A Finger Vein Identification Method Based on Template Matching

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Abstract. New methods for extracting vein features from finger vein image and generating templates for matching are proposed. In the algorithm for generating templates, we proposed a parameter-templates quality factor (TQF) - to measure the quality of generated templates. So that we can use fewer finger vein samples to generate templates that meet the quality requirement of identification. The recognition accuracy of using proposed methods of finger vein feature extraction and template generation strategy for identification is 97.14%.

1. Introduction

Biometric identification is a technology that uses human bodies' physiological characteristics to distinguish status of individuals. It is known as the most secure and convenient identification method. Fingerprint identification is the most widely used biometric technology currently. Like fingerprint, finger vein patterns of individuals are also unique and therefore can be used in biometric identification. Compared with fingerprint identification, finger vein identification has several advantages :(1) The characteristics of finger vein will not be affected by wounds or stains on skin; (2) According to medical statistics, about 5% of people's fingerprints can hardly be collected due to physiological defects, while finger vein characteristics are more universal; (3) From a security standpoint, one’s finger vein characteristics can hardly be acquired by others because they lie inside of human body. With these unique advantages, finger vein identification technology is becoming a hot spot in current research. In this study, New methods to extract the features of the finger vein and synthesis templates are adopted. In the algorithm for generating templates, we proposed a parameter-templates quality factor (TQF) - to measure the quality of generated templates. The experimental results show that high recognition accuracy is achieved with proposed finger vein features extraction methods and template generation strategy for identification.

2. Materials and Methods

2.1. Image acquisition

A finger vein acquisition device is used to obtain finger vein image. Finger vein is located beneath the skin. To obtain the finger vein image, near infrared light which can penetrate fingers is selected as the light source. When near-infrared light transmits through fingers, because of the strong absorption effect on the near-infrared light of hemoglobin in the finger vein dark stripes are formed in the transmission light, which are the patterns of the finger vein.

The images acquired are 256 grey levels per pixel and 861×303 pixels in size.
2.2. Finger vein feature extraction

Original images cannot be used for identification directly. Only after a series of image processing procedures to remove redundant information, can we extract the finger vein features for identification.

Step 1 Edge detection. We need to separate fingers from background information. The gray gradient of the image has a mutation at finger edges. By using a Sobel operator to detect finger edges, we can separate finger from background information. To reduce computation cost, all images will be normalized to $45 \times 121$ pixels in size.

Step 2 Vein segmentation. We need to separate fingers veins from other biological tissues in fingers. The gray value of finger veins is always less than that of other biological tissues near it, which means pixels on finger veins have local minimum gray values. Considering this phenomenon, this paper presents a "multi-directional finding method" for finger veins. For a finger vein image $I$, as shown in Fig.1,

Starting with 0 degree (the horizontal direction), according to counter-clockwise order, we search for finger vein pixels which have local minimum gray values every 15 degrees. Results of each search are stored in matrix $I_i$ ($i=1, 2, 3, \cdots, 12$), as shown in Fig.2.

$$I_i(x, y) = \begin{cases} 1, & I(x, y) \text{is finger vein pixel} \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

Searching will be conducted for 12 times in the range of $[0, \pi)$. Then superimposing these 12 matrixes, as shown in Fig.3, we can have $I_{sum}$, namely:

$$I_{sum}(x, y) = \sum_{i=0}^{11} I_i(x, y) \quad (2)$$

Considering the existence of noise, let

$$I'_{sum}(x, y) = \begin{cases} 1, & I_{sum}(x, y) > 1 \\ 0, & \text{otherwise} \end{cases} \quad (3)$$

Then processing graphics operation on $I'_{sum}$, we can get binarized finger vein lines, as shown in Fig.3.
Step 3 Thinning finger vein lines. To reduce computation cost, extracted finger vein lines will be thinned to one pixel wide. Below is the introduction of the thinning algorithm. For pixels in a binarized finger vein image, the gray value of a pixel is 1 if this pixel lies in finger vein lines, otherwise the gray value is 0. For a pixel $P_0$, we define its 8-neighborhood as shown in Fig.4.

$$
\begin{array}{c|c|c|c}
 P_1 & P_2 & P_3 \\
 P_8 & P_0 & P_4 \\
 P_7 & P_6 & P_5 \\
\end{array}
$$

Fig 4. 8-neighborhood of a pixel.

Where $R_i$ is the gray value of $P_i$.

Then we can traverse every nonzero pixel in a binarized finger vein image. A pixel will be deleted (setting its gray value to 0) if the following conditions are satisfied:

$$
\begin{cases}
  1 < n_{\text{number}} < 6 \\
  t_{\text{number}} = 2
\end{cases}
$$

(4)

Where $n_{\text{number}}$ is the number of nonzero neighbors in $P_0$'s 8-neighborhood, that is,

$$
n_{\text{number}} = \sum_{i=0}^{8} R_i
$$

(5)

And $t_{\text{number}}$ is the number of 0-1 transitions in $P_0$'s 8-neighborhood, that is,

$$
t_{\text{number}} = \sum_{i=0}^{8} |R_{i+1} - R_i| \quad (\text{Let } R_{9}=R_8)
$$

(6)

Repeating the above processes until all pixels that need to be get rid of are set to 0. The thinned finger vein features are as shown in Fig.5.

Fig 5. (a) Finger vein lines; (b) finger vein features.

2.3. Generating templates
Due to the inevitable discrepancies of illumination condition, finger position and side movement in each sampling, there are some delicate differences in each vein samples of the same finger. To avoid the impact of discrepancies on identification accuracy, we sample a finger for several times, thus sampling results will contain the information of above discrepancies. Then we abstract finger vein features from these sampling results. Abstracted vein features of one finger will be used to synthesize a feature template. By using this template in the matching process, we can eliminate the influence of above discrepancies on identification accuracy in sampling. Specific steps are: Firstly, sampling procedure will be conduct \( m \) times of one finger. And we abstract \( m \) vein features from the sampling results, vein features are denoted by

\[
C_i (i = 1, 2, \cdots, m) \tag{7}
\]

Then superimpose these vein features, we can have \( C_T \), namely:

\[
C_T(x, y) = \sum_{i=0}^{n} C_i(x, y) \tag{8}
\]

A higher value of a pixel in \( C_T \) indicates a greater probability of vein feature appears in this position. Some pixels in \( C_T \) have relatively small values, which indicates the probabilities of vein feature appears in these positions are not stable. If these pixels involved in matching process, they may affect the accuracy. So these pixels must be eliminated (setting its gray value to 0). Considering this, let

\[
C'_T(x, y) = \begin{cases} 1, & C_T(x, y) > 1 \\ 0, & \text{otherwise} \end{cases} \tag{9}
\]

\( C'_T \) is the synthesized finger vein feature template.

For example, let \( m = 6 \), which means the sampling procedure will be conduct 6 times of one finger. Next, we abstract 6 vein features from the sampling results. Then we superimpose these 6 vein features and get \( C_T \), as shown in Fig.6. After processing \( C_T \) according to equation (9), we can get \( C'_T \), which is the synthesized finger vein feature template of the given finger.

![Fig 6. (a) Vein feature samples of one finger; (b) composition of vein feature samples; (c) template.](image)

The sampling number \( m \) is a critical parameter. If the sampling number too small, the quality of generated template will be poor because of containing inadequate discrepancies. However, if the sampling number too large, the sampling time will increase significantly while the recognition accuracy will not improve much. In order to determine the appropriate value of \( m \), we proposed an indicator-Template quality factor (TQF) - to measure the quality of generated template. TQF is defined as

\[
\text{TQF} = \frac{n_1}{n_0} \cdot 100 \tag{10}
\]
Where $n_1$ is the number of nonzero pixels in $C_r$, $n_2$ is the number of nonzero pixels in $C_T$.

TQF indicates the randomness and certainty of finger vein’s occurrence at a certain position in the template. If TQF is too small, the generated template will contain too much randomness while lack of certainty, therefore cannot be used for matching. A relatively larger TQF indicates the generated template contains adequate certainty. In practice, TQF increased with the increment of samples involved in generating the template. However, too large a value of TQF will lower the recognition accuracy because the template has little tolerance, and will obviously increase the sampling time. Using a different number of samples to generate templates and comparing the recognition accuracy of those templates, we found that the template quality can achieve the recognition accuracy when the TQF value is 35. Strategies for generating templates are: Firstly, we use 3 samples to generate a template, if the TQF no less than 35, the template is available. Otherwise, we add one more sample and generate a new template. Repeating above steps until the TQF of generated template is no less than 35.

2.4. Matching strategy

We use modified Hausdorff distance (MHD) to match samples and templates. MHD is defined as in equation (11)

$$H(A, B) = \frac{1}{N_A} \sum_{a \in A} \min_{b \in B} ||a - b||$$

(11)

Where point set A contains all nonzero pixels of a template in sequential order, point set B contains all nonzero pixels of a feature sample in sequential order. $a$ and $b$ are elements from points A and B. $||a - b||$ represents the Euclidean distance between point sets A and B. $H(A, B)$ indicates the similarity between point sets A and B, the less $H(A, B)$ is, the more similar point sets A and B are.

For a new finger vein feature sample needs to be identified, we calculate the MHD between it and every saved template. Then we compare calculated MHD values and find out the minimum MHD value. Template that corresponding to the minimum MHD value will be identified as the matching template of input vein feature sample. The advantage of this method is that it can overcome the deflection and inclination of fingers in each sampling. To ensure the accuracy of recognition, a finger to be recognized needs to be sampled 3 times. Thus we can extract 3 finger vein feature samples for this finger. Each sample will be processed with the method previously mentioned to identify its matching template. Recognition will not success unless more than one results out of three are the same.

Footnotes

Footnotes should be avoided whenever possible. If required they should be used only for brief notes that do not fit conveniently into the text.

3. Experiment result

To test the performance of the proposed method, 35 subjects provide their finger vein images. Each finger was sampled 10 times across different sessions. All finger vein images are from the finger vein acquisition device we designed. Each pixel of images has 256 grey levels. Images are scaled into 45 × 121 pixels.

All sampled images are processed into finger vein features. Each finger has 10 features, we randomly select 7 of them to generate a template, and the remaining 3 feature are used for testing. The recognition accuracy of our matching strategy is 97.14%.
The distribution of Hausdorff distances in each test is shown in Fig.7. X axis indicates the Hausdorff distance, and the Y axis indicates the percentage of the corresponding distance. As shown in Fig.8, if samples match templates, the Hausdorff distance values are mainly distributed in the region of 5 to 15, if samples mismatch templates, the Hausdorff distance values are mainly distributed in the region of 20 to 60. These two distribution curves barely intersect with each other, indicating that this method can effectively distinguish between different finger vein samples.

4. Conclusion

In this study, a new finger vein identification method based on template matching is proposed. Firstly, we use a finger vein acquisition device to obtain finger vein image. Secondly, a series of image processing procedures are carried out to extract the features of finger vein. New methods for extracting finger vein features and generating templates for matching are proposed. Template quality factor (TQF) is proposed as an indicator to measure the quality of generated template. The similarity between sample and each feature template is determined by the modified Hausdorff distance (MHD). Experimental results show that this matching method has high accuracy.

Though the database used in this study is relatively small, and it is inadequate to confirm that this method has high recognition accuracy in the process of mass population (in terms of million users). The experimental results do indicate that finger vein recognition, as a new recognition technology, is feasible and of great long term potential. With continuous research, finger vein identification technology will be developed more mature, and will be able to be applied to many situations of social production and the lives of people.

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