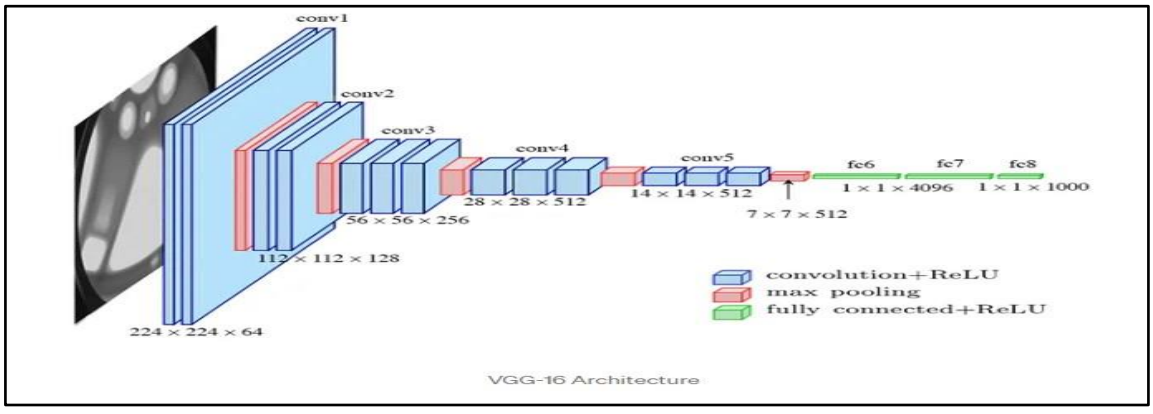

Figure II. 7: Base VGG-16 architecture design

- Freezing VGG16 Weights: The pre-trained weights of the VGG16 model are frozen to preserve learned representations and prevent overfitting.
- Flatten Layer: The extracted features are flattened into a 1D vector.

- Fully Connected Layers: The flattened features are passed through dense layers, serving as the classifier to predict blood groups.
- Output Layer: The final dense layer produces class probabilities using softmax activation.
- Compilation: The model is compiled with an optimizer, loss function, and evaluation metrics.

By using the VGG16 architecture and transfer learning, the model benefits from pre-learned visual patterns, making it more effective in classifying fingerprint images for blood group prediction. The freezing of weights prevents overfitting and the fully connected layers adapt the features for accurate classification. The compiled model is ready for training and evaluation.

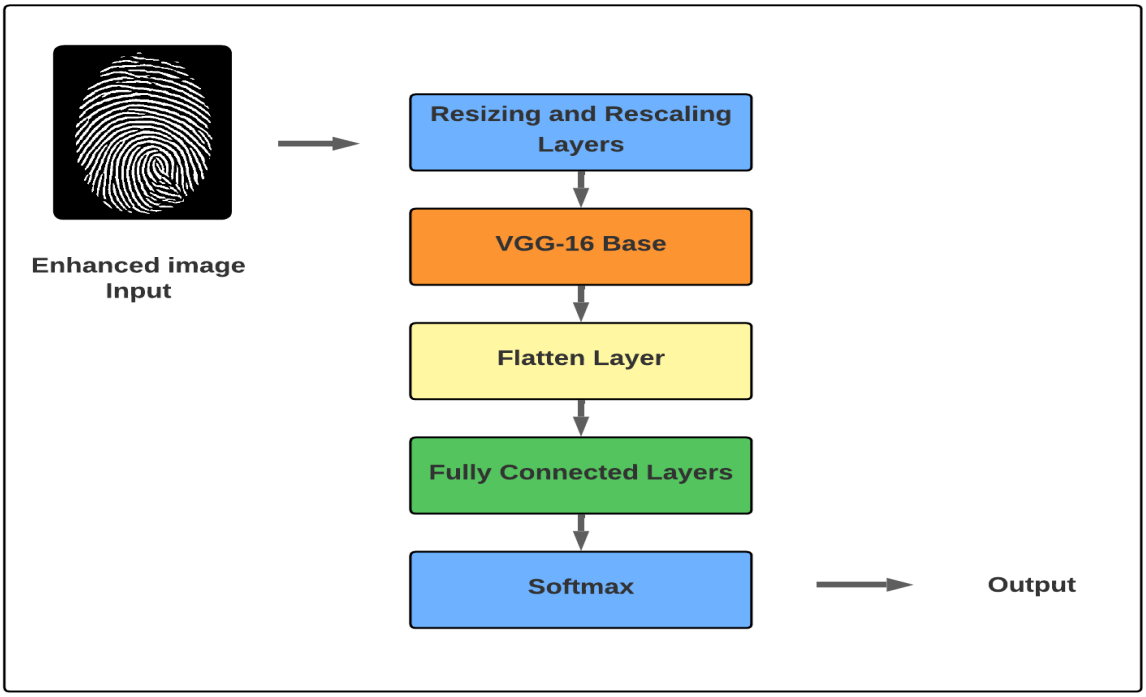

Figure II. 8: Our VGG-16 model architecture design

2.5.4 CNN Model

Convolutional Neural Network (CNN) architecture is a popular deep learning technique for pattern recognition and image analysis. Because of their capacity to automatically learn and extract pertinent features from the input data, CNNs have a significant advantage when it comes to predicting blood group from fingerprints. The CNN architecture that was employed in our study to determine blood group from fingerprint images is presented in this section.

A. Model Layers:

The CNN architecture consists of several key layers, each playing a crucial role in the feature extraction and classification process. The initial layers, such as the input layer and the resize-and-rescale layer, provide the necessary structure and normalization for the input fingerprint images. The subsequent convolutional layers are responsible for learning and detecting meaningful patterns or features from the images. These layers apply multiple filters with different weights to capture different aspects of the fingerprint patterns, such as ridgelines, ridge endings, and bifurcations. The ReLU activation function introduces non-linearity, allowing the network to model complex relationships between these learned features.

The max pooling layers follow the convolutional layers and serve to reduce the spatial dimensions of the feature maps. By selecting the maximum value within each pooling window, the layers downsample the feature maps while preserving the most salient information. This pooling operation helps to enhance the network's robustness to small variations in the fingerprint images and improve computational efficiency.

The flatten layer turns the 2D feature maps into a 1D vector so that the subsequent fully connected layers can process the newly discovered features. The dense, fully connected layers, which also complete the final mapping to the predicted blood groups, provide higher-level representations. The first dense layer uses the ReLU activation function to introduce non-linearity, whereas the output layer uses the softmax activation function to produce the probabilities for each blood group class.

B. Parameter Selection and Optimization:

The precise architecture of CNN-including the quantity of filters, kernel sizes, and dense units-is chosen using a combination of domain knowledge and experimentation. These

parameters play a crucial role in how well the network can capture and represent the discriminative features related to blood group prediction from fingerprints. Hyperparameter optimization techniques like grid search or random search can also be used to locate the ideal configuration that maximizes the model's performance.

The architecture is then trained using a suitable optimization algorithm, such as categorical cross-entropy as the task-appropriate loss function and stochastic gradient descent (SGD) or Adam (in our model). As the model is trained to minimize loss, the weights and biases of the network are modified in accordance with the gradients computed using backpropagation. The diagram below depicts the architecture of our model:

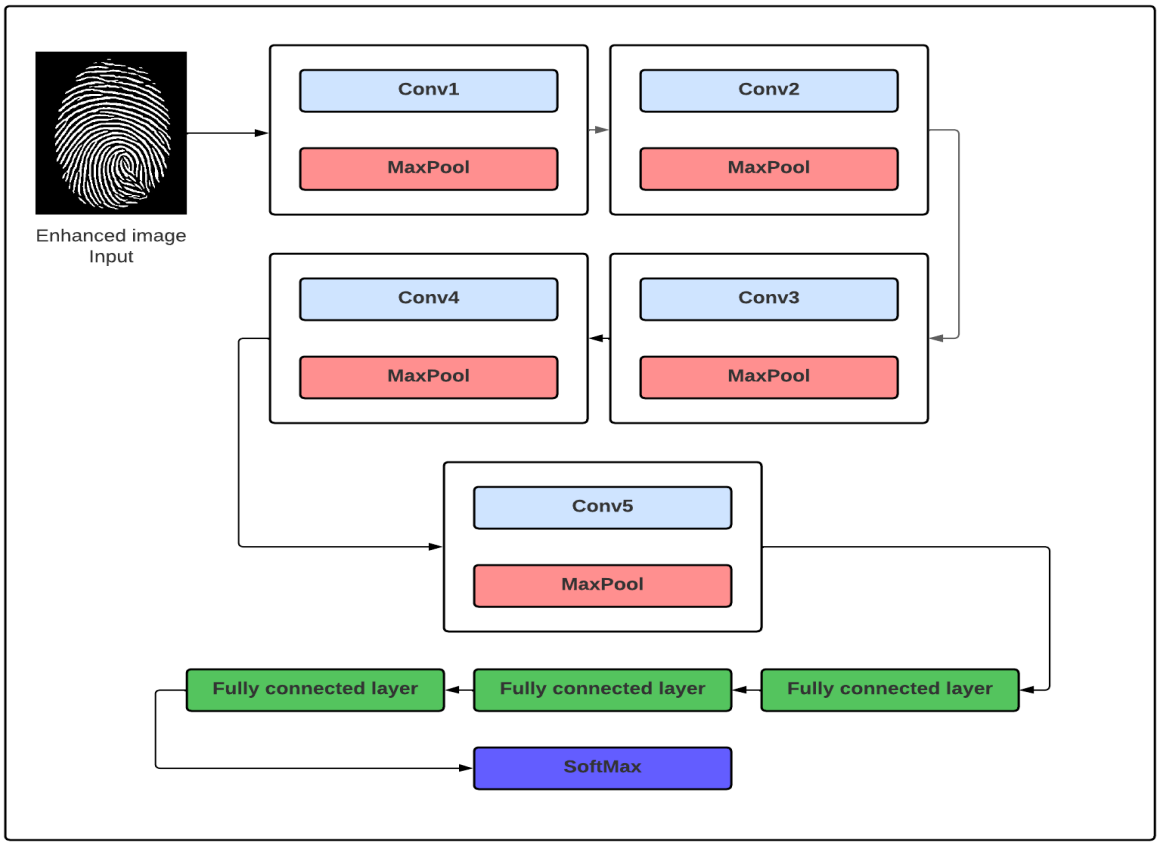

Figure II. 9: Proposed CNN architecture design

2.6. Conclusion

This chapter looked at the techniques and deep learning methodology we utilized in our research to predict blood types from fingerprints. The two key areas on which we focused were data collection and model architecture choices. We discussed the challenges of data collection, such as people's reluctance to provide their fingerprints and the dearth of certain blood kinds. We were nonetheless able to gather a respectable dataset of blood types and fingerprint patterns in spite of these difficulties. This dataset serves as the foundation for training and testing our deep learning models.

We then got into choosing the model architecture. We took into account a number of popular deep learning models, such as the VGG-16, AlexNet, ResNet, and build our CNN model. Each model's performance in picture classification tasks is influenced by its unique architectural features, such as the number and kinds of layers. By detailing the function of certain layers, parameters, and approaches used for fingerprint analysis and blood type prediction, we gave deep insights into the architecture of each model.

Chapter 3 will now concentrate on the application and outcomes of our investigation. We will give thorough explanations of the training procedure. Also, we will provide the findings from testing each model on our dataset and training it. We will use performance measures like accuracy, precision, and recall evaluating how well each model predicts blood types from fingerprints. The outcomes will be thoroughly analyzed and compared, which will reveal important information about the hypothesis "Possibility of predict blood group from fingerprint".

Chapter 03:
Implementation and results

Chapter III Implementation and Results

3.1 Introduction

This chapter presents the implementation details and results of our study on predicting blood groups from fingerprints using deep learning techniques. We discuss the training process, present the obtained results, conduct comparisons, and provide insights into the relationship between fingerprint characteristics and blood group prediction.

We begin by introducing the implementation environment, including the programming language, frameworks, and hardware specifications utilized. Next, we delve into the training process, covering the dataset used, preprocessing steps, and training parameters. We then present the results, evaluating the performance using relevant metrics and visualizations. Discussions and comparisons follow, analyzing the strengths and weaknesses of our approach and comparing it to previous studies or methods.

In summary, this chapter provides an overview of our implementation and the results obtained. By examining the training process, discussing the findings, and conducting comparisons, we gain insights into predicting blood groups from fingerprints. These findings contribute to the advancement of biometric recognition and healthcare applications.

3.2 Development Environment

3.2.1 Anaconda

By enhancing package management and deployment, the open-source Anaconda distribution for Python and R seeks to simplify scientific computing. Python is a powerful, free, and interpreted programming language that may be used for a wide range of tasks. It provides a platform with a comprehensive collection of pre-installed packages and tools commonly used in data analysis, machine learning, and scientific research. Anaconda makes configuring and managing the development environment easier by providing a user-friendly package manager and environment management system. Data scientists, academics, and developers regularly utilize it due to its ease of use, accessibility of packages, and compatibility with a range of operating systems [21].

3.2.2 PyCharm

The robust integrated development environment (IDE) PyCharm was created especially for Python programming. It is created by JetBrains and offers a variety of features and tools to boost productivity and simplify Python development. Among the features offered by PyCharm are support for a number of Python frameworks and libraries, intelligent code analysis, debugging tools, and version control integration [22].

Python code can be efficiently written, tested, and debugged using PyCharm's user-friendly interface. It provides sophisticated coding support, such as syntax highlighting, code formatting, and code navigation, which facilitates the writing of clear, well-structured code. Additionally, the IDE offers project management capabilities that let programmers control dependencies, carry out unit tests, and deploy applications in packaged form.

In addition, PyCharm provides integration with well-known web development frameworks, such as Django, Flask, or FastApi, which we will use in our work and offers specialized support for web development projects. Additionally, it supports database integration, allowing developers to access databases and use SQL queries inside the IDE.

3.3 Programming Language and Libraries

3.3.1 Python

In the area of deep learning, Python is a high-level programming language that stands out for a number of reasons. Both newcomers and seasoned programmers can benefit from how simple and easy to understand it is to learn and use. TensorFlow, PyTorch, and Keras are just a few of the deep learning libraries and frameworks that Python is home to, all of which offer robust tools and pre-built functions for rapid model development. Additionally, Python's adaptability enables seamless integration with other technologies and tools frequently used in deep learning pipelines, including libraries for data manipulation like NumPy and Pandas and visualization libraries like Matplotlib. For projects like ours, the language's interpreted nature and interactive development environment facilitate quick prototyping and experimentation [23].

3.3.2 Libraries Used

1) TensorFlow

TensorFlow is a powerful software that can greatly assist us in our project of predicting blood groups from fingerprints. It offers a comprehensive framework for building deep learning models, allowing us to design a neural network specifically tailored to our task. With TensorFlow's image processing capabilities, we can enhance fingerprint images, extract relevant features, and preprocess the data to improve accuracy. Additionally, TensorFlow's efficient training algorithms and optimization techniques enable us to train our model on labeled fingerprint datasets, while GPU acceleration speeds up computations. By leveraging TensorFlow's capabilities, we can develop a robust prediction model that accurately analyzes fingerprints and predicts blood groups [24].

2) Keras

On top of TensorFlow, Keras is a high-level neural network API written in Python. It offers a simple and straightforward interface for creating deep learning models. By providing a variety of pre-built layers, activation functions, and optimization techniques, Keras makes it easier to build and train neural networks. Keras can be useful in constructing and training our model for our study on inferring blood types from fingerprints. With Keras, you can quickly build a convolutional neural network (CNN) architecture that is suitable for image classification applications. We can evaluate the effectiveness of our blood type prediction model on hidden fingerprint data thanks to Keras, which also makes model assessment and prediction possible. Keras gives us power with its simplicity and connection with TensorFlow [25].

3) Matplotlib

We utilized Matplotlib in our project for its powerful data visualization capabilities. Matplotlib is a widely-used plotting library in Python that allows us to create a variety of visualizations, including charts, graphs, histograms, and scatter plots. In the context of predicting blood groups from fingerprints, Matplotlib enables us to visualize the distribution and patterns of different blood groups within our dataset. We can generate informative plots to understand the relationship between fingerprint features and blood group outcomes. This visualization aids in exploring the data, identifying any potential trends or patterns, and gaining insights into the predictive capabilities of our model. Additionally, Matplotlib allows us to present our findings effectively, making it easier to communicate the results of our project to

stakeholders and researchers. By incorporating Matplotlib into our project, we enhance our ability to analyze and interpret the data, contributing to the overall success and comprehensibility of our blood group prediction system [26].

4) NumPy:

NumPy is a crucial component in our project as it provides efficient numerical computing capabilities and array manipulation. With NumPy, we can easily process and manipulate multi-dimensional arrays, enabling us to extract features from fingerprint images, perform statistical analysis, and streamline our data processing pipeline. Its powerful mathematical functions and operations enhance the accuracy and efficiency of our blood group prediction system [27].

3.4 Training and Results

In this section, we present the training and results of our blood group prediction models. We have trained four different models (VGG16, ResNet, AlexNet, and a custom CNN) using various datasets, including fingerprints from different sources. Also we evaluate the models on an independent test dataset using metrics such as accuracy, precision, recall, and F1 score. We compare the performance of the different models and datasets to identify the most effective combinations.

Through this section, we display the accuracy of our models in predicting blood groups from fingerprints. The results provide insights into the performance of each model and the impact of dataset variations.

3.4.1 ALexNET

"AlexNet" is the first model that will be trained and assessed. We will use a variety of fingerprint datasets to train it, including "right-hand fingerprints alone," "left-hand fingerprinting only," "fingerprints from both hands combined," and "modified fingerprints," among others. This is done to account for all potential outcomes and produce unmistakable outcomes. The model's parameters are listed below:

- **Epochs:** The number of times the fingerprint images dataset is passed through the model during training. on this model we gonna put it 15.

- **Batch size:** batch size it the number of training examples "fingerprints images" that processed together in one iteration. We gonna put it 32.

- **Optimizer (Adam):** Adam is an optimization algorithm commonly used for training deep learning models. It stands for Adaptive Moment Estimation. Adam maintains adaptive learning rates for each parameter by keeping track of past gradients and their magnitudes. It combines the advantages of two other optimization algorithms, AdaGrad and RMSProp, to efficiently converge to a good set of weights for the model.

- **Activation function (ReLU):** ReLU stands for Rectified Linear Unit and is an activation function commonly used in neural networks. It introduces non-linearity into the network by transforming the weighted sum of inputs into an output value. ReLU activation returns the input as the output if it is positive, and zero otherwise. It helps the model learn complex patterns and improves the network's ability to model non-linear relationships between inputs and outputs.

```
Model: "sequential_2"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 sequential_1 (Sequential)   (None, 256, 256, 3)       0

 conv2d (Conv2D)             (None, 62, 62, 96)        34944

 max_pooling2d (MaxPooling2D  (None, 30, 30, 96)       0
 )

 conv2d_1 (Conv2D)           (None, 26, 26, 256)       614656

 max_pooling2d_1 (MaxPooling  (None, 12, 12, 256)      0
 2D)

 conv2d_2 (Conv2D)           (None, 10, 10, 384)       885120

 conv2d_3 (Conv2D)           (None, 8, 8, 384)         1327488

 conv2d_4 (Conv2D)           (None, 6, 6, 256)         884992

 max_pooling2d_2 (MaxPooling  (None, 2, 2, 256)        0
 2D)

 flatten (Flatten)           (None, 1024)              0

 dense (Dense)               (None, 4096)              4198400

 dropout (Dropout)           (None, 4096)              0

 dense_1 (Dense)             (None, 4096)              16781312

 dropout_1 (Dropout)         (None, 4096)              0

 dense_2 (Dense)             (None, 2)                 8194

=================================================================
Total params: 24,735,106
Trainable params: 24,735,106
Non-trainable params: 0
_________________________________________________________________
```

Figure III. 1: AlexNet Model Summary

After training the model with these settings on two datasets (the first is collection of fingerprint of both hands and the second it only fingerprints of left hand), we observed the following results, represented by accuracy and loss rates on the F1 scale.

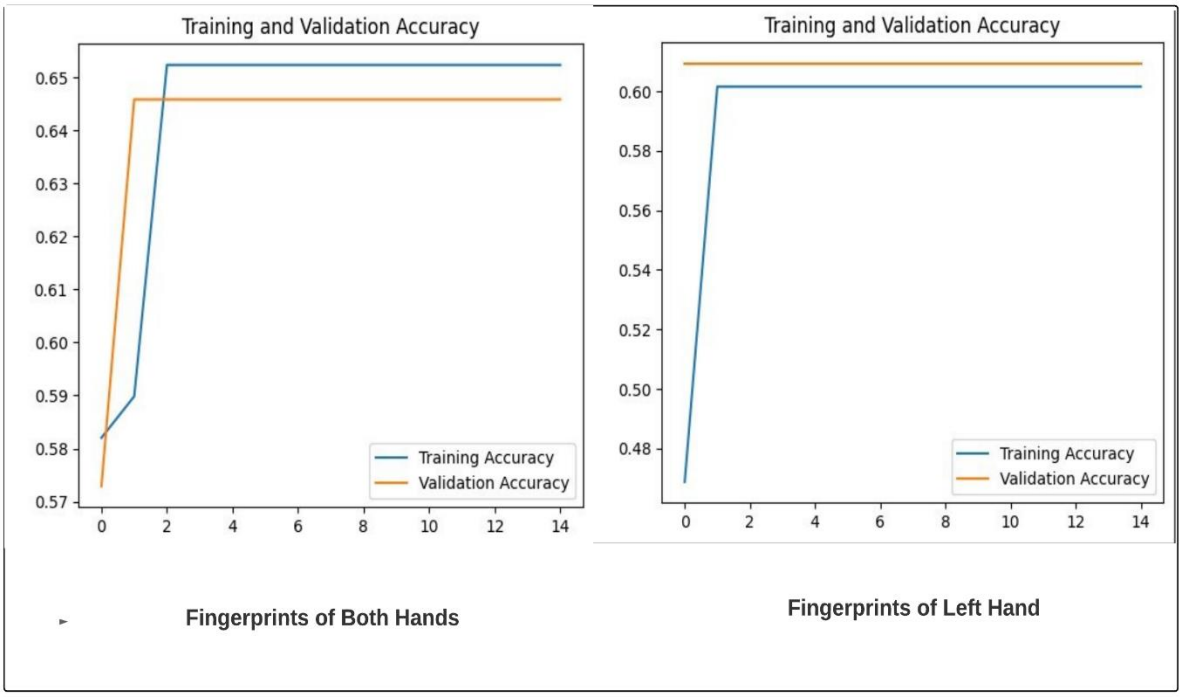

Figure III. 2: Training and Validation Accuracy

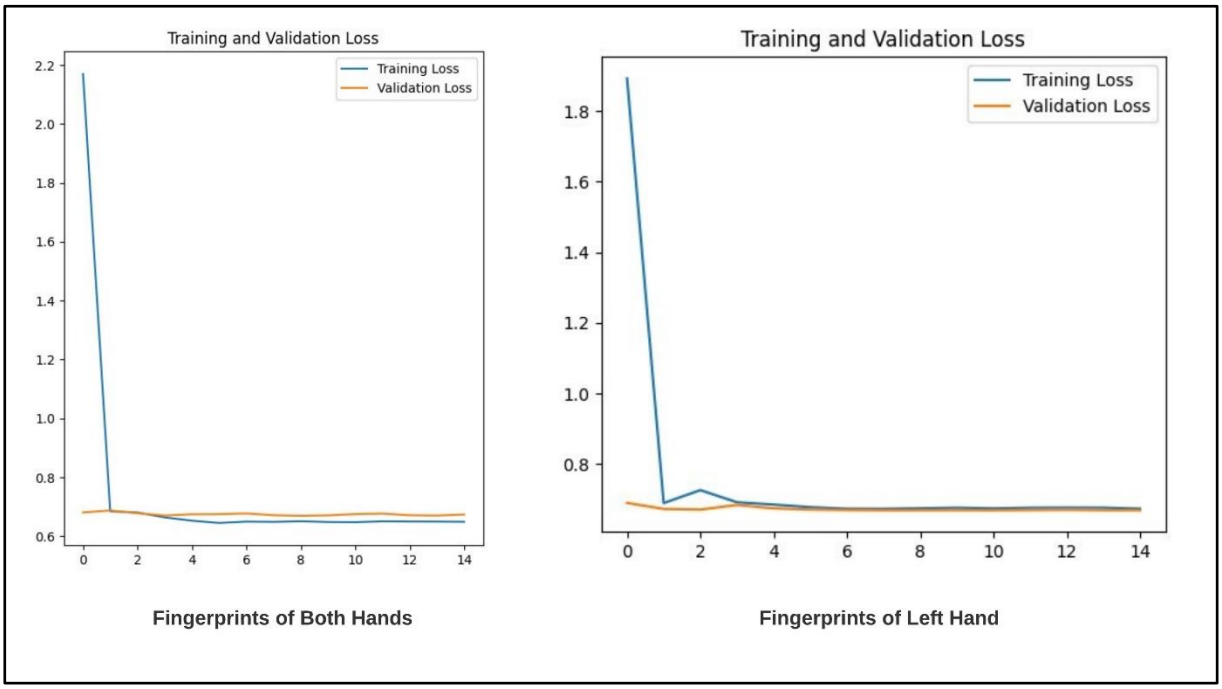

Figure III. 3: Training and Validation Loss

After training and evaluating, this some result of model prediction of different fingerprints:

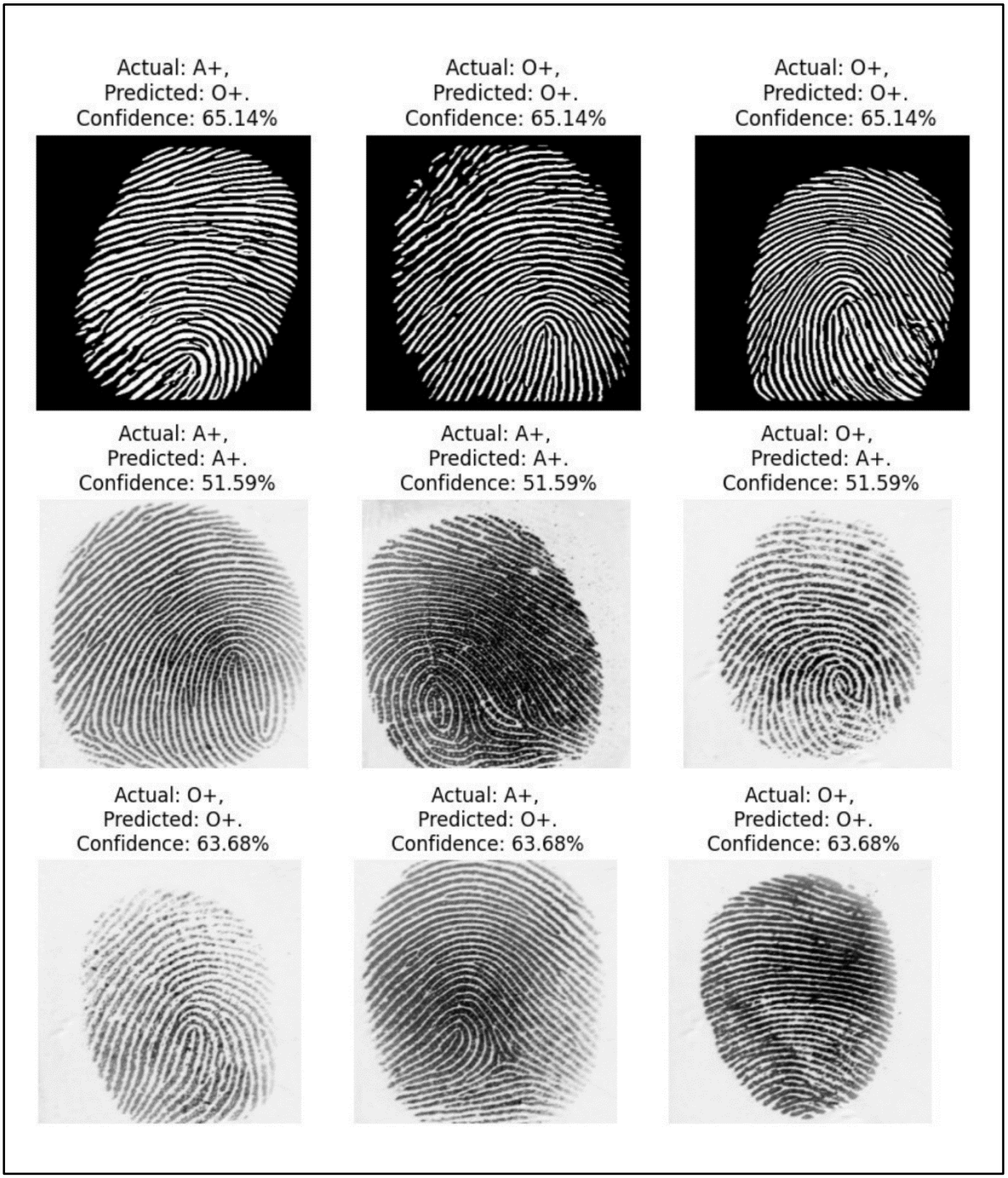

Figure III. 4: AlexNet Prediction of Blood Group

3.4.2 VGG-16

VGG-16 it going to be the second model that we will trained and assessed, the model's parameters are listed below:

- Epochs: we going to put it 15.
- Batch size**:** batch size will be 32.
- Optimizer: optimization algorithm = ‘Adam’.
- Activation function: it will be ReLU.

Layer (type)	Output Shape	Param #
sequential (Sequential)	(None, 350, 350, 3)	0
vgg16 (Functional)	(None, 10, 10, 512)	14714688
flatten (Flatten)	(None, 51200)	0
dense (Dense)	(None, 4096)	209719296
dense_1 (Dense)	(None, 4096)	16781312
dense_2 (Dense)	(None, 2)	8194

Total params: 241,223,490
Trainable params: 241,223,490
Non-trainable params: 0

Figure III. 5: VGG-16 Model Summary

After training the model with these settings on two datasets (the first is collection of fingerprint of both hands and the second it only fingerprints of left hand), we observed the following results, represented by accuracy and loss rates on the F1 scale.

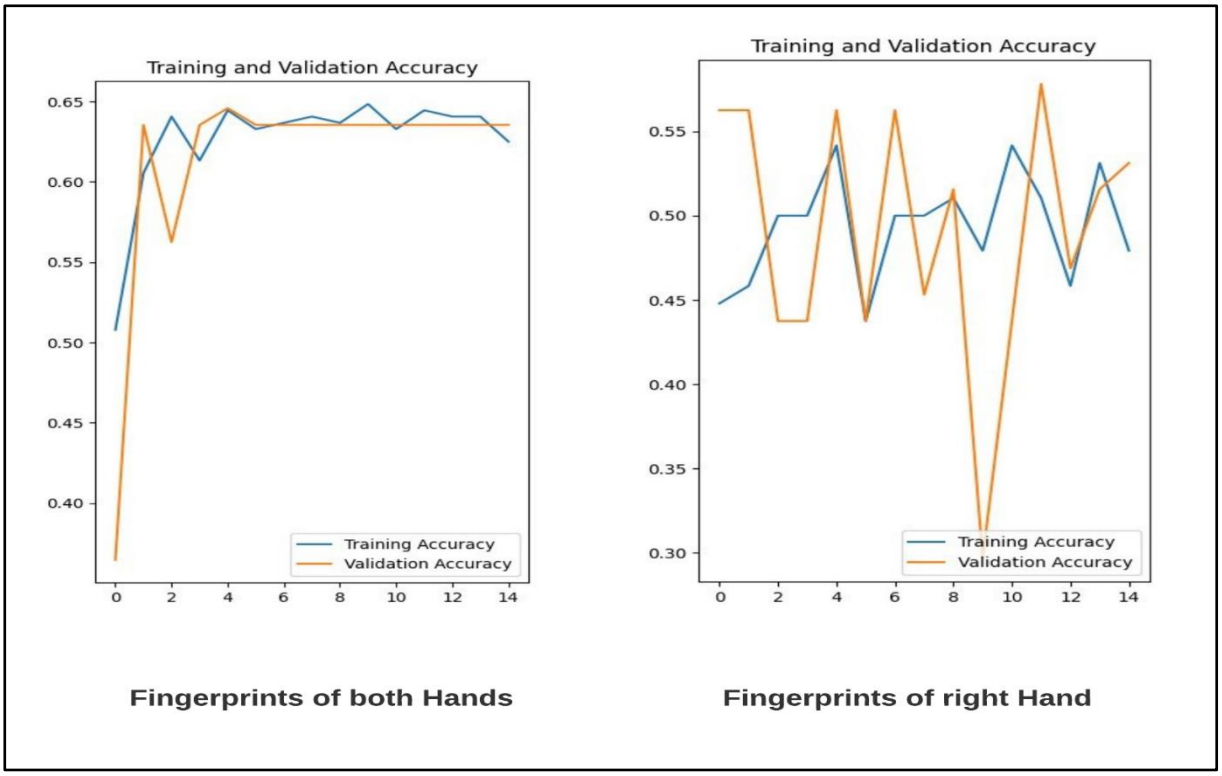

Figure III. 6: Training and Validation Accuracy

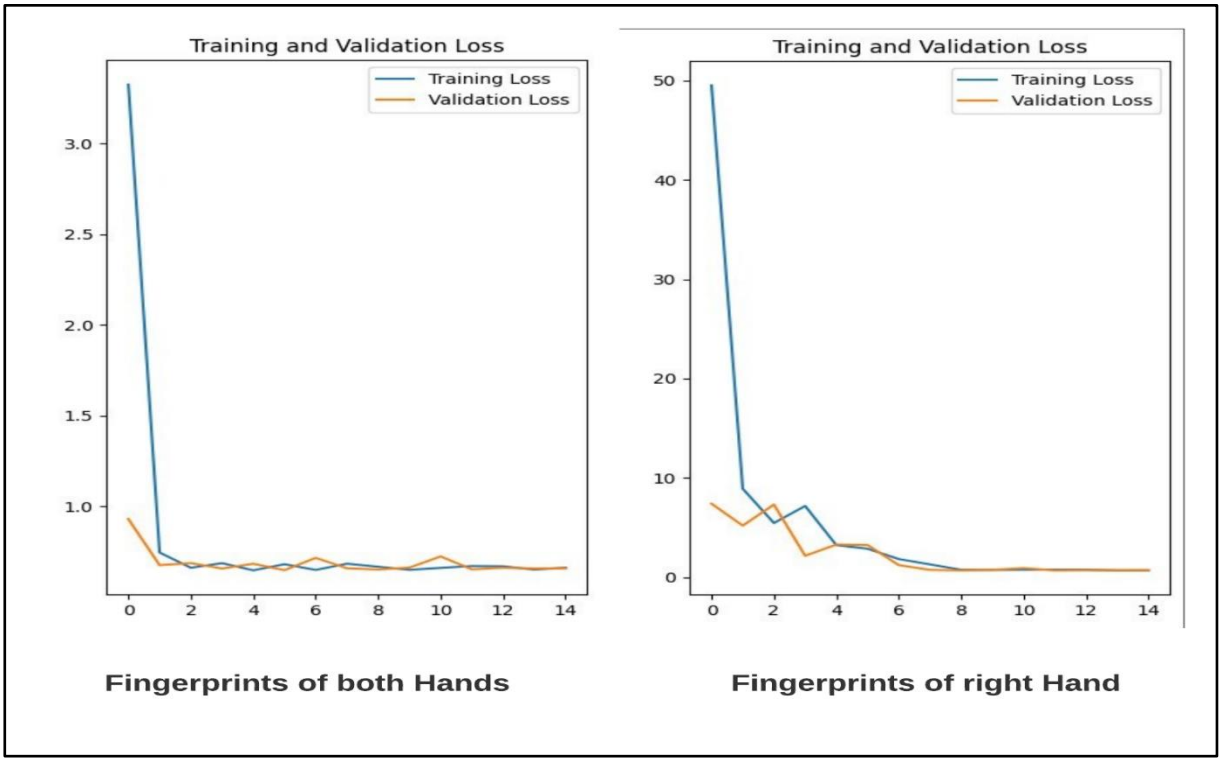

Figure III. 7: Training and Validation Loss

After training and evaluating, this some result of model prediction of different fingerprints:

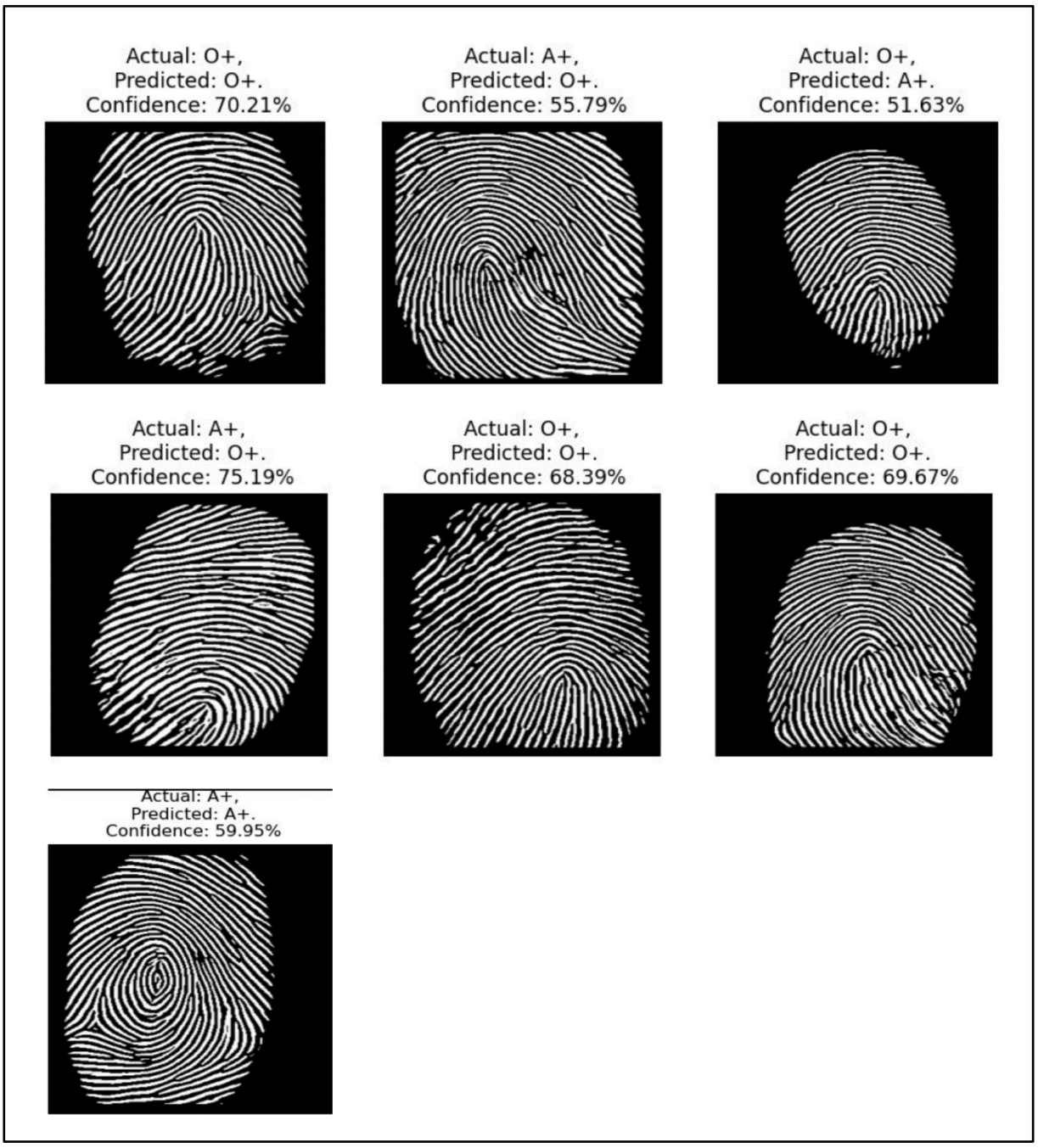

Figure III. 8: VGG-16 Prediction of Blood Group

3.4.3 ResNet

ResNet it going to be the third model that we will trained and assessed, the model's parameters are listed below:

- Epochs: we going to put it 40.
- Batch size**:** batch size will be 32.
- Optimizer: optimization algorithm = ‘Adam’.
- Activation function: it will be ReLU.

```
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 sequential (Sequential)     (None, 350, 350, 3)       0

 vgg16 (Functional)          (None, 10, 10, 512)       14714688

 flatten (Flatten)           (None, 51200)             0

 dense (Dense)               (None, 4096)              209719296

 dense_1 (Dense)             (None, 4096)              16781312

 dense_2 (Dense)             (None, 2)                 8194

=================================================================
Total params: 241,223,490
Trainable params: 241,223,490
Non-trainable params: 0
_________________________________________________________________
```

Figure III. 9: ResNet Model Summary

After training the model with these settings on two datasets (the first is collection of fingerprint of both hands and the second it only fingerprints of left hand), we observed the following results, represented by accuracy and loss rates on the F1 scale.

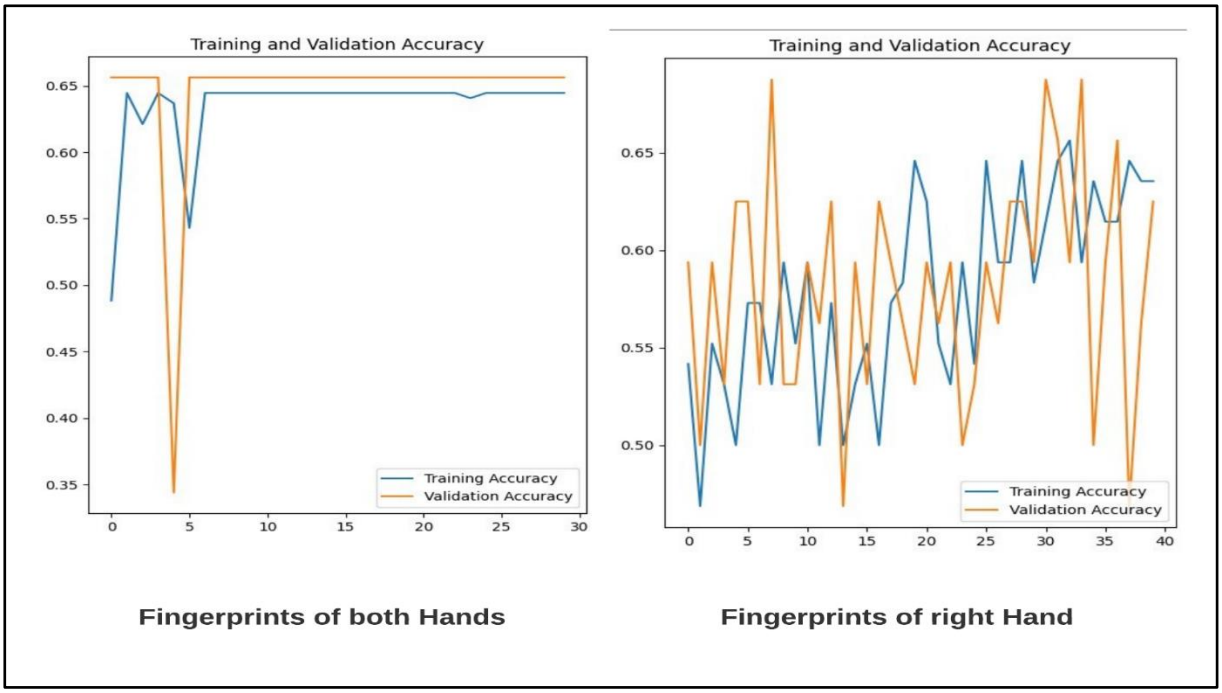

Figure III. 10: Training and Validation Accuracy

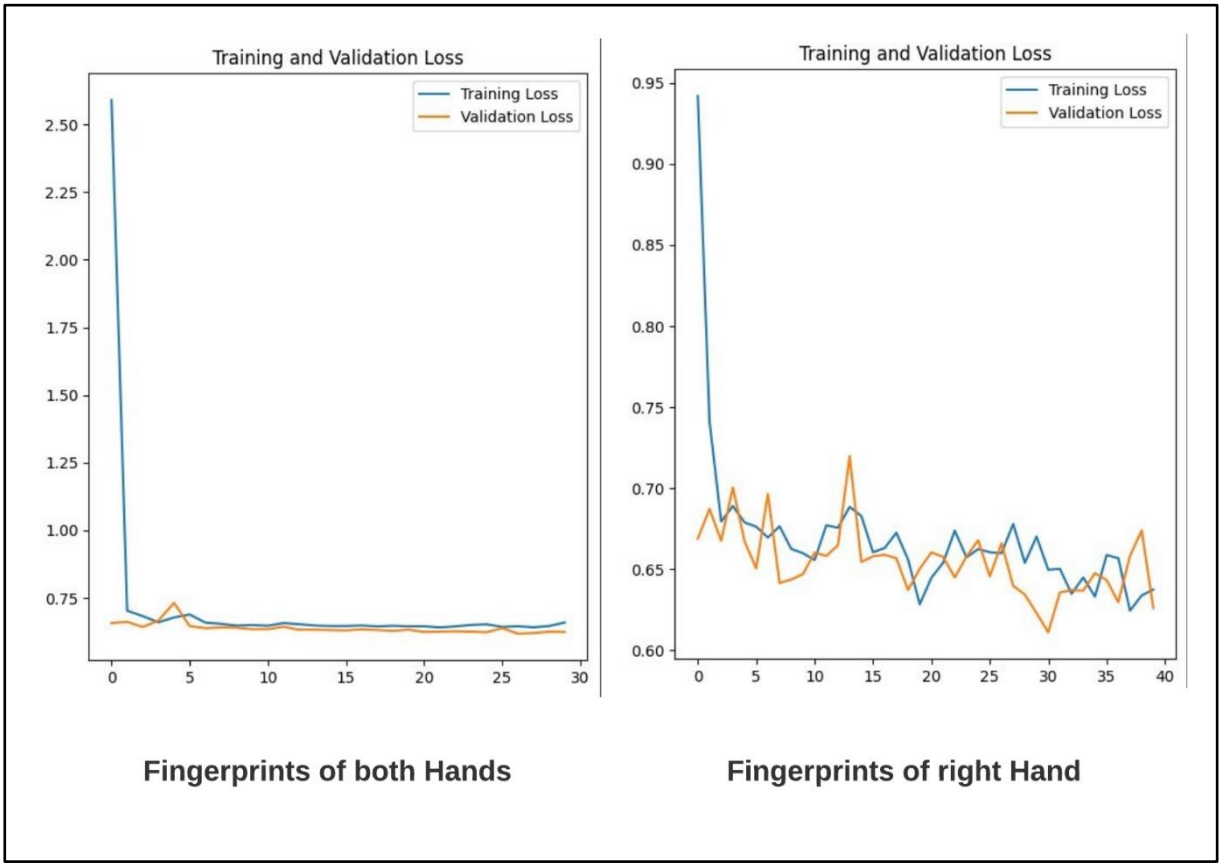

Figure III. 11 : Training and Validation Loss.

After training and evaluating, this some result of model prediction of different fingerprints:

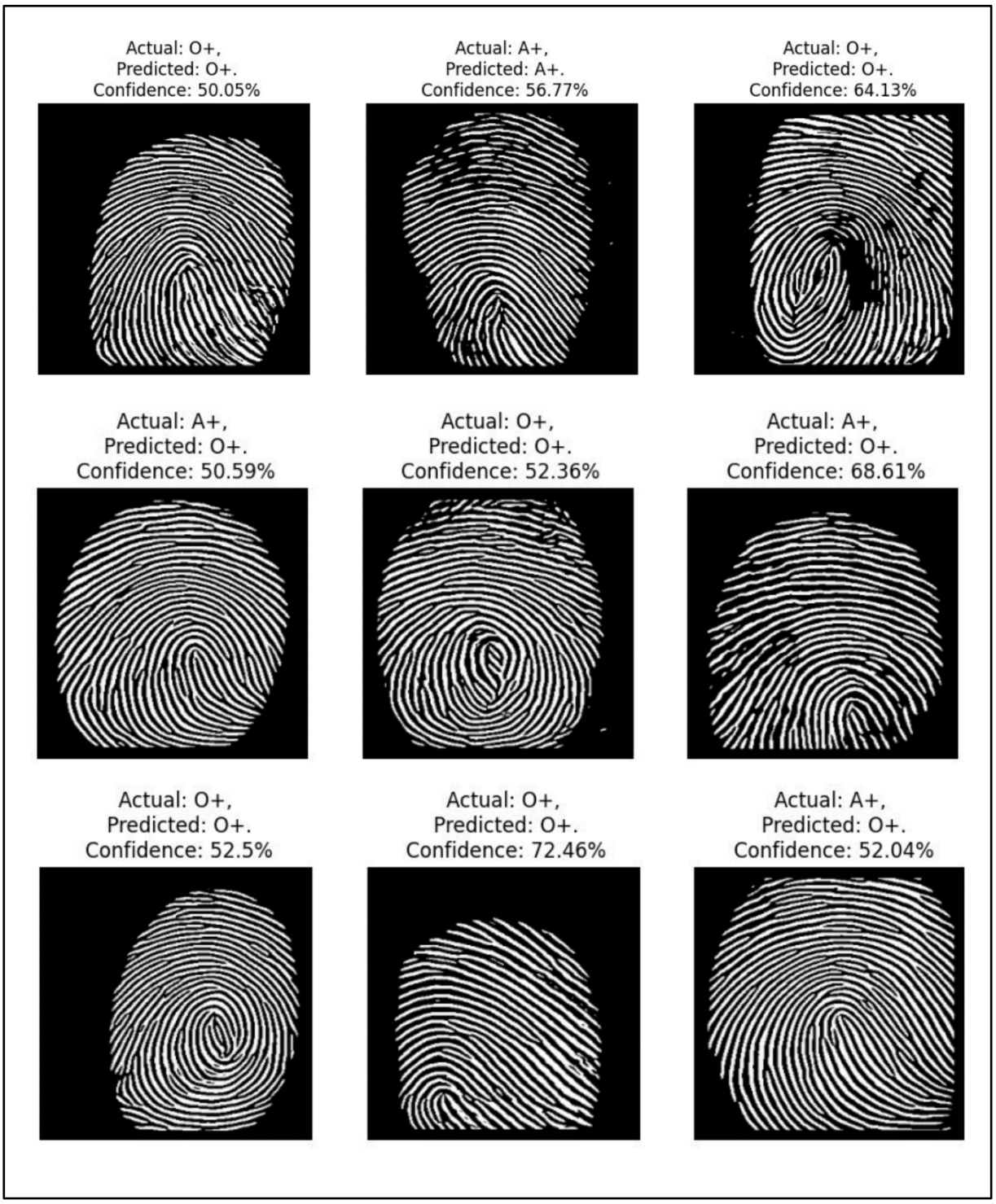

Figure III. 12: ResNet Prediction of Blood Group

3.4.4 CNN

The CNN model that we build it going to be the fourth model that we will trained and assessed, the model's parameters are listed below:

- Epochs: we going to put it 15.
- Batch size**:** batch size will be 32.
- Optimizer: optimization algorithm = ‘Adam’.
- Activation function: it will be ReLU.

```
Model: "sequential_3"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 sequential (Sequential)     (None, 256, 256, 3)       0

 conv2d_4 (Conv2D)           (32, 254, 254, 32)        896

 max_pooling2d_4 (MaxPooling  (32, 127, 127, 32)       0
 2D)

 conv2d_5 (Conv2D)           (32, 125, 125, 64)        18496

 max_pooling2d_5 (MaxPooling  (32, 62, 62, 64)         0
 2D)

 conv2d_6 (Conv2D)           (32, 60, 60, 128)         73856

 max_pooling2d_6 (MaxPooling  (32, 30, 30, 128)        0
 2D)

 conv2d_7 (Conv2D)           (32, 28, 28, 256)         295168

 max_pooling2d_7 (MaxPooling  (32, 14, 14, 256)        0
 2D)

 conv2d_8 (Conv2D)           (32, 12, 12, 256)         590080

 max_pooling2d_8 (MaxPooling  (32, 6, 6, 256)          0
 2D)

 flatten_1 (Flatten)         (32, 9216)                0

 dense_2 (Dense)             (32, 512)                 4719104

 dropout_1 (Dropout)         (32, 512)                 0

 dense_3 (Dense)             (32, 2)                   1026

=================================================================
Total params: 5,698,626
Trainable params: 5,698,626
Non-trainable params: 0
```

Figure III. 13: CNN Model Summary

After training the model with these settings on two datasets (the first is collection of fingerprint of both hands and the second it only fingerprints of left hand), we observed the following results, represented by accuracy and loss curves

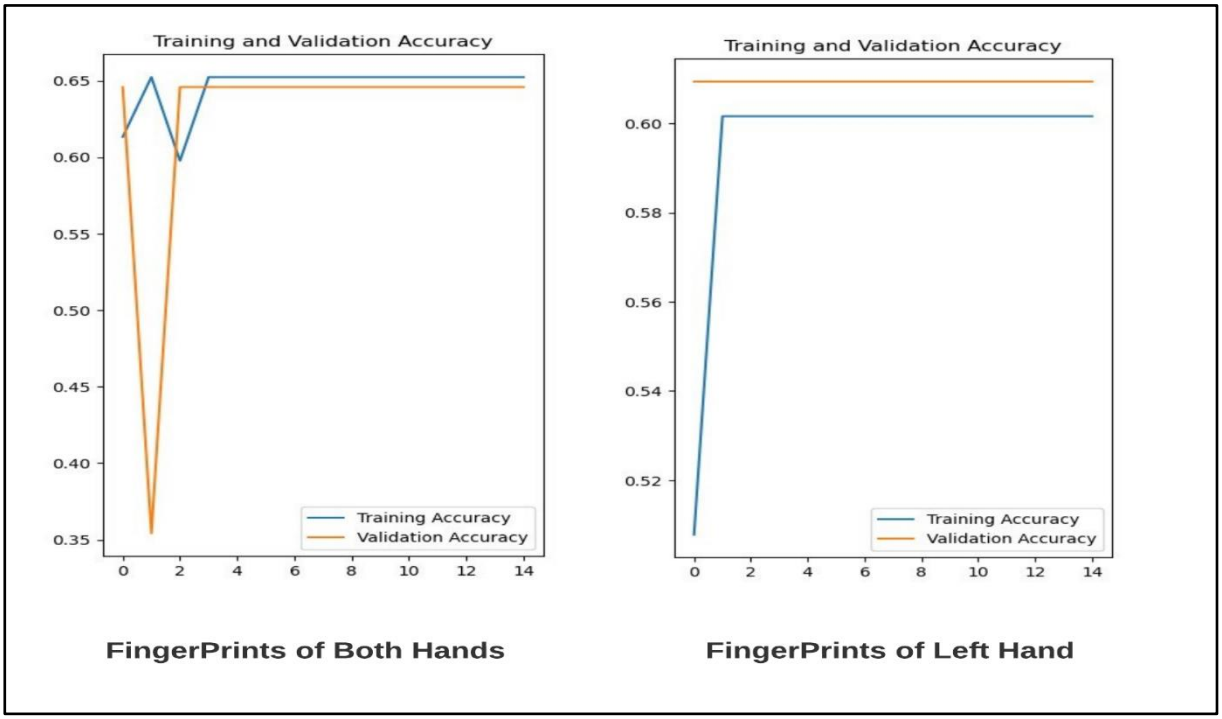

Figure III. 14: Training and Validation Accuracy

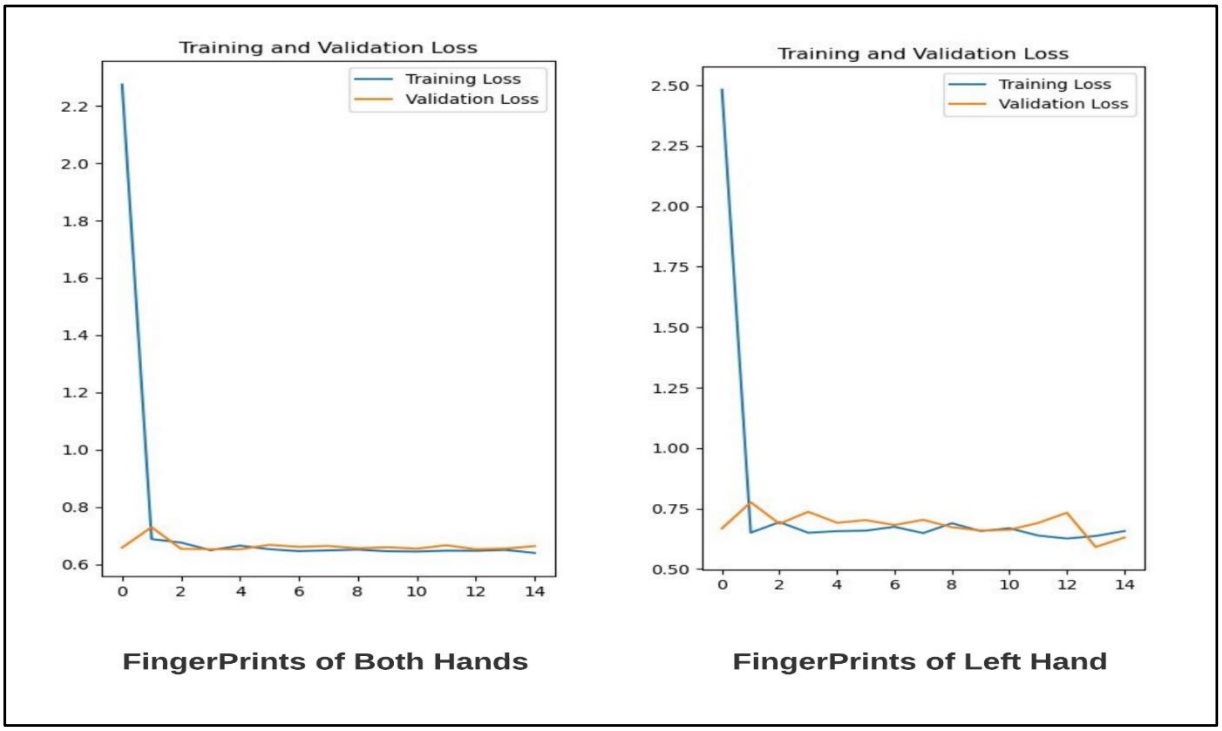

Figure III. 15: Training and Validation Loss

After training and evaluating, this some result of model prediction of different fingerprints:

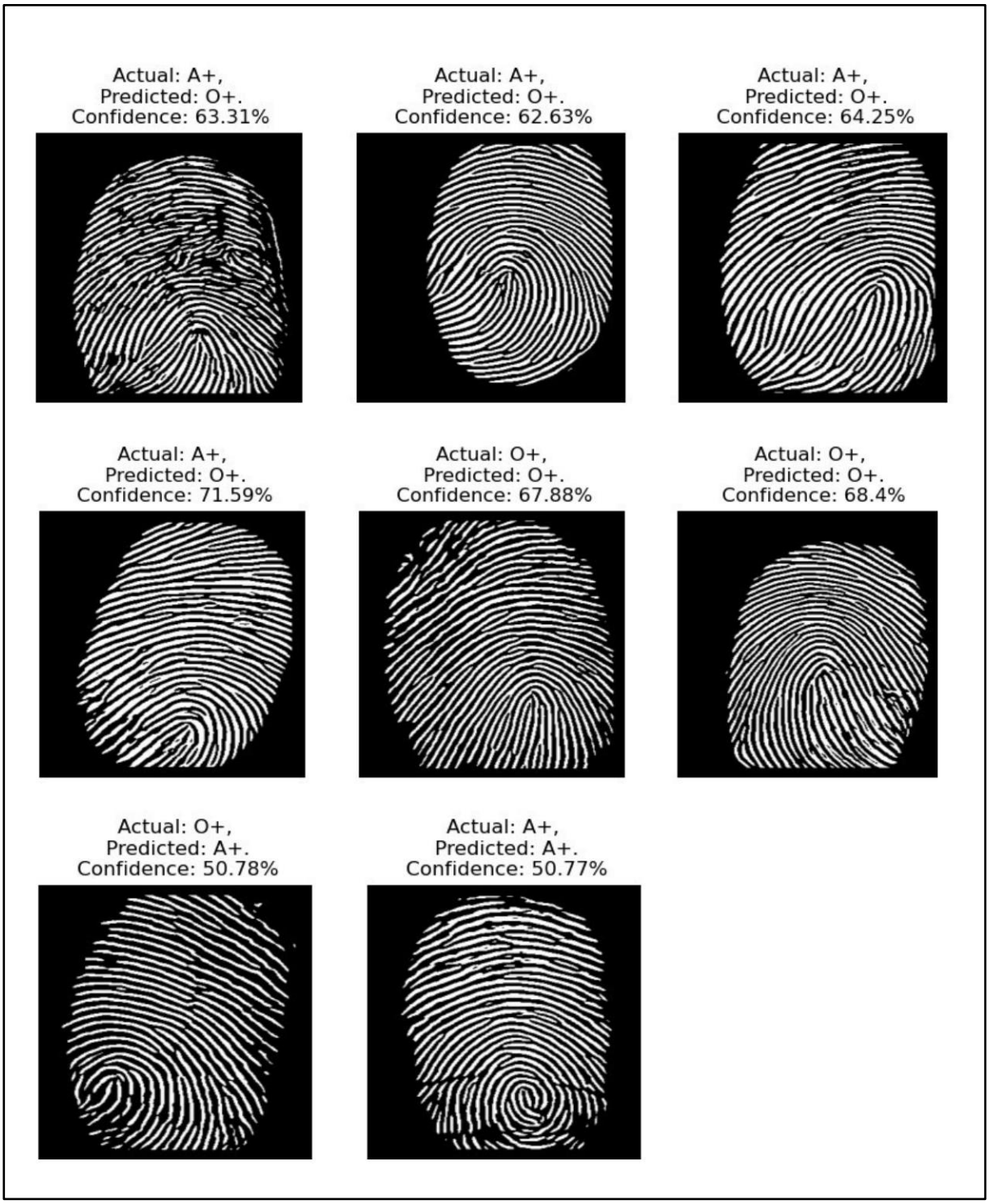

Figure III. 16: CNN Prediction of Blood Group

The Figure below (Figure III.17) describe the accuracy of our models with two kind of dataset “one hand and both hand”.

Figure III. 17: Comparative statistics of Models

3.5 Discussions

The outcome of our study was unexpected and somewhat discouraging, as the accuracy achieved by the four models (VGG, ResNet, AlexNet, and the CNN) did not surpass 0.76, even after extensive exploration and training. This suggests that the models were not able to effectively capture the distinguishing fingerprint signals associated with blood groups.

One possible explanation for the limited accuracy could be the lack of clear and consistent fingerprint patterns that are exclusively associated with specific blood groups. When examining the statistics of fingerprint types, we observed that the distribution of fingerprint patterns across different blood groups was not significantly distinct. For example, in the group O, which is the most common blood group, we found that 54% of fingerprints exhibited loop patterns, 31% had whorl patterns, and 15% had arch patterns. These proportions were not significantly different from the fingerprint pattern distributions in other blood groups.

Furthermore, our findings revealed that certain fingerprint indications believed to be associated with particular blood groups were present in the fingerprints of individuals with

group O+ blood. This suggests that relying solely on fingerprint characteristics to predict blood type may not be reliable, as the presence of these indications does not necessarily indicate a specific blood group.

The limitations and challenges encountered during data collection also contributed to the suboptimal results. We faced difficulties in collecting a diverse dataset of fingerprints, as many individuals were hesitant to provide their fingerprints for the study. Additionally, the availability of certain blood types, particularly rare blood types, was limited, resulting in an imbalance in the dataset.

Based on these findings, it becomes evident that the current understanding of fingerprint anatomy and the science of fingerprint recognition may not provide sufficient information to accurately predict blood types. The lack of consistent and distinguishing fingerprint signals associated with blood groups poses a significant challenge in developing reliable prediction models.

3.6 Conclusion

In this chapter, we discussed the implementation details and outcomes of our project, which employed deep learning models to predict blood types from fingerprints. Our goals were to evaluate the effectiveness of various model architectures and investigate the viability of employing fingerprint traits as blood type markers.

We trained and evaluated four deep learning models: VGG, ResNet, AlexNet, and a custom CNN model. These models were trained on various datasets, including fingerprints from the right hand, both hands, and other combinations, to encompass all possible scenarios. The training process involved preprocessing the data, augmenting the dataset, and optimizing the model parameters.

We gathered performance indicators such as accuracy, precision, recall during the training and assessment phases to evaluate each model's propensity for prediction. In order to uncover any potential relationships, we also performed statistical research on the distribution of fingerprint patterns among various blood types.

Despite our rigorous efforts, the results obtained were below our expectations. The accuracy achieved by the models did not exceed 0.76, indicating the difficulty of accurately predicting blood types based solely on fingerprint characteristics. Our models exhibited random behavior, and we found no substantial evidence of consistent and distinguishing fingerprint signals associated with specific blood groups.

In conclusion, our project demonstrates the complexities and limitations in predicting blood groups from fingerprints using deep learning models. While our models were trained on diverse datasets and architectures, the results did not yield conclusive evidence to support the reliable prediction of blood types solely based on fingerprint characteristics.

General Conclusion

Our work concludes that it is currently not possible to predict blood types from fingerprints using deep learning algorithms. Despite being trained on a wide range of scenarios and possibilities, the models, including VGG, ResNet, AlexNet, and the suggested CNN, could not attain appreciable accuracy, with the maximum accuracy not exceeding 0.76.

The absence of clear and consistent fingerprint patterns exclusively associated with specific blood groups, coupled with the presence of similar indications across different blood groups, challenges the assumption that fingerprints alone can reliably predict blood types. These findings highlight the complexity of the relationship between fingerprints and blood groups and the limitations of current fingerprint recognition techniques.

To improve the accuracy of blood group prediction from fingerprints, future research should consider exploring alternative approaches or integrating complementary data sources. For instance, incorporating genetic information or other biometric data alongside fingerprints may enhance the prediction models' performance.

Further investigations are needed to advance our understanding of the underlying factors that influence fingerprint characteristics and their potential association with blood types. Such advancements may enable the development of more accurate and reliable methods for predicting blood groups from fingerprints.

It should mention also During the data collection process, several challenges and limitations were encountered. One of the primary difficulties involved obtaining an adequate amount of fingerprint data due to privacy concerns and hesitancy from participants. This limited the size and diversity of the dataset, potentially impacting the generalizability of the blood group prediction model. Additionally, the imbalanced distribution of blood types within the collected dataset, with a majority of A+ and O+ samples and underrepresentation of other blood types, may affect the model's accuracy in predicting less prevalent blood groups. Despite these challenges, efforts were made to ensure data privacy, obtain informed consent, and maximize the dataset's diversity. However, it is important to acknowledge these limitations, as they may affect the generalizability and reliability of the blood group prediction model. Future work

should focus on expanding the dataset, engaging with a more diverse participant pool, and collaborating with healthcare facilities or blood banks to access a wider range of blood types.

Until advancements are made in the understanding of fingerprint anatomy and the science of fingerprint recognition, it remains unfeasible to accurately predict blood types based on fingerprints. Further research and exploration are needed to explore alternative approaches or consider complementary data sources to improve the accuracy of blood group prediction.

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