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# Point Grouping Method for Finger Vein Recognition

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**ABSTRACT** In finger vein recognition, vein points-based methods classified the image points into vein points and non-vein points and only measured the vein points for the recognition. All points-based methods utilized the features of all points regardless of the difference of vein points and non-vein points. This paper proposes a point grouping method for finger vein recognition by integrating the advantages of the above-mentioned two kinds of methods. In the proposed method, all image points are considered in the recognition, and the points are classified into multiple groups in both feature extraction and similarity measurement. The matched (unmatched) points are separately found from each group pair of the enrolled image and the probe and are fused to obtain the similarity (dissimilarity) score. Moreover, we incorporate the idea of the point grouping into two popular finger vein recognition methods and devise the corresponding point grouping assisted methods, namely, point grouping assisted anatomy structure analysis-based vein extraction and point grouping assisted Gabor. The experimental results on finger vein databases demonstrate the efficacy of the point grouping assisted methods. The equal error rate values of our point grouping methods are lower about 1% than their base methods on SDUD in the multiple templates' mode and on HKPUD in the single template mode.

**INDEX TERMS** Finger vein recognition, point grouping, PG-ASAVE, PG-Gabor.

## I. INTRODUCTION

Finger vein recognition, a physiological characteristic-based biometric technique, utilizes the vessels in finger palmar side to perform identity authentication. Compared with other physiological traits, e.g., face and fingerprint, and behavioral traits, e.g., voice and gait, the vessels underneath the skin, (e.g., finger vessels [1] and wrist vessels [2]), are more robust to spoof attack. Finger vein images are usually captured by the near-infrared light. The hemoglobin in the vein vessels can intensively absorb the near-infrared light, but the light can easily transmit other finger tissues, which brings another advantage to finger vein recognition, i.e., living body identification [1]. This imaging way also results in lower gray level of vein points than non-vein points, and therefore finger vessels appear as dark lines in the captured images.

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In the past years, lots of methods have been developed for finger vein recognition. According to the features, the methods can be classified into vein points based methods and all image points based methods. Vein points based methods first segmented vein pattern from the image, and the similarity of the enrolled and probe vein patterns was measured by the ratio of overlapped vein points to all vein points. The second kind of methods utilized the features of all image points in the recognition, and the Hamming distance and the Euclidean distance were separately used for the binary feature and the real feature in similarity measurement.

Each kind of the above methods has its strengths and weaknesses. In detail, as the finger vessels have the uniqueness, the vein pattern in the first kind of methods has high discrimination, and has advanced the performance of finger vein recognition. However, it is hard to extract vein pattern from low-quality images. Additionally, other discriminative features, extracted in vein pattern segmentation, were generally

ignored, for example, the non-vein points, the feature values and the orientations of all image points. Although the features of all image points were considered in the second kind of methods, the features may not be used in an efficient way. In similarity measurement, the similarity (dissimilarity) of one probe feature value and one enrolled feature value with same location in the feature matrixes or vectors was measured, and the similarities (dissimilarities) of all value pairs were fused to give the final score. However, the probe feature value may be from one vein point (non-vein point), and the enrolled feature value may be from one non-vein point (vein point).

By combining the strengths and overcoming the weaknesses of two kinds of methods, we try to extract and group the features of all points in an image, and match the points in group pair between two images. We also incorporate the idea of point grouping into two popular finger vein recognition methods (i.e., ASAVE and Gabor), and devise the corresponding point grouping assisted methods (i.e., PG-ASAVE and PG-Gabor). In feature extraction of PG-ASAVE and PG-Gabor, we extract features of all points for one image and group the points based on their feature orders. In similarity measurement, the overlapped points and the non-overlapped points in each group pair of two images are separated based on the point locations, and the overlapped points are further grouped into the genuinely matched points and the unmatched points based on the point orientations. The matched (unmatched) points of all group pairs are fused to obtain the similarity (dissimilarity) score. The proposed methods are tested on three public databases, and the experimental results prove the efficacy of the methods.

The novelties of our paper are listed: (1) The point grouping assisted methods are proposed for finger vein recognition by integrating the advantages of vein points based methods and all points based methods. (2) The proposed methods extract both vein points and non-vein points as the image features. (3) The vein points and the non-vein points are separately classified into multiple groups, and the group-wise similarity measurement is used to explore more discriminative information.

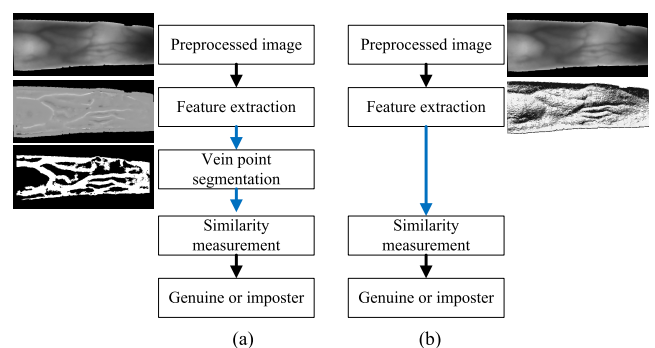
The rest of this paper is organized as follows: Section 2 describes the related works, and Section 3 introduces the idea of point grouping. In section 4, we give a detailed description of the point grouping and the point grouping assisted methods. The experimental results are reported in Section 5, and finally we conclude the paper in Section 6.

## II. RELATED WORK

As we introduced, there are two kinds of finger vein recognition methods, i.e., vein points based methods and all image points based methods. Lots of vein points based methods were proposed for segmenting vein pattern from the image, such as, repeated line tracking [3], maximum curvature [4], Gabor [5], curvature in Radon space [6], anatomy structure analysis-based vein extraction

(ASAVE) [7]. In addition, some features, e.g., histogram of oriented gradient (HOG) [8], neighbor pattern coding (NPC) [9], vein vector fields [10] and tri-branch structure [11], were extracted from the vein points to enhance the recognition performance of this kind of methods.

In all image points based methods, the typical feature extraction methods include local binary pattern (LBP) [12], polarized depth-weighted binary direction coding [13], double competitive pattern [14], competitive coding [15], discriminative binary code [16], discriminative binary descriptor [17], cross section asymmetrical coding [18], and fusion of soft biometric and primary feature (e.g., LBP and HOG) [19]. Recently, deep networks also have been used in finger vein recognition, including the integration of convolutional neural network (CNN) and fully convolutional network (FCN) [20], light CNN [21], two-stream CNN [22], and CNN [23].



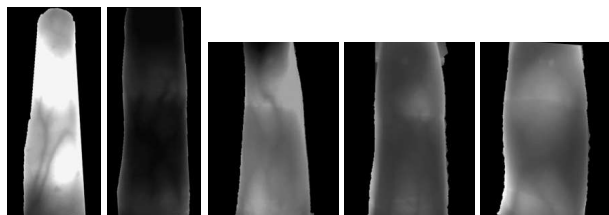
**FIGURE 1.** The flowcharts of (a) vein points based method and (b) all image points based method. Noting that the feature values in (a) have been normalized into [0,255] for easy observation.

The flowcharts of two kinds of methods are given in Fig. 1. From the figure we can see that two kinds of methods both extract feature values for all points of one image. The difference is that, the methods in (b) utilize the features of all points, not only the vein points in (a), to perform the recognition. More specifically, the vein points based methods in (a) employ 0 or one experiential threshold to binarize the feature value. Then the points with value 1 are taken as vein points, and used in matching for the recognition.

## III. PROBLEM ANALYSES

Recent years, vein points based methods have advanced finger vein recognition, and shown promising recognition performance. Although the finger vessels have uniqueness, this kind of methods are not robust to the image quality. We illustrate some low-quality images in Fig. 2. The figure shows that, the amount of finger vessels captured in the image is small, and it is not easy to extract the thin vessels and the vessels in low-contrast image region. So, only using the vein points may not be enough for the recognition.

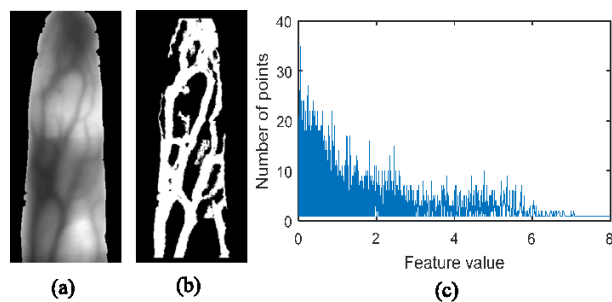
One feasible solution for the above problem is exploring more discriminative features like all image points based methods. Some features have been extracted but not used



**FIGURE 2.** Examples of low-quality finger vein images. The first two images are from HKPUD, and the others are from SDUD.

in vein points based methods, which include the non-vein points, the feature values of all points, and the orientation map.

- 1) About the non-vein points: As we introduced above, all non-vein points are ignored in vein points based methods. However, the optical characteristics of skin and subcutaneous tissue revealed by the near-infrared light have been used in hand vein recognition, and the experimental results showed that they are helpful for the recognition [24].
- 2) About the feature values: All vein points are evaluated equally in matching of vein points based methods. It should be noted that the feature values of vein points may vary largely. For example, the feature values of vein points in one image, extracted by ASAVE, vary from 0.0002 to 8.0955, and we give the distribution of these feature values in Fig. 3. Generally, thick vein backbone has bigger feature values than thin vein sub-branch, and the center points of one vein branch have bigger feature values than the points on two sides of the branch. Therefore, grouping the image points based on feature values and matching all image points in group-wise may explore more discriminative information from finger vein image.
- 3) About the orientation map: The orientation map labels the orientation of each point in finger vein image. In palmprint recognition, orientation codes [25], [26] have been used and achieved promising performance. Similar to the palmprint, finger vessels have obvious orientations, and the growth orientations of finger



**FIGURE 3.** Example of feature value distribution. (a) Preprocessed finger vein image; (b) Extracted vein pattern; (c) Distribution of feature values on vein points.

vessels, especially the vein sub-branches, have big randomness [27]. So, for two vein branches with same location, we may use their orientations to differentiate them.

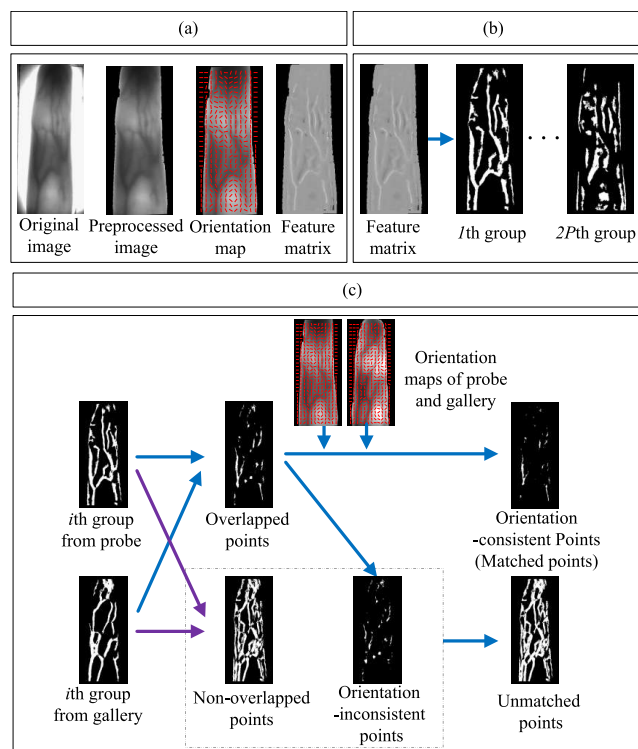
In total, we try to employ the feature values of all image points in recognition like all image points based methods, and group the feature values by the feature value order and point orientation like the classification of vein points and non-vein points in vein points based methods.

#### IV. PROPOSED METHODS

By combining the advantages of vein points based methods and all image points based methods, we propose the point grouping for finger vein recognition. Here, we present the proposed point grouping framework, and introduce the point grouping assisted recognition methods.

##### A. POINT GROUPING FRAMEWORK

The proposed point grouping framework is illustrated in Fig. 4, which consists of three main steps: (a) finger vein image representation, (b) point grouping by feature order in feature extraction, and (c) point grouping by feature location and orientation in similarity measurement. The finger vein image we listed is from Hong Kong Polytechnic University, and the finger region is labeled by the preprocessing method in [5]. The orientation map and the feature matrix in (a) are



**FIGURE 4.** Flowchart of the proposed point grouping framework. It should be noted that the feature matrix has been normalized into [0,255] for easy observation. In addition, we take  $i$ th group pair as an example to show the point grouping in similarity measurement.

extracted by our recent ASAVE [7]. In (b) and (c), the point grouping is performed in feature extraction and similarity measurement. In following subsections, we will main present the details of the point grouping.

### 1) POINT GROUPING IN FEATURE EXTRACTION

In this subsection, we introduce how to group the image points by the feature value order. The point grouping by the feature value order is inspired by the extraction of vein pattern from finger vein image, in which the image points are grouped into the vein points and the non-vein points based on the imaging characteristic of finger vessels. The distribution of vein points varies largely with the finger, which is used for the recognition. Here, the image points will be classified into multiple groups based on their feature values, and the distributions of image points in all groups will be used for the recognition.

Given the feature matrix, we use the feature value order to classify the image points into different groups. In particular, a finger vein image is first divided into vein pattern and non-vein region. Then, the points in the vein pattern are sorted by their feature values in an ascending order, and the points in non-vein region are sorted in the same way. Last, the vein pattern and the non-vein region are separately classified into  $P$  groups of same size. The reason of distinguishing vein pattern from non-vein region before the point grouping by the feature value order is that, we want to keep the inherent distribution of vein pattern, and do not mix the vein points and the non-vein points by the feature value order.

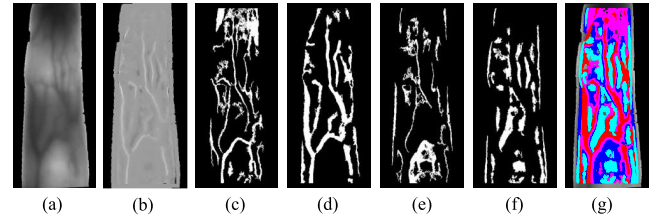
Formally, denoting the feature matrix of one finger vein image by  $F$ , we use an experiential threshold to divide the finger vein image into vein pattern and non-vein region. In most methods, 0 is used as the threshold. (See [3]–[5], [7] for the details). The feature vectors of vein points and non-vein points are separately denoted by  $V_v$  and  $V_n$ :

$$V_v = \{F(x, y) | F(x, y) > 0\} \quad (1)$$

$$V_n = \{F(x, y) | F(x, y) \leq 0\} \quad (2)$$

The points in two vectors are sorted by their feature values in an ascending order for the subsequent calculation of the grouping thresholds.

As we classify the vein points (non-vein points) into  $P$  size-uniform groups, the percentage of the points in each group is  $(100/P)\%$ . For example, we group the vein points into 2 groups, and the percentage of the points in each group is 50%. More specifically, the points with feature values in top 50% are classified into the first group, and the points with feature values in last 50% are classified into the second group. In this example, the grouping threshold is the feature value of the point, which is sorted at the position of 50% in the cumulative percentages of all points. So, the thresholds for  $P$  groups are the feature values of the points sorted at  $(100/P)\%$ ,  $(100/2P)\%$ , ...,  $(100/(P-1)P)\%$  of the cumulative percentages.



**FIGURE 5.** Example of the feature value based point grouping. (a) Preprocessed image; (b) Normalized feature matrix; (c)-(f) The classified four groups; (g) Four groups labeled by different colors.

For  $l$ th point in the sorted vector  $V_v$ , its cumulative percentage can be computed by:

$$C(l) = \frac{\text{num}(V_v \leq V_v(l))}{L}, l = 1, 2, \dots, L \quad (3)$$

in which  $L$  is the number of points in  $V_v$ , and the function  $\text{num}()$  counts the points whose feature values meet the condition. With the cumulative percentages, we can obtain the grouping thresholds  $t_i, i = 1, 2, \dots, P - 1$ :

$$t_i = V_v(C = (100/(i * P))\%) \quad (4)$$

The cumulative percentages and the grouping thresholds of the non-vein points in  $V_n$  can be computed in the same way.

Last, we use the grouping thresholds to group the vein points into  $P$  groups,  $VP_i, i = 1, 2, \dots, P$ :

$$VP_1(x, y) = \begin{cases} 1, & \text{if } 0 < F(x, y) \leq t_1 \\ 0, & \text{otherwise} \end{cases} \quad (5)$$

$$VP_i(x, y) = \begin{cases} 1, & \text{if } t_{i-1} < F(x, y) \leq t_i \\ 0, & \text{otherwise,} \end{cases} \quad (6)$$

$i = 2, 3, \dots, P - 1$

$$VP_P(x, y) = \begin{cases} 1, & \text{if } F(x, y) > t_{P-1} \\ 0, & \text{otherwise} \end{cases} \quad (7)$$

Similarly, the non-vein points can also be classified into  $P$  groups,  $NP_i, i = 1, 2, \dots, P$ . In total, we can get  $2P$  groups for one finger vein image, denoted by  $FP = \{VP, NP\}$ , i.e.,  $FP_i, i = 1, 2, \dots, P, P + 1, \dots, 2P$ . Fig. 5 shows an example of the feature value based point grouping. In this example,  $P=2$ , and the feature matrix is extracted by ASAVE [7].

### 2) POINT GROUPING IN SIMILARITY MEASUREMENT

By the point grouping in feature extraction, we can separately get  $2P$  groups from the enrolled image and the probe. This subsection classifies the points in each pair of the enrolled group  $FP_i^e$  and the probe group  $FP_i^p$  into the matched points and the unmatched points by the point location and the point orientation.

The existing matching method only seeks the overlapped points and the non-overlapped points of the probe and the enrolled vein patterns based on the locations of vein points, and the overlapped (non-overlapped) points are used in the calculation of similarity (dissimilarity) score. In other words, the point locations are used to group the enrolled vein points

and the probe vein points into the overlapped class and the non-overlapped class. The points in the non-overlapped class are definitely unmatched. However, the points in the overlapped class may not be genuinely matched, as their orientations may be different. In addition, only the vein points, without the non-vein points, are considered in the existing methods.

We try to employ the point orientation to further group the points in the overlapped class of all group pairs into the matched class and the unmatched class. It is mainly enlightened by the orientation characteristic of finger vessels. The anatomical studies [27], [28] found that finger vessels have a network-like distribution. In the vessel network, vein direction largely varies on the bifurcation points of multiple vein branches, and vein direction may have a big variation even in one vein branch. So, one probe vein point and one enrolled vein point with same location in two images may have different orientations. As far as we know, it is the first time to employ the orientation map of finger vein image to enhance the similarity measurement.

The orientation map of an image can be estimated in feature extraction of vein points based methods, which labels the orientation of each point. We calculate the difference of two orientation maps, and seek the genuinely matched points by the orientation difference. Noting that there are two differences of two orientations, i.e., the clockwise difference and the anticlockwise difference. The minor one of two differences is used here. Moreover, it is strict to set 0 as the threshold of orientation difference in grouping the matched points and the unmatched points. Generally, finger vein image is captured in a contactless and unrestrained way. The randomness of finger placement in image capturing causes the finger deformations in genuine images, which can vary the point orientation. Therefore, to be robust to finger deformations, we use a threshold bigger than 0 to grouping the points.

We formally denote the probe groups and the enrolled groups by  $FP_i^p, i = 1, 2, \dots, P, P + 1, \dots, 2P$  and  $FP_i^e, i = 1, 2, \dots, P, P + 1, \dots, 2P$ . For one probe group  $FP_i^p$  and one enrolled group  $FP_i^e$ , we first classify their points into the overlapped class and the non-overlapped class by the point locations. The points in the overlapped class are calculated by (8), and the points in the non-overlapped class are calculated by (9).

$$O_i = FP_i^p * FP_i^e \quad (8)$$

$$N_i = FP_i^p \otimes FP_i^e \quad (9)$$

in which  $*$  and  $\otimes$  denote the dot product and the exclusive-OR operator separately. The points in  $O_i$  with value 1 are the overlapped points, and the points in  $N_i$  with value 1 are the non-overlapped points.

Then, we further group the overlapped points into the genuinely matched class and the unmatched class by the point orientation. Assuming the orientation maps of the probe and the enrolled image are denoted by  $ori^p$  and  $ori^e$ . The

orientation difference is computed by

$$ori_{diff} = \min(ori_d, 180 - ori_d) \quad (10)$$

$$ori_d = \text{abs}(ori^p - ori^e) \quad (11)$$

The points with orientation differences lower than a predefined threshold  $ori_{thr}$  can be found by:

$$lab\_match(x, y) = \begin{cases} 1, & \text{if } ori_{diff}(x, y) \leq ori_{thr} \\ 0, & \text{otherwise} \end{cases} \quad (12)$$

We can obtain the genuinely matched points by

$$M_i = O_i * lab\_match \quad (13)$$

The unmatched point can be also obtained by

$$Non\_M_i = N_i + O_i * \overline{lab\_match} \quad (14)$$

in which the operator  $\overline{\quad}$  denotes the logical NOT operation. The matched points of all group pairs can be calculated, and denoted by  $M_i, i = 1, 2, \dots, 2P$ . Similarly, the unmatched points of all group pairs can also be obtained, which is denoted by  $Non\_M_i, i = 1, 2, \dots, 2P$ .

## B. POINT GROUPING ASSISTED VEIN POINTS BASED METHODS

We incorporate the idea of point grouping into two popular vein points based recognition methods (i.e., ASAVE and Gabor), and devise the corresponding point grouping assisted ASAVE (i.e., PG-ASAVE) and point grouping assisted Gabor (i.e., PG-Gabor).

### 1) POINT GROUPING ASSISTED ASAVE

In vein pattern extraction by ASAVE [7], the orientation map is first estimated by the least mean square orientation estimation algorithm [29] to label the orientation of each image point. With the estimated orientation map, the curvature value (i.e., the feature value) of each point is calculated on one cross-sectional profile of this point, which is perpendicular to the point direction.

Our improvements to ASAVE focus on the point grouping by the order of the curvature values in feature extraction and the point grouping by the locations and orientations of points in similarity measurement. Specifically, the curvature values are used as feature values in the point grouping. Firstly, 0 is used as the curvature threshold to separate the vein points from the non-vein points by the formulas (1) and (2). Then, the curvature thresholds can be estimated by the formula (4) for point grouping. Last, based on the curvature thresholds, the points in finger vein image are classified into  $2P$  groups.

We use the ratio of the matched vein points to all vein points as the similarity score of two vein patterns for ASAVE. The overlapped points in each group pair can be calculated by the formula (8), and the genuinely matched points are further picked out from the overlapped points by the formula (13), in which  $22.5^0$  is used as the orientation threshold.

By the above calculations, we can obtain the matched points of each group pair, based on which we will calculate

the similarity score of two images. Let  $Num_i^m$  be the number of the matched points in the  $i$ th pool pair. The number of the matched points in all group pairs can be calculated by:

$$Num^m = Num_1^m + \dots + Num_i^m + \dots + Num_{2P}^m \quad (15)$$

The similarity score of two images is finally defined:

$$Sim\_score = \frac{Num^m}{Num\_image} \quad (16)$$

in which  $Num\_image$  is the total number of points in one finger vein image.

## 2) POINT GROUPING ASSISTED GABOR

Multiorientation Gabor filters were defined for vein pattern extraction in [5]. For each image point, it can get multiple convolution response values, and the maximum among these values is used as the feature value for vein pattern extraction.

Our improvements to Gabor include the point grouping by the order of the convolution response value in feature extraction and the point grouping by the location and orientation of points in similarity measurement. In detail, 0 is used as the convolution response threshold to separate the vein points from the non-vein points. Based on the estimated convolution response thresholds by the formula (4), the vein points and the non-vein points are respectively classified into  $P$  groups. The steps in feature extraction are similar with those in the point grouping assisted ASAVE.

In similarity measurement, PG-Gabor has three differences with PG-ASAVE: a) The orientation map need to be estimated based on the maximal convolution response value of each point, while the orientation map is estimated ahead of feature extraction in PG-ASAVE; b) The estimated orientation values are discrete, while the orientation values in PG-ASAVE is continuous; and c) The dissimilarity score is measured for PG-Gabor, while the similarity score is used in PG-ASAVE. These differences related steps, i.e., the orientation estimation, the difference calculation of discrete orientation and the calculation of dissimilarity score, will be introduced in details.

For the enrolled image and the probe, the unmatched points in each group pair includes the non-overlapped points, detected by the formula (9), and the overlapped points with big orientation differences. We pick out the unmatched points from the overlapped points based on the orientation maps of two images. Assuming Gabor filters, with eight orientations, i.e.,  $i\pi/8$ ,  $i = 1, 2, \dots, 8$ , are convoluted with one image, and eight response matrices, denoted by  $f_i(x, y)$ ,  $i = 1, 2, \dots, 8$ , can be obtained. The orientation of one point is the one that produces the biggest response value, and the index  $i$  ( $i = 1, 2, \dots, 8$ ) of this orientation is stored into the orientation map as follows:

$$ori(x, y) = \arg \max(f_i(x, y)), i = 1, 2, \dots, 8 \quad (17)$$

There are one clockwise difference and one anticlockwise difference between two orientation indexes, the minor one is used. The minor orientation index difference between the

probe orientation map  $ori^p$  and the enrolled orientation map  $ori^e$  is computed:

$$ori_{diff} = \min(ori_d, 8 - ori_d) \quad (18)$$

in which  $ori_d$  can be computed by the formula (11). With the orientation index difference, we use 1 as the threshold to pick out the unmatched points from the overlapped points, and all the unmatched point in the  $i$ th pool pair can be calculated by the formula (14).

Finally, we calculate the dissimilarity score of two images. By the above calculations, we can obtain the unmatched points of each group pair, and the number of the unmatched points in the  $i$ th group pair is denoted by  $Num_i^u$ . The number of the unmatched points in all group pairs can be calculated by:

$$Num^u = Num_1^u + \dots + Num_i^u + \dots + Num_{2P}^u \quad (19)$$

The dissimilarity score of two images is defined as follows:

$$Dis\_score = \frac{Num^u}{Num\_finger} \quad (20)$$

in which  $Num\_finger$  is the point number of the overlapped finger region in two finger vein images.

## C. DISCUSSION

In this subsection, we discuss the relationship between our point grouping assisted methods and the existing two kinds of finger vein recognition methods, i.e., vein points based methods and all image points based methods.

- 1) **Relationship with the vein points based methods.** Existing vein points based methods separate the vein points from the non-vein points, however, our point grouping assisted methods classify the image points into multiple groups. So, the existing vein points based methods can be seen as a two-group point grouping assisted methods. Moreover, the vein points based methods only employ the point locations to group the vein points from two images into the overlapped class and the non-overlapped class in similarity measurement. Our main improvement is further seeking the genuinely matched points and the unmatched points from the overlapped points based on the point orientations, which can produce a more reasonable similarity (dissimilarity) score.
- 2) **Relationship with the all image points based methods.** Existing all image points based methods inspire us to employ both the vein points and the non-vein points in recognition. However, there are two main differences between the all image points based methods and our methods. The all image points based methods take all points in one image as a group, and measure the similarity (dissimilarity) of the real-value features in image-wise. Our methods divide the points in one image into multiple groups, and measure the similarity (dissimilarity) of the binary features in group-wise. In other words, although all images points are used

in both two kinds of methods, the existing methods directly employ the real-value features of one image in recognition, but our methods classify the points in one image into multiple groups based on the feature values and measure the distribution difference of points in each group pair.

## V. EXPERIMENTS

Here, we evaluate the effectiveness of our proposed point grouping assisted methods for finger vein recognition.

### A. DATABASES

We use three public finger vein databases in our experiments. The first one is from the Hong Kong Polytechnic University (abbreviated to HKPUD) [5]. It contains 3, 312 finger vein images from the index finger and the middle finger of 156 volunteers. Each of the first 210 fingers has 12 images, and each of other 102 fingers has 6 images. The size of each image is  $513 \times 256$  pixels, and the finger region in image is labeled by the preprocessing method in [5]. The size of the preprocessed image is  $485 \times 215$  pixels as the noise region on the image borders is removed.

The second database we used is from Shandong University (abbreviated to SDUD) [30]. It has 3, 816 finger vein images from the index finger, the middle finger and the ring finger of two hands of 106 volunteers. Each of 636 fingers has 6 images. Each image has  $320 \times 240$  pixels, and our prior image preprocessing method [31] is used in finger segmentation. The preprocessed image has the same size with the original image.

The last database is opened by Chonbuk National University (abbreviated to MMCBNU) [32]. It has 6,000 images from 600 fingers. All images are 8-bit gray level BMP files with a resolution of  $640 \times 480$  pixels. Finger region in a raw image is labeled by the preprocessing method in [31].

### B. EXPERIMENTAL CONFIGURATION

Three main experiments are designed. First, we test the effect of the group number  $P$  on the recognition performance and choose the best value for the following experiments. Second, we evaluate the effectiveness of the point grouping, including the effectiveness of the point grouping in feature extraction, the effectiveness of the point grouping in similarity measurement and the comparison between the point grouping assisted methods and their base methods. Third, the comparison between the point grouping assisted methods and typical state-of-the-art methods are performed.

Two types of experiments are performed: single template mode and multiple templates mode. In single template mode, the images of each finger are used as the enrolled template one by one, and the corresponding remainders are used as the probe. In multiple templates mode, one image per finger is selected as the probe, and the others are used as the enrolled templates, which is repeated six times and the average performance is reported. For the consistency of three databases, 6 images of each finger are used in the experiments.

The equal error rate (EER) is used to evaluate the recognition performance of all considered methods. The EER is the error rate when the false acceptance rate (FAR) is equal to the false rejection rate (FRR). The method, who achieves lower EER value, has better recognition performance.

### C. SELECTION OF GROUP NUMBER

Here, we test the effect of the group number  $P$  on the recognition performance by varying  $P$  from 1 to 4, with 1 as the interval. The experiment is conducted on HKPUD in both the single template mode and the multiple templates mode. The feature values, extracted by ASAVE, are used in the point grouping. As the group number is only used by the point grouping in feature extraction, the ratio of overlapped points to all points in one image is used in similarity measurement. The EER values with different group numbers on vein points and non-vein points are separately listed in Table 1 and Table 2.

TABLE 1. EER values(%) with different group numbers on vein points.

Group number	1	2	3	4
Single template	7.04	<b>6.33</b>	6.34	6.69
Multiple templates	1.97	<b>1.07</b>	1.05	1.18

TABLE 2. EER values(%) with different group numbers on non-vein points.

Group number	1	2	3	4
Single template	6.62	<b>6.28</b>	6.45	6.48
Multiple templates	1.55	<b>1.28</b>	1.28	1.43

From the results in two tables, we can see that the best recognition performance achieves on both vein points and non-vein points when the group number is 2. The point grouping explores more discriminative information from the vein points and non-vein points, which enhances the recognition performance. Considering that more time costs will be spent with a bigger number of groups, in the following experiments, both the vein points and the non-vein points in one image are classified into 2 groups. In other words, the points in one image are classified into 4 groups.

### D. EVALUATION OF POINT GROUPING

The effectiveness of the point grouping is tested on both HKPUD and SDUD. On HKPUD and SDUD, Gabor filters [5] and ASAVE [7] are separately employed to extract the feature values. In addition, single template is used on HKPUD, and multiple templates are used on SDUD. For ASAVE method, the ratio of the overlapped points to all points in one image is used as the similarity score of two images. For Gabor filters, the ratio of the non-overlapped points to all points in finger region is used as the dissimilarity score.

1) EVALUATION OF POINT GROUPING IN FEATURE EXTRACTION

Firstly, the point grouping in feature extraction is tested. The grouped image points are compared with the image points without grouping, and the experimental results are given in Table 3.

TABLE 3. Recognition performance comparison between image points and grouped image points.

Feature	EER (%)	
	HKPUD	SDUD
Vein points	11.69	3.71
Grouped vein points	<b>10.93</b>	<b>2.85</b>
Non-vein points	9.88	3.09
Grouped non-vein points	<b>9.79</b>	<b>2.57</b>
All image points	9.93	3.03
Grouped all image points	<b>7.81</b>	<b>2.38</b>

The results reveal that the point grouping in feature extraction can improve the recognition performance of the vein points, the non-vein points, and even all image points, which is mainly attributed to that the point grouping in feature extraction enlarges the differences of the features from the imposter images. For example, one vein point in an image may be incorrectly matched with one vein point with same location in one imposter image by the traditional location based similarity measurement. The feature value based point grouping has ability to prevent this mistake, as two points may be classified into different groups based on the feature values, and one point in the first group of an image will be never matched with one point in the second group of another image.

Moreover, the results also tell us that the combination of the vein points and the non-vein points (i.e., all image points) achieves lower EER value than the vein points and the non-vein points. It proves that the non-vein points are discriminative in the recognition, and therefore employing all image points in a right way is better than only using the vein points for the finger vein recognition. It is also should be noted that, the better performance on SDUD over HKPUD is attributed to multiple enrolled templates.

2) EVALUATION OF POINT GROUPING IN SIMILARITY MEASUREMENT

Secondly, we test the performance of the point grouping in similarity measurement. The comparison between the point grouping in only feature extraction and the point grouping in both feature extraction and similarity measurement is conducted, and the experimental results are reported in Table 4.

From Table 4, we can observe that the point grouping in both feature extraction and similarity measurement achieves better recognition performance than the point grouping in only feature extraction for all three kinds of features on both two databases. Such performance improvement is mainly attributed to the orientation based point grouping in similarity measurement. More specifically, our similarity measurement methods further seeks the orientation-unmatched

TABLE 4. Effectiveness of point grouping in similarity measurement. (Noting that FE denotes feature extraction, and SM denotes similarity measurement.)

Feature	Point grouping	EER(%)	
		HKPUD	SDUD
Vein points	in only FE	10.93	2.85
	in both FE and SM	<b>10.31</b>	<b>2.44</b>
Non-vein points	in only FE	9.79	2.57
	in both FE and SM	<b>8.94</b>	<b>2.30</b>
All image points	in only FE	7.81	2.38
	in both FE and SM	<b>6.93</b>	<b>2.03</b>

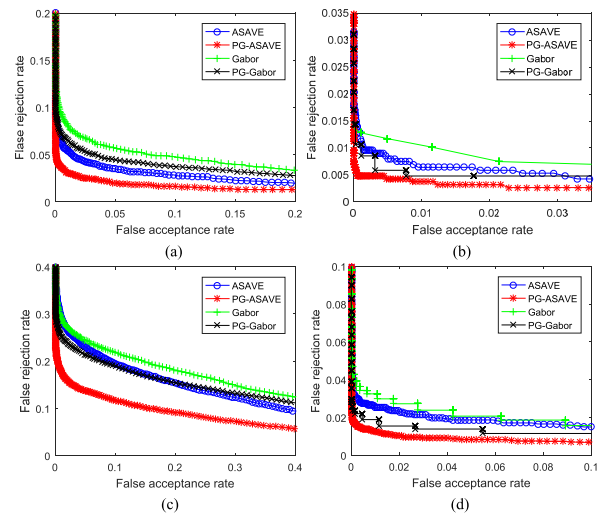


FIGURE 6. ROC curves of point grouping assisted methods and their base methods. (a) Single template and (b) Multiple templates on HKPUD; (c) Single template and (d) Multiple templates on SDUD.

points from the location-overlapped points, used in traditional similarity measurement, and therefore both the location-non-overlapped points and the orientation-unmatched points increase the difference of imposter images.

The experimental results also reveal that, all image points achieve better recognition performance over the vein points and the non-vein points when the point grouping is used in both feature extraction and similarity measurement.

3) COMPARISON OF POINT GROUPING ASSISTED METHODS AND THEIR BASE METHODS

Lastly, we make a comparison between the point grouping assisted methods, (i.e., PG-ASAVE and PG-Gabor), and their base methods, (i.e., ASAVE and Gabor). The image calibration [7] is performed for all considered methods. The ROC curves of all methods are illustrated in Fig. 6, and the corresponding EER values are reported in Table 5.

The results show that PG-ASAVE and PG-Gabor achieve better performance than their based methods on two databases and in two modes. The better performance is mainly from: (a) our methods employ more image points in recognition than ASAVE and Gabor. In detail, the vein points and the non-vein points in each image are both employed in PG-ASAVE and PG-Gabor, but ASAVE and Gabor only use



**TABLE 5. EER(%) comparison between point grouping assisted methods and their base methods.**

Database	Mode	ASAVE	PG-ASAVE	Gabor	PG-Gabor
HKPUD	Single template	3.77	<b>2.52</b>	5.52	<b>4.57</b>
	Multiple templates	0.70	<b>0.43</b>	0.98	<b>0.45</b>
SDUD	Single template	16.68	<b>11.31</b>	18.56	<b>16.35</b>
	Multiple templates	2.09	<b>1.10</b>	2.58	<b>1.35</b>

the vein points for the recognition. (b) The feature value, location, orientation based point grouping in our methods enlarges the difference between imposter images. In ASAVE and Gabor, the enrolled point and the probe point with same location are seen as matched. However, these points in the same group and with both same location and same orientation are seen matched in PG-ASAVE and PG-Gabor. In other words, more discriminative features are used in our methods for differentiate the imposter images.

### E. COMPARISON WITH STATE-OF-THE-ART METHODS

In this section, we make a comparison between our PG-ASAVE and PG-Gabor and the state-of-the-art finger vein recognition methods, including all image points based methods (i.e., competitive code and discriminative binary code), vein points based methods (i.e., repeated line tracking, maximum curvature, Gabor filters and ASAVE), and vein feature based methods (i.e., tri-branch structure and HOG).

#### 1) EER COMPARISON WITH STATE-OF-THE-ART METHODS

The EER comparison is firstly conducted in multiple templates mode on all three databases. The image calibration is performed in this experiment. Noting for the discriminative binary code [16] and tri-branch structure [11], the first three images of each finger are used for learning and other three images are used for testing. The EER values of all considered methods are given in Table 6.

**TABLE 6. EER(%) comparison between proposed methods and the state-of-the-art methods.**

Method	EER (%)		
	HKPUD	SDUD	MMCBNUD
Competitive code [15]	1.28	2.56	2.48
Discriminative binary code [16]	1.44	-	-
Repeated line tracking [3]	3.32	5.85	5.74
Maximum curvature [4]	2.41	3.65	2.69
Gabor filters [5]	0.98	2.58	2.42
ASAVE [7]	<b>0.38</b>	1.39	0.62
Gabor+Tri-branch structure [11]	0.75	4.04	1.14
Maximum curvature+HOG [8]	2.60	2.22	1.79
Proposed PG-Gabor	0.45	1.35	0.71
Proposed PG-ASAVE	0.43	<b>1.10</b>	<b>0.42</b>

It can be revealed by the experimental results that the point grouping assisted methods achieve the best performance on SDUD and MMCBNUD, and can catch up with the best state-of-the-art method (i.e., ASAVE) with very small gaps (i.e., 0.05% and 0.07%) on HKPUD. Both the discriminative features and the group-wise similarity measurement of our methods contribute to the promising performance. In detail, (1) All

image points, including the vein points and the non-vein points, are considered in the recognition; and (2) The image points are classified into multiple groups based on the feature value, location and orientation of the points, and the group-wise similarity measurement powerfully explores the discrimination of the image points. For example, two points in two images with same location may have different feature values, and two points in two image with same location and same feature value may have different orientations. These points cannot be matched in our methods, but there is big probability that the traditional methods matched them incorrectly owing to same location or/and same feature value.

In traditional vein points based methods and vein feature based methods, only vein points are used for the recognition, and lots of discriminative information (i.e., the non-vein points and the orientation map) are totally ignored in [3]–[5], [7], [8], and [11]. However, ASAVE achieves almost same EER values with our methods on three databases. The main reason is that this method fuses the vein backbone and the vein network at score-level, which brings the promising recognition performance.

The inferior performance of all image points based methods may be caused by the traditional image-wise similarity measurement. Although the feature values of all image points are used, the image-wise similarity measurement measures the similarity of features only based on feature locations. However, for two feature values with same location in feature matrix, one feature value may be from the vein point, and the another feature value may be from the non-vein point. So, the proposed group-wise similarity measurement is more powerful than the traditional image-wise similarity measurement.

#### 2) TIME COMPARISON WITH STATE-OF-THE-ART METHODS

Secondly, the time costs of the proposed methods and the best state-of-the-art method (i.e., ASAVE) are compared on the first image of each finger in HKPUD. This experiment is performed by MATLAB2016 on a PC with CPU 3.60GHz and 12.00G memory. It should be noted that the image calibration is considered in similarity measurement. The computational time of feature extraction per image and the time of similarity measurement per image pair are summarized in Table 7.

The table shows that our methods spend less time than ASAVE in both feature extraction and similarity measurement. In our methods, the time spent by vein network extraction of ASAVE is avoided, and the time-consuming elastic matching of ASAVE is replaced by the binary operation based similarity measurement, which save the computational time.

**TABLE 7. Time cost (in second) comparison between proposed methods and the best state-of-the-art method. (Noting that FE denotes feature extraction, and SM denotes similarity measurement.)**

Method	FE	SM	Total
ASAVE	0.4257	0.0585	0.4842
PG-Gabor	0.2476	0.0384	0.2860
PG-ASAVE	0.3864	0.0346	0.4210

Based on the experimental results about EER comparison and time comparison, it can be summarized that, (1) our PG-Gabor and PG-ASAVE achieves better recognition performance than most of the-state-of-the-art methods; and (2) our methods can catch up with the best state-of-the-art method, and speed less computational time than the best method.

## VI. CONCLUSION AND FUTURE WORK

This paper proposes and incorporates the idea of point grouping into vein points based methods to devise two point grouping assisted methods (i.e., PG-ASAVE and PG-Gabor) for finger vein recognition. The point grouping assisted methods combine the vein points and the non-vein points in feature extraction, and combine of the point location and the point orientation in similarity measurement. In details, all image points are considered in the group-wise similarity measurement, which explores more discriminative information than the traditional image-wise similarity measurement and vein points based similarity measurement. Additionally, the enrolled point and the probe point with same location and same orientation, not with only same location in the traditional methods, are seen matched, which enlarges the difference of imposter images. The experimental results prove that our proposed methods outperform most of the existing methods.

There is an interesting direction of future work, i.e., how to incorporate the idea of point grouping into all image points based methods. The feature values in the vein points based methods can be used in the extraction of vein points and non-vein points, and in the grouping of all image points. However, it is dubious about the point grouping by the feature values extracted by the all image points based methods (e.g., local binary pattern and competitive code).

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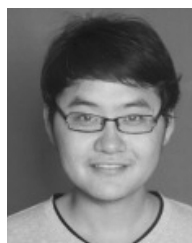
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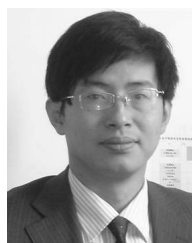
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