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Human identification based on vein structure in Sclera

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Abstract: The main objective of this project is sclera vein recognition. Sclera vein recognition is used for human identification. It poses a challenge because sclera vessel patterns are often dense and/or saturated and, most importantly, the vessel structure in the sclera is complex and has deformation. The blood vessel patterns of sclera show rich and unique details. Here, a new sclera vein recognition method using a two-stage approach for registration and matching is proposed. The sclera vein recognition system includes sclera segmentation, feature enhancement, feature extraction and feature matching. Before matching, the mask's file should be aligned and the overlap of these masks was calculated as a new mask. Y shape descriptor to narrow the search range to increase the matching efficiency, which is a new feature extraction method. The proposed method dramatically improves the matching efficiency without compromising recognition accuracy.

Index Terms: Sclera vein recognition, Feature extraction, sclera feature matching, sclera matching.

1. INTRODUCTION

The sclera is the opaque and white outer layer of the eye. The blood vessel structure of sclera is formed randomly and is unique to each person, which can be used for human's identification. The new sclera descriptor – the Y shape sclera feature-based efficient registration method and the "Weighted Polar Line (WPL) descriptor" and coarse to fine two-stage matching process are proposed here. These approaches make the process most efficient.

2. RELATED WORK

2.1. Overview of Sclera vein recognition

Each user should provide one or more samples of biometric data. These samples are stored as a template in database. When the user attempt to authenticate, the biometric they provide is then compared with the stored template. The system assesses whether the sample is similar to the template. If similar, it judged to be a match. The acquired image undergoes the following process. Image pre-processing, sclera segmentation, feature enhancement, feature extraction, and feature matching (Figure 1).

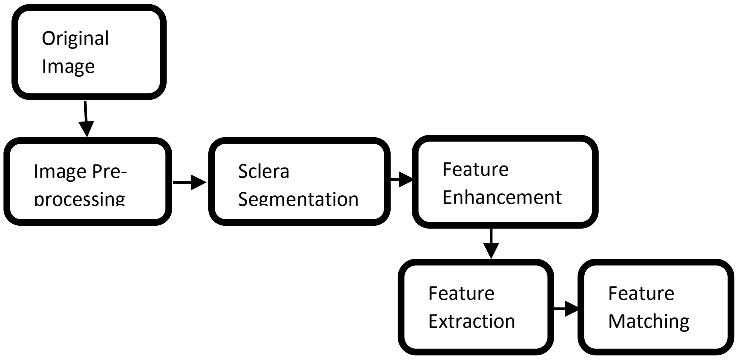


Figure 1 Diagram of the typical sclera vein recognition approach.

2.2. Image pre-processing

Pre-Processing is a technique of enhancing the data images prior to computational processing. Pre-processing methods use a small neighborhood of a pixel in an input image to get a new brightness value in the output image. Such pre-processing operations are also called **filtration**. To remove low frequency background noise in the image, Wiener2 filter is used.

2.3. Sclera segmentation

Sclera image segmentation is the next step in sclera vein recognition. It is a process of partitioning a digital image into multiple segments i.e. Set of pixels. Here, k-means clustering algorithm is used for sclera vein segmentation. Clustering is a process of partitioning a group of data points into a small number of clusters. It is a simple and easiest way to classify a given data set through a certain number of clusters (k-no. of clusters). Define k-number of centroids, one for each cluster. Centroids placed far away from each other. Then take each point belonging to a given data set and associate it to the nearest centroid. When no point is pending, an early grouping is done. Then recalculate k-new centroids.

$$\text{Objective function J} = \sum_{j-1}^{k}\sum_{i-1}^{x}\left(x_i - c_j\right)^2 \qquad (1)$$

Euclidean distance is used to assign a point to a cluster. Calculate distance from data point to each cluster.

2.4. Feature enhancement:

After sclera segmentation, it is necessary to enhance and extract the sclera features since the sclera vein patterns often lack of contrast, and are hard to detect. The following techniques are used for enhancement.

1. Gabor filter
2. Histogram equalization

2.4 a Gabor filter

Gabor filters are used for vascular pattern enhancement. Sclera area is very reflective and hard to be accurately focused. Therefore the sclera vascular pattern is often blurry and low contrast. Gabor filters, which are Gaussian weighted sinusoids, are good method for enhancement. Since the vascular pattern is multi orientations, Directional Gabor filters are used.

$$G(x,y,\vartheta,s) = e^{-\pi}((x-x_0)^2+(y-y_0)^2)/s^2$$

$$X \quad e^{-2\pi i}(\cos\vartheta\,(x-x_0)+\sin\vartheta\,(y-y_0)) \quad (2)$$

Where,

(x_0, y_0) = center frequency of the filter

s = variance of the Gaussian

ϑ = angle of sinusoidal modulation

Image is first filtered.

$I_F(x, y, \vartheta, s) = I(x,y) * G(x,y,\vartheta,s)$

$I_F(x,y,\vartheta,s)$= Gabor Filter image at orientation θ and scale

I(x,y) = Original intensity image

$G(x,y,\vartheta,s)$ = Gabor Filter

The filter is constructed such that if the vein width is 4 pixels wide, the filter band width will be 3, 4 and 5 pixels respectively.

2.4 b Histogram equalization:

Histogram equalization is to enhance the contrast of the sclera image by adjusting the intensity. It is a graphical representation of the no of pixels in an Image as a function of their intensity. It is made up of bins, which represents certain intensity value range. It is an intensity transformation that transforms the distribution of the pixel intensity values into a uniform or nearly uniform distribution. Two concepts used are Probability Mass Function (PMF) and Cumulative Distributive Function (CDF).

2.5. Line descriptor based sclera vein recognition method:

The matching segment of the line-descriptor based method is a bottleneck with regard to matching speed. After segmentation, vein patterns were enhanced by a bank of directional Gabor filters. Binary morphological operations are used to thin the detected vein structure down to a single pixel wide skeleton and remove the branch points. The line descriptor is used to describe the segments in the vein structure. Figure 2 shows a visual description of the line descriptor. Each segment is described by three quantities: the segments angle to some reference angle at the iris center θ, the segments distance to the iris center r, and the dominant angular orientation of the line segment $\emptyset$.

The descriptor is,

$$S = (\theta\ r\ \emptyset)^T \qquad (3)$$

The individual components of the line descriptor are calculated as:

$$\theta = \tan^{-1}\left(\frac{y_l - y_i}{x_l - x_i}\right) \qquad (4)$$

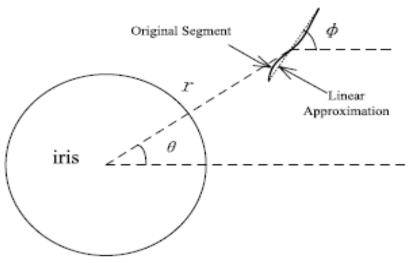


Figure 2 The sketch of parameter of segment descriptor

$$r = \sqrt{(y_l - y_i)^2 + (x_l - x_i)^2} \quad \text{and}$$

$$\emptyset = \tan^{-1}\left(\frac{d}{dx} f_{line}(x)\right) \qquad (5)$$

Here $f_{line}(x)$ is the polynomial approximation of the line segment, (x_l, y_l) is the center point of the line segment, (x_i, y_i) is the center of the detected iris, and S is the line descriptor. In order to register the segments of the vascular patterns, a RANSAC-based algorithm is used to estimate the best-fit parameters for registration between the two sclera vascular patterns. For the registration algorithm, it randomly chooses two points – one from the test template, and one from the target template. It also randomly chooses a scaling factor and a rotation value, based on a priori knowledge of the database. Using these values, it calculates a fitness value for the registration using these parameters. After sclera template registration, each line segment in the test template is compared to the line segments in the target template for matches. In order to reduce the effect of segmentation errors, we created the weighting image (Figure 3) from the sclera mask by setting interior pixels in the sclera mask to 1, pixels within some distance of the boundary of the mask to 0.5, and pixels outside the mask to 0. The matching score for two segment descriptors is calculated by:

$$M(S_i, S_j) = \begin{cases} w(S_i)w(S_j), & d(S_i, S_j) \le D_{match} \text{ and } |\emptyset_i - \emptyset_j| \le \emptyset_{match} \\ 0 & else, \end{cases} \qquad (6)$$

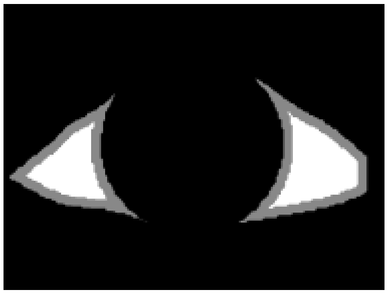


Figure 3 Weighted polar image

where S_i and S_j are two segment descriptors, $m(S_i, S_j)$ is the matching score between segments S_i and S_j, $d(S_i, S_j)$ is the Euclidean distance between the segment descriptors center points, D_{match} is the matching distance threshold, and $\emptyset_{match}$ is the matching angle threshold. The total matching score, M, is the sum of the individual matching scores divided by the maximum matching score for the minimal set between the test and target template. That is, one of the test or target templates has fewer points, and thus the sum of its descriptors weight sets the maximum score that can be attained.

$$M = \frac{\sum_{(i,j \in Matches)} m(S_i, S_j)}{min(\sum_{i \in Test} w(S_i), \sum_{j \in Target} w(S_j))} \qquad (6)$$

Here *Matches* is the set of all pairs that are matching, *Test* is the set of descriptors in the test template and *Target* is the set of descriptors in the target template.

3. PROPOSED MODELLING

3.1. Y Shape sclera feature for efficient registration

Currently, the registration of two sclera images during matching is very time consuming. To improve the efficiency, a new descriptor — the Y shape descriptor is proposed, which can greatly help improve the efficiency of the coarse registration of two images and can be used to filter out some non-matching pairs before refined matching. Within the sclera, there can be several layers of veins. The motion of these different layers can cause the blood vessels of sclera show different patterns. But in the same layers, blood vessels keep some of their forms. As present in Figure 5, the set of vessel segments combine to create Y shape branches often belonging to same sclera layer. When the numbers of branches is more than three, the vessels branches may come from different sclera layers and its pattern will deform with movement of eye. Y shape branches are observed to be a stable feature and can be used as sclera feature descriptor. To detect the Y shape branches in the original template, we search for the nearest neighbors set of every line segment in a regular distance, classified the angles among these neighbors.

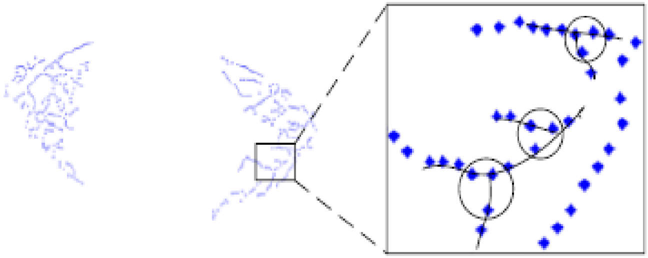


Figure 4 The Y shape vessel branch in sclera.

If there were two types of angle values in the line segment set, this set may be inferred as a Y shape structure and the line segment angles would be recorded as a new feature of the sclera. There are two ways to measure both orientation and relationship of every branch of Y shape vessels: one is to use the angles of every branch to x axle, the other is to use the angels between branch and iris radial direction. The first method needs additional rotation operating to align the template.

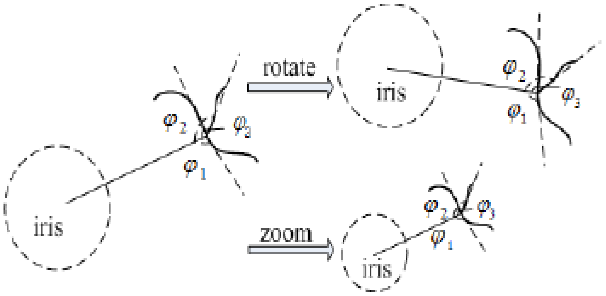


Figure 5 Rotation and scale invariant character of Y shape vessel branch

Here, we employed the second method. As Figure 5 shows, $\emptyset_1$ $\emptyset_2$ and $\emptyset_3$ denote the angle between each branch and the radius from pupil center. Even when the head tilts, the eye moves, or the camera zooms occurs at the image acquisition step, the $\emptyset_1$ $\emptyset_2$, and $\emptyset_3$ are quite stable. To tolerate errors from the pupil center calculation in the segmentation step, we also recorded the center position (x, y*)* of the Y shape branches as auxiliary parameters. So in our rotation, shift and scale invariant feature vectors are defined as: Y *(*$\emptyset_1$,$\emptyset_2$,$\emptyset_3$, x& y*)*. The Y-shape descriptor is generated with reference to the iris center. Therefore, it is automatically aligned to the iris centers. It is a rotational- and scale- invariant descriptor.

3.2. WPL sclera descriptor

The line descriptor is extracted from the skeleton of vessel structure in binary images (Figure 6). The skeleton is then broken into smaller segments. For each segment, a line descriptor is created to record the center and orientation of the segment. This descriptor is expressed as $s(x, y, \emptyset)$, where (x, y) is the position of the center and $\emptyset$ is its orientation. Because of the limitation of segmentation accuracy the descriptor in the boundary of sclera area might not be accurate and may contain spur edges resulting from the iris, eyelid, and/or eyelashes. To be tolerant of such error, the mask file .is designed to indicate whether a line segment belongs to the edge of the sclera or not. When matching, the registration RANSAC type algorithm was used to randomly select the corresponding descriptors and the transform parameter between them was used to generate the template transform affine matrix. After every templates transform, the mask data should also be transformed; and new boundary should be calculated to evaluate the weight of the transformed descriptor. This results in too many convolutions in processor unit.

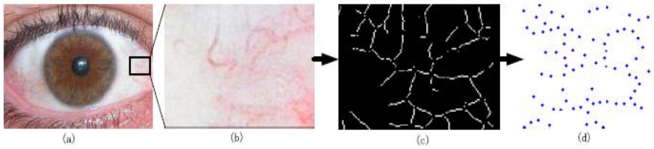


Figure 6 Line descriptor of the sclera vessel pattern. (a) An eye image. (b) Vessel patterns in sclera. (c) Enhanced sclera vessel patterns. (d) Centers of line segments of vessel patterns.

To reduce heavy data transfer and computation, we designed the weighted polar line (WPL) descriptor structure, which includes the information of mask and can be automatically aligned. We extracted the relationship of geometric feature of descriptors and store them as a new descriptor. We use a weighted image created via setting various weight values according to their positions. The weight of those descriptors who are beyond the sclera are set to be 0, and those who are near the sclera boundary are 0.5 and interior descriptors are set to be 1. In our work, descriptors weights were calculated on their own mask by the CPU only once. The calculating result was saved as a component of descriptor. The descriptor of sclera will change to $\mathbf{s}(x, y, \emptyset, w)$, where, w denotes the weight of the point and the value may be 0, 0.5, 1. To align two templates, when a template is shifted to another location along the line connecting their centers, all the descriptors of that template will be transformed. It would be faster if two templates have similar reference points. If we use the center of the iris as the reference point, when two templates are compared, the correspondence will automatically be aligned to each other since they have the similar reference point. Every feature vector of the template is a set of line segment descriptors composed of three variable (Figure 2) the segment angle to the reference line which went through the iris center, denoted as θ; the distance between the segments center and pupil center which is denoted as r ; the dominant angular orientation of the segment, denoted as $\emptyset$. The descriptor vector becomes $\mathbf{s}(x, y, r, \theta, \emptyset, w)$.

The left and right parts of sclera in an eye may have different registration parameters. For example, as an eyeball moves left, the left part sclera patterns of the eye may be compressed while the right part sclera patterns are stretched. These two parts are treated separately for different deformation.

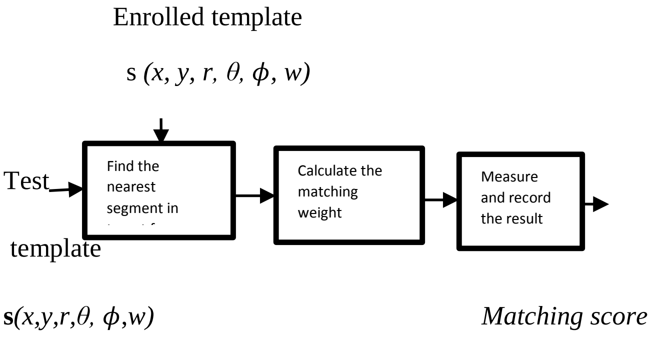


Figure 7 Simplified sclera matching steps.

Matching score from the output is recorded. After reorganizing the structure of descriptors, the mask information is added into the new descriptor. The simplified sclera matching steps are given in figure 7.

3.3. Matching process

To improve the matching process, coarse-to-fine two-stage matching process is proposed. In the first stage, we matched two images coarsely using the Y-shape descriptors, which is very fast to match because no registration was needed. The matching result in this stage can help filter out image pairs with low similarities. After this step, it is still possible for some false positive matches. In the second stage, we used WPL descriptor to register the two images for more detailed descriptor matching including scale- and translation invariance. Combining these two stages, the matching program can run faster and achieve more accurate score.

Stage I: Matching with Y shape descriptor

To match two sclera templates, we searched the areas nearby to all the Y shape branches. The search area is limited to the corresponding left or right half of the sclera in order to reduce the searching range and time. The distance of two branches is defined by using the angle between the each branch and the polar from pupil center in each descriptor. The number of matched pairs and the distance between Y shape branches centers are stored as the matching result.

$$n_{i=1,}\ d_{i=}\ d_{\varphi}(\ y_{tei},\ y_{tai}) \qquad (7)$$

$$\text{Matching score} = \frac{2\sum ni - a\sum di}{\max(Ni..Nam)} \qquad (8)$$

$$d_{\emptyset}(y_{tei} y_{taj}) = \sqrt{(\emptyset_{io}-\emptyset_{jo})^2 + (\emptyset_{i1}-\emptyset_{j1})^2 + (\emptyset_{i2}-\emptyset_{j2})^2} \qquad (9)$$

$$d_{xy}(y_{tei}, y_{taj}) = \sqrt{(x_i-x_j)^2 + (y_i-y_j)^2} \qquad (10)$$

Here, y_{tei} and y_{taj} are the Y shape descriptors of test template T_{te} and target template T_{ta} respectively. d_{φ} is the Euclidian distance of angle element of descriptors vector. d_{xy} is the Euclidian distance of two descriptor centers. n_i and *di* are the matched descriptor pairs' number and their centers distance respectively. t_{φ} is the distance threshold and t_{xy} is the threshold to restrict the searching area. We set t_{φ} to 30 and t_{xy} to 675 in the experiment. The number of matched pairs *ni* and the distance between Y shape branches centers *di* are stored as the matching result. Here, α is a factor to fuse the matching score which was set to 30 in our study. *Ni* and *Nj* is the total numbers of feature vectors in template *i* and *j* separately. The decision is regulated by the threshold t: if the sclera's matching score is lower than t, the sclera will be discarded. The sclera with high matching score will be passed to the next more precisely matching process.

Stage II: Fine matching using WPL descriptor

The WPL descriptor reveals more vessel structure detail of sclera than the Y shape descriptor. The variation of sclera vessel pattern is nonlinear because: 1) when acquiring an eye image in different gaze angle, the vessel structure will appear nonlinear shrink or extend because eyeball is spherical in shape. And, 2) sclera is made up of four layers: episclera, stroma, lamina fusca and endothelium. There are slightly differences among movement of these layers. The WPL descriptor matching is designed to tolerant possible errors in pupil center detection in the segmentation step and to tolerant some deformation of sclera patterns in the matching step. Finally, the total matching score is minimal score of two transformed result divided by the minimal matching score for test template and target template.

4. RESULTS AND DISCUSSIONS

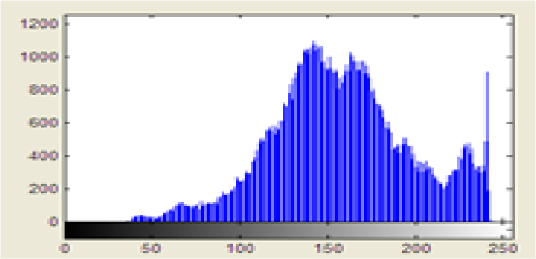
In existing system line descriptor-based method for sclera vein recognition is used. The matching step (including registration) is the most time consuming step in this sclera vein recognition system, which costs about 1.2 seconds to perform a one-to-one matching. Using Y shape descriptor, it takes 56.8 second to compare an 1168x1168 pair template. The Equal Error Rate (EER) of this stage is not very accurate. However, it can be used as a filtering method to select most likely matching templates to compare in the next step, Stage II. To balance the matching speed and accuracy, different strategies are adopted to select the possible template after

Stage I. The matching only using Stage II achieves the most accurate result; however it would take longest time.

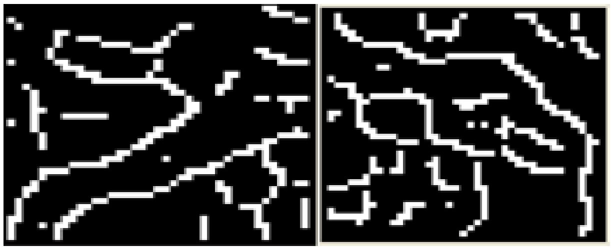
For the line descriptor based method, the EER is 3.386%, the area under the curve (AUC) is 97.5%. For the Y shape descriptor based method, the EER =3.052%, AUC = 98.6%. At the same time, this method achieves a 769 times speed improvement. If we filter 23.3% of pairs from the Stage I, the speed would be further improved to be 805 times. The proposed Y shaped descriptor based method could dramatically improve the speed without compromising the recognition accuracy.

a) Input image

b) Filtered image



c) Histogram equalization



d) Detected sclera edges

e) Matched image

5. CONCLUSION

In this paper, a new Y shape descriptor method with a two stage approach for registration and matching is proposed. We designed the Y shape descriptor to narrow the search range to increase the matching efficiency, which is a new feature extraction method. We developed the WPL descriptor to tolerant possible errors in pupil center detection and deformation of sclera patterns in the matching step. The proposed method dramatically improves the matching efficiency without compromising recognition accuracy. In future, matching efficiency will be improved further.

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