Local binary patterns for a hybrid fingerprint matcher

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ABSTRACT

In this work, we present a novel hybrid fingerprint matcher system based on local binary patterns. The two fingerprints to be matched are first aligned using their minutiae, then the images are decomposed in several overlapping sub-windows, each sub-window is convolved with a bank of Gabor filters and, finally, the invariant local binary patterns histograms are extracted from the convolved images.

Extensive experiments conducted over the four FVC2002 fingerprint databases show the effectiveness of the proposed hybrid approach with respect to the well-known Tico's minutiae matcher and other image-based approaches. Moreover, a BioHashing approach have been designed using the proposed fixed-length feature vector and very interesting performance has been obtained by combining it with the Tico's minutiae matcher.

1. Introduction

Main approaches proposed in the literature for the fingerprint automatic verification may be roughly classified as minutiae-based, correlation-based or image-based (for a good survey see Ref. [1]).

Most of the approaches are minutiae-based: the matching between two fingerprints is based on the alignment of their sets of minutiae extracted from the fingerprint images. One of the most known minutiae-based approaches is the method proposed by Tico and Kuosmanen [2], which aligns two sets of minutiae considering the directional image around the minutiae.

In correlation-based fingerprint matching [3], the template and query fingerprint images are spatially correlated to estimate the degree of similarity between them.

The image-based approaches extract a feature vector from the grey-level image of the fingerprint and the matching decision is made using only these feature vectors. A well-known image-based technique is the FingerCode [4], which extracts the features by applying Gabor Filters in the region around the fingerprint core point. The main problem of this approach is to obtain a reliable core detection. In Refs. [5,6] two FingerCode variants are proposed, where the fingerprint images are first aligned using the overall minutiae information; experimental results show that using minutiae for aligning image pairs makes an image-based approach more robust than using the core point. Another image-based method proposed in Ref. [7] extracts the features from an integrated wavelet and Fourier–Mellin transformed image.

None of the image-based approaches proposed in the literature gains performance comparable to the minutiae-based ones; anyway they are an interesting choice in case of images of low quality, where the minutiae-based methods cannot obtain a reliable minutiae detection.

Several techniques have been proposed in the literature to handle the presence of non-linear distortions and noise in the fingerprint image (see Ref. [1] Section 4.5; [8–10]). In our previous works [8–10], we have partitioned the region of interest around the core point in smaller sub-images, in order to bound the effects of image variations and distortion to some of the sub-images, and thus, to better preserve and represent the local information. The features extracted from each sub-image were used for creating a template, and different matchers were trained, one for each sub-image, to be finally combined by a fusion rule.

In this paper we propose a hybrid approach where fingerprints are pre-aligned using minutiae, and then image-based features are extracted by invariant local binary patterns (LBP) from the fingerprint image convolved with Gabor filters [11]. The feature extraction is performed locally: the fingerprint image is first divided into several sub-windows, then a segmentation step is performed in order to discard the background, finally each sub-window is convolved with a bank of Gabor filters and LBP are calculated. The comparison between the unknown fingerprint and the stored template is performed by the average Euclidean distance calculated among the correspondent couples of foreground sub-windows.

Experimental results conducted over the four FVC2002 fingerprint databases show the effectiveness of the proposed approach with respect to other Gabor-based methods [4,5,8–10].

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Another important advantage of the proposed feature extraction approach is related to the fixed length of the feature vector, which makes this approach suitable to be coupled with a BioHashing method. In fact, since BioHashing requires a fixed length feature vector, it cannot be easily applied to a minutiae-based method.

BioHashing [12] is a verification method based on iterated inner products between tokenised pseudo-random number (generated by a Hash key) and the user specific biometric features; the resulting user specific compact code is named "BioHash code". The main drawback reported for BioHashing [13,14] is the low performance when an "impostor" B steals the hash key or the pseudo-random numbers of A and tries to authenticate as A. An accurate experimental analysis [15] revealed that the primary weakness of the base approach was in the length of the BioHash code (which is bounded by the dimension of the feature space). Therefore an improved BioHashing approach [15] has been proposed, which performs well also in the worst test case, when always an "impostor" steals the Hash key.

The feature vector proposed in this work has fixed dimension and it is long enough to be coupled with BioHashing; such BioHashing approach experimentally confirms optimal results when the hash key is not stolen and gains good performance also in the worst test case (when always an "impostor" steals the hash key). Another interesting result has been obtained by combining the image based approach with a minutiae-based one: the fusion by the sum rule of the well-known Tico's minutiae matcher [2] and the new BioHashing matcher proposed in this work gains very valuable performance in all the tested data sets.

The paper is organized as follows: in Section 2 we give an overview of the proposed hybrid system, presenting the details of the new feature extraction approach; in Section 3 we briefly review the improved BioHashing approach; and in Section 4 we present and discuss some experimental results. Finally we draw our conclusions in Section 5.

2. System overview

The first step of the novel hybrid matcher is the enhancement. Since the input image may be noisy, it is first enhanced in order to improve the clarity of the ridges and furrow structures using the technique described in Ref. [16], which proposes a Fourier domain based block-wise contextual filter approach for enhancing fingerprint images. Then, the unknown fingerprint is aligned to the stored model using the minutiae (as in Refs. [5,6]). For feature extraction the image is decomposed in several sub-windows with fixed dimensions; only the foreground sub-windows are retained, according to a segmentation procedure described in Ref. [4]. The feature extraction (see Section 2.1) for each sub-window consists in the convolution with a bank of Gabor filters and in the calculation of the LBP histograms from the convolved images; the feature vector is obtained by

concatenating the LBP histograms. Finally, the comparison between corresponding sub-windows from the unknown, aligned fingerprint and the stored model is performed by calculating their Euclidean distance; the matching value for two fingerprints is the (average distance of their corresponding sub-windows)×(−1).

In Fig. 1 a functional schema of pre-processing and feature extraction for the novel hybrid matcher (named GLBP) is reported.

2.1. Feature extraction

The image is divided in possibly overlapping sub-windows of fixed dimension $d \times d$. Each sub-windows is first resized to a dimension of 25×25 (to reduce the computation time) and then convolved with a bank of g Gabor filters at different scales and orientations. Before and after the convolution, each sub-window is normalized to fixed mean and variance using the method proposed in Ref. [17]. Finally, the LBP histogram[1] is calculated for each convolved image.

The $LBP_{P,R}$ operator [18] is a truly grayscale invariant measure that is obtained from a pixel $\mathbf{x}$ and its symmetric neighbor set of P pixels placed on a circle radius of R (Fig. 2). A binary pattern $LBP_{P,R}$ is calculated by considering the difference between the gray value of the pixel $\mathbf{x}$ from the gray values of the circularly symmetric neighborhood; when a neighbor does not fall exactly in the center of a pixel its value is obtained by interpolation. The LBP histogram of dimension n (usually $n = P + 2$) is obtained considering all the binary patterns of a given image. In this work we have tested the three configurations proposed in Ref. [18]: ($P = 8$; $R = 1$; $n = 10$), ($P = 16$; $R = 2$; $n = 18$) and ($P = 24$; $R = 3$; $n = 26$).

Since fingerprints are susceptible of several variations mainly due to the presence of skin distortions and of different skin quality, such as dry or moist or dirty skin, we consider that LBP histograms could be particularly suited for the fingerprint identification problem. In fact, in Ref. [19] it is shown that the LBP histogram is very robust in terms of grayscale variations; it is invariant against any monotonic transformation of the grayscale and it is possible to achieve rotation invariance by simply incorporating a fixed set of rotation invariant patterns.

Moreover we argued that the application of Gabor filters (which have been extensively used in fingerprints) before LBP could make the feature extraction more discriminant with respect to the direct application to gray-levels. In fact the images obtained as response to the application of bank of Gabor filters contain a more detailed information about the local orientation and scales of the ridge lines, with respect to the grey-level image. Therefore coupling LBP and Gabor filtering allows to extract a set of features that can reflect the local information of each filer, thus enhancing the representation power of the spatial histogram greatly. In Fig. 3 we show two sub-windows that are matched considering the Gabor filters feature extraction, but are not matched considering the proposed feature extraction based on the LBP extracted from the Gabor filtered image.
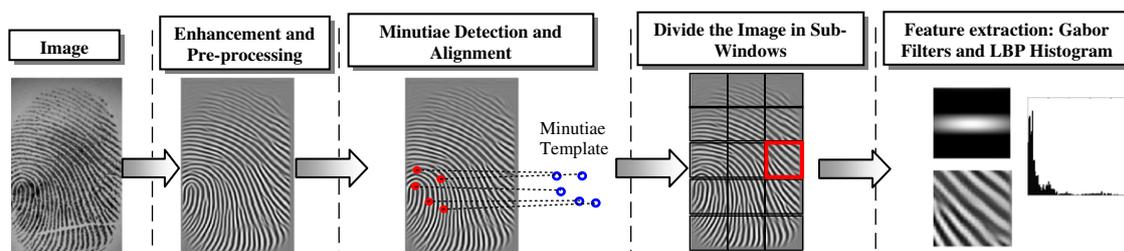

Fig. 1. A functional schema of pre-processing and feature extraction of the novel hybrid matcher.

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[1] The Matlab implementation is available at http://www.ee.oulu.fi/mvg/page/lbp_matlab.
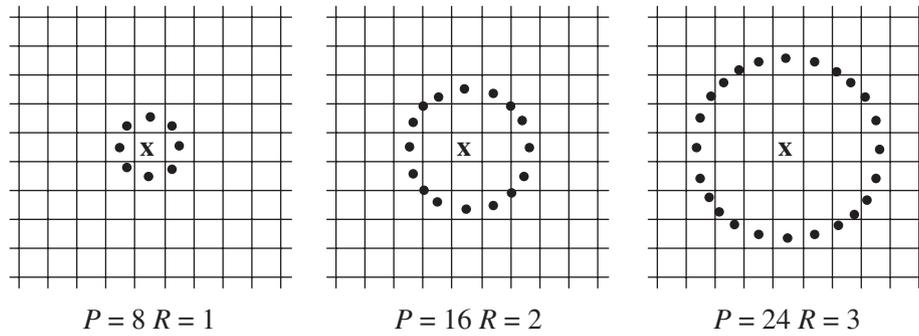
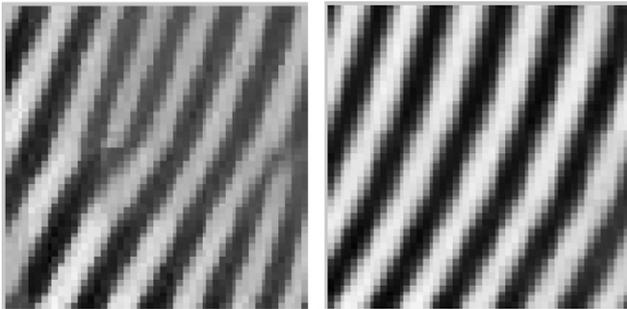**Fig. 2.** LBP neighbor sets for different (P, R).

Fig. 3. Sub-windows matched by the Gabor based method but they are not matched considering the proposed approach.

In conclusion, the idea of coupling LBP and Gabor filtering in fingerprint analysis is motivated by the fact that the frequency and orientation of the ridge lines in each local sub-window of a fingerprint are very important for the matching in order to reduce the influence of noise; this means that using good features for representing the local regions of the fingerprints can make the matching more robust against noise and other local variations. The comparative results reported in Tables 3 and 4 (Section 4) confirm the effectiveness of our method.

In conclusion, for each sub-window, a $n \times g$-dimensional feature vector is obtained, where n is the number of bins in the LBP histogram and g the number of Gabor filters. In Fig. 4 an example of feature extraction is presented related to a single Gabor filter; the final vector is obtained from the concatenation of the histograms from g filtered images.

3. BioHashing

BioHashing [12,20] can be perceived as a feature transformation that calculates a vector of bits, named BioHash code, starting from a biometric feature vector and a given seed (the Hash key). The biometric vector data $\mathbf{x} \in \Re^n$ is reduced down to a bit vector $\mathbf{b} \in \{0,1\}^m$ with m the length of the bit string ($m=n$ in this paper), via a uniform distributed pseudo-random numbers generated by giving a secret seed. To reduce the dependence of performance on the parameter m an improved version of BioHashing proposed in Ref. [15] is adopted (see Fig. 5) and applied to the feature vector extracted from each sub-window.

The improved algorithm for generating the BioHash code is the following:

(1) The biometric vectors $\mathbf{x}$ is normalized by its module, in this way the scalar product is within the range $[-1, 1]$ (Normalization).

(2) Given the Hash key $\mathbf{K}$ repeat for k times (Space Augmentation) the following generation steps:
  (2.1) Generate a set of linearly independent pseudo random vectors $\mathbf{r}_i \in \Re^n$, $i = 1, \ldots, m$.
  (2.2) Orthonormalize the basis $\mathbf{r}_i$ by Gram–Schmidt, obtaining an orthonormal set of vectors $\mathbf{or}_i$, $i = 1, \ldots, m$.
  (2.3) Compute the inner products between the biometric feature vector $\mathbf{x}$ and $\mathbf{or}_i$ ($\langle \mathbf{x} | \mathbf{or}_i \rangle$), $i = 1, \ldots, m$ and compute b_i ($i = 1, \ldots, m$) as $b_i = \begin{cases} 0 & \text{if } \langle \mathbf{x} | \mathbf{or}_i \rangle \leqslant \tau \\ 1 & \text{if } \langle \mathbf{x} | \mathbf{or}_i \rangle > \tau \end{cases}$, where τ is a threshold varying τ between $\tau_{\max}$ and $\tau_{\min}$, with p steps of $\tau_{\text{step}} = (\tau_{\max} - \tau_{\min})/p$ (τ Variation).

(3) The results of the procedure is a set of $k \times p$ BioHash codes $\mathbf{b}_j$ which are concatenated and compared by the Hamming distance.

4. Experiments and discussion

Experiments have been conducted on the four fingerprint databases from FVC2002 [21], each containing 800 images from 100 individuals, according to the FVC2002 testing protocol, which consists in the following matching attempts:

- *genuine recognition attempts*: the template of each impression is matched against the remaining impressions of the same individual, but avoiding symmetric matches;
- *impostor recognition attempts*: the template of the first impression is matched against the first impression of the remaining individuals, but avoiding symmetric matches.

The performance has been measured by means of the equal error rate (EER) [21] and the area under the receiver operating characteristic curve (AUC) [22]. EER is the error rate when the frequency of fraudulent accesses (false acceptance rate) and the frequency of rejections of people who should be correctly verified (false rejection rate) assume the same value. The receiver operating characteristic (ROC) is a two-dimensional measure of classification performance that plots the probability of classifying correctly the genuine examples against the rate of incorrectly classifying impostors examples. The AUC is a scalar performance indicator which can be interpreted as the probability that the system will assign a higher score to a randomly picked genuine example than to a randomly picked impostor sample.

For the minutiae based alignment and to implement the minutiae based approach proposed by Tico and Kuosmanen [2], the minutiae were extracted from the fingerprint according to the approach proposed in the Matlab CUBS fingerprint toolbox[2] (for the data sets

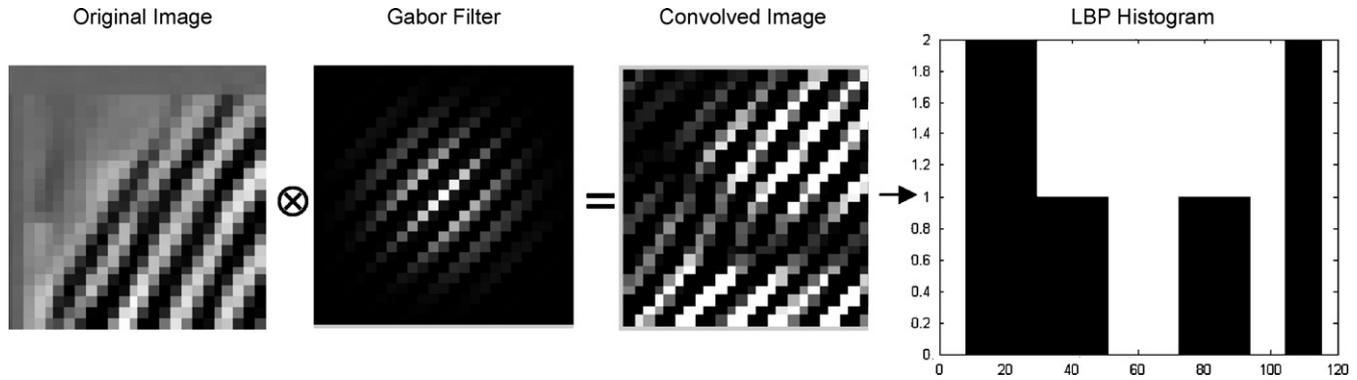---

[2] http://www.cubs.buffalo.edu.

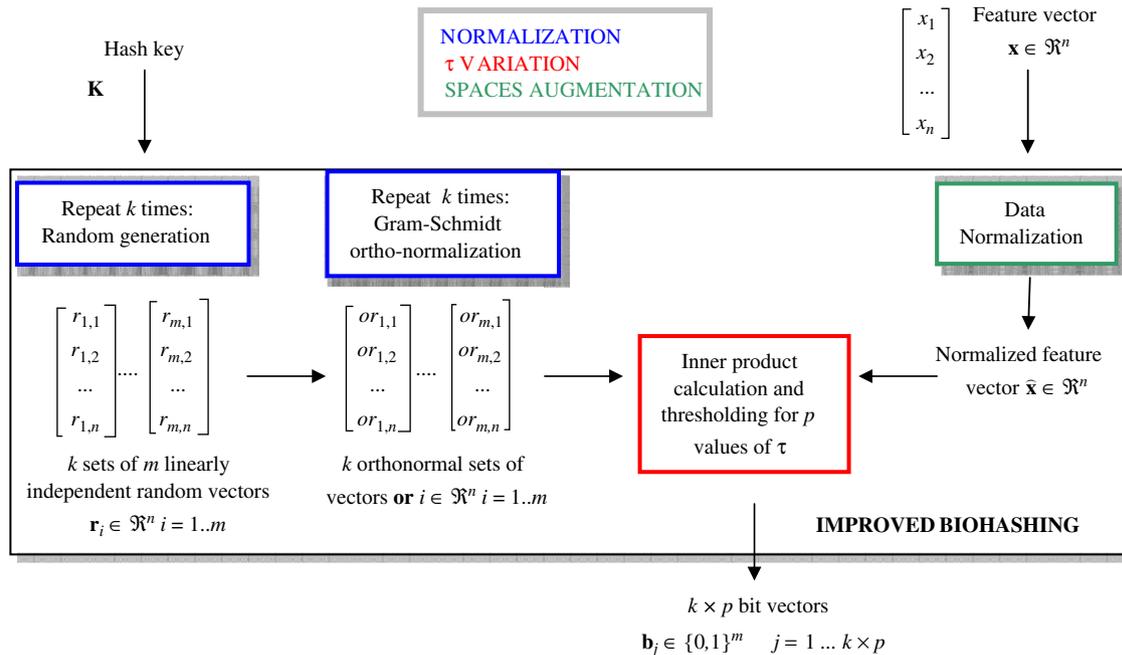Fig. 4. Feature extraction by Gabor + LBP (histogram of $n = 10$ bins).

Fig. 5. The improved BioHashing method (from Ref. [15]).

DB1, DB3 and DB4); while for DB2 we used a more accurate commercial method.[3]

The first group of experiments, whose results are reported in Tables 1 and 2, are aimed at parameter estimation. Several values for the sub-windows dimension d are tested with and without overlap (in this case two consecutive sub-windows overlap for the 50% of their area). Moreover, different values of the number n of bins in the LBP histogram and different banks of Gabor filters are tested: two scales and two angles ($0°$ and $90°$), four scales and four angles ($0°$, $45°$, $90°$ and $135°$), six scales and six angles ($0°$, $30°$, $60°$, $90°$, $120°$ and $150°$).

From these tests it is clear that the best tested configuration of parameters is $d = 50$, $g = 16$ and $n = 10$ with overlap. The choice of small sub-windows with a certain amount of overlap among them allows to extract information from the local structure of the fingerprint patterns, and thus makes the approach more robust to local variations (e.g. due to skin distortions). As the Gabor filters are concerned our results confirms that the bank composed by four scales

Table 1
EER obtained by GLBP as a function of the parameters d, g and n

Window size (overlap)	# Gabor filters	LBP bins	DB1	DB2	DB3	DB4
30 (N)	4×4	10	4.0	3.5	9.8	**4.4**
30 (Y)	4×4	10	4.0	3.3	9.0	4.5
50 (N)	4×4	10	3.8	3.1	9.9	6.7
50 (Y)	4×4	10	**3.7**	**2.4**	**6.9**	**4.4**
70 (N)	4×4	10	**3.7**	4.1	9.7	9.9
70 (Y)	4×4	10	4.0	**2.4**	7.8	6.1
50 (Y)	2×2	10	4.0	3.9	7.1	4.9
50 (Y)	4×4	10	**3.7**	**2.4**	**6.9**	**4.4**
50 (Y)	6×6	10	4.1	2.8	7.5	**4.4**
50 (Y)	4×4	10	**3.7**	**2.4**	6.9	**4.4**
50 (Y)	4×4	18	**3.7**	3.0	7.3	6.7
50 (Y)	4×4	26	4.0	3.2	**6.6**	7.0

and four angles, which is the most used in the literature, is the best for this problem.

The second group of experiments are aimed at validating our feature extraction approach and at comparing the new hybrid matcher with a minutiae based matcher. To this aim, in Tables 3 and 4 the

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[3] http://www.biometrika.it. It processes only images acquired from a property scanner.

Table 2
AUC obtained by GLBP as a function of the parameters *d*, *g* and *n*

Window size (overlap)	# Gabor filters	LBP bins	DB1	DB2	DB3	DB4
30 (N)	4 × 4	10	1.00	0.75	3.30	1.10
30 (Y)	4 × 4	10	1.00	0.76	3.60	0.97
50 (N)	4 × 4	10	1.20	0.49	3.60	1.80
50 (Y)	4 × 4	10	**0.80**	**0.37**	**2.40**	**0.96**
70 (N)	4 × 4	10	2.00	0.66	4.00	4.20
70 (Y)	4 × 4	10	1.60	0.47	2.50	2.05
50 (Y)	2 × 2	10	0.85	0.80	**2.40**	1.20
50 (Y)	4 × 4	10	**0.80**	**0.37**	**2.40**	**0.96**
50 (Y)	6 × 6	10	0.85	0.44	**2.40**	1.12
50 (Y)	4 × 4	10	**0.80**	**0.37**	2.40	**0.96**
50 (Y)	4 × 4	18	1.00	0.50	2.40	1.60
50 (Y)	4 × 4	26	1.00	0.55	**2.00**	2.00

Table 3
Comparison among EER obtained by different matchers

EER	DB1	DB2	DB3	DB4
Minu	4.0	1.6	7.1	7.7
GLBP	**3.7**	**2.4**	**6.9**	**4.4**
Gabor	6.0	5.2	7.8	6.3
LBP	7.0	6.2	9.9	7.5

Table 4
Comparison among AUC obtained by different matchers

AUC	DB1	DB2	DB3	DB4
Minu	1.80	0.56	3.03	2.30
GLBP	**0.80**	**0.37**	**2.40**	**0.96**
Gabor	1.50	1.00	3.30	2.00
LBP	2.10	1.70	3.75	2.60

EER and the AUC, respectively, obtained by the following matchers are reported:

- MINU, Tico's minutiae matcher.
- GLBP, our approach with parameters *d* = 50 (Y), *g* = 16 and *n* = 10.
- GABOR, a Gabor-based fingerprint matcher, where the image is divided in sub-windows as described in Section 2 (*d* = 50 (Y)) and the features extracted from each sub-window are the standard deviations of the image convolved with a bank of *g* = 16 Gabor filters (similarly to Ref. [6]). The similarity between two feature vectors is evaluated by their Euclidean distance.
- LBP, a reduced version of GLBP, where the LBP histogram (*n* = 10) for each sub-window (*d* = 50 (Y)) is calculated directly from the grey-level image. The similarity between two feature vectors is evaluated by their Euclidean distance.

The experiments confirm the validity of the idea of combining Gabor filters and LBP histograms for feature extraction in fingerprint and put in evidence that the simple LBP approach also, which is certainly much faster than Gabor, has interesting verification performance. Moreover the most interesting research finding is the superiority of our hybrid approach with respect to a minutiae matcher: this unexpected result is strictly related to the choice of small overlapping sub-windows and to the effectiveness of the extracted features.

Finally the third and last group of experiments is addressed at evaluating BioHashing applied to the feature vector based on LBP histograms. Notice that a BioHashing approach requires a fixed length feature vector, therefore cannot be easily applied to a minutiae-based method. In the experiments in Tables 5 and 6 the performance obtained by the Tico's minutiae matcher (Minu), our BioHashing

Table 5
EER obtained by the Tico's minutiae matcher (Minu), our BioHashing matcher (BH) and their combination using sum rule (FUS)

EER	DB1	DB2	DB3	DB4
Minu	4	1.6	7.1	7.7
BH	3.3	2.5	5.8	4.3
FUS	**2.0**	**1.1**	**4.2**	**3.1**

Table 6
AUC obtained by the Tico's minutiae matcher (Minu), our BioHashing matcher (BH) and their combination using sum rule (FUS)

AUC	DB1	DB2	DB3	DB4
Minu	1.80	0.56	3.03	2.30
BH	0.65	0.43	1.84	1.03
FUS	**0.50**	**0.29**	**1.49**	**0.54**
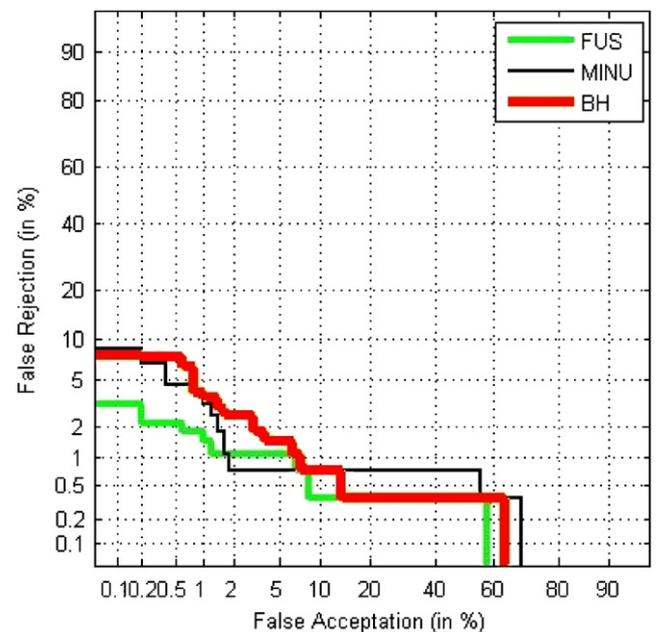
Fig. 6. The DET curve obtained on DB2 by some tested approaches.

matcher (BH) and their combination using sum rule (FUS) are reported, related to the worst test case when always an "impostor" steals the hash key (since an optimal result of 0% EER has always been obtained when the key is not stolen, except for Minu). These experiments confirm what already stated in other works [13,15,20] that the fusion among a BioHashing matcher and a pure biometric approach is extremely useful to improve the performance also in cases when the hash key is stolen.

Finally, in order to confirm the benefits of our method, the DET curve has been considered. The DET curve [23] is a two-dimensional measure of classification performance that plots the percentage of false acceptation against the percentage of false rejection. In Fig. 6 the DET curves obtained in DB2 by MINU, BH and FUS methods, in the worst case of always stealing of the hash key, are plotted. The graph shows the effectiveness of the BioHashing matcher also when the BioHash key is stolen; anyway the method FUS gains the best performance.

5. Conclusions

In this work we present a novel hybrid fingerprint matcher where the feature extraction is based on the local calculation of LBP histograms on the result of Gabor filtering of the image. The resulting feature vectors have very desirable properties: they are quite robust to noise (due to both Gabor and LBP), to small skin distortion distortions (mainly because they are extracted from local windows) and they are suitable for BioHashing (they are fixed-length vectors). Extensive experiments conducted over the four FVC2002 fingerprint databases show that: (i) the proposed feature extraction outperforms the wide-used Gabor filters, (ii) the hybrid matcher gains performance comparable with the well-known Tico's minutiae matcher, (iii) the novel feature vector can be used in a BioHashing approach which outperforms the stand-alone biometric matcher also in the worst test case when always an "impostor" steals the hash key and obtains a 0% EER when the key is not stolen and (iv) a further performance improvement can be obtained by combining the BioHashing matcher with the Tico's minutiae matcher.

Since the proposed approach, as all the image-based methods for fingerprint verification, is quite computationally expensive (few seconds for matching), a possible direction for future research is to perform a sub-window selection (e.g. based on the quality of the pattern) to reduce the number of sub-windows to be processed.

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