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Abstract

Finger vein recognition systems have gained more popularity recently, and it is one of the most reliable biometric modality. Finger veins are present inside the finger, and its pattern is not known which makes it hard to spoof. In addition, it's known to produce high accuracy, permanence and reliable for person identification/ recognition. Because of these advantages, finger vein recognition has already been implemented in financial sectors of Brazil, China, Japan and Poland. With the increased use of Biometric systems for large scale application like Unique ID project (AADHAAR) in India and border control projects, there is a need for indexing methods to narrow down the search space in large scale databases. So, It is essential to have a good indexing scheme for finger vein as widely used in real life scenarios. As of now, there is only one method based on the local sensitive hashing (LSH) to search in large-scale databases. The main limitations of LSH are, it depends on the choice of hash functions and memory required to store the hash tables will grow according to the size of the database. It is not a feasible solution to use for real life scenarios where, database scaling is required.

In this work, we presented finger vein indexing and retrieval schemes based on unsupervised clustering. To this extent, we investigated three different clustering schemes namely K-means, K-medoids with binary & real-valued features and self organizing maps (SOM) neural networks with real-valued features. The proposed schemes are experimentally verified with the large scale heterogeneous finger vein database comprised of 2850 unique identities constructed using seven different finger vein databases. The obtained results demonstrated the efficacy of the proposed schemes for large scale finger vein applications in real life scenarios.

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Jayachander Surbiryala June, 2015

Acronyms and Abbreviations

CLAHE Contrast-Limited Adaptive Histogram Equalization DFT Discrete Fourier Transform **EER** Equal Error Rate FAR False Accept Rate FRR False Reject Rate FTA Failure-to-Acquire Rate HiGFVDB Høgskolen i Gjøvik Finger Vein Database ISO International Organization for Standardization LSH Local Sensitive Hashing MCC Minutiae Cylinder Code MCP Maximum Curvature Points MV Minutiae Vicinity NBL Norwegian Biometric Laboratory NIR Near Infra-Red OF Orientations & Frequencies OTP One Time Password PIN Personal Identification Number PNR Penetration Rate PSE Pre-Selection Error PSFC Pre-selection of features & comparison ROI Region of Interest SMR Spectral Minutiae Representation SOM Self Organizing Maps SOTA State-of-the-art UID Unique ID

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1 Introduction

In this chapter, we discuss about the work carried out in this thesis with problem description, motivation and justification. All research questions addressed in this thesis are presented and main contributions of this thesis are outlined briefly.

1.1 Topic

Biometric systems are used for identification and authorization of users in many day to day applications. Biometrics gained more popularity because of its convenience and the increased need for security over the last decade. With the usage of large number of real-time applications, users need to remember many passwords or carry access control cards/ keys to workplaces. Biometric recognition systems are replacing the password and PIN (personal identification number) based authentication systems because of the advantages provided by biometric systems such as : individual using the system don't have to remember any passwords, PIN's and no need to carry access control cards or keys to gain the access to the applications or workplaces.

Finger vein recognition systems have gained more popularity recently, and it is one of the most reliable biometric recognition systems. It has many advantages compared to other modalities in biometrics such as the finger veins are present inside finger, hard to spoof, and it requires subjects co-operation to steal the finger veins samples. There exist no experimental evidence showing that finger veins are prone to changes or morphing over a long period. Finger veins are robust and unique to every individual and they are distinctive for all the fingers of the same person [11].

1.2 Keywords

H.2.0.b Information Technology and Systems, Database Management, General, Database design, modeling and management.

H.3.1.c Information Technology and Systems, Information Storage and Retrieval, Context Analysis and Indexing, Indexing methods.

H.3.3.a Information Technology and Systems, Information Storage and Retrieval, Information Search and Retrieval, Clustering.

H.2.8.e Information Technology and Systems, Database Management, Database Applications, Feature extraction or construction.

K.6.5.a Computing Milieux, Management of Computing and Information Systems, Security and Protection, Authentication.

1.3 Problem description

Finger vein recognition has gained more popularity recently because of the advantages provided by these systems, as a result some of the countries like Brazil, China, Japan and Poland have already deployed the vein recognition systems in their financial sectors to increase the security for their transactions. With the greater use of biometric systems for large scale application like Unique ID (UID) project in India

[12], there is a need for indexing methods to narrow down the search space for finger vein identification in large-scale databases. Indexing is crucial in large scale databases as it improves the performance of the system and identification of the subjects will be faster within the narrow search space for real-time applications.

Even though there exist a finger vein indexing technique [13], proper analysis of the scheme was not presented in terms of the pre-selection error (PSE) rate and penetration rate (PNR). The analysis of the technique in terms PSE and PNR will help in understanding the usability in real time large scale finger vein applications. So we analyze the state-of-the-art finger vein indexing method in terms PSE and PNR. We will check whether the performance of the finger vein systems can be improved with any other schemes.

1.4 Motivation and justification

With the increased use of finger vein recognition systems in real time applications, there is a need for narrow down the search space in large scale finger vein databases. This narrow search space can be achieved with a proper indexing method for finger vein samples, rather than a comprehensive search on the whole database. There is only one method [13], which has been proposed to search in the marginal database instead of the entire database. In this research, we will explore new finger vein indexing methods using unsupervised clustering methods to confine the search to a subset of the database instead of the whole database.

Implementing indexing process will have following benefits in large-scale finger vein databases:

- **Narrow search space**, can be used to locate particular subject quickly in a small set of subjects instead of an exhaustive search on the complete database.
- Faster comparisons, as there will be less number of operations at the system level.
- Scalability, easy to incorporate new subjects.

1.5 Research questions

Research Question 1 Does the present state-of-the-art (SOTA) indexing technique performance suffice for large scale finger vein applications?

The present finger vein indexing method based on locality-sensitive hashing (LSH)[13] for narrowing the search space in finger vein database has not been evaluated in terms of pre-selection error(PSE) rate and penetration rate (PNR). In this work, we intend to assess the performance of the LSH[13] in terms of PSE and PNR to measure the applicability for large scale finger vein applications.

Research Question 2 Is unsupervised clustering of finger vein samples useful for narrowing down the search space in large scale finger vein application?

We explore the unsupervised clustering schemes such as, 1) K-means [14], 2) K-medoids [15] and 3) Self-organizing Map (SOM) neural network [16] for narrowing the search space in large scale finger vein databases. The performance of these unsupervised clustering will be presented in terms of PSE and PNR to measure the suitability for large-scale finger vein applications.

Research Question 3 Does the proposed unsupervised clustering techniques with 1) binary features and 2) real features will be useful in real life scenarios?

Based on the narrowing down the search space in the large scale finger vein databases using the unsupervised clustering techniques, in this work we compare the results achieved by the unsupervised clustering using binary and real features with the SOTA technique. Further, we discuss the usability of these techniques for real life scenarios.

1.6 Contributions

The main contributions of this thesis are:

- 1. Data collection using the in-house finger vein sensor [11].
- 2. Proposed a robust ROI extraction across the six finger vein databases.
- 3. Proposed two unsupervised clustering techniques using binary features of finger vein samples: (1) K-means [14] and (2) K-medoids [15]
- 4. Proposed three unsupervised clustering techniques using real features for finger vein samples namely: (1) K-means [14] (2) K-medoids [15] and (3) Self-Organizing Map (SOM) neural network [16].
- 5. Comprehensive analysis on a large scale database of 2850 unique identities and performance are benchmarked with the existing finger vein indexing scheme based on LSH [13]. All the results are presented following the ISO/IEC 19795-1:2005 to produce a comprehensive analysis of the proposed finger vein indexing technique.

1.7 Structure Of Dissertation

This thesis is organized as follows: in Chapter 2, we present an overview of the general biometric system, biometric characteristics along with various biometric modalities. Chapter 3 presents well-established indexing techniques used for face, fingerprint, iris and ear traits and presented the SOTA finger vein indexing method. In Chapter 4, details of various finger vein databases used in this thesis are presented along with the distribution of the finger vein samples across the development, training, and testing data sets. The proposed finger vein indexing schemes using unsupervised clustering are discussed in Chapter 5 and Chapter 6 quantitative results are presented following the ISO/IEC 19795-1:2005 standard. Based on the results significant findings are presented in Chapter 7. Chapter 8 presents the interpretation of the obtained results, analysis to answer all the research questions and future work.

2 Biometrics

In the Chapter 1, we presented the introduction to the thesis work carried out along with problem description, motivation, research questions and contributions. In this chapter, we introduce the biometric with an explanation some of the basic terms, modules of the general biometric system, effects on the biometric systems performance for various reasons and properties of biometric characteristics are presented along with short introduction to the different biometric traits.

2.1 Introduction

Biometrics refers to the science of relating the human characteristics to identify the individuals based on their biological or behavioral traits. Biometrics authentication is used in many modern day applications for access control, identification, and verification of individual based on different characteristics possessed by humans. Face, fingerprint, iris, retina, gait, keystroke, signature, hand/finger geometry, voice, ear, palm-print and hand/finger vein patterns are various traits used for identification of individuals [17, 18]. Use of biometrics in many day to day applications has been increasing with large-scale biometrics applications. These applications can include very confidential data related to individuals, organizations or national security. Still many of the real-time applications need a reliable identification system. e.g. Online banking and credit cards still rely on old methods for identification of the users.

The primary task in the identity management systems is the verification of the individual with the claimed identity. This is required because the person who needs to have access to the network is a genuine user, not an imposter with the access to confidential data. Traditional methods of identification includes knowledge-based (what you remember e.g., passwords, pins) and token-based (what you possess, e.g., Bank chips or tokens, One time password (OTP) sent to mobile) methods, but these things can be easily lost, manipulated, stolen or taken control by threatening users. Security provided by these can be easily compromised. These problems can be solved with biometrics identity management using their biological traits (who you are) [19]. In some of the application, two of these factors can be combined to have high level of security. Such systems are known as a dual-factor authentication systems.

2.2 Verification and Identification

Biometrics systems can be operated in verification or identification mode depending on the application. In verification mode, the system will validate the identity of the person by comparing the biometric data with stored biometric template data which is stored in the database module. This is 1:1 comparison. In identification mode, the system will compare the individual biometric sample with the all the user templates of the system that are present in the database for a match. Here, the system compares one to many comparisons to identify the user.

2.3 General Biometric System

Biometric systems mainly works on the principle of pattern recognition of the biometric trait from the individual, where system extracts the features from the traits and compares the features with the stored

features in the database associated with the same person. Based on the comparison results, specific actions will be taken. An overview of the general biometric system can be visualized as Figure 1 along with the illustrates the information flow between the various subsystems during the enrollment, identification, and verification [20].



Figure 1: Components of general biometric system (taken from ISO/IEC: TR 24741 [1])

2.3.1 Data capture

A biometric device which can acquire the raw biometric data from an individual when their traits are presented in front of the system. Data capture mainly works by using the sensor module. For example, to obtain vein samples from the hand we need to have a sensor that is capable of capturing the vein patterns using the near infra-red (NIR) illumination onto the hand. The sensor module is the place where humans interact with the system, so this module needs to be stable and robust for good performance of the system. Poor design of the sensor module may result in high failure-to-acquire rate (FTA) and, therefore, low user acceptability because of the inconvenience caused by the system.

2.3.2 Data storage

Data storage module acts as a repository for the biometric system. From all the enrolled user templates, the features will be extracted and stored in the enrollment database along with other personal information related to the individuals.

2.3.3 Matching

In matching module, the extracted features will be compared with one or more stored templates present in the database and similarity or matching scores will be passed to the decision module. The score represents the degree of similarity between the features and template/s. For verification one matching score will be given, whereas for the identification many matching scores will be given.

2.3.4 Decision

Based on the matching scores, decision-making module either accepts/ rejects for verification and identifies the person based on the extracted features. For verification, when the matching score exceeds the required threshold with the presented biometric trait features to the available template features. Whereas, for the identification list of all possible identities of the person can be generated based on the threshold limits.

There will be some hidden modules apart from these four modules, which help for proper functioning of the Biometric Systems:

- **Transmission:** module will transfer the samples or features between the different modules.
- **Signal processing:** module will be used to extract the features from the collected biometric sample. This module includes feature extraction and quality assessment. The quality of the biometric data acquired using the sensor module is determined to check the usability of the samples collected for next step in the system. If the quality of the data obtained is not of sound quality, the subject needs to present the biometric data again to the sensor module. If the quality of the data samples is good, biometric data will be processed and set of features will be extracted to enroll (during enrollment, this feature set will be stored in the database and it is referred as template) or identify the individual (by comparing to template present in the database) based on the traits presented to the system.
- Administration: module takes care of the implementation and usage of the biometric system.
- Interface: module may be used in applications, to show the response of the system.

2.4 Performance of a biometric system

Performance of the biometric system can vary for several reasons :

- 1. Changes in the sensor (e.g. sensor malfunction)
- 2. Alterations in biometric traits (e.g. cuts in fingerprints)
- 3. Imperfect sensing conditions (e.g. wet fingerprints or diseased fingerprints)
- 4. Changes in surroundings (e.g. illumination changes on face images) and
- 5. Variations while interacting with the sensor (e.g., partial fingerprints or half face images).

In these scenarios, the biometric traits from the same user don't match the other sample. A Perfect match between the two features might indicate spoofing (replay attack) on the system. The difference observed in the biometric features of an individual is known as intra-class variation and difference between the biometric features sets related to two different individuals is referred as an inter-class variation.

2.5 **Biometric characteristics**

Different biometric characteristics are used in many of the applications based on their requirement and convenience because of their pros and cons. Jain et al. [18] [19] have listed the seven factors that decide the usability of the biological or behavioral traits in biometric applications.

- 1. Universality: Every person using the system or application should possess characteristics.
- 2. Uniqueness: Trait should be different (unique) among all people using the system.

- 3. Permanence: The biometric trait should not change over the period, it should remain stable. A biometric trait that changes over the time significantly may not be useful.
- 4. Measurability/ Collectability: It should be easy to collect the biometric data using the sensor without any inconvenience to the person using the system. Moreover, it should be easy to process the collected raw data for pre-processing for extracting the features representing the trait.
- 5. Performance: Which refers to the accuracy of the system in recognition with the speed. The system should have less number of errors while operating.
- 6. Acceptability: The biometric trait needs to be accepted in the target group that uses the application, and they are willing to present their trait to the system.
- 7. Circumvention: The biometric trait should be very hard to counterfeit using artefacts

But none of the biometric traits will not be able meet all the requirements for the applications in real time. Based on the requirements, the specific biometric trait will be used [18]. A short introduction to some of the biometric traits are given below:

Face

Face recognition is a non-interfering method, and facial features are mostly used by humans to distinguish one human to the other. Application of facial recognition can be static or dynamic, i.e. controlled or uncontrolled identification of individuals with various backgrounds. The more popular approaches for face recognition are based on [18]:

- 1. The location and outline of the facial features, such as eyes, nose and lips and their relationships based on the spatial characteristics,
- 2. Overall analysis of the face as a weighted combination of recognized faces.

If the facial images are captured with different pose or illumination, they have difficulty in matching the face images. For a facial recognition system to work properly in real time, system should be capable of [18]:

- 1. Detect, weather face is present in the captured image
- 2. Locate the face in the image, if there is a face in the image and
- 3. Extract the face images from any pose and illumination.

Fingerprint

Fingerprints are the pattern of ridges and valleys which are present on the surface of the fingertips that are formed during the initial days of baby and remain unaltered during the lifetime of a human. Fingerprints have been used for person identification for many decades by humans. The identification of the users using the fingerprints is very high [21]. Based on the experimental analysis, it has been concluded that fingerprints of identical twins does not match. But, fingerprints of a small group of people (e.g. manual workers, they might have some cuts on the finger and fingerprints will not be same) may not be useful for identification [18].

Hand geometry

Recognition systems based on hand geometry takes many factors into consideration like the shape, size and length of the fingers. Authentication systems based on hand geometry are easy to use and affordable. External factors like climate changes will not affect the performance of the system. But, these systems can not be used in large scale application, as the geometry of the hand can be same for many people in large population and it is not stable with the children, who's hand geometry changes very often [22] [18].

Palmprint

Palm of the human hand contains ridges and valleys same as a fingerprint, along with principal lines and wrinkles that can be used for the identification of users [23].

Iris

Iris is the circular region in the eye surrounded by the pupil (dark part in the center of the eye) and the sclera (white part of the eye) on the other side. The iris texture is formed during the first two years of a baby. This iris texture can be used for the identification of individuals [24]. Iris recognition accuracy and speed is fast, and it can be implemented in large-scale systems for identification based on the textures of the iris. Iris pattern is unique to all humans, even for the identical twins. Iris recognition systems will have a very low false accept rate (FAR), but false reject rate (FRR) could be high when compared to other biometric traits [18].

Keystroke

Keystroke dynamics is a behavioral biometric; it is the typing rhythm of a person while using the keyboard of a computer system or laptop. Typing pattern of an individual can change because of several reasons like state of the person (i.e. emotional state), position of the keyboard with respect to the user, over the time user, might improve his typing skills, etc. On the other hand, keystrokes dynamics of a person can be observed without any special equipment, as this information can be captured while the user is using the system with a software program. This keystroke information permits the "continuous verification" of a user even after logging in to the computer system or laptop [25] [18].

Signature

The way each person sign his/her name is a unique characteristic of that person. It is one of the accepted methods of authentication for legal and commercial transactions. Signature is a behavioral trait that change over a period and it can be influenced by several factors like surrounding (where the document is signed), emotional condition of the person. Even when the same person signs continuously his/her signature can vary significantly [18].

Voice

Voice trait is a combination of biological and behavioral trait. Voice is based on mouth, vocal, nasal and lips, which are part of the biological characteristics of the voice and these are invariant for a person, but the speech which is behavioral characteristic changes over the time because of age, medical circumstances and emotional feelings like anger, sorrow etc. Voice cannot be used in large scale applications for identification because of it's not unique. The main drawback of the voice based recognition systems is that it is prone to background noise [26] [18].

Gait

Gait is the way in which an individual walks, and it is one of the behavioral trait that can be used to identify the person at a distance. This can be used in surveillance for the identification of individual based on their walking style. But, the gait of an individual can be changed or affected by the choice of footwear (especially for a woman), clothing, surface, etc. [18].

Finger Vein

Among the various biometric traits, finger vein biometrics has gained popularity in biometric systems because of the many advantages provided by these systems such as, 1) easy to capture the finger veins using the NIR light source and sensor capable of capturing 2) distinctive features of the individuals 3) high verification rates and 4) very hard to spoof [3]. Because of these advantages some of the countries have adopted the vein recognition systems into their financial sectors.

3 Indexing

In the Chapter 2, we have discussed general biometric systems, the performance of the biometric systems, biometric characteristics and various biometric traits. In this chapter, we present some of the indexing techniques used for face, fingerprint, iris and ear modalities. State-of-the-art (SOTA) indexing technique for finger vein will be explained, and detailed discussion of indexing on various modalities is not covered, as this is beyond the scope of this thesis.

3.1 Introduction

The importance of indexing and retrieval is increasing continuously in biometric applications with the increase in large-scale biometrics systems for government projects in real time like unique identity management system (AADHAR) [12] in India. Indexing techniques helps us to retrieve the relevant information required with minimum resources, fewer comparisons and within small time. Indexes are used by the system to find the information more quickly; these indexes are created using indexing techniques. The word "Index" is derived from the Latin word "indicare" ¹ to point or indicate, but the actual meaning has changed over the time [27].

Although, classification and indexing are interrelated; they are not completely same. Organizing the details of information in some structure is known as classification, whereas the index is a link that connects the different subjects to same reference related to the subject's information. The main purpose of indexing is to access information efficiently from the database, which can be used for any purposes like identification, verification, retrieval of personal information, etc. A perfect indexing leads to the correct and accurate retrieval of information [27]. Indexing techniques are used in large scale databases to reduce the search space in real time biometric applications. Some of the indexing techniques are presented below for face, fingerprint, iris, and ear.

3.1.1 Face indexing

There are many indexing techniques for matching the face samples in large-scale databases. Gyaourova et al. [28, 29] have proposed a method using match scores, which has demonstrated excellent results for face indexing in terms of PSE rate. Vikram et al. [30] have explored the face indexing with spatial similarity using Kd-trees. Further, Abate et al. [31] and Kaushik et al. [32] have used discrete fourier transform (DFT) and modified geometric hashing respectively for face indexing. Table 1 shows the SOTA performance of few existing face indexing schemes.

3.1.2 Fingerprint indexing

Fingerprint is one of the oldest biometric modalities used for identification from the early days of 20th century. Because of it's widespread use, there has been a lot of research carried out in fingerprint indexing. Yuan et al. [33] have proposed a fingerprint retrieval that is based on minutiae triplet using locality sensitive hashing (LSH) and it has demonstrated the sound performance of the system with zero PSE rate.

¹http://www.perseus.tufts.edu/hopper/morph?l=indicare&la=latin

		Dat	Results			
Author	Technique used	Name	Subjects	No of	(PSE/ PNR)	
				samples		
Vikrom at al. [20]	Kd traa	ORL face	40	400	10.0/5.0	
Vikialli et al. [50]	Ku-uee	database				
		private	135	1/185		
Abote et al [21]	Discrete Fourier	database	155	1405	0/-	
Abate et al. [31]	transform (DFT)	private	1820	20020		
		database	1020	20020	L	
Kaushik at al [22]	Modified geometric	FERET	103	206	0/	
Kauslik et al. [52]	hashing	database	105	200	0/-	
Guaguraya et al. [20]	Matah anama	FERET	1012	2024		
Gyaourova et al. [29]	Watch scores	database	1012	2024	-	
		FERET	1010	-	0/30	
Gyaourova et al. [28]	Match scores	database				
	Watch scores	FRGC face	568	-	0/86	
		database				

Table 1: Some of the face biometric indexing approaches

Cappelli et al. have presented two indexing techniques based on orientations & frequencies (OF) and minutiae cylinder code (MCC) in [34] with lower PNR. Li et al. [35] have used minutiae vicinity-index (MV-Index) and minutia cylinder code-index(MCC-Index) to generate MV-MCC fusion scores to retrieve the fingerprint faster from the database and in [36, 37] they have used geometric hashing of fingerprint samples for faster retrieval. There are two recent survey articles [38, 39] on fingerprint classification. For more details regarding the fingerprint indexing and classification, the reader can refer [38] [39]. Table 2 shows the performance of some of the fingerprint indexing schemes in terms of PSE and PNR.

		Databa	Results		
Author	Technique used	Name	Subjects	No of	(PSE/ PNR)
				samples	
	Orientations & Frequ-	FVC2000 DB2		800	1/6 1
Cappelli	encies (OF)-Idx		-	800	1/0.1
et al. [34]	Minutiae Cylinder			800	1/2 0
	Code (MCC)-Idx	FVC2000 DB2	-		1/3.9
		NIST SD27 (good)		88	0/43
		NIST SD27		170	0.4/50
Vuon	LSH	(bad & ugly)		170	9.4/50
et al. [33]		FVC 2000 DB2	-	800	0/22
		FVC 2002 DB1	-	800	0/9.9
		FVC 2004 DB1	-	800	0/11.7
		FVC 2004 DB1	-	800	4/2.61
Jayaraman	Geometric	FVC 2004 DB2	-	800	5/2.33
et al. [36]	hashing	FVC 2004 DB3	-	800	6/1.95
	Minutiae Vicinity-	FVC 2004 DB1 a	100	800	10.0/26
	Index (MV-Index)	FVC 2004 DB2 a	100	800	10/32.33
T:	MCC Index	FVC 2004 DB1 a	100	800	10.0/7
et al. [35]	MCC-IIIdex	FVC 2004 DB2 a	100	800	10.0/15
	MV MCC fusion	FVC 2004 DB1 a	100	800	10/1.19
	WIV-WICC IUSION	FVC 2004 DB2 a	100	800	10/2.4
Wang	Geometric	FVC 2002 DB1	100	800	1.0/3
et al. [37]	Hashing	NIST DB14	2700	5400	18.0/1

Table 2: Some of the fingerprint biometric indexing approaches

3.1.3 Iris indexing

U. Jayaraman et al. [40] have proposed a method using Kd-tree with iris color and texture for indexing, which provides a non-uniform distribution of indices has shown a good performance. Dey et al. [41] have used gabor energy features for indexing and in [42, 43] iris codes have been used for indexing of iris

samples with different techniques. Further, the indexing approach developed by Mehrotra et al. in [44] K-means clustering, and it has demonstrated good performance in iris indexing. Some of the iris biometric indexing methods are presented in Table 3 along with the performance of the system.

		Dat	Results			
Author	Technique used	Name	Subjects	No of	(PSE/ PNR)	
				samples		
Invergmen et al. [40]	Kd tree	UPOL	94	384	2/2.0	
Jayaraman et al. [40]	Ku-uee	UBIRIS	372	1860	1.3/8.3	
		BATH	25	1000	1.8/11.3	
		CASIA-V3-	240	2(20	<u> </u>	
Dey et al. [41]	Gabor wavelet	Interval	249	2039	0.7/14.3	
		CASIA-V4-	1000	20000	0 2/16 2	
		Thousand	1000		9.3/10.3	
		MMU2	100	995	14.8/13.5	
		WVU	244	3099	4/10.3	
Droopoo [0]	Wavalat and as	CASIA-V4-	1000	20000	51	
FIOEliça [9]	wavelet codes	Thousand			51-	
		UBIRIS.v2	-	11102		
Jayaraman et al. [43]	Iris Code Hashing	CASIA-V3-	240	2655	5 02/10 62	
		Interval	249	2033	3.93/10.03	
Mahrotro at al [44]	k means clustering	BATH	50	2000	0/3	
Memoria et al. [44]	K-means clustering	CASIA-V3	249	2655	4.0/28	

Table 3: Some of the iris biometric indexing approaches

3.1.4 Ear indexing

There exists minimal research on the ear indexing. Liu et al. [45] have presented angle indexing method for the ear samples indexing in a database, which has achieved zero PSE with small PNR. Chen et al. [46] and Pflug et al. [47] has proposed ear indexing using K-d tree and K-means clustering respectively. U. Jayaraman et al. [48] has introduced a technique with enhanced geometric hashing and pyramid tree indexing technique which has been explored for ear in [49]. The performance of the existing ear indexing schemes are presented in Table 4.

3.2 State-of-the-art (SOTA) Finger Vein indexing

Finger vein patterns are unique to every subject, and they are distinct from one finger to other in the same hand. To identify the subjects correctly we need to have the features from the finger veins, which are discriminative in nature when compared to the others subjects. These features need to be extracted for identification of subject using the indexing methods from the database. As of now, there is only one method which has been proposed to narrow the search space using local sensitive hashing (LSH) [13]

		D	Results			
Author	Technique used	Name	Subjects	No of	(PSE/ PNR)	
				samples		
Chan at al [46]	K d trae	UND	302	604	4.25/35	
Chen et al. [40]	K-u uee	UCR	155	902	4.65/35	
	K-means clustering	UND-J2	415	1800		
Pflug et al. [47]		AMI	100	700	0.99/47.1	
		IITK	125	494		
Linet al $[45]$	Angle indexing	private	500	2000	0/0 60	
	Angle Indexing	database	500	2000	0/9.09	
Maity et al. [49]	Pyramid tree indexing	UND-J2	415	-	3.13/-	
Javaraman at al [48]	Enhanced Geometric	UTV	150	1200	0/	
Jayaraman et al. [40]	Hashing		130	1200	0/-	

Table 4: Some of the ear biometric indexing approaches

and it uses the repeated line tracking method [2] for feature extraction. A brief overview of these two techniques are presented below.

3.2.1 Repeated line tracking

In repeated line tracking as a feature extraction technique for finger vein patterns, prominent line patterns in finger vein image are obtained by looking for all lines iteratively [2]. The line tracking is started at several points on the captured image to confine dark pixels corresponding to the vein. Starting point for line tracking and the moving direction attributes are chosen as a unique random pair. The direction of progress is decided based on the curvature of the line with the help of moving direction attributes. The number of points on the space are collected to obtain adequate amount of predetermined number.

Line tracking starting at any pixel in the captured image is known as "current tracking point", and tracking is done by moving a pixel along the dark line in the image. The intensity of the adjacent pixels around the current tracking point will be checked. Figure 2 shows the relation between the current tracking point (xc, yc) and adjacent pixels in the image. If 'p' is a pixel adjacent to the current tracking point as shown in the Figure 2. Cross-sectional profile s-p-t looks like a valley, based on this, we can know if the current tracking point is present on a dark line. The direction of the line can be determined based on the intensity values of the valley by changing the θ i, which gives the deep valley at that angle. Then, the current tracking point will be modified to the neighboring pixel 'p'. If there are no dark pixels adjacent to the current tracking point is classified as background. Further, we pick a new tracking point at another position on the image and repeat the process.

3.2.2 Local Sensitive Hashing (LSH)

The central idea of LSH is to use the hash functions so that the chances of matching two samples (or images) which are highly similar and highly different in hamming space. LSH works by creating large



current tracking point(xc,yc)

Figure 2: Dark-line detection using repeated line tracking (taken from [2])

number of hash functions, for each of the hash functions the input sample will be hashed to add to the buckets. Once the subject has been added to the bucket, it becomes a pair with the existing subjects in that bucket and forms a candidate list for the bucket. In other words, if two subjects gets added into the same bucket for one or more hash functions they form a candidate list for that bucket.

Main limitations of the LSH are outlined as below:

- 1. LSH purely depends on the choice of hash functions.
- 2. We need to tune all hash functions and buckets in each hash function so that we will have relatively few subjects in a bucket (We will end up having more number of buckets).
- 3. If we have more number of buckets, we may add the similar type of subjects to different buckets and while retrieving we might end up searching in a different bucket.
- 4. Memory required to store the hash tables will increase with the size of the database.

4 Finger Vein Database

In the Chapter 3, we presented some of the indexing techniques used for face, fingerprint, iris and ear modalities along with the state of the art (SOTA) finger vein indexing technique. In this chapter, we discuss the various finger vein databases used in this thesis along with the number of participants, age distribution, and gender distribution. The distribution of the finger vein samples from different databases for development, training, and testing data sets are presented.

4.1 Existing Databases of Finger Vein and HiGFVDB

In this work, we have constructed a heterogeneous database by using the finger vein samples from seven different available databases. Out of which five databases are publicly available: (1) FVUSM [50] (2) ICFVR [6] (3) PloyU [8] (4) SDUMLA-HMT [9] (5) Vera [5] and two private databases (6) HiGFVDB [3, 4] (7) UTFVP [7]. Table 5 shows the total numbers of subjects, number of fingers from each participant, total number of samples for each finger, data collection carried in number of sessions and total number of samples present in database.

Database	Number of	Total No of	Total No of	Total No of	Total No of
	sessions	Subjects	Fingers	Samples	Samples in
				for each finger	complete database
ICFVR [6]	1	#	310	5	1550
FVUSM [50]	2	123	492	6	5904
HiGFVDB [3, 4]	1	130	520	10	5200
SDUMLA-HMT [9]	1	106	636	6	3816
PolyU [8]	2	156	312	6	3744
UTFVP [7]	2	60	360	2	1440
VERA [5]	1	110	220	2	440

Table 5: Finger vein databases used in this work

4.1.1 PolyU

PolyU [8] finger vein database has been collected at Hong Kong Polytechnic University during April 2009 - March 2010 at their campus. This database consists of 3744 finger vein samples collected from 156 subjects in bitmap (*.bmp) format in two sessions. Among the captured subjects 93%, of them are younger than 30 years and remaining were older than this. They have collected the database in two sessions with an average interval of 2 months. In each session, all the subjects have presented their two fingers for data collection, and six samples are collected from each finger in both the sessions. So in each session $156 \times 2 \times 6 = 1872$ finger vein samples are collected from 156 subjects. PolyU finger vein database

can be obtained from http://www4.comp.polyu.edu.hk/~csajaykr/fvdatabase.htm.

4.1.2 VERA

Vera finger vein database has been built using the sensor presented in [51]. Vera database consists of 440 finger vein images collected in portable network graphics(png) format from 110 subjects whose 2 finger veins are collected in a single session with 2 samples from each finger. The database consists 70 male and rest of them (40 subjects) are female aging are between 18 and 60. Vera finger vein database can be downloaded from the idiap research institute by requesting the access to their database from the page https://www.idiap.ch/dataset/vera-fingervein/.

4.1.3 ICFVR

The 8th IAPR International Conference on Biometrics (ICB 2015) has been organized between 19-22 May 2015. Ran Xian from AILAB, Peking University has held Finger Vein Recognition competition during October 2014 and provided four data sets namely DS0, DS1, DS2 and DS3 data sets consisting of finger vein samples of 10, 100, 100, and 100 fingers respectively in bmp format. For each finger, there were five images in the 4 data sets constituting to 50 samples in DS0, 500 samples in DS1, 500 samples in DS2 and 500 samples in DS3. We have merged these 4 data sets and formed the ICFVR (International Conference on Biometrics Finger Vein Recognition) database. So, the final database consists of 310 fingers and 1550 finger vein samples. DS0, DS1, DS2 and DS3 datasets are downloaded during October 2014 from http://rate.pku.edu.cn/ [6].

4.1.4 UTFVP

University of Twente finger vein database (UTFVP) [7] is collected from 60 subjects at University of Twente during the years 2011 and 2012. The database has been collected in two sessions with an average time gap of 15 days. From each subject, they have collected the finger vein samples from the index, middle and ring fingers of both the hands and each finger samples are collected twice in a session in png format. 44 subjects in the database are male and remaining 16 subjects are female. UTFVP data set contains 82% of subjects in the age group of 19–30, the rest of the volunteers are older than 30. UTFVP is a private database, provided to us for research purpose only.

4.1.5 SDUMLA-HMT

SDUMLA-HMT [9] finger vein database has been created using the sensor designed at Wuhan University. From each of the volunteer, they have collected the finger vein samples from the index, middle and ring fingers of both hands and from each finger they have collected six finger vein samples. SDUMLA-HMT database contains $106 \times 6 \times 6 = 3816$ finger vein samples collected from 106 subjects and all the samples are stored in bmp format. SDUMLA-HMT can be downloaded from the link http://mla.sdu.edu.cn/sdumla-hmt.html.

4.1.6 FVUSM

Finger Vein USM (FVUSM) [50] database samples are collected from 83 males and 40 females at Universiti Sains Malaysia. Age group of these 123 subjects were in the range of 20 to 52 years. The index finger and middle finger of left and right hands are collected from all the volunteers resulting in a total of $123 \times 4 = 492$ unique finger. From each finger, they have collected six finger vein samples in a session, and they have collected the data from 123 subjects in two sessions. A total of $492 \times six \times 2 = 5904$ finger

vein samples are collected in two sessions, and all samples are stored in the joint photographic experts group (jpg) format. FVUSM database contains the extracted ROI images using the method presented in [50]. FVUSM database can be downloaded from the link http://blog.eng.usm.my/fendi/?page_id=262.

4.1.7 HiGFVDB

Høgskolen i Gjøvik Finger Vein Database (HiGFVDB) collection is carried out at Norwegian Biometric Laboratory (NBL) Gjøvik for a duration of 3 months (August 2014 - October 2014) using the sensor [11, 3, 4]. HiGFVDB consists of finger vein images collected from 96 male and 34 female subjects. From each subject, we have collected finger vein data from the index and middle fingers of both the hands resulting four different fingers for each subject, and we have collected ten samples from each finger. All the finger vein samples are stored in the bmp format. HiGFVDB contains $130 \times 4 \times 10 = 5200$ finger vein samples collected from 520 unique fingers of 130 subjects.

4.2 Database construction

This new heterogeneous finger vein database is comprised of 685 plus subjects that resulted in 2850 unique finger veins. Since each finger vein is unique, we consider each finger vein as the unique enrollment that resulted in 2850 unique identities and each of these unique identities has 2 samples (first two samples of each finger). Thus, the whole database used in this work is comprised of 5700 finger vein samples. Table 6 shows the distribution of the subjects as well as fingers from 7 different finger vein databases used to construct a single heterogeneous database.

Database	Total No of	Total No of	Data Partition		
	Subjects	Fingers	Development	Training	Testing
ICFVR [6]	#	310	76	150	84
FVUSM [50]	123	492	0	200	292
HiGFVDB [3, 4]	130	520	36	150	334
SDUMLA-HMT [9]	106	636	0	250	386
PolyU [8]	156	312	83	100	129
UTFVP [7]	60	360	0	150	210
VERA [5]	110	220	78	75	67
Total	685+#	2850	273	1075	1502

Table 6: Heterogeneous database construction using seven databases

4.2.1 Performance evaluation protocol

In order to effectively evaluate the database, we divide the whole database into three independent (or nonoverlapping) datasets namely: development, training, and testing. The development data set is comprised of 273 unique identities with $273 \times 2 = 546$ finger vein samples. The development database is used only to tune the parameters of the ROI extraction as well as the proposed feature extraction scheme. The training data set is comprised of 1075 identities that will result in $1075 \times 2 = 2150$ finger vein samples used only to build the cluster space using either K-means or K-medoids or SOM neural network. Lastly, the testing data set is comprised of 1502 unique identities that are used solely to report the performance of the proposed indexing and retrieval scheme. The testing data set is further divided into two groups namely gallery and probe. Since each identity has two samples, we assigned the first sample to the gallery and second sample to probe. Finally, the data partition into development, training, and testing is repeated for 10 times and average of the results are reported.
5 Proposed finger vein indexing schemes

In the Chapter 4, we presented the various databases used in this thesis work along with the details of the database construction such as, number participants, age and gender distribution. Heterogeneous database construction is discussed with distribution of finger vein samples into development, training and testing data sets. In this chapter, we will present the proposed finger vein indexing schemes with unsupervised clustering.

Figure 3, shows the block diagram of the proposed finger vein indexing and retrieval scheme based on unsupervised clustering. The proposed method has been structured using five different functional blocks namely: (1) Region of Interest (ROI) extraction (2) pre-processing (3) Feature extraction (4) Building indexing space (5) Retrieval of the probe identity. In the following sections, we discuss each of these steps in detail along with the unsupervised clustering techniques.



Figure 3: Block diagram of the finger vein indexing using unsupervised clustering

5.1 Region of Interest (ROI) extraction

The idea of the ROI extraction and pre-processing is to extract the interest region from the finger vein sample that can solely represent the vein pattern and then we enhance the extracted ROI to improve the visibility of the vein pattern. Since we have combined 7 different databases which are captured in different conditions to form a single large database, the ROI extraction is needs to be robust for the changes across the database. In this work, we detect the ROI based on the boundary of the finger. Given the Finger vein image I_{Fv} , we first perform the binarization using Otsu's thresholding. The binarized finger vein image I_{Fv} is further processed to fill the holes using morphological reconstruction. In the next step, we locate the center of the image $C_{Ib}(x, y)$, we then consider the column corresponding to $C_{Ib}(x, y)$ then find the first discontinuity along rows on both the direction to get outer edge of the finger. Let the outer boundary point be represented as $U_c(x, y)$ and lower boundary point be represented as $L_c(x, y)$. In the next step, we fix the ROI by discarding 40 pixels on either side of the finger starting from $U_c(x, y)$ and $L_c(x, y)$. Finally ROI is corrected for the translation and rotation using affine transform as mentioned in [11]. Figure 4 shows the ROI extraction from different databases adopted in this work.



Figure 4: Illustration of ROI extraction on six different finger vein databases used in this work (a) HiGFVDB [3, 4] (b) VERA [5] (c) ICFVR [6] (d) UTFVP [7] (e) PolyU [8] (f) SDUMLA-HMT [9]

5.2 Pre-processing

The pre-processing operation involves in enhancing the finger vein sample by adjusting the contrast by using contrast-limited adaptive histogram equalization (CLAHE) [52]. CLAHE works on image by dividing it in to the small tiles. Each tile of the image is enhanced by adjusting the contrast. Then all the tiles of the image will be combined to form the enhanced image. Figure 5 shows the pre-processed finger vein enhanced sample from raw ROI image. Finally, the enhanced finger vein images are resized to 128×512 pixels in order to compensate for the different resolution across the databases.



Figure 5: Pre-processing of the raw finger vein image to get Enhanced finger vein sample

5.3 Feature extraction techniques

After enhancing the finger vein samples using CLAHE [52], we need to extract the finger vein features from the finger vein samples. In this thesis, we have used Maximum Curvature method [10] (for binary features) and proposed a new feature extraction method based on block wise encoding of the Maximum Curvature points for real features.

5.3.1 Maximum Curvature method

In this work, we adopted Maximum Curvature method [10] as a binary feature extraction technique for finger vein samples. Explanation of the method includes a general procedure used for the extraction of finger vein samples as we are using maximum curvature for extracting the binary features and real features (refer to Section 5.3.2). It consists of three main steps.

Step 1 Center positions of vein extraction: Center positions of finger veins are extracted using the cross-sectional profiles of the finger-vein image. Cross-sectional profile shows the vein pattern as dent because of the darker pixels in the surrounding the vein pattern and these curves will have large curvatures can be seen in Figure 6. For any finger vein image I, intensity of the pixel (x, y) is I(x, y). If P_i(z) is a cross sectional profile from I(x, y) at a position z. The mapping function T_{rs} can be defined as I(x, y) = T_{rs}(P_i(z)). Curvature, κ(z) can be written as,

$$\kappa(z) = \frac{d^2 P_i(z)/dz^2}{\{1 + (dP_i(z)/dz)^2\}^{\frac{3}{2}}}$$
(5.1)

Based on the value of $\kappa(z)$ profile can be classified as concave($\kappa(z)$ positive) or convex($\kappa(z)$ negative) profile $P_i(z)$ (Figure 7). The local maximum values of $\kappa(z)$ in each of the concave area is calculated and these points basically represent the center of the veins. All these points represent the local maximum points in the profile. Then, scores will be assigned to the plane (V) center positions based on the $\kappa(z)$ and width of the vein i.e. where we have the concave profile in the image. Which represents the vein pattern in the image I. To get the complete vein patter in the image I, all the profiles in four directions are analyzed. Then, all the center positions of the vein are calculated by local maximum curvatures.

• Step 2 Connecting of the vein centers based on intensity: If the center positions of the vein have large values, then line will be drawn connecting the centers of veins. Otherwise, the intensity of the pixels will be normalized.



Figure 6: Cross-sectional profile view of veins (taken from [10]).



Figure 7: Relationship among profile, curvature, and probability (taken from [10])

For any pixel (x, y) and its adjacent pixels on either side have large values, line will be drawn connecting the pixels. When (x, y) has small value and pixels on both sides are with large values then the value at (x, y) should be increased to draw the line. If pixel (x, y) has large value compared to

adjacent pixels, then the value should be decreased to remove the noise. This can be represented as,

$$C_{d1}(x,y) = \min\{\max(V(x+1,y), V(x+2,y)) + \max(V(x-1,y), V(x-2,y))\}$$
(5.2)

The calculations are repeated in four directions, which give C_{d1} , C_{d2} , C_{d3} , and C_{d4} . At each point, the maximum is obtained using:

$$G = \max\{C_{d1}, C_{d2}, C_{d3}, C_{d4}\}$$
(5.3)

• Step 3 Removing noise from the Vein pattern: Vascular pattern of the sample is processed with a threshold to eliminate the noise. Threshold value is calculated for each finger vein image based on the median of maximum curvature points. If the pixels on the image with the smaller value than threshold will be removed by making it as background, and the pixels values larger than the threshold forms the vein on the processed image.

5.3.2 Proposed real feature extraction technique

In this work, we propose a new feature extraction scheme for finger vein representation in real space that consists of two main steps namely: (1) Extraction of maximum curvature points [10] (2) Block wise encoding of extracted maximum curvature points. Given the enhanced finger vein image, we extract the maximum curvature points that can accurately represent the vein pattern. In the next step, we divide the maximum curvature points image to 8×8 blocks. We then count the number of white pixels that are present within each block that can represent a new set of feature vector of dimension 1×1024 . Figure 8 illustrates the proposed feature extraction scheme. The main advantage of the proposed feature extraction scheme is in reducing the size of the feature dimension that makes it more appealing for the indexing applications. Furthermore, the proposed feature can be compared using simple correlation rule and thereby overcomes the complex comparison scheme used with the maximum curvature points method that involved in comparing pixel by pixel with several rotation and shifting.

Feature Extraction



Figure 8: Proposed feature extraction scheme

5.4 Unsupervised clustering techniques

In this work, we have investigated three different unsupervised clustering namely: (1) K-means [14] (2) K-medoids [15] and (3) Self Organizing Map (SOM) neural network [16] independently.

5.4.1 K-means clustering

K-means algorithm [14] is used to cluster objects into K partitions based on the common attributes possessed by objects and each object will be added to the cluster with the nearest mean. K will be much smaller compared to the total number of objects. K-means algorithm can applied to objects whose attributes can be mapped to the vector space. The main objective of the K-Means clustering is to achieve the minimum total intra-cluster variance (squared error function).

The value of the 'K' is not fixed, it has to be calculated by training system with training data and centroids of the clusters needs to be created based on the training data which are well separated from each other. For clusters to be well separated, cluster centroids are recalculated for all clusters until convergence or there is no change in their cluster centroids.

K-means clustering algorithm :

- Input : Set of training data points $X_1, X_2, \ldots X_n$ and K (required number of clusters).
- Starts by placing centroids $C_1, C_2, \ldots C_K$ at random locations.
- Repeat the following steps until convergence :
 - 1. For each data point X_i for i = 1, 2, ... n.
 - find the distance between the centroid C_j for j = 1, 2, ..., K and X_i . Assign X_i to the cluster j where the distance is minimum.

$$C_{j} \leftarrow \arg\min_{j} \sum_{j=1}^{K} \sum_{i=1}^{n} ||X_{i} - C_{j}||^{2}$$
 (5.4)

2. For each cluster $j = 1, 2, \ldots K$.

calculate the new centroid C_j , which will be the mean of all data points X_i assigned to the cluster j in the previous step.

$$C_{j}(m) = \frac{1}{n_{j}} \sum_{l=1}^{n_{j}} X_{l}(m)$$
(5.5)

Where, m will the dimension of the input data and n_j is the number data samples added to the cluster j.

Stop: When none of the data points changes the cluster membership i.e. cluster centroids are fixed.

5.4.2 K-medoids clustering

K-medoids algorithm [15] also works similar to the K-means algorithm [14]. Suppose we have n objects with p variables which needs to be clustered in ot K clusters (K < n). The distance between the two objects can given as

$$d_{ij} = \sqrt{\sum_{l=1}^{p} (X_{il} - X_{jl})^2}$$
(5.6)

where, i = 1, 2, ..., n; j = 1, 2, ..., n.

K-medoids clustering algorithm :

- Selecting the intial medoids
 - 1. calculate the distance between the all object pairs (d_{ij}) .
 - 2. Then, calculate the V_i for all the objects

$$V_{j} = \sum_{i=1}^{n} \frac{d_{ij}}{\sum_{l=1}^{n} d_{il}}$$
(5.7)

- 3. Sort the list V_i 's and choose the K smallest values as initial medoids.
- 4. Assign all the objects to the closest medoid.
- 5. Calculate the sum of the distances for all the mediods from their objects.
- Then, we need to update the medoids. Based on the object in the cluster which has smaller distance to other objects. Update the medoid with to new calculated medoid.
- Assigning the objects to medoids 1. Assign the each object to cluster with smallest distance and get the cluster result. 2. Calculate the sum of all obejects distance from their medoids. If the sum of the distances is equal to the previous one Stop the alogrithm as medoids are fixed. Otherwise, go to step 2.

5.4.3 Self Organizing Map (SOM) neural network

Self Organizing Map (SOM) neural network [16] is used to automatically cluster the data. All neurons will be assigned with some random weights before starting the training. Every data object $X_1, X_2, ..., X_n$ is presented to every neuron repeatedly. With the repetition of training data, the neurons in a SOM network attempt to become like the input data presented to them. When the neuron receives the training data, neuron weights are adjusted with the data values. Learning parameters will determine how much the neurons needs to be adjusted. Neurons not only adjust themselves to the data, but also adjust the neighboring neurons as well.

Self-Organizing Map algorithm :

1. For each input object calculate the distance from all neurons and select the neurons with small distance as winner W_{winner}

$$W_i \leftarrow \arg\min \|X_k - W_i\| \tag{5.8}$$

where, k = 1, 2, ... n will be the training objects, W_i is wait of the neuron i, i = 1, 2, ... j and j is the number of neurons in SOM network.

2. Update the weights of each neuron as,

$$W_{i} = W_{i} + \alpha h(W_{winner}, W_{i}) \parallel X_{k} - W_{i} \parallel$$

$$(5.9)$$

where, α will be the learning rate or learning parameters, h will be the neighbor function to determine neighbor's of neuron.

3. Repeat the process until the map converges.

5.5 Indexing and Retrieval using unsupervised clustering

In this section, we present the details of indexing and retrieval space built for three unsupervised clustering techniques discussed in the Section 5.4 using the extracted features from the raw finger vein samples (refers to Section 5.3) along with the data sets used for both the spaces. Figure 9 shows representation of the indexing space and retrieval space built using the unsupervised clustering.



Figure 9: Schematic representation of indexing and retrieval using unsupervised clustering

5.5.1 Building indexing space

In this work, the clustering is performed on the training data set (refer Section 4.2.1 for experimental protocol). Thus, given the training data set, we adopt unsupervised clustering method (one at a time) that can output the K cluster centroids as $\{C_1, C_2, ..., C_K\}$. In the next step, we build the indexing by assigning each of the enrolled subject sample to any one of the clusters $\{C_1, C_2, ..., C_K\}$ based on the closest distance to the cluster center. To this extent, we have used the gallery samples from the testing database (refer Section 4.2.1 for experimental protocol). The gallery set represent one image for each subject. Thus, for each gallery image GE_{fv} from the testing data set, we first extract the features F_{GE} . We then compute the distance between F_{GE} and the K cluster centroids as $d_i = ||F_{GE} - C_i||$, i = 1, 2, ..., K. We then label the gallery image that represent individual subject (or identity) with cluster indices corresponding to the minimum distance. We use Hamming distance for the binary features and Euclidean distance for the real features.

5.5.2 Retrieval of the probe identity

The probe identity retrieval involves in computing the label of the input probe image on which the matching subject (or identity) is obtained by performing the database search corresponding to the cluster associated with the computed gallery label. Given the probe sample PE_{fv} from a test data set, we first perform the feature extraction step to obtain F_{PE} . We then compute the distance d_{Pi} between F_{PE} and the K clusters centers as $d_{Pi} = ||F_{PE} - C_i||$, i = 1, 2, ..., K (Hamming distance for binary features and Euclidean distance for real features are used). Then, the probe sample is assigned to the cluster corresponding to the minimum distance. In this way, the search is confined to the gallery samples associated with the computed cluster indices. Finally, the retrieval process will output a list of gallery identities L_g corresponding to the selected cluster indices.

Finger Vein Indexing using Unsupervised Clustering

6 Experimental Results

In the Chapter 5, we presented finger vein indexing and retrieval schemes based on unsupervised clustering using (1) K-means [14] (2) K-medoids [15] and (3) SOM [16]. In this chapter, we present the experimental results of the proposed unsupervised clustering techniques. The quantitative results of the proposed indexing and retrieval schemes are presented in terms of Pre-selection error (PSE) rate and Penetration Rate (PEN) following the International Organization for Standardization (ISO) [20]. PSE is defined as per ISO as "pre-selection error that occurs when the corresponding enrollment template is not in the preselected subset of candidates when a sample from the same biometric characteristic on the same user is given"[20].

The pre-selection error rate is defined as the probability of the probe image $PE_{f\nu}$ is not assigned to the same cluster as the corresponding identity $GE_{f\nu}$ in the gallery set. Let $CL_P \in \{C_1, C_2, ..., C_K\}$ be the cluster label of the probe image $PE_{f\nu}$ and L_{PE} be the corresponding list of the gallery images retrieved from the database. Let $CL_G \in \{C_1, C_2, ..., C_K\}$ be the cluster label of the gallery image $GE_{f\nu}$ corresponding to the same identity $PE_{f\nu}$ then [20] [47]:

$$PSE = 1 - \frac{1}{m} \sum_{i=1}^{m} Hit(PE_{fv})$$
 (6.1)

and

$$\operatorname{Hit}(\operatorname{PE}_{fv}) = \begin{cases} 1 & \operatorname{CL}_{P} \subseteq \operatorname{CL}_{G} \\ 0 & \text{otherwise} \end{cases}$$
(6.2)

PNR is defined as per ISO as "penetration rate measure of the average number of pre-selected templates as a fraction of the total number of templates"[20]. The penetration rate can be defined as follows [20] [47]:

$$PEN = \frac{1}{m} \sum_{i=1}^{m} \frac{|L_{PE}|}{n}$$
(6.3)

Where, n is the number of images in gallery set, m indicates the number of samples in probe set.

6.1 Results of proposed finger vein indexing schemes

The results of the proposed finger vein indexing and retrieval based on the un-supervised clustering are investigated with three different well established schemes like K-means [14], K-medoids [15] and Self Organizing Map (SOM) neural network [16] independently. In case of K-means and K-medoids, the performance largely depends on the initialization. Hence, both K-means and K-medoids clustering schemes are run for 500 times with a different set of initialization and finally we pick the one with the smallest sum of distances between all feature vectors and the respective cluster centers.

In this work, we present the results of unsupervised clustering for (1) binary features: extracted using the MCP [10] and (2) real features: with the proposed feature extraction technique.

6.1.1 Based on binary features

In this section we will present the results based on the MCP features [10] with (1) Single cluster search: where we confine our search to the single cluster (2) Multi-cluster search: in which we allow the search to expand to multiple clusters.

6.1.1.1 Single cluster search

Table 7 shows the quantitative results of the proposed indexing and retrieval on the single cluster search using binary features extracted using MCP [10]. Table 7 also indicates the results with different number of clusters (K). Thus, based on the experiments carried out on the single cluster search, the binary MCP features with K-means clustering have demonstrated the best performance when K = 2 with PSE/PEN = 9.38/73.53(%). Where as K-medoids has achieved the best performance when K = 2 with PSE/PEN = 16.91/64.08(%)

Clustering	Feature	Error	Number of Clusters (K)								
Method	Extraction	Rates (%)	K=2	K=3	K=4	K=5	K=6	K=7	K=8		
K-Means MCP [MCP [10]	PSE	9.38	10.18	20.9	16.37	19.9	22.56	24.16		
	MCF [10]	PEN	73.53	72.85	55.07	64.76	56.06	53.19	46.69		
K-Medoids	MCP [10]	PSE	16.91	28.36	28.36	28.36	28.36	28.36	28.36		
		PEN	64.08	43.80	43.80	43.80	43.80	43.80	43.80		

Table 7: Performance of the Single cluster search in terms of PSE/PEN (%) with binary features

6.1.1.2 Multi-Cluster Searching

In multi-cluster search , we extend the search to multiple clusters to explore the impact of multi-cluster search. Table 8 indicates the quantitative results of the multi-cluster search with binary features (with Number of clusters $N_c = 8$) that shows the performance of the best performing scheme (on single cluster based search with binary features) based on K-means, K-medoids and also we compare the performance with the existing state-of-the-art scheme based on repeated line tracking [2] and Locality Sensitive hashing (LSH) [13]. Following observation are made on the results: (1) The pre-selection rate quickly drops with multi-cluster search but increases the penetration rate. (2) MCP based on K-means shows the best result with PSE/PNR = 2.53/86.43(%). However, state of the art technique (LSH) demands more penetration rate to achieve pre-selection error rate of less than 3%. Performance of the K-medoids is not comparable, as we can see that penetration rate at any number of clusters is almost 100% with zero pre-selection error rate, which is same as sequential search.

Figure 10 shows the performance (PSE/PNR (%)) of the multi-cluster search on K-means and K-medoids clustering scheme using the binary features. Here we can clearly see that K-medoids clustering scheme performance with respect to the K-means. Later has performed very will and with the increased in number of clusters from right to left the penetration rate increases.

6.1.2 Based on real features

In this section we will present the results based on the proposed feature extraction technique with (1) Single cluster search: we search in single cluster (2) Multi-cluster search: we allow the search in multiple

Clustering	Feature	Error	Number of Clusters Searched (Nc)							
Method	Extraction	Rates (%)	Nc=2	Nc=3	Nc=4	Nc=5	Nc=6	Nc=7	Nc=8	
K Moone	MCB [10]	PSE	17.97	6.12	2.53	0.53	0.53	0.53	0.53	
K-Ivicalis	MCF [10]	PNR	62.57	75.02	86.43	99.48	99.48	99.43	99.43	
K Madaida	MCB [10]	PSE	0	0.06	0.06	0.06	0.06	0.06	0.06	
K-Weddius	WEI [10]	PNR	100	99.95	99.95	99.95	99.95	99.95	99.95	
Indexing	Feature	Error			Nun	ber of Table	s (T)			
Method	Extraction	Rates (%)	T=2	T=3	T=4	T=5	T=6	T=7	T=8	
LSH [13]	Repeated Line	PSE	92.5433	86.4181	84.8202	84.6871	83.2224	78.6951	77.9627	
	Tracking [2]	PNR	5.3228	6.1304	10.7618	13.5364	14.7107	16.5731	23.8645	

Table 8: Performance of the Multi-cluster search in terms of PSE/PEN (%) with binary features



Figure 10: Tradeoff between PSE and PNR using binary MCP features on K-means and K-medoids

clusters. We first present the quantitative results of the proposed feature extraction technique.

6.1.2.1 Quantitative results of the proposed real feature extraction scheme

The quantitative results of the proposed feature extraction scheme are given in this section. Since the proposed feature extraction is derived based on Maximum Curvature Points (MCP) [10], it is reasonable to compare the results of the proposed scheme with MCP. Table 9 shows the results of the comparative performance of the proposed scheme on six different publicly available finger vein database. Here, it can be observed that, the proposed scheme emerged as the best method on all six databases. This indicates the efficacy of the proposed scheme on the finger vein recognition. Thus, the proposed scheme not only represent the compact feature length but also demonstrated the improved performance over MCP [10].

Databasa	EER (%)						
Database	MCP [10]	Proposed Method					
ICFVR [6]	13.24	6.85					
FVUSM [50]	3.25	1.95					
UTFVP [7]	16.12	10.42					
HiGFVDB [3, 4]	1.13	0.20					
PloyU [8]	1.05	0.78					
HMV [9]	2.93	1.98					

Table 9: Quantitative performance of the proposed scheme

We will present the finger vein indexing and retrieval based on the un-supervised clustering using the real features. As explained K-means and K-medoids clustering schemes are run 500 times to choose the cluster centroids with smallest distance between the features and centroids. Further, we have also carried out the Silhouette measure [14] to fix the optimum number of clusters. Figure 11 shows the variation of the average Silhouette measure versus number of clusters (K) that indicates the smaller values of K results in more coherent clusters than large values of K. However, in case of SOM neural network clustering we followed the experimental procedure to try with various values of clusters and then to choose the one that yield the best PSE and PEN.

6.1.2.2 Single cluster search

Table 10 presents the quantitative results of the proposed indexing and retrieval on the single cluster search with the real features. Table 10 also shows the results with different number of clusters (K). In order to present the comprehensive comparison of the proposed feature extraction scheme we compare the results with most recent finger vein feature extraction scheme based on the improved Spectral Minutiae Representation (SMR) [11]. We particularly choose the SMR as it is most recent method that have demonstrated good performance and also provide the real number features that will fit well to our proposed indexing framework.

As observed from the Table 10, the penetration rate (PEN) decreases with increase in number of clusters (K). When comparing the performance of SMR with the proposed scheme, the best performance is noted with the proposed scheme. The SMR features shows the good performance when K = 4 while the proposed scheme shows the best performance when K = 3. Among the three different cluster schemes



Figure 11: Illustration of the Silhouette measure on K-means and K-medoids

 Table 10: Performance of the proposed finger vein indexing and retrieval scheme in terms of PSE/PEN

 (%) on single cluster search

Clustering	Feature	Error	Number of Clusters (K) /							
Method	Extraction	Rates (%)	Number of Nodes in case of SOM (K)							
Wiethou	Extraction	Kates (70)	K=2	K=3	K=4	K=5	K=6	K=7	K=8	
	SMR [11]	PSE	11.98	12.64	22.7	24.56	25.76	25.96	27.16	
K Means	Switc[11]	PEN	63.75	61.37	35.67	32.82	32.64	31.47	31.01	
IX-Ivicalis	Proposed	PSE	0.13	7.58	10.31	11.98	13.24	17.9	18.7	
	rioposed	PEN	83.96	42.48	28.85	22.16	18.84	15.1	13.2	
	SMR [11]	PSE	17.17	22.76	21.57	33.62	39.88	33.62	44.14	
SOM		PEN	54.3	38.76	36.57	26.2	22.01	25.3	17.05	
30101	Proposed	PSE	0.13	7.78	10.05	11.18	18.01	18.2	20.23	
	rioposed	PEN	80.46	41.85	27.93	22.37	17.63	15.39	14.8	
	SMD [11]	PSE	0	0	0	0	0	0	0	
K-Medoids	SIMIC [11]	PEN	100	100	100	100	100	100	100	
	Proposed	PSE	20.7	28.62	31.62	35.75	38.28	39.88	40.61	
	Toposed	PEN	50.17	34.23	28.04	22.84	19.31	17.24	16.24	

investigated in this work, the use of K-means and SOM clustering schemes shows better results when compared with K-Medoids clustering scheme. Further, the K-means and SOM clustering will show similar performance.

Thus, based on the experiments carried out on the single cluster search, the proposed real feature extraction scheme with K-means clustering have demonstrated the best performance with PSE/PEN = 7.58/42.48(%). Further, the use of SOM has also indicated the competent performance with PSE/PEN = 7.78/41.48(%).

6.1.2.3 Multi-Cluster Searching

In this experiment, we extend the search to multiple clusters to explore the impact of multi-cluster search. Table 11 indicates the quantitative results of the multi-cluster search (with Number of clusters $N_c = 8$) that shows the performance of the best performing scheme (on single cluster based search) based on K-means and least performing scheme based on K-medoids and also we compare the performance with the existing state-of-the-art scheme based on repeated line tracking and Locality Sensitive hashing (LSH) [13]. Following are the important observation on the results: (1) The pre-selection rate quickly drops with multi-cluster search but increases the penetration rate. (2) The proposed scheme based on K-means shows the best result with PSE/PNR = 0.98/52.88(%). However, other schemes based on K-medoids and LSH demands more penetration rate to achieve pre-selection error rate of less than 1%.

Clustering	Feature	Error			Number of	Clusters Sea	arched (Nc)		
Method	Extraction	Rates (%)	Nc=2	Nc=3	Nc=4	Nc=5	Nc=6	Nc=7	Nc=8
	SMD [11]	PSE	11.65	7.19	3.72	1.59	0.53	0	0
K Moone	SWIK [11]	PNR	62	74.58	83.55	89.81	95.12	100	100
]	Proposed	PSE	5.59	2.46	0.98	0.466	0.19	0	0
	Floposed	PNR	26.92	39.96	52.88	65.82	78.49	91.14	100
SMD [11]		PSE	0	0	0	0	0	0	0
K Medoids	SWIK [11]	PNR	100	100	100	100	100	100	100
K-Ivicuolus	Proposed	PSE	21.63	11.98	6.12	2.86	0.86	0.26	0
	Floposed	PNR	31.49	45.97	59.93	72.72	84.24	94.09	100
Indexing	Feature	Error			Nun	nber of Table	s (T)		
Method	Extraction	Rates (%)	T=2	T=3	T=4	T=5	T=6	T=7	T=8
LSH [13]	Repeated Line	PSE	92.5433	86.4181	84.8202	84.6871	83.2224	78.6951	77.9627
	Tracking [2]	PNR	5.3228	6.1304	10.7618	13.5364	14.7107	16.5731	23.8645

Table 11: Performance of the proposed fing	er vein indexing	and retrieval	scheme in t	erms of PSE	PEN
(%) 01	n multi-cluster se	earch			

Figure 12 shows the performance (PSE/PNR (%)) of the proposed feature extraction scheme with existing SOTA feature extraction scheme based on SMR on multi-cluster search on using K-means clustering. The number of cluster N_c to be searched increases from right to left. It can be observed that, the proposed feature extraction scheme shows the outstanding performance to achieve the tradeoff between PSE/PNR.

Figure 13 shows the performance (PSE/PNR (%)) of the proposed feature extraction scheme on multicluster search on K-means and K-medoids clustering scheme. Here also the number of cluster N_c to be searched increases from right to left. It can be observed here that the use of the K-means clustering has



Figure 12: Convergence rate of pre-selection rate and penetration rate tradeoff with proposed feature extraction and SMR on multi-cluster searching with $N_c = 8$ using K-means

demonstrated the best performance over K-mediods clustering scheme in multi-cluster search.



Figure 13: Tradeoff between PSE and PNR using proposed scheme on K-means and K-medoids

7 Discussion

In the Chapter 6, we presented the experimental results of the proposed unsupervised clustering schemes using binary and real features. In this chapter, we will discuss the various findings based on the results from the Chapter 6.

To this extent, we have used the maximum curvature points for binary features and introduced a new finger vein real feature extraction scheme based on the block-wise counting of maximum curvature points. We have introduced the finger vein indexing scheme based on unsupervised clustering using three independent methods namely: K-means, K-medoids and Self-Organizing Map (SOM) neural network. We then performed the extensive experiments on the large scale finger vein database with 2850 identities for binary and real features using both single and multi-cluster search strategy that showed the best performance of MCP (binary features) and the proposed real feature extraction scheme with K-means clustering.

In summary, following are the main observations based on the experiments:

- The proposed ROI extraction works efficiently on the six different finger vein databases.
- The proposed new real feature extraction scheme on finger vein biometric demonstrated the best performance when compared with a well established state of the art (SOTA) scheme based on Maximum Curvature Points (MCP) on 6 different finger vein databases. Furthermore, the proposed real features are compact, discriminative and robust that made suitable for building the indexing space.
- We have introduced the unsupervised clustering based finger vein indexing and retrieval scheme. We
 have investigated three different unsupervised clustering schemes using K-means, K-medoids and
 Self-Organizing Maps (SOM) neural network. We have also compared the proposed method with real
 feature extraction scheme with the existing SOTA scheme using Spectral Minutiae Representation
 (SMR).
- K-means single cluster search using binary features has achieved good performance when number of clusters K = 2 with PSE/PNR = 9.38/73.53(%) and K-medoids has achieved best performance with PSE/PEN = 16.91/64.08(%) when number of clusters K = 2.
- Multi-cluster search with K-means has achieved best performance when Nc = 4 with PSE/PNR = 2.53/86.43(%) for the binary features. Whereas K-medoids performance was comparable with the sequential search of the database.
- The single cluster search strategy presented in this work indicates the best performance of the proposed real feature extraction scheme with K-means clustering with a PSE/PNR = 7.58/42.48(%). Furthermore, the use of SOM also shows the encouraging results with a PSE/PNR = 7.78/40.85(%) when number of cluster K = 3. But, the use of K-medoids fails to produce the good results.
- The use of multi-cluster search further improves the pre-selection error rate at the cost of increased

penetration rate with the real features. The experimental results also demonstrates the best performance of the proposed K-means clustering with a PSE/PNR = 0.98/52.88(%) when compared with existing SOTA scheme based on LSH [13] and K-medoids has taken a taken a huge penetration rate in the database to achieve the same PSE with a PSE/PNR = 0.86/84.24(%).

• Finger vein indexing scheme using the real-valued features has achieved the best performance with K-means clustering using single cluster search and multi-cluster search. Even the performance of the SOM is comparable with the K-means single cluster search. Whereas finger vein indexing scheme using binary features has achieved the best performance with K-means clustering both single and multi-cluster search but the performance of this system is not comparable to the real- valued feature based finger vein indexing.

8 Conclusions and Future work

In this thesis, we have collected Høgskolen i Gjøvik Finger Vein Database (HiGFVDB) using an inhouse sensor [11] from 130 participants. A new robust Region of Interest (ROI) extraction technique has been proposed which works across different databases. We have investigated new schemes for finger vein indexing using unsupervised clustering techniques with binary features and real features. We have also evaluated the existing state of the art finger vein indexing technique. An extensive set of experiments are carried out on the large scale finger vein database which has been constructed from the seven different databases with 2850 unique finger samples collected using different sensors. Results of the proposed unsupervised clustering schemes are presented with binary features, real features and compared with the SOTA indexing technique.

8.1 Conclusion

In this section, we present an analysis of all the research question, with an explanation in terms of achieved results.

Research Question 1 Does the present state-of-the-art (SOTA) indexing technique performance suffice for large scale finger vein applications?

Based on the experimental results presented in the Chapter 6, it is clearly visible that SOTA indexing technique has a significant pre-selection error (PSE) rate with considerable penetration rate (PNR). With the increase in total number of tables, the PSE decreases along with a rise in PNR. SOTA indexing technique requires a large number of tables to achieve small PSE. But for any indexing method to be used in large-scale finger vein applications, we need to have less PSE, less PNR and need to use same amount of space required for the database without any redundancy of the finger vein samples. To increase the performance of SOTA indexing technique in terms of PSE, we need to increase the of number tables, which lead to the redundancy of the finger vein samples across the tables. Thus, the SOTA indexing technique performance is not acceptable for large scale finger vein applications.

Research Question 2 Is unsupervised clustering of finger vein samples useful for narrowing down the search space in large scale finger vein application?

In order to answer this question, we have analyzed three unsupervised clustering schemes for indexing of finger vein samples namely: 1) K-means, 2) K-medoids and 3) Self-Organizing Map (SOM) neural network and results are presented in Chapter 6. The indicated results clearly show the better performance as compared to the SOTA indexing technique in terms of PSE and PNR. It has been experimentally demonstrated, that the unsupervised clustering of finger vein samples will be useful for narrowing down the search space in large scale finger vein application. **Research Question 3** Does the proposed unsupervised clustering techniques with 1) binary features and 2) real features will be useful in real life scenarios?

The proposed unsupervised clustering techniques in this work has demonstrated the superiority in terms of the PSE and PNR over the SOTA indexing technique. Even though the performance of the unsupervised clustering with binary features has shown good results compared to the SOTA, unsupervised clustering with real features outperform both of them. As finger vein biometric systems are used in many of the real-time application, it would be appropriate to incorporate the unsupervised clustering technique with the proposed real feature extraction technique. Furthermore, the proposed real features are compact and show good performance over SOTA feature extraction techniques. Conclusively, it can be argued that the Proposed unsupervised clustering techniques with real features can be used in real life scenarios for large scale finger vein applications.

8.2 Future work

The proposed techniques in this work have indicated the significance and applicability for finger vein indexing in real life scenarios. An interesting study in this regard would apply the proposed technique on very large scale finger vein databases to measure the PSE and PNR. This large-scale study shall indicate the strengths and shortcomings of the proposed techniques which shall help in improving the algorithms for making them robust. Another important aspect of the future work shall be to explore new feature extraction techniques to reduce the PSE and PNR as compared to the values obtained from proposed unsupervised clustering techniques.

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A Additional Experiments

A.1 Pre-selection of features & comparison (PSFC)



Figure 14: Schematic representation of PSFC using small set of features

In this method, for the given probe sample we perform the features extraction to obtain F_{I_P} . Then, we need to select the P (%) features for retrieving the candidate list. These features can be selected in three ways, namely: 1)First, 2) Last and 3) Random P (%) of features out of the total features. For selecting the random features, random numbers are generated and used across the gallery and probe samples for feature selection. Then, hamming distance between the gallery and probe samples calculated with same set of features $D_i = ||P(G_{I_i}) - P(F_{I_P})||$ for i = 1, 2, 3 ... n. Where, n is the number of images in gallery set. If the hamming distance is less than the threshold(T), gallery sample will be added to the candidate list. An overview of the proposed scheme is given in Figure 14.

A.1.1 Experimental Results

we search based on the selected number of features (P %) from both gallery and probe samples, instead of searching with complete set of features. Table 12 illustrates the quantitative results with PSFC. Based on the experiments we have following observations:

- 1. With the increase in the threshold(T), decreases the pre-selection error rate. Which can be clearly seen in Figure 15 for various P% of features.
- 2. With the increase in the threshold also increases the number of pre-selected samples for each probe, Figure 16 shows the tradeoff between the number of pre-selected samples to threshold for different set of features.
- 3. Best performance of PSFC is achieved with T = 0.12 and P = 30(%) of features with PSE = 9.58 / 9.85 / 8.05 for first / last / random features with less number of gallery samples for identification.

Threshold (T)	Fastures (D %)		PSE		Average 1	Average no of samples for a probe			
Threshold (1)	reatures (r %)	First	Last	Random	First	Last	Random		
	30	95.8	99.6	99.8	0.042	0.003	0.001		
0.02	40	97.86	99.66	99.86	0.021	0.003	0.001		
0.02	60	99.66	99.86	99.86	0.003	0.001	0.001		
	80	99.66	99.86	99.86	0.003	0.001	0.001		
	30	79.76	93.47	90.94	0.38	0.06	0.09		
0.04	40	83.95	92.41	90.87	0.17	0.07	0.09		
	60	88.81	94.8	91.27	0.11	0.05	0.08		
	80	87.68	93.8	90.87	0.12	0.06	0.09		
	30	62.58	72.7	71.17	6.49	0.46	0.28		
0.06	40	64.98	71.5	71.03	1.23	0.28	0.28		
0.00	60	70.37	75.29	71.5	0.29	0.24	0.28		
	80	69.97	73.56	71.63	0.3	0.26	0.28		
	30	43.74	50.19	54.12	74.78	7.93	0.48		
0.08	40	45.33	52.13	54.79	24.88	1.72	0.46		
0.08	60	53.72	56.65	54.86	0.89	0.44	0.45		
	80	53.26	55.85	54.52	0.55	0.44	0.46		
	30	25.03	26.56	29.62	380.33	126.09	11.26		
0.1	40	25.96	27.76	30.75	241.48	70.79	9.16		
0.1	60	30.35	32.88	30.42	39.31	6.18	8.14		
	80	30.02	32.42	30.09	28.83	2.59	8.17		
	30	9.58	9.85	8.05	918.22	701.1	565.99		
0.12	40	10.65	9.85	8.32	802.61	646.58	513.99		
0.12	60	11.31	11.85	8.32	504.06	312.36	515.79		
	80	9.52	10.58	8.18	571.59	309.01	521.01		
	30	1.39	1.39	0.59	1423.3	1430.29	1466.71		
0.15	40	1.19	0.73	0.59	1418.63	1454.97	1464.08		
0.15	60	0.93	0.59	0.59	1408.16	1439.3	1466.23		
	80	0.46	0.73	0.59	1451.59	1452.23	1465.42		
	30	0	0	0	1501.93	1501.98	1502		
0.2	40	0	0	0	1501.97	1502	1502		
0.2	60	0	0	0	1501.98	1502	1502		
	80	0	0	0	1501.99	1502	1502		

Table 12: Performance of the PSFC in terms of PSE (%) and Average number of samples for a probe with threshold (T) and features (P%)



Figure 15: Tradeoff between T and PSE with PSFC with (a) 30% (b) 40% (c) 60% (d) 80% of features



Figure 16: Relation between T and number of pre-selected samples for each probe with (a) 30% (b) 40% (c) 60% (d) 80% of features with PSFC

Finger Vein Indexing using Unsupervised Clustering

B Finger vein indexing based on binary features

A scientific paper communicating the results based on the binary features for finger vein indexing using K-means unsupervised clustering and pre-selection of features & comparison (PSFC) is presented in this section. This paper has been accepted for publication in CVCS2015 (http://colourlab.no/events/cvcs2015) and shall be published in IEEE Proceedings of CVCS2015, Gjøvik, Norway.

Finger vein indexing based on binary features

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Abstract-Finger vein indexing refers to the process of creating clusters of finger vein samples based on the extracted features from the image. In large scale finger vein identification, the input probe image needs to be compared with a large set of gallery images to match the identity. Clusters can be used to confine the process of identity match of the images present in the gallery to the probe sample of the same cluster. In this work, we explored a new finger vein indexing and retrieval scheme with K-means clustering and pre-selection of features & comparison(PSFC). For a input probe sample, the centroid with the smallest distance will be chosen and compare with them for identification with K-means and P% of features (First, Last and Random) are compared with gallery samples features to choose for identification with PSFC. Extensive set off experiments are carried on a large scale data set of 2850 unique subjects created using publicly available finger vein databases. Single cluster search with K-means clustering demonstrated the performance with pre-selection error of 9.38%(hit rate of 90.62%), Multi-cluster search with K-means clustering has achieved best performance with pre-selection error of 2.53% (hit rate of 97.47%) and PSFC has demonstrated the efficiency with pre-selection error of 9.58/9.85/8.05% (hit rate of 90.42/90.15/91.95%)for first/last/random features.

I. INTRODUCTION

Biometric systems are used to identify the individuals based on their physiological or behavioral characteristics. In physiological characteristics, finger vein biometrics are gaining more popularity because of several advantages 1) It is very easy to capture the finger veins using the Near infra-red devices and 2) it is very hard spoof finger veins, because of their presence under human skin and no one know their patterns without capturing them using the sensor [1]. Because of these advantages, Finger vein biometric systems are adopted into the financial sectors in some of the countries.

With the increased use of finger vein systems in financial sectors, identification of users using these applications requires to search the complete database for correct recognition. This problem can be solved with the help indexing and retrieval of the user search space, which can help in narrowing the search space. So, decision can be taken based on the subset of the search space instead of comparing to all users present in complete database.

To the best of our knowledge, there was only one research carried out by D. Tang et al. [2] to address the finger vein retrieval with the binary features. R. Raghavendra et al. [3] has explored the finger vein indexing using the real features, which is beyond the scope of this work. In this [2] initial study of finger vein indexing using binary features has used the repeated line tracking [4] feature extraction method and Local Sensitive Hashing (LSH) as the indexing method. Experimental results in [2] show good results, but it requires high amount of memory to store the hash tables with increase in size of the database. So, in this work, we introduced a new finger

vein indexing technique using K-means clustering and Preselection of features & comparison(PSFC) based on binary finger vein features. The main contribution of this work are (a) new finger vein indexing and retrieval framework based on K-means clustering [5] (b) PSFC framework with minimum set of features and (c) new diversified finger vein database is constructed from seven publicly available finger vein databases and experiments are performed on this new database of 2850 unique subjects which shows the efficiency of the proposed methods.

The paper is organized into four sections: the first section, is the Introduction. Section II describes the proposed Finger vein indexing using K-means clustering and PSFC, Section III present the details of database construction, discuss the obtained results and comparative analysis of the proposed methods with state-of-the-art schemes and finally Section IV draws the conclusion.

II. PROPOSED METHODS

The proposed methods consists of three main components, namely: (1) Region of Interest (ROI) extraction and preprocessing (2) Feature extraction using maximum curvature method (MCM) (3) Proposed schemes. Each of these components are outlined in the following section.

A. Region of Interest (ROI) extraction and pre-processing



Fig. 1: ROI extraction on one of the finger vein sample from the database

The goal of the ROI extraction is to acquire the prominent details from the finger where the vein patterns are present. Then enhance these extracted ROI samples to intensify the vascular patterns. ROI extraction has to be robust across the seven databases. In this work, we extract the ROI based on the boundaries of finger vein samples. We have adopted the method described in [1] for translation and rotation to align the finger. For the given Finger vein sample S_v , samples are re-sized to 200 x 600 pixels to bring the same resolution across the data sets. We perform the binarization of re-sized finger vein samples RS_v using Ostus thresholding. In the next step, we locate the center of the binarized finger vein sample $C_{BRS}(x,y)$, then we travel along the column of $C_{BRS}(x,y)$ to find boundary of finger in both directions $B_1(x, y)$ and $B_2(x, y)$. Then, we fixed the ROI by discarding 20 pixels on both sides of the finger from $B_1(x, y)$ and $B_2(x, y)$, 40 pixels



Fig. 2: Schematic representation of finger vein indexing using K-means clustering

from tip of the finger and 20 pixels from fourth side of the sample. Figure 1 shows the ROI extraction adopted in this work.

The pre-processing step involves improving and equalizing contrast of the finger vein pattern using CLAHE [6]. The improved finger vein samples I_{Sv} are re-sized to 128 x 512 pixels to make ROI samples of all subjects to same resolution.

B. Feature extraction using Maximum Curvature method

In this work, we adopted Maximum Curvature method [7] as feature extraction technique for finger vein samples, which has demonstrated very good results in identification. It consists of three main steps. 1) Center positions of finger veins are extracted using the curvatures of veins, based on the adjacent pixel on both sides of the pixel. 2) If the pixels have large values, then line will be drawn connecting the pixels. This operation is performed in all four directions at each pixel and maximum value is obtained. 3) Vascular pattern of the sample is processed with a threshold to eliminate the noise.

C. Proposed schemes

In this section we present the two schemes based on the 1)K-means clustering and 2) pre-selection of features & comparison.

1) Finger vein indexing using K-means clustering: Figure 2 shows the block diagram of the proposed indexing and retrieval scheme for finger vein using K-means clustering. Clustering and retrieval covers the building of indexing space and retrieval of the probe identity from the gallery.

Building clustering: After extracting the features from samples, we need to cluster them to build an indexing space. In this work, we have explored K-means [5] unsupervised clustering. Initially on training data set performed the K-means clustering to get the K cluster centroids $C_1, C_2, C_3 \dots C_K$. Then, indexing space has been created by assigning each subjects enrollment sample to one of the clusters $C_1, C_2, C_3 \dots C_K$ based on the distance to the cluster centroids. To achieve this, we have used testing data set gallery samples, which consists of enrollment sample for each subject. First we extract the features $F_{GI_{Sv}}$ for all the gallery samples GI_{Sv} in testing database. Then, we calculate the distance between the K cluster centroids and $F_{GI_{Sv}}$ as $D_i = ||C_i - F_{GI_{Sv}}||$ for $i = 1, 2, 3 \dots K$. Finally, the gallery sample of a subject will be added to a cluster where the distance between the cluster centroid and subject is minimal.

Retrieval of the probe identity: Identity retrieval includes the computation of a cluster for the input probe sample for which a matching subject from gallery of all subjects is obtained from database. For the given probe sample PS_v from the testing data set, first we perform ROI extraction and pre-processing to obtain I_{PSv} . We then perform the features extraction to get F_{I_P} . Next step is to calculate the distance D_{P_i} between K cluster centroids and F_{I_P} as $D_{P_i} = ||C_i - F_{I_P}||$ for $i = 1, 2, 3 \dots K$. Then, the probe sample will be assigned to a cluster with minimum distance. By this, searching of probe sample will be confined to the gallery samples associated with subset of all gallery samples present in specific cluster. Finally, the retrieval method will match the identities in the gallery from the selected cluster indices. An overview of the identity retrieval for probe images is given in Figure 2.



Fig. 3: Schematic representation of PSFC using small set of features

Database	Total No. of Subjects	Total No. of Fingers	Data Partition				
Database	Total NO OF Subjects	Total No of Filigers	Development	Training	Testing		
ICFVR [8]	#	310	76	150	84		
FVUSM [9]	123	492	0	200	292		
HiGFVDB [10], [11]	130	520	36	150	334		
HMV [12]	106	636	0	250	386		
PolyU [13]	156	312	83	100	129		
UTFVP [14]	60	360	0	150	210		
VERA [15]	110	220	78	75	67		
Total	685+#	2850	273	1075	1502		

TABLE I: Finger vein databases used to construct the database

2) Pre-selection of features & comparison (PSFC): In this method, for the given probe sample we perform the features extraction to obtain F_{I_P} . Then, we need to select the P (%) features for retrieving the candidate list. These features can be selected in three ways, namely: 1) First, 2) Last and 3) Random P (%) of features out of the total features. For selecting the random features, random numbers are generated and used across the gallery and probe samples for features selection. Then, hamming distance between the gallery and probe samples calculated with same set of features $D_i = ||P(G_{I_i}) - P(F_{I_P})||$ for $i = 1, 2, 3 \dots n$. Where, n is the number of images in gallery set. If the hamming distance is less than the threshold(T), gallery sample will be added to the candidate list. An overview of the scheme is given in Figure 3.

III. EXPERIMENTAL RESULTS

This section will present the results of the new proposed finger vein indexing and retrieval scheme with K-means clustering. The quantitative results are analyzed using the Pre-Selection Error rate (PSE) and Penetration Rate (PEN) for the proposed indexing scheme [16] [17]. The pre-selection error rate occurs when the corresponding enrolled template is not present in the pre-selected subset of subjects when a sample from the same subject's biometric characteristic is given.

Let $CL_P \in \{C_1, C_2, \ldots, C_K\}$ be the cluster label of the probe image PI and L_{PI} be the corresponding list of the gallery images retrieved from the database. Let $CL_G \in \{C_1, C_2, \ldots, C_K\}$ be the cluster label of the gallery image GI corresponding to the same identity PI then [16] [17]:

 $PSE = 1 - \frac{1}{m} \sum_{i=1}^{m} Hit(PI)$

and

$$Hit(PI) = \begin{cases} 1 & CL_P \subseteq CL_G \\ 0 & otherwise \end{cases}$$
(2)

Where, m indicates the number of probe set.

The penetration rate is nothing but how much database has been searched to retrieve the list [16] [17]:

$$PEN = \frac{1}{m} \sum_{i=1}^{m} \frac{|L_{PI}|}{n}$$
(3)

Where, n is the number of images in gallery set.

A. Database construction

In this work, we have constructed a database from publicly available seven different finger vein databases, which are collected using different finger vein sensors: (a) ICFVR [8] (b) FVUSM [9] (c) HiGFVDB [10], [11] (d) HMT [12] (e) ployU [13] (f) UTFVP [14] (g) Vera [15]. This new diversified finger vein database is comprised of 2850 unique finger vein samples resulting in 2850 subjects from 685+ users. Since each database has different number of samples, we have considered first 2 samples for each finger from all the seven databases. Construction of the database from 7 different finger vein databases can be seen in Table I along with distribution of samples between the development, training and testing data sets without any overlap of samples. Usage of the each data set and its purpose will be explained below.

B. Performance evaluation of the system

The database has been divided in to three data sets 1) development, 2) training and 3) testing with independent subjects is each set. The development data set is used for tuning the parameters for ROI extraction, which contains 546 finger vein samples associated to 273 distinct subjects in complete database. The training data set holds 2150 finger vein samples related to 1075 different subjects by randomly selecting the fixed number of subjects from all the databases, which is used to build the cluster centroids using K-means algorithm. As the cluster centroids depends on the initialization, the K-means procedure is set to run 500 times with dissimilar centroids. Out of these 500 centroids, we choose the set where the distance between the features and cluster centroids sum is smallest. Then, the remaining finger vein samples are used in the testing data set, which comprises of 1502 unique subjects used to evaluate the performance. For each subject in testing data, one of the image is taken in to the gallery data set and other image in to the probe data set.

C. Results and discussion

(1)

All results presented in this section are based on the new database which has been created. In this work, we present the quantitative results of the proposed methods 1) K-means Single Cluster Search 2) K-means Multi-Cluster Search and 3) PSFC.

TABLE II: Performance of the Single cluster search in terms of PSE/PEN (%) with proposed K-means indexing and retrieval scheme

NGD II	Number of clusters (K)									
MCP + K-means	K = 2	K = 3	K = 4	K = 5	K = 6	K = 7	K = 8	K = 9	K = 10	K = 15
PSE	9.38	10.18	20.9	16.37	19.9	22.56	24.16	29.63	31.55	14.91
PNR	73.53	72.85	55.07	64.76	56.06	53.19	46.69	40.71	36.11	58.74

TABLE III: Performance of the Multi-cluster search in terms of PSE/PEN (%) with proposed K-means indexing and retrieval scheme

	D D (0)	Number of clusters (Cn)								
Method	Error Rates (%)	Cn = 2	Cn = 3	Cn = 4	Cn = 5	Cn = 6	Cn = 7	Cn = 8		
	PSE	17.97	6.12	2.53	0.53	0.53	0.53	0.53		
MCP + K-means	PNR	62.57	75.02	86.43	99.48	99.48	99.43	99.43		
	D D (0)			Numl	per of table	s (Tn)				
Method	Error Rates (%)	Tn = 2	Tn = 3	Tn = 4	Tn = 5	Tn = 6	Tn = 7	Tn = 8		
	PSE	92.54	86.41	84.82	84.68	83.22	78.69	77.96		
LSH + Repeated Line Tracking [2]	PNR	5.32	6.13	10.76	13.53	14.71	16.57	23.86		

TABLE IV: Performance of the PSFC in terms of PSE (%) and Average number of samples for a probe with threshold (T) and features (P%)

Threshold (T)	Fastures (D %)		PSE		Average no of samples for a probe			
Threshold (1)	reatures (1 70)	First	Last	Random	First	Last	Random	
	30	95.8	99.6	99.8	0.042	0.003	0.001	
0.02	40	97.86	99.66	99.86	0.021	0.003	0.001	
0.02	60	99.66	99.86	99.86	0.003	0.001	0.001	
	80	99.66	99.86	99.86	0.003	0.001	0.001	
	30	79.76	93.47	90.94	0.38	0.06	0.09	
0.04	40	83.95	92.41	90.87	0.17	0.07	0.09	
0.04	60	88.81	94.8	91.27	0.11	0.05	0.08	
	80	87.68	93.8	90.87	0.12	0.06	0.09	
	30	62.58	72.7	71.17	6.49	0.46	0.28	
0.06	40	64.98	71.5	71.03	1.23	0.28	0.28	
0.00	60	70.37	75.29	71.5	0.29	0.24	0.28	
	80	69.97	73.56	71.63	0.3	0.26	0.28	
	30	43.74	50.19	54.12	74.78	7.93	0.48	
0.08	40	45.33	52.13	54.79	24.88	1.72	0.46	
0.08	60	53.72	56.65	54.86	0.89	0.44	0.45	
	80	53.26	55.85	54.52	0.55	0.44	0.46	
	30	25.03	26.56	29.62	380.33	126.09	11.26	
0.1	40	25.96	27.76	30.75	241.48	70.79	9.16	
0.1	60	30.35	32.88	30.42	39.31	6.18	8.14	
	80	30.02	32.42	30.09	28.83	2.59	8.17	
	30	9.58	9.85	8.05	918.22	701.1	565.99	
0.12	40	10.65	9.85	8.32	802.61	646.58	513.99	
0.12	60	11.31	11.85	8.32	504.06	312.36	515.79	
	80	9.52	10.58	8.18	571.59	309.01	521.01	
	30	1.39	1.39	0.59	1423.3	1430.29	1466.71	
0.15	40	1.19	0.73	0.59	1418.63	1454.97	1464.08	
0.15	60	0.93	0.59	0.59	1408.16	1439.3	1466.23	
	80	0.46	0.73	0.59	1451.59	1452.23	1465.42	
	30	0	0	0	1501.93	1501.98	1502	
0.2	40	0	0	0	1501.97	1502	1502	
0.2	60	0	0	0	1501.98	1502	1502	
	80	0	0	0	1501.99	1502	1502	



Fig. 4: Tradeoff between T and PSE with PSFC with (a) 30% (b) 40% (c) 60% (d) 80% of features



Fig. 5: Relation between T and number of pre-selected samples for each probe with (a) 30% (b) 40% (c) 60% (d) 80% of features with PSFC
1) Single cluster search: where we search in single cluster and Table II illustrates the indexing and retrieval on the Kmeans single cluster search with MCP as feature extraction method. Based on the experiments conducted on the single cluster search, best performance is achieved when K = 2 with PSE/PNR = 9.38/73.53(%).

2) Multi-Cluster Searching: we allow the search in multiple clusters and choose cluster with the minimum distance. Table III illustrates the quantitative results with K-means multiple cluster search (Number of clusters Cn = 8) and we compare the performance with the state-of-the-art scheme based on repeated line tracking as feature extraction scheme and Locality Sensitive hashing (LSH) for indexing and retrieval [2]. Based on the experiments we have made following observations. 1) With the increase in the number of clusters in multi-cluster search increases the penetration rate with the decrease of pre-selection error rate. 2) best performance of K-means multi-cluster search is achieved when Cn = 4 with PSE/PNR = 2.53/86.43(%). Where as, with LSH it requires more number of tables (Tn) to achieve the same pre-selection error rate of less than 3%.

3) Pre-selection of features & comparison (PSFC): we search based on the selected number of features (P %) from both gallery and probe samples, instead of searching with complete set of features. Table IV illustrates the quantitative results with PSFC. Based on the experiments we have following observations. 1) With the increase in the threshold(T), decreases the pre-selection error rate. Which can be clearly seen in Figure 4 for various P% of features. 2) With the increase in the threshold also increases the number of preselected samples for each probe, Figure 5 shows the tradeoff between the number of pre-selected samples to threshold for different set of features. 3) Best performance of PSFC is achieved with T = 0.12 and P = 30(%) of features with PSE = 9.58/9.85/8.05 for first/last/random features with less number of gallery samples for identification.

IV. CONCLUSION

In this work, we present a new finger vein indexing and retrieval based on K-means clustering with single cluster search, multi-cluster search and PSFC. A rigorous set of experiments are carried out on diversified data set constructed using the seven publicly available databases with 2850 unique identities corresponding to 685+ users. Finally, we have the following observations. In this work, we present a new finger vein indexing and retrieval based on K-means clustering with single cluster search, multi-cluster search and PSFC. A rigorous set of experiments are carried out on diversified data set constructed using the seven publicly available databases with 2850 unique identities corresponding to 685+ users. Finally, we have the following observations.

- K-means single cluster search has achieved performance when K = 2 with PSE/PNR = 9.38/73.53(%).
- Multi-cluster search with K-means has achieved best performance when Cn = 4 with PSE/PNR = 2.53 / 86.43(%).

- Pre-selection of features & comparison has achieved best performance when T = 0.12 and P = 30(%) of features with PSE = 9.58/9.85/8.05 for first/last/random features.
- State-of-the-art technique LSH [2] requires more number of tables (Tn) to achieve the same pre-selection error rate.

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Finger Vein Indexing using Unsupervised Clustering

C An efficient finger vein indexing scheme based on unsupervised clustering

A scientific paper communicating the results based on the real features using the proposed feature extraction technique for finger vein indexing using unsupervised clustering techniques K-means [14], Kmedoids [15] and Self-Organizing Map (SOM) neural network [16] is presented in this section. This paper has been published in proceedings of IEEE ISBA2015 (http://www.isba2015.org/), Hong Kong, China.

An efficient finger vein indexing scheme based on unsupervised clustering

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Abstract

Finger vein recognition has emerged as the robust biometric modality because of their unique vein pattern that can be captured using near infrared spectrum. The large scale finger vein based biometric solutions demand the need of searching the probe finger vein sample against the large collection of gallery samples. In order to improve the reliability in searching for the suitable identity in the large-scale finger vein database, it is essential to introduce the finger vein indexing and retrieval scheme. In this work, we present a novel finger vein indexing and retrieval scheme based on unsupervised clustering. To this extent we investigated three different clustering schemes namely K-means, K-medoids and Self Organizing Maps (SOM) neural networks. In addition, we also present a new feature extraction scheme to extract both compact and discriminant features from the finger vein images that are more suitable to build the indexing space. Extensive experiments are carried out on a large-scale heterogeneous finger vein database comprised of 2850 unique identities constructed using seven different publicly available finger vein databases. The obtained results demonstrated the efficacy of the proposed scheme with a pre-selection rate of 7.58% (hit rate of 92.42%) with a penetration rate of 42.48%. Further, the multi-cluster search demonstrated the performance with pre-selection error rate of 0.98% (hit rate of 99.02%) with a penetration rate of 52.88%.

1. Introduction

Finger vein biometrics has rapidly gaining popularity for its potential characteristics useful for human identification/recognition. The finger vein pattern can be captured by penetrating the Near-Infrared Light (NIR) on the finger that will be absorbed significantly by the haemoglobin than by the surrounding tissues. Figure 1 (a) shows the region of interest from finger vein pattern captured with NIR illu-



Figure 1: Finger vein image (a) ROI of finger vein (b) Enhanced finger vein

mination and Figure 1 (b) shows the enhanced finger vein pattern. Furthermore, the use of finger vein biometrics offers an advantage of being contactless and difficult to spoof as the vein pattern is hidden inside the skin. This enables the adaptation of the finger vein biometric based identification solution in a wide range of banking application especially in the Asian counties. The finger vein biometrics has received remarkable progress from recent decades that resulted in various feature extraction schemes that mainly includes Maximum Curvature points (MCP) [8], Wide Line Detector (WLD) [3], Repeated Line Tracking (RLT) [7], Spectral Minutiae Representation (SMR) [2] and improved Spectral Minutiae Representation [13]. These feature extraction schemes have demonstrated very good accuracy in building a ginger vein based identification solution.

Inspite of many finger vein recognition schemes most of the analysis is limited to the small scale database. With the growing requirements of the large scale national ID programs, for example, India's UID project [15] using biometrics has imposed the challenges that include not only the robustness but also the accuracy for reliable identification. Under these circumstances, the biometric based identification solution need to search for the biometric reference in a large-scale database by ensuring a very high recognition accuracy. The natural way of addressing this situation is by introducing the indexing and retrieval scheme that can simply reduce the search space by selecting the number of likely candidates from the large scale database to facilitate the comparison and decision on the smaller dimension space.

Even though the finger vein indexing and retrieval problem was not studied extensively, there exist only one work [16] that address the finger vein retrieval problem. In [16],

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preliminary study on the finger vein indexing is presented using the repeated line tracking as the feature extraction scheme and Locality Sensitive Hashing (LSH) as the indexing scheme. Experimental results indicated in [16] shows the improvement in the query time at the cost of reduced hit rate when compared to the linear search. Even though the choice of LSH for finger vein is appealing, it demands the tuning of hyper-parameters and also the memory requirement to store the hash table that will grow according to the size of the database as well as the choice of hash function. Thus, in this work we introduced a novel finger vein solution using unsupervised clustering and present the in-depth analysis on the same. The novelty and main contribution of this paper can be summarized as follows:

- We present a novel finger vein indexing and retrieval framework based on unsupervised clustering. To this extent, we investigated three different clustering schemes like: (1) K-means [6] (2) K-medoids [10] and Self Organizing Map (SOM) neural network [4] independently.
- We present a new finger vein feature extraction scheme by exploring a block wise counting of Maximum Curvature points (MCP) that will result in compact feature representation suitable for indexing.
- Extensive experiments are carried out on a large scale database of 2850 unique identities constructed using seven different publicly available finger vein databases. The obtained results demonstrated the efficacy of the proposed finger vein indexing and also the proposed finger vein feature extraction scheme.

The paper is organized as follows: Section 2 present the proposed framework on finger vein indexing and feature extraction scheme, Section 3 reports the experimental results, comparison with existing state-of-the-art (SOTA) schemes and also in-depth analysis of the proposed scheme. Finally, Section 4 draws the conclusion.

2. Finger vein indexing using unsupervised clustering

Figure 2 shows the block diagram of the proposed finger vein indexing and retrieval scheme based on unsupervised indexing. The proposed method can be structured using four different functional blocks namely: (1) Region of Interest (ROI) extraction and pre-processing (2) Feature extraction (3) Building indexing space (4) Retrieval of the probe identity. In the following, we discuss each of these steps in detail.

2.1. Region of Interest (ROI) extraction and preprocessing

The idea of the ROI extraction and pre-processing is to extract the interest region from the captured finger that can solely represent the vein pattern and then to enhance the extracted ROI to improve the visibility of the vein pattern. Since we have combined 7 different publicly available databases that exhibits different capturing conditions to form a single large database, the ROI extraction is expected to be robust for these changes. In this work, we detect the ROI based on tracing the boundary of the finger. Given the Finger vein image I_{Fv} , we first perform the binarization using Otsu's thresholding. The binarized finger vein image Ib_{Fv} is further processed to fill the holes using morphological reconstruction. In the next step, we locate the center of the image $C_{Ib}(x, y)$, we then consider the column corresponding to $C_{Ib}(x, y)$ then find the first discontinuity along rows on both the direction to get outer edge of the finger. Let the outer boundary point be represented as $U_c(x, y)$ and lower boundary point be represented as $L_c(x, y)$. In the next step, we fix the ROI by discarding 40 pixels on either side of the finger starting from $U_c(x, y)$ and $L_c(x, y)$. Finally ROI is corrected for the translation and rotation using affine transform as mentioned in [13]. Figure 3 shows the ROI extraction from different databases adopted in this work.

The pre-processing operation involves in enhancing the finger vein by adjusting the contrast by using CLAHE [21]. Figure 2 shows the enhanced finger vein ROI images. Finally, the enhanced finger vein images E_{fv} are resized to 128×512 pixels in order to compensate for the different resolution across the databases.

2.2. Proposed feature extraction

In this work, we propose a new feature extraction scheme for finger vein representation that consists of two main steps namely: (1) Extraction of maximum curvature points [8] (2) Block wise encoding of extracted maximum curvature points. Given the enhanced finger vein image E_{fv} , we extract the maximum curvature points that can accurately represent the vein pattern. In the next step, we divide the maximum curvature points image to 8×8 blocks. We then count the number of white pixels that are present within each block that can represent a new set of feature vector of dimension 1×1024 . Figure 3 illustrates the proposed feature extraction scheme. The main advantage of the proposed feature extraction scheme is in reducing the size of the feature dimension that makes it more appealing for the indexing applications. Furthermore, the proposed feature can be compared using simple correlation rule and thereby overcomes the complex comparison scheme used with the maximum curvature points method that involved in comparing pixel by pixel with several rotation and shifting.



Figure 2: Block diagram of the finger vein indexing using unsupervised clustering



Figure 3: Illustration of ROI extraction on seven different finger vein databases used in this work (a) HiGFVDB [14, 12] (b) FVUSM [9] (c) VERA [17] (d) UTFVP [18] (e) ployU [5] (f) HMV [20]

2.3. Building indexing space

Once the feature extraction is performed, the next step is to cluster these extracted features to build a cluster space.

In this work, we have investigated three different unsupervised clustering namely: (1) K-means [6] (2) K-medoids [10] and Self Organizing Map (SOM) neural network [4] independently. The clustering is performed on the training dataset (refer Section 3.2 for experimental protocol). Thus, given the training dataset, we adopt unsupervised clustering method (one at a time) that can output the K cluster centroids as $\{C_1, C_2, \ldots, C_K\}$. In the next step, we build the indexing by assigning each of the enrolled subject sample to any one of the clusters $\{C_1, C_2, \ldots, C_K\}$ based on the closest distance to the cluster center. To this extent, we have used the gallery samples from the testing database (refer Section 3.2 for experimental protocol). The gallery set represent one image for each subject. Thus, for each gallery image GE_{fv} from the testing data set, we first extract the features F_{GE} . We then compute the distance between F_{GE} and the K cluster centroids as $d_i = ||F_{GE} - C_i||$, $i = 1, 2, \ldots, K$. We then label the gallery image that represent individual subject (or identity) with cluster indices corresponding to the minimum distance.

2.4. Retrieval of the probe identity

The probe identity retrieval involves in computing the label of the input probe image on which the matching subject (or identity) is obtained by performing the database search corresponding to the cluster associated with the computed gallery label. Given the probe sample PE_{fv} from a

test data set, we first perform the feature extraction step to obtain F_{PE} . We then compute the distance d_{Pi} between F_{PE} and the K clusters centers as $d_{Pi} = ||F_{PE} - C_i||$, i = 1, 2, ..., K. Then, the probe sample is assigned to the cluster corresponding to the minimum distance. In this way, the search is confined to the gallery samples associated with the computed cluster indices. Finally, the retrieval process will output a list of gallery identities L_g corresponding to the selected cluster indices.

3. Experimental results

In this section, we present the experimental results of the proposed finger vein indexing and retrieval scheme. The quantitative results of the proposed scheme is presented in terms of Pre-Selection Error rate (PSE) and Penetration Rate (PEN) following the ISO standard [1] [11]. The pre-selection error rate is defined as the probability of the probe image PE_{fv} is not assigned to the same cluster as the corresponding identity GE_{fv} in the gallery set. Let $CL_P \in \{C_1, C_2, \ldots, C_K\}$ be the cluster label of the probe image PE_{fv} and L_{PE} be the corresponding list of the gallery images retrieved from the database. Let $CL_G \in$ $\{C_1, C_2, \ldots, C_K\}$ be the cluster label of the gallery image GE_{fv} corresponding to the same identity PE_{fv} then [1] [11]:

$$PSE = 1 - \frac{1}{m} \sum_{i=1}^{m} Hit(PE_{fv})$$
 (1)

and

$$Hit(PE_{fv}) = \begin{cases} 1 & CL_P \subseteq CL_G \\ 0 & otherwise \end{cases}$$
(2)

The penetration rate can be defined as follows [1] [11]:

$$PEN = \frac{1}{m} \sum_{i=1}^{m} \frac{|L_{PE}|}{n}$$
(3)

Where, n is the number of images in gallery set, m indicates the number of probe set.

3.1. Finger vein database

In this work, we have constructed a heterogeneous dataset by including the finger vein images from seven different publicly available databases: (a) UTFVP [18] (b) ICFVR [19] (c) HMT [20] (d) FVUSM [9] (e) ployU [5] (f) Vera [17] (g) HiGFVDB [14, 12]. This new heterogeneous finger vein database is comprised of 685 plus subjects that resulted in 2850 unique finger veins. Since each finger vein is unique, we consider each finger vein as the unique enrollment that resulted in 2850 unique identities and each of these unique identities has 2 samples. Thus, the whole database used in this work is comprised of 5700 finger vein samples. Table 1 shows the distribution of the subjects as well as fingers from 7 different finger vein database.

Database Total No	Total No	Total No	Data Partition			
	of Subjects	of Fingers	Devel-	Training	Testing	
			-opment			
UTFVP [18]	60	360	0	150	210	
ICFVR [19]	#	310	76	150	84	
HMV [20]	106	636	0	250	386	
FVUSM [9]	123	492	0	200	292	
PolyU [5]	156	312	83	100	129	
VERA [17]	110	220	78	75	67	
HiGFVDB [14, 12]	130	520	36	150	334	
Total	685+#	2850	273	1075	1502	

Table 1: Statistics of the finger vein databases used to construct a heterogeneous finger vein database

3.2. Performance evaluation protocol

In order to effectively evaluate the database, we divide the whole database into three independent (or nonoverlapping) datasets namely: development, training and The development dataset is comprised of 273 testing. unique identities with $273 \times 2 = 546$ finger vein samples. The development database is used only to tune the parameters of the ROI extraction as well as the proposed feature extraction scheme. The training dataset is comprised of 1075 identities that will result in $1075 \times 2 = 2150$ finger vein samples used only to build the cluster space using either K-means or K-medoids or SOM neural network. Lastly, the testing dataset is comprised of 1502 unique identities that are used solely to report the performance of the proposed indexing and retrieval scheme. The testing dataset is further divided into two groups namely gallery and probe. Since each identity has 2 samples, we assigned first sample to gallery and second sample to probe. Finally, the data partition into development, training and testing is repeated for 10 times and average of the results are reported.

3.3. Results and discussion

We first present the quantitative results of the proposed feature extraction scheme. Since the proposed feature extraction is derived based on Maximum Curvature Points (MCP) [8], it is reasonable to compare the results of the proposed scheme with MCP. Table 2 shows the results of the comparative performance of the proposed scheme on six different publicly available finger vein database. Here, it can be observed that, the proposed scheme emerged as the best method on all six databases. This indicates the efficacy of the proposed scheme on the finger vein recognition. Thus, the proposed scheme not only represent the compact feature length but also demonstrated the improved performance over MCP [8].

We now present the results of the proposed finger vein

Clustering Method	Feature Extraction	Error Pates (%)	Number of Clusters (K) / Number of Nodes in case of SOM (K)						
	Teature Extraction	Enor Rates (70)	K=2	K=3	K=4	K=5	K=6	K=7	K=8
K-Means	SMR [13]	PSE	11.98	12.64	22.7	24.56	25.76	25.96	27.16
		PEN	63.75	61.37	35.67	32.82	32.64	31.47	31.01
	Proposed	PSE	0.13	7.58	10.31	11.98	13.24	17.9	18.7
		PEN	83.96	42.48	28.85	22.16	18.84	15.1	13.2
SOM	SMR [13]	PSE	17.17	22.76	21.57	33.62	39.88	33.62	44.14
		PEN	54.3	38.76	36.57	26.2	22.01	25.3	17.05
	Proposed	PSE	0.13	7.78	10.05	11.18	18.01	18.2	20.23
		PEN	80.46	41.85	27.93	22.37	17.63	15.39	14.8
K-Medoids	SMD [12]	PSE	0	0	0	0	0	0	0
	51VIK [15]	PEN	100	100	100	100	100	100	100
	Proposed	PSE	20.7	28.62	31.62	35.75	38.28	39.88	40.61
	Toposed	PEN	50.17	34.23	28.04	22.84	19.31	17.24	16.24

Table 3: Performance of the proposed finger vein indexing and retrieval scheme in terms of PSE/PEN (%) on single cluster search

Table 2: Quantitative performance of the proposed scheme

Databasa	EER (%)				
Database	MCP [8]	Proposed Method			
ICFVR [19]	13.24	6.85			
FVUSM [9]	3.25	1.95			
UTFVP [18]	16.12	10.42			
HiGFVDB [14, 12]	1.13	0.20			
ployU [5]	1.05	0.78			
HMV [20]	2.93	1.98			

indexing and retrieval based on the un-supervised clustering. In order to generate the clusters, we have investigated three different well established schemes like K-means [6], K-medoids [10] and Self Organizing Map (SOM) neural network [4] independently. In case of K-means and Kmedoids, the performance largely depends on the initialization. Hence, both K-means and K-medoids clustering schemes are run for 500 times with a different set of initialization and finally we pick the one with the smallest sum of distances between all feature vectors and the respective cluster centers. Further, we have also carried out the Silhouette measure [6] to fix the optimum number of clusters. Figure 4 shows the variation of the average Silhouette measure versus number of clusters (K) that indicates the smaller values of K results in more coherent clusters than large values



Figure 4: Illustration of the Silhouette measure on K-means and K-medoids

of K. However, in case of SOM neural network clustering we followed the experimental procedure to try with various values of clusters and then to choose the one that yield the best PSE and PEN.

In this work, we present the two set of results based on (1) Single cluster search: where we confine our search to the single cluster (2) Multi-cluster search: in which we allow the search to expand to multiple clusters.



Figure 5: Analysis of clusters based on confusion matrix from (a) SOM (b) K-means (c) K-Medoids

Single cluster search Table 3 shows the quantitative results of the proposed indexing and retrieval on the single cluster search. Table 3 also indicates the results with different number of clusters (K). In order to present the comprehensive comparison of the proposed feature extraction scheme we compare the results with most recent finger vein feature extraction scheme based on the improved Spectral Minutiae Representation (SMR) [13]. We particularly choose the SMR as it is most recent method that have demonstrated good performance and also provide the real number features that will fit well to our proposed indexing framework.

As observed from the Table 3, the penetration rate (PEN) decreases with increase in number of clusters (K). When comparing the performance of SMR with the proposed scheme, the best performance is noted with the proposed scheme. The SMR features shows the good performance when K = 4 while the proposed scheme shows the best performance when K = 3. Among the three different cluster schemes investigated in this work, the use of K-means and SOM clustering schemes shows better results when compared with K-Medoids clustering scheme. Further, the K-means and SOM clustering will show similar performance.

In order to better interpret the results, we have included the confusion table obtained from three different clustering schemes with number of clusters K = 5 in Figure 5. It can observed here that, the use of K-medoids clustering scheme (see Figure 5 (c)) shows larger pre-selection rate because of their misclassification between all clusters. With K-means clustering scheme (see Figure 5 (b)) the error rate is contributed mainly because of misclassification between cluster 3 and 5 while with SOM (see Figure 5 (a)) the error rate is contributed mainly because of misclassification between cluster 1 and 2.

Thus, based on the experiments carried out on the single cluster search, the proposed feature extraction scheme with K-means clustering have demonstrated the best performance with PSE/PEN = 7.58/42.48(%). Further, the use of SOM has also indicated the competent performance with PSE/PEN = 7.78/41.48(%).

Multi-Cluster Searching In this experiment, we extend the search to multiple clusters to explore the impact of multi-cluster search. Table 4 indicates the quantitative results of the multi-cluster search (with Number of clusters $N_c = 8$) that shows the performance of the best performing scheme (on single cluster based search) based on K-means and least performing scheme based on Kmedoids and also we compare the performance with the existing state-of-the-art scheme based on repeated line tracking and Locality Sensitive hashing (LSH) [16]. Following are the important observation on the results: (1) The preselection rate quickly drops with multi-cluster search but increases the penetration rate. (2) The proposed scheme based on K-means shows the best result with PSE/PNR = 0.98/52.88(%). However, other schemes based on Kmedoids and LSH demands more penetration rate to achieve pre-selection error rate of less than 1%.

Figure 6 shows the performance (PSE/PNR (%)) of the proposed feature extraction scheme with existing SOTA feature extraction scheme based on SMR on multi-cluster search on using K-means clustering. The number of cluster N_c to be searched increases from right to left. It can be observed that, the proposed feature extraction scheme shows the outstanding performance to achieve the tradeoff between PSE/PNR.

Figure 7 shows the performance (PSE/PNR (%)) of the proposed feature extraction scheme on multi-cluster search on K-means and K-medoids clustering scheme. Here also the number of cluster N_c to be searched increases from right to left. It can be observed here that the use of the K-means clustering has demonstrated the best performance over K-mediods clustering scheme in multi-cluster search.

Thus, based on the above presented extensive experiments the use of proposed feature extraction scheme together with proposed indexing and retrieval scheme has demonstrated the improved performance when compared with the existing scheme based on LSH and there by

Table 4: Performance of the proposed finger vein indexing and retrieval scheme in terms of PSE/PEN (%) on multi-cluster search

Clustering Method Feature	Eastura Extraction	Error Potos (%)	Number of Clusters Searched (Nc)						
	reature Extraction	Error Kates (70)	Nc=2	Nc=3	Nc=4	Nc=5	Nc=6	Nc=7	Nc=8
K-Means —	SMR [13]	PSE	11.65	7.19	3.72	1.59	0.53	0	0
		PNR	62	74.58	83.55	89.81	95.12	100	100
	Proposed	PSE	5.59	2.46	0.98	0.466	0.19	0	0
		PNR	26.92	39.96	52.88	65.82	78.49	91.14	100
K-Medoids	SMD [13]	PSE	0	0	0	0	0	0	0
	SIVIK [15]	PNR	100	100	100	100	100	100	100
	Proposed	PSE	21.63	11.98	6.12	2.86	0.86	0.26	0
		PNR	31.49	45.97	59.93	72.72	84.24	94.09	100
Indexing Method	Eastura Extraction	Error Datas (%)	Number of Tables (T)						
Indexing Method	Feature Extraction	EIIOI Kales (70)	T=2	T=3	T=4	T=5	T=6	T=7	T=8
D.Tang [16] Re	Perseted Line Treeking	PSE	92.5433	86.4181	84.8202	84.6871	83.2224	78.6951	77.9627
	Repeated Line Tracking	PNR	5.3228	6.1304	10.7618	13.5364	14.7107	16.5731	23.8645



Figure 6: Convergence rate of pre-selection rate and penetration rate tradeoff with proposed feature extraction and SMR on multi-cluster searching with $N_c = 8$ using Kmeans

emerged as the best finger vein indexing and retrieval scheme.

4. Conclusion

In this paper, we present a new scheme for finger vein indexing and retrieval based on unsupervised clustering. To this extent, we have introduced a new finger vein feature extraction scheme based on the block wise counting of maximum curvature points. We then introduced the finger vein indexing scheme based on unsupervised clustering using three independent methods namely: K-means, K-medoids and Self Organizing Map (SOM) neural network. We then



Figure 7: Tradeoff between PSE and PNR using proposed scheme on K-means and K-medoids

performed the extensive experiments on the large scale finger vein database with 2850 identities using both single and multi-cluster search strategy that shows the best performance of the proposed feature extraction scheme with K means clustering. In summary, following are the main observations:

• The proposed new feature extraction scheme on finger vein biometric demonstrated the best performance when compared with a well-established state-of-theart scheme based on Maximum Curvature Points (MCP) on 6 different publicly available finger vein databases. Furthermore, the proposed features are compact, discriminative and robust that made suitable for building the indexing space.

- We have introduced the unsupervised clustering based finger vein indexing and retrieval scheme. We have investigated three different unsupervised clustering schemes using K-means, K-mediods and Self Organizing Maps (SOM) neural network. We have also compared the proposed method of feature extraction scheme with the existing SOTA scheme using Spectral Minutiae Representation (SMR).
- The single cluster search strategy presented in this work indicates the best performance of the proposed feature extraction scheme with K-means clustering with a PSE/PNR = 7.58/42.48(%). Furthermore the use of SOM also shows the encouraging results with a PSE/PNR = 7.78/40.85(%) when number of cluster K = 3. But, the use of K-medoids fails to produce the good results.
- The use of multi-cluster search further improves the pre-selection error rate at the cost of increased penetration rate. The experimental results also demonstrates the best performance of the proposed K-means clustering on the proposed features with a PSE/PNR = 0.98/52.88(%) when compared with existing SOTA scheme based on LSH [16].

Thus, based on the above results, the proposed finger vein indexing and retrieval scheme emerged as the potential scheme suitable for real life application.

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