Accurate 3D Finger Knuckle Recognition Using Auto-Generated Similarity Functions

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Abstract-Contactless 3D finger knuckle is an emerging biometric identifier, which can provide a promising alternative for personal identification. To maximize its potential, feature representation and matching are the two critical components towards high performance. A recent pioneering work is limited by its preliminary design of the feature descriptor and the tailormade similarity function. Although this method demonstrates decent recognition performance, there is room for improvement. This paper advances the state-of-the-art method by introducing a new curvature based feature descriptor and a method to compute the similarity functions based on the statistical distribution of the encoded feature space. Our proposed feature representation utilizes an insight in 3D geometry for accurately encoding the curvature information. When computing the similarity between a pair of templates, we compute the similarity function from the probability mass distributions of the encoded feature space. Our proposed approach is scalable to templates with different sizes, and more importantly outperforms the state-of-the-art methods significantly, which is demonstrated in a publicly available database of 3D finger knuckle. In addition, we also demonstrate the generalizability of our approach by evaluating on other publicly available biometric datasets of similar patterns, i.e. 3D palmprint and finger vein.

Index Terms—hand biometrics, 3D finger knuckle recognition, feature extraction, templates matching

I. INTRODUCTION

 $\mathbf{B}_{\mathrm{which}}$ leads to enormous solutions to modern civilian applications. Among various biometric identifiers, the use of finger knuckle images [1-4] has attracted increasing attention recently probably due to its decent recognition accuracy, efficiency, and the high convenience of acquiring hand biometric images. This emerging technology can be deployed in conjunction with the popular fingerprint recognition systems and can provide a range of applications such as authentication for immigration check, unlocking computers as well as online transactions. One of the popular research trends in biometrics attempted to incorporate 3D domain with the widely explored 2D intensity domain, because such domain contains rich information meanwhile those 3D images are usually more robust and illumination invariant. This approach has been studied in a wide range of biometric research work such as 3D fingerprint [5], 3D palmprint [6-8, 28, 43-45], 3D face [9-10],

TABLE I		
SUMMARY OF KEY DIFFERENCES BETWEEN A STATE-OF-THE-ART METHOD		
AND OUR PROPOSED APPROACH.		

	Surface Gradient Derivatives (TPAMI20)	This Paper
Feature Extraction	Using the derivatives of surface gradient	Using 3D geometry of surface normal vectors
Feature Comparison	Using a hand-crafted similarity function	Using a similarity function generated from statistical distributions
Recognition Accuracy	High	Very high
Computational Complexity	Low	Slightly higher

3D ear [11-12] and recently also 3D finger knuckle [13]. However, there is plenty room for improvement on utilizing 3D finger knuckle as a promising biometric identifier.

In order to maximize the potential of contactless 3D finger knuckle in biometric recognition, feature representation and matching are the two critical components towards high performance. A recent pioneering work on 3D finger knuckle recognition [13] introduced a simple feature descriptor using the surface gradient derivatives computed from 3D surface normal images in two principal directions, i.e. horizontal and vertical. The feature templates with sizes two-bits per pixel are compared by using a hand-crafted similarity function with the considerations of partially similar because the two binary encodings for a pixel are not necessarily equally important [14]. Similarity functions in this paper refer to the pixelwise mapping function for computing the similarity score between a pair of discrete template values. An example of such function can be referred to Table 2 in [13]. Although this method demonstrates decent recognition performance, there is room for improvement. For example, this method only considers the curvature features in two directions. Furthermore, the introduced similarity function is tailor-made for the proposed two-bits feature representation and cannot adapt to other feature representation with different sizes, e.g. four-bits per pixel. In short, this method has a limited flexibility and scalability to feature representation with larger sizes, which can be a bottleneck for further development. With the increasing demand for security requirements in modern applications, more



Fig. 1. Overview of the key technical components introduced in this paper. The hemispheres associated with surface normal vectors v_1 and v_2 represents the range of possible surface normal directions. The similarity function is represented by a matrix of size 16×16 where each entry refers to a pixelwise similarity score for a possible matching case, displayed using a jet colour map.

accurate, scalable and generalizable solutions are highly desirable.

A. Our Work and Key Contributions

This paper advances the state-of-the-art 3D finger knuckle recognition method in two-folds, i.e. enhancing both the feature representation and matching. Firstly, we develop a new feature descriptor based on 3D geometry, which is capable for accurately describing curvature features of 3D finger knuckle surfaces in multiple directions. When increasing the number of considered directions, the feature representation can encode more discriminative characteristics. However, when the size of feature templates increases, it is more difficult to develop a similarity function for comparing a pair of feature templates. If Hamming distance is employed, the recognition performance will be limited by the ineffective similarity function because the two binary encodings for curvature refers to convex and concave, which can be of unequal importance, e.g. concave regions in 3D finger knuckle indicates the line patterns and therefore they are expected to weight more. Alternatively, if we design a similarity function with the consideration of partially similar as in [13], the size of the similarity function grows exponentially with the size of the feature templates. For examples, if the feature template is of size 1-bit per pixel, comparing a pair of such pixels constitutes to four possible matching cases ('00', '01', '10', '11'). In [13], the feature template is of size 2-bits, which constitutes to sixteen possible matching cases. When we attempt to increase the size of the feature templates to 4-bits per pixel, a similarity function with 256 possible matching cases must be considered. Therefore, we develop a new approach for computing the similarity function based on the statistical distribution of the encoded feature space. Table I summarizes the key differences between the state-of-the-art 3D finger knuckle recognition method and our proposed approach. Figure 1 shows an overview of the key technical components introduced in this paper. Implementation codes for the proposed approach are also made available [33].

Key contributions of this paper can be summarized as follows:

(i) This paper introduces a new feature representation approach for accurately encoding 3D finger knuckle surface patterns. The proposed approach utilizes an insight in 3D geometry that, for a pair of neighboring surface normal vectors, the distance between their heads is shorter than the distance between their tails if the surface is concave. In contrast, the distance between their heads is longer than the distance between their tails if the surface is convex. Therefore, we can distinguish whether a local shape is convex or concave along a specified direction and encode the curvature information as binary templates of preferable sizes for further comparisons. The size of this feature representation can be scalable, depending on the number of considered directions in respective applications.

(ii) This paper also addresses another critical problem, i.e. what is the best similarity function for matching binary templates. When computing the similarity between a pair of binary templates, it is a common approach to compute the averages of pixelwise outcomes from exclusive-or operators, i.e. Hamming distance, which is adopted as one of the most reliable computation by many state-of-the-art feature descriptors in biometrics [5, 8, 19]. However, this approach lies on an assumption that the two encodings for a pixel, e.g. zero and one, are equally important so that matching a pair of zeropixels and a pair of one-pixels produce the same outcome, i.e. zero. However, this assumption may not be true, especially for palmprint and finger knuckle features. For examples, a research [14] on palmprint and finger knuckle recognition developed a binary feature descriptor for encoding line and non-lines regions. It is shown that despite both regions provide helpful information for discriminating identities, a pair of one-pixels (lines regions) indicates a higher confidence for similarity than a pair of zero-pixels (non-lines regions). Another research [13] on finger knuckle recognition introduced a similarity function accommodating two-bits per pixel per feature template with the considerations of partially similar when matching a pair of zeropixels. However, these methods either require an extensive

parameter tuning procedure or cannot adapt to other feature descriptors, which limits their generalizability and scalability to feature template with larger sizes. Therefore, we develop a new method for computing the similarity function from the probability mass distributions of the encoded feature space (i.e. frequencies observed in each of the possible feature values). Our proposed approach is scalable to binary templates with different sizes.

(iii) The effectiveness of our proposed approach is validated on a publicly available database of 3D finger knuckle. Our approach outperforms the state-of-the-art methods significantly. In addition, we also demonstrate the generalizability of our approach by evaluating on other publicly available biometric datasets of similar patterns, i.e. 3D palmprint and finger vein. Our approach is generalizable to different biometrics.

Rest of this paper is organized as follows: Section II reviews the related work of the 3D finger knuckle recognition problem. Section III presents the technical detail of our proposed feature representation. Section IV discusses the technical detail of our approach to compute the similarity function. Section V presents the comparative experimental results on three publicly available databases of 3D finger knuckle, 3D palmprint and finger vein. Section V concludes this paper and outline the possible future research work.

II. RELATED WORK

Contactless 3D finger knuckle is one of the most exciting and emerging biometric identifiers due to its capability to offer decent accuracy, efficiency and convenience. The use of such images for biometric recognition has recently attracted increasing attentions. The first attempt to use this biometric identifier was in a research studying finger dorsal surfaces for biometric recognition [20]. However, the recognition performance with 3D finger knuckle images was not compelling, probably because of the low-resolution 3D images and the generic feature descriptor employed, i.e. the Shape Index [21-22], for extracting 3D finger knuckle features. Another more recent work [13] developed a new 3D finger knuckle database and investigated several important aspects of 3D finger knuckle recognition including the effective feature extraction methods, the possibility of spoofing attacks, and the individuality of this biometric identifier. It can be observed that there are enormous potentials of using this emerging biometric identifier for personal recognition. However, there are plenty room for improvement. For instance, the proposed feature descriptor utilized a limited amount of information, e.g. simple gradients are computed in only two directions. In addition, the introduced similarity function is rather hand-crafted and is neither generalizable to other feature templates nor scalable to different sizes of feature templates.

While there is a lack of research work on 3D finger knuckle recognition, many promising related work can be referenced to the literatures of conventional finger knuckle recognition [1-4] and 2D/3D palmprint recognition [6-8, 15-17, 34-35]. A survey paper [1] comprehensively summarized previous research work on finger knuckle recognition. On the other hand, *Surface Code*

[7], *Binary Shape* [8] and collaborative representation-based framework (CR_L2) [6] provided promising baselines for 3D palmprint recognition. These methods can also be applied on the problem addressed in this paper, 3D finger knuckle recognition. However, the surface gradient derivative (*SGD*) feature descriptor [13] further advance those methods and achieved the state-of-the-art recognition performance in 3D finger knuckle recognition.

Besides the mainstream of developing feature descriptors, similarity measure is also an important problem in image retrieval [42], texture recognition [27, 36] and biometric recognition [15, 23-24, 39-40]. For example, over a billion people worldwide have been enrolled in iris recognition systems using binarized templates [18]. While binarized feature representation is widely employed to describe various biometrics, Hamming distance is widely adopted for computing the similarity function between a pair of binary templates. Such examples can be observed from a range of biometric feature descriptors, e.g. Surface Code [7] and Finger Surface Code [5] describe a palmprint and a fingerprint respectively using fourbits per pixel; Binary Shape [8] and UniNet [19] describe a palmprint and an iris pattern respectively using one-bit per pixel. Since the importance of two levels (e.g. zero and one pixels) during the binary template encoding may not be equal, adjusting the outcome score for matching a pair of zero/one pixels may offer higher recognition performance. Such problem has been firstly investigated in a reference [41] and further verified in another recent work [14] on biometrics, which develops a weighted similarity function so that the matching for a pair of one-pixels (line region) worth more attention. Another work [13] further developed a similarity function for its twobits feature representation with the consideration of partial similarity for matching a pair of zero-pixels (non-line region). However, there are no systematic studies to scientifically determine/formulate an appropriate similarity function for matching binary templates with unequal importance in the encodings.

III. FEATURE REPRESENTATION FOR 3D FINGER KNUCKLE

This section presents the technical detail of our proposed scalable feature representation for 3D finger knuckle recognition. An ideal feature representation can encode the most discriminative information, meanwhile can tolerate a certain level of noise. For finger knuckle recognition, it is expected that the most discriminative information lies in the irregular finger knuckle lines with varying thickness, which constitute to a unique biometric pattern for each individual. However, it is challenging to accurately detect those lines due to the existence of noises such as illumination variations. With the help from 3D information in addition to the 2D intensity images, it is relatively easier to detect those lines because of the association with valley/concave regions. Such 3D information can be considered as a set of 3D surface normal vectors. However, that reconstructed 3D information from intensity images generally contains errors inherited from illumination noises and 3D estimations. It is yet challenging to accurately distinguish whether a region is convex, or concave given the set

of surface normal vectors. A recent research on 3D finger knuckle recognition [13] attempted to utilize the derivative of surface normal gradient for the decision of convex or concave shapes. Therefore, it is motivated to further investigate the possibility of an improved feature representation.

To begin with, consider a pair of unit surface normal vectors, denoted as v_1 and v_2 . We utilize an insight in 3D geometry that, for a pair of neighboring surface normal vectors, the distance between their heads is shorter than the distance between their tails if the surface is concave. In contrast, the distance between their heads is longer than the distance between their tails if the surface is convex. Let the 3D coordinate of the tail of v_1 to be (x_1^0, y_1^0, z_1^0) and the elements of v_1 to be (x_1^1, y_1^1, z_1^1) . Therefore, the 3D coordinate of the head of v_1 is $(x_1^0 + x_1^1, y_1^0 + y_1^1, z_1^0 + z_1^1)$. Similarly, let the 3D coordinate of the tail of v_2 to be (x_2^0, y_2^0, z_2^0) , the elements of v_2 to be (x_2^1, y_2^1, z_2^1) , and the 3D coordinate of the head of v_2 is $(x_2^0 + x_2^1, y_2^0 + y_2^1, z_2^0 + z_2^1)$. We first compute the distance between their tails as follows:

$$d_0 = \sqrt{(x_1^0 - x_2^0)^2 + (y_1^0 - y_2^0)^2 + (z_1^0 - z_2^0)^2}$$
(1)

Next, the distance between their heads is computed as:

$$d_{1} = \sqrt{ (x_{1}^{0} + x_{1}^{1} - x_{2}^{0} - x_{2}^{1})^{2} + (y_{1}^{0} + y_{1}^{1} - y_{2}^{0} - y_{2}^{1})^{2} + (z_{1}^{0} + z_{1}^{1} - z_{2}^{0} - z_{2}^{1})^{2} }$$
(2)

These variables can be observed in the center part of Figure 1. In order to detect the irregular finger knuckle lines, we can encode the corresponding condition, i.e. concave/valley regions, when the distance between their heads is shorter than the distance between their tails, i.e. if $d_1 < d_0$. Therefore, the feature value *f* can be easily computed as:

$$f = \begin{cases} 1 & , \ d_1 < d_0 \\ 0 & , \ d_1 \ge d_0 \end{cases}$$
(3)

For a local region, we can iteratively consider a pair of neighboring surface normal vectors and compute the feature value f. For examples, in each sliding window of size 3×3 , taking the pair of surface normal vectors from the left and right can enable the computation of the feature value f in horizontal directions, while taking the pair of surface normal vectors from the top and bottom can enable the computation of the feature value f in vertical directions. For a 3D surface normal image. each considered direction constitute to one-bit binary feature image. Therefore, the final size of the feature template depends on the number of considered directions. This feature representation method can produce an arbitrary size of the feature template for further comparison. In our applications on 3D finger knuckle and 3D palmprint, we considered four directions, i.e. horizontal, vertical and both diagonal directions. The method of comparing the similarity between a pair of feature templates will be discussed in the following section.

IV. FEATURE MATCHING USING A SIMILARITY FUNCTION

A. Similarity Function Formulation

This section presents a scientific approach for computing the similarity function for comparing a pair of binary feature templates. Our hypothesis is that, the encoding with lower



Fig. 2. Probability mass functions of three situations: ideally random, ideally matched and ideally non-matched.

density deserves more attention. For instance, when the binary encodings with one correspond to line regions of palmprint/finger knuckle patterns and the encodings with zero correspond to the non-line/background regions, line regions are usually less dense than non-line regions and the matching for a pair of one-pixels can result a higher confidence for similarity than the matching for a pair of zero-pixels. With such an insight, we attempt to model the similarity function with the considerations of densities of each of the encodings. Our approach attempts to compute the probability mass functions for three ideal situations: ideally random, ideally matched and ideally non-matched; and utilizes these probabilities for computing the final similarity function.

In our applications on 3D finger knuckle and 3D palmprint, we considered four directions, which constitutes to feature templates of size four-bits per pixel. In order to improve clarity for presenting this model, it is better to deliver the necessary components using a more simplified version. Therefore, in the analysis of this section, we select a state-of-the-art feature descriptor [13], which describe a 3D finger knuckle using a feature template with two-bits per pixel. The feature templates with size β bits per pixel ($\beta = 2$) constitute to 2^{β} (i.e. 4) possible feature representations, i.e. '00', '01', '10', '11'. Let X be a random variable for the 2^{β} possible feature representations and x_{ii} be the random values for $X, i, j \in \{0,1\}$. The probability mass function of the random variable X can be easily observed from the average occurrences of each possible feature representations in the training samples.

$$\boldsymbol{p}_{\boldsymbol{X}}(\boldsymbol{x}_{ij}) = \boldsymbol{P}(\boldsymbol{X} = \boldsymbol{x}_{ij}) \tag{4}$$

When matching a pair of templates A and B, each with β -bits per pixel, there are $2^{2\beta}$ (i.e. 16) possible matching cases for each pixel. Let A and B be the random variables for the four possible feature representations in templates A and Brespectively, and a_{ij} and b_{ij} be the random values for A, B, $i, j \in \{0,1\}$. We first consider the ideally random situation. Let R be a random variable for the $2^{2\beta}$ possible matching cases when templates A and B are of random, and r_{ijkl} be the random values for $R, i, j, k, l \in \{0,1\}$. The probability mass function of the random variable R can be computed as:

$$\boldsymbol{p}_{\boldsymbol{R}}(\boldsymbol{r}_{ijkl}) = \frac{\boldsymbol{p}_{\boldsymbol{A}}(a_{ij}) \times \boldsymbol{p}_{\boldsymbol{B}}(b_{kl}) + \boldsymbol{p}_{\boldsymbol{A}}(a_{kl}) \times \boldsymbol{p}_{\boldsymbol{B}}(b_{ij})}{2}$$
(5)

$$=\frac{p_X(x_{ij}) \times p_X(x_{kl}) + p_X(x_{kl}) \times p_X(x_{ij})}{(6)}$$

$$= \boldsymbol{p}_{\boldsymbol{X}}(x_{ij}) \times \boldsymbol{p}_{\boldsymbol{X}}(x_{kl}) \tag{7}$$

Secondly, we consider the ideally matched situation, i.e. all feature representations between the two templates are the same. Let *M* be a random variable for the $2^{2\beta}$ possible matching cases when templates *A* and *B* are ideally matched, and m_{ijkl} be the random values for *M*, $i, j, k, l \in \{0,1\}$. The probability mass function of the random variable *M* is:

$$\boldsymbol{p}_{\boldsymbol{M}}(m_{ijkl})$$

$$= \frac{p_{A}(a_{ij}) \times P(B=b_{kl}|A=a_{ij} \& A=B) + p_{A}(a_{kl}) \times P(B=b_{ij}|A=b_{kl} \& A=B)}{2} (8)$$

$$= \begin{cases} \frac{1}{2} \left(p_{A}(a_{ij}) + p_{A}(a_{kl}) \right), & \text{if } i = k \text{ and } j = l \\ 0, & \text{else} \end{cases}$$
(9)

$$=\begin{cases} \boldsymbol{p}_{\boldsymbol{X}}(\boldsymbol{x}_{ij}), & \text{if } i = k \text{ and } j = l\\ 0, & \text{else} \end{cases}$$
(10)

Thirdly, we consider the ideally non-matched situation, i.e. all feature representations between the two templates are different, while having the same distribution as p_X . Let *N* be a random variable for the $2^{2\beta}$ possible matching cases when templates *A* and *B* are ideally non-matched, and n_{ijkl} be the random value for *N*, $i, j, k, l \in \{0,1\}$. The probability mass function of the random variable *N* is:

 $\boldsymbol{p}_{N}(n_{ijkl})$

$$=\frac{p_A(a_{ij})\times P(B=b_{kl}|A=a_{ij}\&A\neq B)+p_A(a_{kl})\times P(B=b_{ij}|A=b_{kl}\&A\neq B)}{2}$$
(11)

$$= \begin{cases} 0, if \ i = k \ and \ j = l \\ \frac{1}{2} \left(p_A(a_{ij}) \times \frac{p_B(b_{kl})}{1 - p_A(a_{ij})} + p_A(a_{kl}) \times \frac{p_B(b_{ij})}{1 - p_A(a_{kl})} \right), else \end{cases}$$
(12)

$$= \begin{cases} 0, & if \ i = k \ and \ j = l \\ \frac{1}{2} \left(\boldsymbol{p}_{X}(x_{ij}) \times \frac{\boldsymbol{p}_{X}(x_{kl})}{1 - \boldsymbol{p}_{X}(x_{ij})} + \boldsymbol{p}_{X}(x_{kl}) \times \frac{\boldsymbol{p}_{X}(x_{ij})}{1 - \boldsymbol{p}_{X}(x_{kl})} \right), else \quad (13) \end{cases}$$

For a better visualization, We compute the probability mass functions of p_R , p_M and p_N using the same training (gallery) feature templates as in [13] and such probabilities are shown in Figure 2.

Next, we attempt to utilize these probabilities for computing the similarity function. Let *U* be a random variable for the $2^{2\beta}$ possible matching cases when templates *A* and *B* are unknown, and u_{ijkl} be the random values for *U*, $i, j, k, l \in \{0,1\}$. The probability mass function of the random variable *U* can be computed from the average occurrences of each possible matching cases in the test samples. We attempted to split the computation of a similar score and a dissimilar score from respective clues in the probability mass functions, e.g. i = k & j = l as a group of 2^{β} (i.e. 4) elements for similarity while the remaining $2^{2\beta} - 2^{\beta}$ (i.e. 12) elements as another group for dissimilarity.

For the group of similarity, it can be observed in the ideally matched situation that $p_M(m_{1111})$ is much smaller than $p_M(m_{0000})$, which implies that if the unknown templates are

from the same class, $p_U(u_{1111})$ is expected to be smaller than $p_U(u_{0000})$. Therefore, instead of considering the absolute masses from $p_U(u_{0000})$, $p_U(u_{0101})$, $p_U(u_{1010})$ and $p_U(u_{1111})$ as the indication of similarity, it is reasonable to consider the relative masses with respect to p_M . The score for the group of similarity can be computed as follows:

$$s_{s} = \frac{1}{2^{\beta}} \sum_{i=0}^{1} \sum_{j=0}^{1} \frac{p_{U}(u_{ijij})}{p_{M}(m_{ijij})}$$
(14)

Similarly, the score for the group of dissimilarity can also be computed as the relative masses with respect to p_N :

$$s_d = \frac{1}{2^{2\beta} - 2^{\beta}} \sum_{i=0}^{1} \sum_{j=0}^{1} \sum_{k=0}^{1} \sum_{l=0, l \neq j \ if \ k=i}^{p} \frac{p_U(u_{ijkl})}{p_N(n_{ijkl})} \quad (15)$$

While adopting the convention that a score with a smaller value means more similar, the final score can be computed as a weighted sum of these two scores:

$$s = \begin{cases} -s_s + s_d , if \ w_s = 0 \ and \ w_d = 0 \\ -w_s \cdot s_s + w_d \cdot s_d , else \end{cases}$$
(16)

where w_s and w_d are two scalars representing the weighting importance between the scores for the group of similarity s_s and dissimilarity s_d . Intuitively, it is reasonable that the clues from the group of similarity, i.e. matching cases '0000', '0101', '1010', '1111', weights more than the clues from the group of dissimilarity, i.e. remaining non-matching cases. We attempt to estimate such weighting from the variances of each group with the probability mass function p_R when templates **A** and **B** are of random. It can be observed that the variance of p_R from the group of similarity is larger than that of dissimilarity, which implies that the scores from the group of similarity is expected to have more dominant effect than the scores from the group of dissimilarity for the determination of whether a pair of templates is similar. In other words, the probability mass in the group of dissimilarity varies less significantly than the probability mass in the group of similarity. Therefore, we attempt to make use of those variances for estimating the respective weights:

$$w_s = \frac{1}{2^{\beta}} \sum_{i=0}^{1} \sum_{j=0}^{1} (\boldsymbol{p}_{\boldsymbol{R}}(r_{ijij}) - \overline{\boldsymbol{p}_{\boldsymbol{R}}})^2$$
(17)

 $w_{d} = \frac{1}{2^{2\beta} - 2^{\beta}} \sum_{i=0}^{1} \sum_{j=0}^{1} \sum_{k=0}^{1} \sum_{l=0, l \neq j \ if \ k=i}^{1} (\boldsymbol{p}_{\boldsymbol{R}}(r_{ijkl}) - \overline{\boldsymbol{p}_{\boldsymbol{R}}})^{2} (18)$

In summary, the final score can be represented as:

$$s = \sum_{i=0}^{1} \sum_{j=0}^{1} \sum_{k=0}^{1} \sum_{l=0}^{1} \frac{p_{U}(u_{ijkl})}{-2^{\beta} w_{s} \cdot p_{M}(n_{ijkl}) + (2^{2\beta} - 2^{\beta}) w_{d} \cdot p_{N}(n_{ijkl})}$$
(19)

If we implement the computations using equation (19), it is required to count the occurrence of all $2^{2\beta}$ possible matching cases, which is quite inefficient. Therefore, we further simplify the equation for more efficient computations. Let Q be the number of pixels in each template. Recall that the probability mass function of the random variable U (the unknown situation), can be computed from the average occurrences of each possible matching cases in the test samples:

$$\boldsymbol{p}_{\boldsymbol{U}}(\boldsymbol{u}_{ijkl}) = P(\boldsymbol{U} = \boldsymbol{u}_{ijkl}) \tag{20}$$

$$= \frac{1}{Q} \sum_{q=1}^{Q} \boldsymbol{h}_{ijkl}(\boldsymbol{A}_{q}, \boldsymbol{B}_{q})$$
(21)



$$\boldsymbol{h_{ijkl}}(\boldsymbol{A}_q, \boldsymbol{B}_q) = \begin{cases} 1, if \left(\boldsymbol{A}_q = ij\right) and \left(\boldsymbol{B}_q = kl\right) \\ 0, else \end{cases}$$
(22)

Substituting equation (21) into (19),

S

$$= \frac{1}{Q} \sum_{q=1}^{Q} \sum_{i=0}^{1} \sum_{j=0}^{1} \sum_{k=0}^{1} \sum_{l=0}^{1} \frac{h_{ijkl}(A_q, B_q)}{-2^{\beta} w_s \cdot p_M(n_{ijkl}) + (2^{2\beta} - 2^{\beta}) w_d \cdot p_N(n_{ijkl})}$$

(23)

For each pixel, there is exactly one case among the $2^{2\beta}$ possible matching cases, therefore this equation can be simplified as:

$$s = \frac{1}{Q} \sum_{q=1}^{Q} \frac{h_{ijkl}(A_q, B_q)}{-2^{\beta} w_s \cdot \boldsymbol{p}_M(n_{ijkl}) + (2^{2\beta} - 2^{\beta}) w_d \cdot \boldsymbol{p}_N(n_{ijkl})}$$
(24)

where $ij = A_q$, $kl = B_q$.

$$s = \frac{1}{Q} \sum_{q=1}^{Q} \boldsymbol{h}_{ijkl}(\boldsymbol{A}_{q}, \boldsymbol{B}_{q}) \cdot \boldsymbol{v}$$
(25)

$$\boldsymbol{v} = \frac{1}{-2^{\beta} w_{s} \cdot \boldsymbol{p}_{\boldsymbol{M}}(n_{ijkl}) + (2^{2\beta} - 2^{\beta}) w_{d} \cdot \boldsymbol{p}_{\boldsymbol{N}}(n_{ijkl})}$$
(26)

Note that \boldsymbol{v} is a vector of length $2^{2\beta}$, which can offer the same computational complexity as both Hamming distance and the partial similarity approach. In our applications on 3D finger knuckle and 3D palmprint, the number of elements of the similar matrix is 256 for the feature templates of size four-bits per pixel. In order to accommodate pose variations in the acquired images, best or the minimum of the match scores resulting from the rotational or translational shifting of the probe template can be employed and is also investigated in our experiments.

B. Theoretical Performance Estimation

In order to ascertain the reliability of performance evaluations, it is highly desirable to evaluate the performances on a large amount of dataset. However, large biometric datasets are not easily available, therefore it is interesting to estimate such recognition performances using a theoretical approach. Similar to earlier references [13, 37], we also develop a binomial/trinomial distribution model consisting of n trails. For the analysis of this section, we select a feature representation of template size one-bit per pixel instead for simplicity, because a template size of two-bits per pixel will result in ten possible outcome scores which is over complicated. When comparing a pair of one-bit templates, Hamming distance will result in two possible outcomes (i.e. '0' and '1') while our approach will result in three possible outcomes, α_1 , α_2 , α_3 . Therefore, a trinomial distribution model consisting of n trails is derived to model the distribution of imposter and genuine matching scores. Let p_1 , p_2 and p_3 represent the probabilities of having the three possible outcome scores respectively; X_1 be the random variable representing the number of times the first outcome α_1 is observed over *n* trails and x_1 be the value for X_1 from each of such trials. X_2 , x_2 X_3 and x_3 are also defined similarly corresponding to α_2 and α_3 . The probability distribution function corresponding to the trinomial random variables is:

$$f_{X_1,X_2X_3}(x_1,x_2,x_3)$$

$$=\begin{cases} \frac{n!}{x_1!x_2!x_3!} p_1^{x_1} p_2^{x_2} p_3^{x_3}, \text{ if } x_1 + x_2 + x_3 = n\\ 0, else \end{cases}$$
(27)

Let *Y* be a random variable representing the matching score between two feature representations.

$$Y = \alpha_1 X_1 + \alpha_2 X_2 + \alpha_3 X_3$$
 (28)

Since the sum of x_1 , x_2 , x_3 is *n*, the dependence of x_1 , x_2 , x_3 can be computed as:

$$x_2 = \frac{\alpha_1 n - \alpha_1 x_3 + \alpha_2 x_2 + \alpha_3 x_3 - y}{\alpha_1} \quad , x_3 \in [0, n]$$
 (29)

$$x_1 = n - x_2 - x_3$$
, $x_3 \in [0, n]$ (30)

Incorporating equations (29)-(30), the probability distribution function for the distribution of scores is:

$$f_Y(y) = \begin{cases} \sum_{x_3=0}^n f_{X_1, X_2, X_3}(x_1, x_2, x_3) & \text{, if } x_1, x_2 > 0\\ 0 & \text{, else} \end{cases}$$
(31)

with the variance as follows: *Var*(*Y*)

$$= \sum_{i=1}^{3} \alpha_{i}^{2} Var(X_{i}) + \sum_{i=1}^{2} \sum_{j=i+1}^{3} 2\alpha_{i} \alpha_{j} Cov(X_{i}, X_{j})$$
(32)

The number of trails n can be computed as follows:

$$n = \left[\frac{Var(Y)}{\sigma^2}\right] \tag{33}$$

In order to obtain the empirical variances for modelling the trinomial distribution, we employ the feature templates of size one-bit per pixel from the finger vein database which the details will be presented in Section V.C. We first model the theoretical distribution of imposter and genuine matching scores to verify the correctness of our implementations. Such estimation is shown in Figure 3(a)/(b). Next, in order to fairly compare the theoretical performance between our approach and the



Fig. 4. Sample Feature Images Employed for the Experiments: (a)/(b) Four-bits Feature Images from two different human subjects in the HKPolyU 3D Finger Knuckle Images Database; (c)/(d) Four-bits Feature Images from two different human subjects in the HKPolyU Contact-free 3D/2D Hand Images Database; (e) One-bit Feature Images from Two subjects in the HKPolyU Finger Image Database.

Hamming distance measure, we set a situation that simulate the number of trails *n* as 1000, and a dataset of 10,000 subjects, each with 10 images, which result in 100,000 ($10,000 \times 10$) genuine and 999,900,000 ($10000 \times 9999 \times 10$) imposter matching scores. The compensation parameter for aligning templates is disabled. The estimation of theoretical performance is shown in Figure 3(c). These theoretical estimations show a promising performance improvement when the densities of zero and one pixels in binary feature templates are unequal (e.g. 0.6419 to 0.3581).

V. EXPERIMENTS AND RESULTS

Our proposed approach outperforms the state-of-the-art methods significantly, which is demonstrated in a publicly available database of 3D finger knuckle. In addition, we also demonstrate the generalizability of our approach by evaluating on other publicly available biometric datasets of similar patterns including 3D palmprint and finger vein. This section presents those comparative experimental results using publicly available databases. In order to ascertain the effectiveness for the verification and identification problems, comprehensive experiments were performed and the experimental results are presented using the receiver operating characteristics (ROC) curve with equal error rates (EER), and cumulative match characteristics (CMC) curve. Moreover, in deployed biometric systems, probe samples can also be acquired from unregistered users and may be incorrectly identified as enrolled users, therefore such open-set identification is widely considered as the more challenging problem. That evaluation was also performed in this paper and the results are presented using False Negative Identification Rate (FNIR) versus False Positive Identification Rate (FPIR) curves. The experimental results presented in this paper are reproducible [33] and are the

evidence to validate the effectiveness, scalability and generalizability of the proposed approach. The feature images from respective databases are shown in Figure 4.

A. Validations using 3D Finger Knuckle Images

The HKPolyU 3D finger knuckle images database [13] is currently the only publicly available dataset providing 3D finger knuckle images. This recently released database can be considered as a benchmark dataset for the evaluation of the performance of 3D finger knuckle recognition. This dataset provides 1410 forefinger images and 1410 middle finger images from 130 subjects, while 105 subjects contain twosession images. Since this dataset is quite small, we acquired more images from another 98 subjects. The combined dataset contains 2508 forefinger images and 2508 middle finger images from 228 subjects, while 190 subjects contain two-session images. Six forefinger images and six middle finger images are available for each subject per session. For the evaluation in this paper, we employ the forefinger knuckle images from the 190 subjects containing two-sessions images. A standard twosession evaluation protocol, which uses the first session images for the training and the second session images for the testing is adopted. This protocol generates 215460 (190×189×6) imposter matching scores and 1140 (190×6) genuine matching scores. As for the open-set identification experiments, 152 subjects (80%) are considered as enrolled users while the remaining 38 subjects (20%) are considered as unenrolled users.

In order to validate the outperforming recognition performance from our proposed approach, we fairly compare our approach with the currently best performing state-of-the-art 3D finger knuckle recognition approach, *SGD* [13] on this enlarged dataset. In addition, we also present comparative experimental results using other state-of-the-art methods which were originally designed for 3D palmprint recognition and can



Fig. 5. Comparative Experimental Results on the HKPolyU 3D Finger Knuckle Dataset: (a) ROC; (b) CMC; (c) FNIR versus FPIR.

be applied on 3D finger knuckle recognition. These baseline methods includes collaborative representation based framework with L1-norm regularizations (CR_L1_DALM) [6], L2-norm regularizations (CR_L2) [6], Binary Shape [8] and Surface Code [7]. For CR_L1_DALM and CR_L2 , we investigate the variations between the reported database employed in [6] and the database employed in this paper. The reported database contain square size images with 128 pixels, it is reasonable to resize and crop our images, without changing the aspect ratio, to be the same size as the images in the reported database, and employ the same parameters provided along with CR_L1_DALM and CR_L2, which is already optimized for their reported database. For Binary Shape, we have optimzed the parameters for the kernel sizes.

Figure 5 shows the comparative experimental results using ROC curves, CMC curves and FNIR versus FPIR curves. It can be observed that our proposed approach significanly outperforms all state-of-the-art methods in all three verification, close-set identification and open-set identification scenarios.

B. Validations using 3D Palmprint Images

While the study of 3D finger knuckle recognition is a research frontier, there is only one database currently publicly available. In order to strengthen the experimental evidence of the proposed approach, demonstrate the effectiveness and generalizability of the proposed method on other similar biometric problems, we also evaluate our method on another contactless 3D biometric database with similar surface patterns. The HKPolyU Contact-free 3D/2D Hand Images Database Version 1.0 [7] contains two-sessions images from 177 subjects (each with five images per session). All images are used for the performance evaluation. We also adopt a standard two-session evaluation protocol, which uses the first session images for the training and the second session images for the testing, which generates 885 (177 \times 5) genuine and 155760 (177 \times 176 \times 5) imposter matching scores. For the open-set identification experiments, 142 subjects (80%) are considered as enrolled users while the remaining 35 subjects (20%) are considered as unenrolled users.

The selection of baseline methods for performance comparison is based on the strong evidence that those methods offer superior performance on this evaluated database [7] as well as the availability of implementation codes. We compare our method with a recently published method (*SGD* [13]), as well as methods developed by other researchers

(*CR_L1_DALM* [6], *CR_L2* [6], *Binary Shape* [8] and *Surface Code* [7]). We further improve the reported experimental results of the best performing method (*SGD*) in [13] by also considering the rotational shifting, denoted as "*SGD (TPAMI20) with rotate*" to ensure fairness in the comparisons.

Figure 6 shows the comparative experimental results using ROC curves, CMC curves and FNIR versus FPIR curves. It can be observed that our proposed approach achieved the best performance among all the baseline methods in all three verification, close-set identification and open-set identification scenarios, which again validates the theoretical arguments presented in Section III and IV.

C. Supportive Evidence using Finger Vein Images

The key purpose of this section is to show that the proposed similarity function can be incorporated with other methods based on binary templates, which are often the most effective and popular choice for the deployment due to the compact size. faster matching and higher resistance to noise. The HKPolyU Finger Image Database Version 1.0 [38] contains 1260 finger vein images acquired from 105 subjects. Similar to previous experiments in the original reference and this paper, we also adopt a standard two-session evaluation protocol as. This evaluation protocol consider the first session images from 105 subjects, each with six images as the training/gallery set, while the second session images as the testing set, resulted in 630 (105×6) genuine and 65520 $(105 \times 104 \times 6)$ imposter matching scores. Since the image from this database is not 3D, our proposed feature representation using surface normal vectors is not applicable. Instead, we integrate our similarity model into the baseline method with the database, using Even Gabor with morphological operation [38] which can describe a finger vein patterns using one-bit per pixel. Since this baseline method employed Hamming distance as the similarity measure, it is judicious to incorporate the proposed similarity function and compare the performance with and without such incorporation, which shows the effectiveness against the widely employed Hamming distance measure.

Figure 7 shows the comparative experimental results using ROC curves, CMC curves and FNIR versus FPIR curves. It can be observed that our proposed approach offers a noticeable performance improvement. Since the employed feature template is of size 1-bit per pixel, the advantage of our proposed similarity function is less obvious than applying on a feature template of larger size, e.g. four-bits per pixel as in the 3D finger knuckle and 3D palmprint recognition experiments.



Fig. 6. Comparative Experimental Results on the HKPolyU Contact-free 3D/2D Hand Images Dataset: (a) ROC; (b) CMC; (c) FNIR versus FPIR.



Fig. 7. Comparative Experimental Results on the HKPolyU 3D Finger Image Database: (a) ROC; (b) CMC; (c) FNIR versus FPIR.

However, we show that without the need of parameter tuning, our proposed approach can automatically compute a better similarity function than the widely employed Hamming distance measure.

VI. CONCLUSIONS AND FURTHER WORK

This work introduces a new approach for accurately encoding the curvature features generated from the 3D finger knuckle surfaces and a method to automatically generate more effective similarity function based on the statistical distribution of the encoded feature space. The proposed feature representation utilizes an insight in 3D geometry that, for a pair of neighbouring surface normal vectors, the distance between their heads is shorter than the distance between their tails if the surface is concave. Therefore, we can distinguish whether a local shape is convex or concave along a specified direction and encode the curvature information as binary templates of preferable sizes for further comparisons. When encoding the curvature feature in four directions, there will be ± 22.5 degrees of tolerance to rotation. This feature representation is also expected to be robust to translation as such variations do not alter the surface curvature.

This paper also addresses another critical problem, i.e. what is the best similarity function for matching binary templates. When computing the similarity between a pair of binary templates, instead of employing the widely adopted Hamming distance approach which lies on an assumption that the binary encodings for a pixel are equally important, we compute a similarity function from the probability mass distributions of the encoded feature space (i.e. frequencies observed in each of the possible feature values). Our proposed approach is scalable to binary templates with different sizes. The effectiveness of our proposed approach is validated on a publicly available database of 3D finger knuckle. Our approach outperforms the state-of-the-art methods significantly. In addition, we also demonstrate the generalizability of our approach by evaluating on other publicly available biometric datasets of similar patterns, i.e. 3D palmprint and finger vein. Our approach is generalizable to different biometrics.

While providing a scientific and theoretical approach for this emerging biometric problem, it is also interesting to investigate the popular deep learning approaches, which have been actively developed for many applications while convolutional neural network (CNN) based methods are one of the leading state-ofthe-art in computer vision related tasks such as object recognition [25], instance segmentation [26] as well as biometric recognition [19, 29-30]. However, such approaches require relatively a large amount of training data and hyper parameter tuning when comparing to the conventional mathematical approaches. Furthermore, such approaches are also susceptible to adversarial attacks [31-32]. In order to compare with such approaches on specific biometric problem, customized development is required. For example, the success of a recent iris recognition research [19] requires the considerations of biometric aspects including the use of binary templates and the bit-shifting strategy for matching the templates. In this paper, we focus on advancing the current state-of-the-art 3D finger knuckle method from a mathematical perspective. The development of integrating theoretical concepts into interpretable deep learning models for learning structural patterns and similarities will be a promising future work in this area. In addition, if a finger sample is significantly

deformed, the proposed feature descriptor may suffer. Such significant deformations are not considered in this work as we reasonably assume that a user has interest in biometrics-based access while presenting his/her 3D finger. Further research work is required to address such problems with large scale 3D finger knuckle databases that includes images from significantly deformed fingers.

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