

HUMAN RECOGNITION BY FINGER VEINS

Peter Lisák

Master Degree Programme (2), FIT BUT

E-mail: xlisak00@stud.fit.vutbr.cz

Supervised by: Radim Dvořák

E-mail: idvorak@fit.vutbr.cz

Abstract: In this paper a new method for human recognition by finger veins pattern is proposed. Identification method is based on a distribution of vein templates into classes by clustering. Patterns are vectors containing extracted features got by sampling of the finger vein contours. The vector space of templates is clustered by the combination of genetic algorithm and k-means clustering.

Keywords: biometrics, human recognition, finger veins, verification, identification, clustering, genetic algorithms.

1 INTRODUCTION

In the last decade we can observe a great boom in biometrics. There are many kinds of biometrics devices and methods, which can be used for recognition. Vein technology is one of them, but belongs to these less developed. Despite this fact, it has a great potential to become one of the most used because of its characteristics such as contactless, accuracy, portability, security and price. During solving of the problem, we have found only a couple of the published verification methods, but no identification method. These methods are usually derived from the fingerprint technologies [1]. The proposed identification method in this work enhances the development of the finger vein recognition device. The project is a part of research performed by research group STRaDe at Faculty of Information Technology, Brno University of Technology. The existing prototype of the capturing device using far infrared radiation as well as the method for finger vein extraction are present there.

2 PROPOSED RECOGNITION METHOD

The method is especially developed for the vein images preprocessed by existing method of the STRaDe group. The image contains a thinned contours of the veins. Because of the used thinning method, there are only vertical contours [2]. To construct a template we need to extract some features from vein image. The vein contour is supposed to be a feature and it is transformed into feature vector by sampling. The finger contour in combination with the vein pattern is supposed to be the second case of feature set. There are two options for creating vectors - bit or integer. In case of bit vector, zero means that no vein occurs in sampling window and vice versa. Samples of integer vector contain a number of vein contour pixels in sampling windows. To compare templates to each other, several dissimilarity measures were tested and used for bit vectors and distance measures for integer vectors. For comparison and measuring of distance, formulas such as Jaccard, Dice, Sokal-Sneath, Euclidean or Cosine distance are used [3]. The result comparison score is the average of scores of all templates belonging to the same finger vein pattern enrolled in the database. Integer vector templates are used for clustering and bit vector templates for comparison. You can notice that integer vector template is convertible into bit vector template. One considerable disadvantage of pattern-based comparison is a proper alignment of templates. In the comparison mode two templates can be adjusted by moving and rotating into the different positions to get the best measure score. But it cannot be used for the identi-

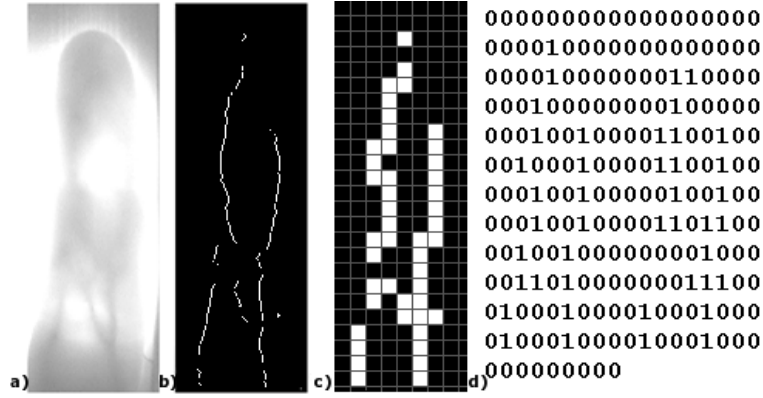


Figure 1: a) original image, b) thinned vein contour, c) example of sampling, d) example of bit vector template.

fication. So we also intend the second approach. According to the finger contour a finger axis is found by linear regression. Then the axis with finger is centered and got upright by affine transformation.

As a result of identification process the identity is assigned to an unknown pattern according to known templates in the database. The simplest way is to compare an unknown pattern with each in the database, but this approach is very time and resource consuming. Therefore, the principle of proposed method is to select the group of candidate templates. As was said, vein features are encoded in the templates as vectors. These vectors lie in the multidimensional space, which is divided into classes by the clustering method named k-means. K-means algorithm is sensitive to the initial choice of centroids. The space of combinations is too large to be explored, therefore, we have used genetic algorithm (GA) to search the optimal solution. We specified several conditions:

- robustness of clusters - inner distance of cluster should be minimal and outer one maximal
- templates of one finger vein pattern enrolled in the database should be in one cluster and a count of items in clusters should be similar to each other

GA checks the conditions and finds the optimal count and distribution of classes using its fitness function. A small population and few generations are needed to find the optimal solution. To constrain a count of clusters, the following formula was specified for theoretical optimal count:

$$\operatorname{argmin}_{k>0} \left(k + \frac{m \cdot n}{k} \right), \quad (1)$$

where k is a count of clusters, n is a count of fingers in the database and m is a count of templates for one finger enrolled in the database. After clustering the database of templates is ready for identification. At first we find a cluster, in which an unknown template belongs to most probably one. Then it is compared with every template in the cluster sequentially assuming that an unknown user was enrolled in the database previously.

3 EXPERIMENTS

For testing and experiments there was the finger vein pattern database of 36 fingers with 3 templates for one finger. Existing of 3 templates for one finger is used for 3-fold cross-validation testing, where a couple of templates is enrolled in the database and the third one is user's attempt for verification or identification. First we were searching the proper size of the sampling window (2×2 , 4×4 and 6×6

Features		Veins				Veins+Contour		
Alignment		none	automatic	adjusted	manual	none	automatic	adjusted
Jaccard	FNMR ¹	61.11%	22.22%	4.63%	0.00%	68.52%	25.00%	14.81%
	FMR ²	0.05%	0.13%	0.08%	0.08%	0.21%	0.08%	0.03%
Cosine	FNMR	59.26%	24.07%	5.56%	1.85%	78.70%	27.78%	17.59%
	FMR	0.21%	0.40%	0.11%	0.03%	0.19%	0.13%	0.16%

Table 1: The results of comparison test with sampling window 4×4 .

pixels). Size 4×4 gave the best results. Then we tried the alignment approaches previously proposed and to choose the best measures for identification. In Table 1 the best result measures are presented.

In our case the optimal value of k is approximately 8.5 according to Formula 1. So we constrained the count of clusters from 7 to 10. Ten runs were performed for every fold of 3-fold cross-validation test. Cosine distance was used in k-means and Jaccard dissimilarity for the sequence comparison. Because of simplicity and the small size of the testing database, we did not specify any exact threshold for the result comparison score. So the template with the best comparison score is claimed as a searched identity. Identification with the manually aligned database is set as a reference one and it expresses the accuracy of proposed method. However, in the common practise this kind of alignment is evidently unusable. The effort is to eliminate an inequality in the alignment by an automatic process. Using our automatized alignment approach we managed to search only about 6 finger veins to identify the searched one with the accuracy 82.63% of the true answer. Nevertheless, there is still space for the improvement as the results of manual alignment show in Table 2.

Features	Veins						Veins+Contour	
Alignment	none		automatic		manual		automatic	
Avg. count of clusters	8.17		8.63		8.70		8.57	
Cluster hits	21.57	59.91%	29.77	82.69%	35.53	98.70%	31.17	86.57%
Identification rate	21.50	59.72%	29.74	82.63%	35.53	98.70%	29.57	82.13%
Avg. count of candidates	8.67	24.08%	6.71	18.65%	5.44	15.11%	5.94	16.50%

Table 2: The results of identification test are the average results of 3-fold cross-validation.

4 CONCLUSION

Proposed recognition method and pattern-based comparison were tested. They will be used for next experiments and further improvements. Jaccard dissimilarity has FNMR=4.63%, FMR=0.08% and Cosine distance has FNMR=5.56%, FMR=0.11%. The identification method with automatized alignment has accuracy 82.63%. Additional enhancements are suggested such as image preprocessing, better automatized pattern alignment, template compression and the usage of more testing samples.

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¹FNMR - False Non-Match Rate measures the percent of valid inputs which are incorrectly rejected.

²FMR - False Match Rate measures the percent of invalid inputs which are incorrectly accepted.