Comprehensive Analysis of Spectral Minutiae for Vein Pattern Recognition

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Abstract

Similar to biometric fingerprint recognition, characteristic minutiae points – here end- and branch points – can be extracted from skeletonized veins to distinguish individuals. An approach to extract those vein minutiae and to transform them into a fixed-length, translation and scale invariant representation where rotations can be easily compensated is presented in this paper. The proposed solution based on spectral minutiae is evaluated against other comparison strategies on three different datasets of wrist and palm vein samples. Our analysis shows a competitive biometric performance while producing features that are compatible with state-of-the-art template protection systems. In addition a modified and more distinctive, but not transform or rotation invariant, representation is proposed and evaluated.

1 Introduction

Intended to be a robust approach for liveness detection in fingerprint and hand geometry systems, vein recognition evolved to an independent biometric modality over the last decade [2]. Classically the capturing process can be categorized as a near or a far infrared approach. Vein recognition systems based on the near infrared approach are exploiting differences in the light absorption properties of the de-oxygenated blood flowing in subcutaneous blood vessels and the surrounding tissue. Veins become visible as dark tubular structures. They absorb higher quantities of the near infrared light, that is commonly emitted by LEDs of the sensor, than the tissue. Alternatively in the far infrared approach the heat radiation of the body can be measured[25]: the temperature gradient between the blood vessels carrying the warm blood and the tissue can be measured in this spectrum.

Vein patterns evolve during the embryonic vasculogenesis. Their final structure is mostly influenced by random factors [8]. Scientific research about the uniqueness of vein patterns is sparse and many sources state that vein patterns are unique among individuals. It is also expected that the position of veins is constant over a whole
lifetime [6]. Because vein scanners work contact-less, they are considered to be more hygienic than systems requiring direct physical contact. This makes vein recognition particularly suited for applications in public environments.

Due to the fact that the mesh of blood vessels forming the vein patterns are located underneath the skin, a person’s individual vein patterns is hard to forge; no latent prints are left unintentionally. Offering the same user convenience as fingerprints while being highly secure against forging, vein recognition has been applied in various fields of access control during the last years. Besides this privacy protecting property, there are also privacy concerns reported in vein recognition systems since disease patterns can be read from the biometrics reference images [10]. There are some attempts to prevent the proliferation of sensitive data from biometric references. Firstly to overcome the linkability between different databases and secondly to enable revocation capacities, so that multiple identifiers can be constructed from the same biometric trait. It is not sufficient to simply encrypt biometric templates with classic cryptographic functions since they cannot be compared in the encrypted domain. The goal is to introduce pseudonymous identifiers that cannot be tracked back to the data subject. At the same time profiling should be denied, multiple pseudonymous identifiers of the same data subject should be unlinkable.

An overview of existing biometric template protection systems is given in [3]. The proposed harmonized reference architecture is integrated in the international standard ISO/IEC 24745 Biometric Information Protection and its nomenclature is used throughout this paper. [12] gives a comprehensive introduction to the topic of biometric template security with a focus on template database security. The authors propose a categorization of template protection schemes and discuss pros and cons. One interesting category covers key-binding biometric cryptosystems, they enable the integration of biometric systems into cryptographic protocols. As one advantage the authors mention the tolerance towards intra-user variability and the adaptability through error correction. However, the major drawback described in the paper is that sophisticated comparators cannot be utilized due to requirements on the structure of the feature vectors.

The Fuzzy Commitment Scheme [13] is one of the systems for template protec-
tion falling in this category. It introduced error-correcting codes and cryptographic functions to secure biometric data. The Helper Data Scheme (HDS) \[23, 22\] uses the principle of fuzzy commitments to protect the privacy of biometric features and to satisfy the above-mentioned requirements. It is an extension of classic biometric systems where the extracted feature vectors are further processed. In the scheme the before mentioned restriction applies: no specifically-designed comparator can be used, the feature vectors must be of fixed-length and structure, so that components can be analyzed for reliability and can consistently be reconstructed from biometric data.

Current work in vein recognition is not focused on solving this issue. However in \[14\] a hand vein based authentication system using Delaunay triangulation of minutiae was presented. The approach is based on the extraction of minutiae groups to form triplets as well as a triplet type, determined from the composition of endpoints and bifurcations. The resulting rotation and translation invariant feature vector is variable in length as determined by the number of identified triplets. Other approaches focus on the extraction of local binary patterns or derived versions \[15, 16\], which are dependent on alignment based on minutiae points or a region of interest selection. The feature vectors are of fixed length, but they are not invariant against translation, scaling or rotation.

The goal of this paper is to investigate an algorithm that transforms feature vectors from vein patterns into a fixed-length and structure representation compatible with the Helper Data Scheme without loosing performance compared to the original representation \[11\]. The proposed feature extraction method for vein patterns is based on minutiae points, known from fingerprint recognition, where the position of end- and branch points from the skeletal representation of vein patterns are being used. Due to noise from various sources like the sensor, the biometric trait, or the pre-processing these feature points cannot be reconstructed perfectly; their amount and their position will vary. To overcome these issues an approach called spectral minutiae is applied to the original vein minutiae. This approach was applied very successfully to fingerprint minutiae \[28\].

In this work we further analyse the spectral minutiae for vein recognition: we propose a fast orientation estimator of the minutiae, which are used to encode the com-
plex spectral minutiae (SMC). Further we propose a second normalization method for
the spectra which increases recognition performance at the cost of invariance to affine
transformation of the input data. In addition a mutual information-based compara-
tor is included and investigated. The experimental section covers an extensive set of
investigations: performance for the different types of minutiae is analyzed, statistics
about the computational requirements are provided and score-level fusion techniques
are applied to further increase the biometric performance. The pipeline of the proposed
pre-processing and the feature extraction algorithm is sketched in figure 1, the compar-
ison strategies are shown in figure 2. In bold letters the newly introduced parts are
highlighted, the corresponding sections are given in curly brackets.

The structure of the paper is as follows: beginning with the introduction of the vein
pattern pre-processing and feature extraction system in section 2, the approach of map-
ing those features into a fixed-length, translation and scale invariant representation is
given in section 3. The following section 4 is showing the feasibility of the approach
using simulations over several databases. Details about the databases and the perfor-
ance evaluation are described there as well. In the last section conclusions and future
works are given.

2 Proposed Biometric Vascular Pattern Recognition Sys-
tem

The biometric system based on vein data is introduced in this section. One challenge in
vein recognition systems is to cope with noise and low contrast in the captured images.
Vein image quality is subject to several factors like ambient light, air temperature,
skin color and varying thicknesses of the skin layers and the limbs. As a result of
all these factors sensors usually deliver images suffering from an unfavorable signal
to noise ratio, low contrast and non-uniform brightness. The vein recognition system
has to cope with global and local contrast changes in the image, while suppressing
noise. Therefore, sophisticated image processing is indispensable in order to improve
the images.

Unlike in fingerprint, it is not possible to extract or estimate an orientation field
based on the veins. The veins are sparse compared to the fingerprint ridges and their orientations do not seem to be as strongly correlated. The orientational field in fingerprints can be estimated from gray-scale images and can be used to extract minutiae locations and orientations. In vein recognition the enhanced images must be segmented before an image skeleton representing the topological structure of the data subject’s veins can be extracted. Minutiae feature points are extracted based on this skeleton and will form the input to the spectral minutiae post processing which is introduced in section 3.

2.1 Vein Pattern Pre-Processing

The proposed solution is not performing a region of interest (ROI) selection to be as generic as possible. Therefore, the first step in the pre-processing pipeline is the contrast enhancement.

2.1.1 Contrast enhancement

For the proposed system the images are first enhanced by using adaptive non-local means which was successfully applied to face recognition in [20], followed by the noise suppressing and edge enhancing nonlinear diffusion algorithm [1]. At this point the image is inverted such that veins now appear as high intensity pixels, while tissue between the veins appear as low intensity. The results of the algorithm applied to raw wrist and dorsal hand vein images can be seen in figures 3(b), 4(b) and 5(b).

2.1.2 Segmentation

The multi-scale filter method by Frangi et. al. [9], designed for simultaneous noise and background suppression in medical imaging of vessels, is used as a segmentation method on the vein images. The method searches for tubular structures in the image by analyzing the second order information (Hessian). The second order derivative of a Gaussian kernel generates a probe kernel that can measure contrast inside a defined range in the direction of the derivative. An eigenvalue analysis of the Hessian gives the direction of smallest curvature and thus the direction of the vessel, the eigenvalues can
be used to classify pixels as vessel or background. Figures 3(c), 4(c) and 5(c) show the effect of the method applied to the contrast enhanced images.

2.1.3 Skeletonization

Skeletons are extracted by the fast marching skeletonization algorithm [21]. One advantage of this method is the built-in pruning method, which allows cutting off certain branches from the image skeleton. In fast marching skeletonization, incremental indices are assigned to each pixel on the edge of the figure. Then they are collapsed until only the center line remains. From the difference between two neighboring indices, it can be concluded, how close a skeleton branch is to the center of the figure. The difference between indices at fine-grained branches at the edge of the image skeleton is small, whereas it is large in the center part. These fine-grained branches are most likely artifacts, which were introduced by segmentation errors or noise and can be removed by applying a threshold. The skeleton points where the difference between their indices falls below the threshold are deleted. All other points are kept. Hence, depending on the threshold, more or less of these remote branches are cut off. Examples are shown in figures 3(d), 4(d) and 5(d).

2.2 Feature Point Detection

After extracting the skeletal representation from a vein image, the specific feature points have to be extracted. An efficient and reliable method is proposed in [17]. It is based on convoluting the binary image with a filter consisting of unique power of two values to get unique filter responses for every pattern in the mask size. The end- as well as the branch points of the vascular skeleton can be found by searching for their pre-computed filter response values in the filter response of the image. The extracted minutiae points are overlayed with the corresponding skeletons in figures 3(e), 4(e) and 5(e).

2.3 Orientation Detection

The same approach for extraction the minutiae location can also used to extract the orientations. We propose a fast and reliable method to detect the orientation of minutiae
points in an 8-connected binary image within a 3x3 pixel window size based on [17]. Therefore the mask of the convolution approach has to be adapted as shown in figure 6.

The geometrical interpretation of the approach is straightforward for the endpoints: the orientation is defined as the absolute angle (towards an upwards defined zero angle) facing the direction of the skeletonized vein (Fig. 7). In case of bifurcation or trifurcation points the orientation is defined as the sum of all absolute angles facing the existing veins within modulo 360. It should be noted that neighboring bifurcation patterns (as seen in figure 8), are assigned the maximum distance of 180, which is reasonable since the pairs are geometrically inverse, mirrored on one axis through the center of the mask. The two cases of trifurcation points (the last two patterns) are also distinguished using the mask from figure 6.

After applying the mask to the binarized image, the orientations can be extracted at the positions identified with the algorithm described in section 2.2.

3 Spectral Minutiae

The spectral minutiae representation is a method to represent a fingerprint minutiae set as a fixed-length feature vector, which is invariant to translation, rotation and scaling. This approach enables the combination of minutiae based recognition systems with template protection schemes based on the Helper Data Scheme (HDS) and allow for fast minutiae-based comparison as well. Considering the similar characteristics of vein and fingerprint minutiae patterns, we applied this method to the extracted vein minutiae.

In the following sections, we introduce two spectral minutiae representations to encode the vein minutiae, the first one is solely based on the location of the points and the second one incorporates in addition their orientation. The location-based spectral minutiae representation (SML) approach was presented in [26, 28], the complex spectral minutiae representation (SMC) in [27].
3.1 SML Approach

Assume we have a fingerprint or vein pattern with \( Z \) minutiae. In SML, we code the minutiae locations by indicator functions,

\[
m(x, y; \sigma^2_L) = \sum_{i=1}^{Z} \frac{1}{2\pi \sigma^2_L} \exp\left(-\frac{(x-x_i)^2 + (y-y_i)^2}{2\sigma^2_L}\right),
\]

(1)

with \((x_i, y_i)\) the location of the \( i \)-th minutiae in the image. Thus, in the spatial domain, each minutiae is represented by an isotropic two-dimensional Gaussian function with variance \( \sigma^2 \), illustrated in figure 9(b). In this way the signal is more robust to small variations of the minutiae locations.

Taking the Fourier transform of \( m(x, y; \sigma^2_L) \) and keeping only the magnitude of the Fourier spectrum (in order to make the spectrum invariant to translation of the input), we obtain the location-based spectral minutiae representation

\[
\mathcal{M}_L(\omega_x, \omega_y; \sigma^2_L) = \left| \exp\left(-\frac{\omega_x^2 + \omega_y^2}{2\sigma^2_L}\right) \sum_{i=1}^{Z} \exp(-j(\omega_x x_i + \omega_y y_i)) \right|.
\]

(2)

In order to obtain the final spectral representations, the continuous spectra SML (2) need to be sampled on a polar-logarithmic grid. A polar mapping transforms rotation to translation in the horizontal direction, while a logarithmic mapping transforms scaling to translation in the vertical direction. In the radial direction \( \lambda \), we use \( M = 128 \) samples between \( \lambda_1 \) and \( \lambda_n \). In the angular direction \( \beta \), we use \( N = 256 \) samples uniformly distributed between \( \beta = 0 \) and \( \beta = \pi \). A polar-logarithmic sampling process is illustrated in figures reffig:IJCB11fouriermagnitude and 9(d).

3.2 SMC Approach

As an additional feature specific to minutiae point besides their location, the orientation of the veins in those points can be measured and used. As shown in [27] there are different ways of incorporating the orientation \( \theta \) into the spectral minutiae. We will focus on the SMC approach which yielded better performance on fingerprint data compared
other approaches.

In SMC the minutiae information is encoded as a two-dimensional Gaussian in
the spatial domain as in the SML approach. Additionally each Gaussian is assigned a
complex amplitude based on the orientation of the original minutiae shifting the phase
in the frequency domain. The complex spectral minutiae representation is defined as
the magnitude of the Fourier spectrum:

\[
M_C(\omega_x, \omega_y; \sigma_C^2) = \left| \exp \left( -\frac{\omega_x^2 + \omega_y^2}{2\sigma_C^2} \right) \sum_{i=1}^{\mathcal{Z}} \exp(-j(\omega_x x_i + \omega_y y_i) + j\theta_i) \right|.
\] (3)

The mapping into the polar-logarithmic sampling grid is done as in the case of SML,
the difference being that the parameters for the angular direction are chosen between
\( \beta = 0 \) and \( \beta = 2\pi \), since the SMC is not symmetrical.

3.3 Normalization of Spectra

As described in equation 2 and 3, we want to keep the magnitude of the spectrum. We
used two approaches that return for each imaginary element \( z = a + bj \) of the spectrum
a) the complex modulus as \( \sqrt{a^2 + b^2} \) or b) the real-valued part \( a \) of the spectrum.

Two resulting spectra are shown in figure 10 for SML and SMC in figure 11. The
performance evaluation of approach a) is reflected in table 2 and yields higher error
rates compared to approach b), which is then used further on throughout the paper.

It has to be stated though that approach a) results in an translation and rotation invari-
ant representation in contrast to method b). Depending on the dataset and the layout of
the system approach a) could be more appropriate.

3.4 Comparison Subsystem

Different comparison strategies are considered, the direct and the fast rotation shift
search. Both can be utilized with a correlation or mutual information approach. They
are described in this section.
3.4.1 Direct Comparison

Let $R(m, n)$ and $T(m, n)$ be the two sampled minutiae spectra in the polar-logarithmic domain respectively achieved from the reference sample and test sample (probe sample) – originating from a fingerprint or a vein source. Both $R(m, n)$ and $T(m, n)$ are normalized to have zero mean and unit energy and are of fixed length $M \times N$. As a similarity score, the normalized cross-correlation with zero lag of two minutiae spectra was chosen, which is a common similarity measure in image processing. Therefore, the SML correlation (SML-C) respectively SMC correlations (SMC-C) similarity score between $R$ and $T$ is defined as:

$$S_{DC}^{(R, T)} = \frac{1}{MN} \sum_{m=1, n=1}^{M, N} R(m, n)T(m, n).$$  \hspace{1cm} (4)

3.4.2 Mutual Information-based Comparison

The similarity between $R(m, n)$ and $T(m, n)$ can also be measured by mutual information. In contrast with correlation measure that considers linear relationship, the mutual information from information theory [5] is utilized to quantify the non-linear relationship between the two variables. If we consider two sampled spectra $R(m, n)$ and $T(m, n)$ as vectors as follows: $R(m, n) = (r_1, r_2, ..., r_{MN})$, $T(m, n) = (t_1, t_2, ..., t_{MN})$, then the SML/SMC mutual information (SML-MI/SMC-MI) as similarity score between them is given as:

$$S_{MI}^{(R, T)} = \sum_{i=1}^{MN} \sum_{j=1}^{MN} \frac{p(r_i, t_j)}{p(r_i)p(t_j)} \log \left( \frac{p(r_i, t_j)}{p(r_i)p(t_j)} \right),$$  \hspace{1cm} (5)

where $p(r_i, t_j)$ is the joint probability distribution function of $R$ and $T$; and $p_{r_i}$ and $p_{r_i}$ are the marginal probability distribution functions of $R$ and $T$ respectively.

3.4.3 Fast Rotation Shift Searching

Rotations might not only be a problem in fingerprint recognition but as well in vein recognition, depending on the capture device used for the acquisition. The fast rotation shift search algorithm introduced in [26] makes a costly normalization of the minutiae points unnecessary by compensating for rotations by testing several rotated spectra.
Because we applied the polar-logarithmic transform to the Fourier spectra, rotations become circular shifts in the horizontal direction in our minutiae spectra. We chose to test rotations from $-10^\circ$ to $+10^\circ$ as starting points, which corresponds to circular shifts from -15 units to +15 units in the polar-logarithmic domain.

Let $T_k(m,n)$ be defined as $T(m,n)$ with a circular shift $k$ in the horizontal direction. For each shift attempt, a new similarity score $S^{(R,T_k)}$ is calculated using (4). Finally, the highest score is chosen as the similarity score and the corresponding shift $k$ is recorded as the best shift (that is, the best rotation).

We applied a fast search for the best shift. This algorithm consists of the following steps: (1) 5 circular shifts ($k = -12, -6, 0, 6, 12$) are applied to $T(m,n)$ and the similarity scores $S^{(R,T_k)}$ are calculated. The maximum value of $S^{(R,T_k)}$ is denoted as $S_1$ and its corresponding shift $k$ is denoted as $k_1$; (2) 2 circular shifts ($k = k_1 - 2, k_1 + 2$) are applied to $T(m,n)$, and the similarity scores $S^{(R,T_k)}$ are calculated. The maximum value of $S^{(R,T_k)}$ and $S_1$ is denoted as $S_2$, and its corresponding shift $k$ is denoted as $k_2$; (3) 2 circular shifts ($k = k_2 - 1, k_2 + 1$) are applied to $T(m,n)$, and the similarity scores $S^{(R,T_k)}$ are calculated. The maximum value of $S^{(R,T_k)}$ and $S_2$ is denoted as $S_{\text{final}}$.

Using this fast rotation shift search algorithm, only 9 shift trials need to be tested, instead of 31 shift trials for an exhaustive search. After these steps, the value $S_{\text{final}}$ is recorded as the final similarity score between $R$ and $T$.

The scores can be computed for SML as well as for the SMC approaches, when using the correlation or direct comparison approach we referred to it SML-C-FR and SMC-C-FR, for the mutual information measure we use SML-MI-FR and SMC-MI-FR respectively.

### 4 Experiments

The simulations are designed to examine the performance – measured in Equal Error Rates (EER) – of different comparison strategies used in vein recognition. Three datasets, which main properties are described in table 1, will give a broad basis for
conclusions about the proposed approach of using spectral minutiae as features.

4.1 Databases

The SNIR and SFIR databases were gathered in 2006 in Singapore’s Nanyang Technological University and contain a subset of samples that were used in several publications [24, 25]. The two parts contain 732 back hand vein samples in the near infrared and 173 in the far infrared spectrum from 122 respectively 34 data subjects.

During the experiments, ground truth errors in the SFIR database were discovered, the naming of some files were erroneous, thus imposter comparisons were considered as genuine and vice versa. These errors were resulting in a limited performance of about 2.37% equal error rate using the proposed algorithms with normalization method b) (Sec. 3.3) and the SMM algorithm. The naming errors have been corrected and the corrected version is referred to as SFIR-GT. This version also features inverted images to consider the nature of the far-infrared data.

The third database used for the experiment is referred to as UC3M [18]. It was collected in 2010 in the University Carlos III of Madrid. The dataset consists of 348 vein images in the near infrared spectrum from the wrist areas of 29 data subjects. The dataset was taken under different illumination intensities to optimize the capturing device and does not reflect an operational database.

One limitation of the datasets is that they were captured during only one session, which limits the variability in the signals. In addition the sizes of the databases limit the significance of the results.

4.2 Comparison Strategies

Our selection of comparison strategies covers a range of different features types that are used. We distinguish here between minutiae based approaches and geometrical based ones.

Table 3 shows the comparison strategies used in the simulations, from the literature we selected the Hausdorff distance, Modified Hausdorff (MHD) [25, 7], and Similarity-based Mix-matching (SMM)[4].
<table>
<thead>
<tr>
<th>Property</th>
<th>SNIR</th>
<th>SFIR</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Frequency Band</td>
<td>NIR</td>
<td>FIR</td>
<td>NIR</td>
</tr>
<tr>
<td>Modality</td>
<td>Back of Hand (2)</td>
<td>Back of Hand (2)</td>
<td>Wrist (2)</td>
</tr>
<tr>
<td>Data Subjects</td>
<td>122</td>
<td>34</td>
<td>29</td>
</tr>
<tr>
<td>Sessions</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Images per Session</td>
<td>$2 \times 3$</td>
<td>$2 \times \sim 3$</td>
<td>$2 \times 6$</td>
</tr>
<tr>
<td>Images</td>
<td>732</td>
<td>173</td>
<td>348</td>
</tr>
<tr>
<td>Genuine Comparisons</td>
<td>732</td>
<td>170</td>
<td>870</td>
</tr>
<tr>
<td>Imposter Comparisons</td>
<td>266814</td>
<td>14708</td>
<td>59508</td>
</tr>
<tr>
<td>Resolution (px)</td>
<td>$(644 \times 492)^\perp$</td>
<td>$320 \times 240$</td>
<td>$(640 \times 480)^\perp$</td>
</tr>
<tr>
<td>Depth</td>
<td>8 Bit gray-scale</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 1: Properties of the biometric vein datasets used in the experimental section. $\perp$ Image size reduced by 50% in each spatial dimension for experiments.

The first category is represented by the Hausdorff as well as the MHD algorithms that use the location of the minutiae points directly. The SML algorithm is based on the spectral minutiae representation of the minutiae location, the SMC approach in addition on the orientation. Both are introduced in section 3, for their comparison different approaches are introduced in detail in section 3.4. A correlation (-C) or mutual information (-MI) in combination with the fast rotation (-FR) strategy is used.

Formally the Hausdorff distance between two sets of numbers $A = \{a_1, a_2, \ldots, a_n\}$ and $B = \{b_1, b_2, \ldots, b_m\}$ is defined as

$$S_H(A, B) = \max \left\{ \max_{a \in A} \min_{b \in B} ||b - a||, \max_{b \in B} \min_{a \in A} ||a - b|| \right\}$$

(6)

Where $||b - a||$ is the Euclidean distance between the points $a$ and $b$.

The Modified Hausdorff (MHD) is more resilient to outliers and defined as

$$S_{MHD}(A, B) = \frac{1}{|A|} \sum_{a_i \in A} \min_{b_j \in B} ||a_i - b_j||$$

(7)

Were $|A|$ is the number of elements in $A$.

The Similarity-based Mix-matching (SMM) algorithm proposed by Chen et al. [4] uses geometrical properties of image skeletons and segmented images to overcome problems with affine transformations. It compensates small translation and rotation errors by comparing the segmented version of the reference sample with the image.
skeleton of the test sample. The computational effort is higher than the feature point based approaches.

4.3 Performance Evaluation

The evaluation is based on three databases using the Equal Error Rate (EER) as main metric. The proposed system of pre-processing and feature point detection and orientation estimation from section 2 is used. During the skeletonization approach using the fast marching algorithm, images from the UC3M database are pruned using a radial threshold of 15, whereas the threshold is set to 75 for the other datasets based on an empirical evaluation of the skeleton variability. All other parameters are generic across the datasets.

Within the simulations the full amount of genuine and imposter comparisons were taken into account for the EER calculations and plots as indicated in table 1.

The biometric performance results are summarized in table 3 giving the EER as well as the error margin with a confidence interval of 90%. Table 4 shows the evaluation results of the False Recognition Rate (FRR) at a fixed rate of 0.1% False Acceptance Rate (FAR) and the error margin again at a confidence interval of 90%. The Receiver Operation Characteristics (ROC) are plotted in figure 12 using a logarithmic scale on the x-axis to increase details in the interesting low false positive region.

All proposed algorithms and the ones from the literature are (re-)implemented in Matlab.

<table>
<thead>
<tr>
<th>Comparison</th>
<th>SNIR</th>
<th>SFIR</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hausdorff</td>
<td>34.65%</td>
<td>25.84%</td>
<td>42.50%</td>
</tr>
<tr>
<td>MHD†</td>
<td>1.13%</td>
<td>3.88%</td>
<td>10.61%</td>
</tr>
<tr>
<td>SMM‡</td>
<td>0.27%</td>
<td>2.37%</td>
<td>1.26%</td>
</tr>
<tr>
<td>SML-C-a)♦</td>
<td>1.35%</td>
<td>3.60%</td>
<td>6.13%</td>
</tr>
<tr>
<td>SML-C-FR-a)♦</td>
<td>1.62%</td>
<td>4.33%</td>
<td>5.90%</td>
</tr>
</tbody>
</table>

Table 2: Previous results of the evaluation of the proposed SML in comparison to other comparison strategies in Equal Error Rates. †Modified Hausdorff distance as proposed in [25, 7]. ‡Similarity-based Mix-matching [4]. ♦Normalization as described in section 3.3.
<table>
<thead>
<tr>
<th>Comparison</th>
<th>SNIR</th>
<th>SFIR-GT</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Haussdorff</td>
<td>34.64% ± 1.08%</td>
<td>21.43% ± 2.88%</td>
<td>42.5% ± 1.09%</td>
</tr>
<tr>
<td>MHD†</td>
<td>1.23% ± 0.35%</td>
<td>1.69% ± 0.93%</td>
<td>11.96% ± 1.01%</td>
</tr>
<tr>
<td>SMM‡</td>
<td>0.27% ± 0.17%</td>
<td>0.04% ± 0.02%</td>
<td>1.26% ± 0.35%</td>
</tr>
<tr>
<td>SML-C</td>
<td>0.55% ± 0.24%</td>
<td>0.12% ± 0.03%</td>
<td>5.4% ± 0.71%</td>
</tr>
<tr>
<td>SML-C-FR</td>
<td>0.41% ± 0.2%</td>
<td>0.15% ± 0.04%</td>
<td>4.48% ± 0.65%</td>
</tr>
<tr>
<td>SML-MI</td>
<td>0.82% ± 0.29%</td>
<td>0.06% ± 0.02%</td>
<td>7.35% ± 0.82%</td>
</tr>
<tr>
<td>SML-MI-FR</td>
<td>0.55% ± 0.24%</td>
<td>0.09% ± 0.03%</td>
<td>6.45% ± 0.77%</td>
</tr>
<tr>
<td>SMC-C</td>
<td>0.68% ± 0.26%</td>
<td>0.54% ± 0.53%</td>
<td>5.17% ± 0.69%</td>
</tr>
<tr>
<td>SMC-C-FR</td>
<td>0.55% ± 0.24%</td>
<td>0.57% ± 0.53%</td>
<td>4.37% ± 0.64%</td>
</tr>
<tr>
<td>SMC-MI</td>
<td>0.82% ± 0.29%</td>
<td>0.59% ± 0.53%</td>
<td>8.49% ± 0.87%</td>
</tr>
<tr>
<td>SMC-MI-FR</td>
<td>0.55% ± 0.24%</td>
<td>0.57% ± 0.53%</td>
<td>8.19% ± 0.86%</td>
</tr>
</tbody>
</table>

Table 3: Evaluation of the proposed solution in comparison to other comparison strategies in Equal Error Rates (EER) and the error margin around the EER at a confidence interval of 90%. † Modified Hausdorff distance as proposed in [25, 7]. ‡ Similarity-based Mix-matching [4].

4.3.1 Minutiae Statistics

In addition to the performance evaluation, statistical information regarding the number of extracted minutiae, as well as the skeletons are summarized in table 5.

4.3.2 Computation Statistics

Statistics about the execution time necessary to compute the spectral minutiae and to compare them with the different approaches were collected to give an idea about the general execution-time-wise performance. The test system features an Intel Core i7 processor and 6GB of RAM, Windows 7 as well as MATLAB are 64bit versions. The majority of the code is executed within MATLAB, only the MI comparison is based on a C++ implementation from [19], using the MEX system to integrate it into the MATLAB pipeline.

The code is not optimized for fast runtime and despite the programming language, the times for generating a spectral minutiae representation from a skeletonized image can be approximated around 250-630 ms depending on the number of minutiae points. It seems there is a linear relation between the number of minutiae \( Z \) and the time for the compute of the spectra \( T \), which can be approximated by: \( T \approx 225ms + Z \cdot 2.65ms \).
Table 4: Evaluation of the False Recognition Rate (FRR) at a fixed rate of 0.1% False Acceptance Rate (FAR) and the error margin around the FRR at a confidence interval of 90%. † Modified Hausdorff distance as proposed in [25, 7]. ⊢ Similarity-based Mix-matching [4].

<table>
<thead>
<tr>
<th>Comparison</th>
<th>SNIR</th>
<th>SFIR-GT</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hausdorff</td>
<td>95.77% ± 0.87%</td>
<td>93.45% ± 3.14%</td>
<td>93.45% ± 0.98%</td>
</tr>
<tr>
<td>MHD†</td>
<td>3.56% ± 1.13%</td>
<td>7.14% ± 3.27%</td>
<td>23.1% ± 2.35%</td>
</tr>
<tr>
<td>SMM†</td>
<td>0.27% ± 0.32%</td>
<td>0% ± 0%</td>
<td>1.72% ± 0.73%</td>
</tr>
<tr>
<td>SML-C</td>
<td>1.23% ± 0.67%</td>
<td>0.59% ± 0.96%</td>
<td>10.23% ± 1.69%</td>
</tr>
<tr>
<td>SML-C-FR</td>
<td>1.09% ± 0.63%</td>
<td>1.18% ± 1.36%</td>
<td>8.05% ± 1.52%</td>
</tr>
<tr>
<td>SML-MI</td>
<td>1.64% ± 0.77%</td>
<td>0.59% ± 0.96%</td>
<td>14.14% ± 1.94%</td>
</tr>
<tr>
<td>SML-MI-FR</td>
<td>1.37% ± 0.71%</td>
<td>0.59% ± 0.96%</td>
<td>11.95% ± 1.81%</td>
</tr>
<tr>
<td>SMC-C</td>
<td>0.96% ± 0.59%</td>
<td>1.18% ± 1.36%</td>
<td>10.69% ± 1.72%</td>
</tr>
<tr>
<td>SMC-C-FR</td>
<td>0.82% ± 0.55%</td>
<td>1.18% ± 1.36%</td>
<td>9.31% ± 1.62%</td>
</tr>
<tr>
<td>SMC-MI</td>
<td>1.37% ± 0.71%</td>
<td>1.18% ± 1.36%</td>
<td>16.55% ± 2.07%</td>
</tr>
<tr>
<td>SMC-MI-FR</td>
<td>0.96% ± 0.59%</td>
<td>1.18% ± 1.36%</td>
<td>15.63% ± 2.03%</td>
</tr>
</tbody>
</table>

Table 5: Statistics about the average number of end and bifurcation points, as well as the average skeleton length (in pixels) for the different datasets.

<table>
<thead>
<tr>
<th>Property</th>
<th>SNIR</th>
<th>SFIR/SFIR-GT</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bifurcations</td>
<td>56.93</td>
<td>28.82</td>
<td>87.21</td>
</tr>
<tr>
<td>Endpoints</td>
<td>16.42</td>
<td>18.32</td>
<td>62.01</td>
</tr>
<tr>
<td>Skeleton length</td>
<td>3146.23</td>
<td>2157.4</td>
<td>3594.62</td>
</tr>
</tbody>
</table>

The results are summarized in figures 13 and 14.

4.3.3 Minutiae Type Sets

It is interesting to investigate how reliable the different types of minutiae can be extracted from the samples. A direct measurement is only possible with a ground truth set of minutiae that is not available, therefore we investigated the algorithm performance by means of EER’s.

For the simulations we distinguished three sets of minutiae types as input for the spectral transformation: 1.) using all minutiae points as one concatenated feature vector, not distinguishing between end- or branch points, 2.) only endpoints, 3.) only bifurcations.

The results are summarized in tables 6 and 7, also indicating the confidence interval...
of 90%. In general the SML performance seems to peak when all of the minutiae types are considered. Only in case of the SNIR dataset the performance difference is significant though. The latter holds true for the trend that bifurcations perform better than endpoints.

Considering all minutiae types in one concatenated feature vector can be seen as feature level fusion. In the next subsection, we compare the results against a score level fusion approach.

The proposed orientation estimation algorithm seems to produce minutiae orientations of reasonable quality. The difference in biometric performance of the SML approach (considering only the location of the minutiae) and the SMC approach (considering also the orientation) regarding the different minutiae type sets is statistically insignificant.

<table>
<thead>
<tr>
<th>Type</th>
<th>SNIR</th>
<th>SFIR-GT</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>All minutiae</td>
<td>0.41% ± 0.2%</td>
<td>0.15% ± 0.04%</td>
<td>4.48% ± 0.65%</td>
</tr>
<tr>
<td>Bifurcation</td>
<td>0.55% ± 0.24%</td>
<td>0.59% ± 0.53%</td>
<td>4.14% ± 0.62%</td>
</tr>
<tr>
<td>Endpoints</td>
<td>1.89% ± 0.44%</td>
<td>0.62% ± 0.54%</td>
<td>4.82% ± 0.67%</td>
</tr>
</tbody>
</table>

Table 6: Evaluation of the SML-C-FR method for the different minutiae types (in EER ± 90% confidence interval).

<table>
<thead>
<tr>
<th>Type</th>
<th>SNIR</th>
<th>SFIR-GT</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>All minutiae</td>
<td>0.55% ± 0.24%</td>
<td>0.57% ± 0.53%</td>
<td>4.37% ± 0.64%</td>
</tr>
<tr>
<td>Bifurcation</td>
<td>0.68% ± 0.26%</td>
<td>0.62% ± 0.54%</td>
<td>4.83% ± 0.67%</td>
</tr>
<tr>
<td>Endpoints</td>
<td>2.73% ± 0.52%</td>
<td>0.59% ± 0.53%</td>
<td>4.95% ± 0.68%</td>
</tr>
</tbody>
</table>

Table 7: Evaluation of the SMC-C-FR method for the different minutiae types (in EER ± 90% confidence interval).

### 4.3.4 Score Level Fusion

Different experiments were designed to investigate the potential performance increase that can be achieved using a normalized score fusion approach with equal weighting. The first two experiments are focused on the combination of comparison scores generated using separate spectral minutiae for the different minutiae type sets. The fol-
following three simulations focus on combining the two best performing approaches for each dataset. Experiment 6 fuses the location and complex spectral minutiae scores. In more detail:

- Exp1: Bifurcation + Endpoints using SML-C-FR;
- Exp2: All minutiae + Bifurcation + Endpoints using SML-C-FR;
- Exp3: SNIR – All minutiae SML-C-FR + All minutiae SMM;
- Exp4: SFIR-GT – All minutiae SML-MI + All minutiae SMM;
- Exp5: UC3M – Exp1 + All minutiae SMM;
- Exp6: All minutiae SML-C + All minutiae SMC-C.

Experiment 1 shows that the different datasets are behaving in completely different ways when comparing the feature fusion level with the score fusion approach: The performance of the SNIR database stays constant, in SFIR-GT the performance of score fusion lowers the EER, whereas the performance of the UC3M dataset strongly improves. In experiment 2, the redundancy of a feature level fused score plus scores of the separate features increases the biometric performance for all datasets. Experiments 3-5 show that the classification performance of the most reliable method, the SMM method, can only slightly be improved in case of the SFIR-GT and the UC3M databases. In experiment 6 a slight performance increase compared to the separate evaluations can be noticed using scores from both the SML and SMC approach with

<table>
<thead>
<tr>
<th>Experiment</th>
<th>SNIR</th>
<th>SFIR-GT</th>
<th>UC3M</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exp1</td>
<td>0.55% ± 0.24%</td>
<td>0.45% ± 0.52%</td>
<td>3.11% ± 0.54%</td>
</tr>
<tr>
<td>Exp2</td>
<td>0.41% ± 0.2%</td>
<td>0.07% ± 0.03%</td>
<td>3.33% ± 0.56%</td>
</tr>
<tr>
<td>Exp3</td>
<td>0.27% ± 0.17%</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Exp4</td>
<td>-</td>
<td>0.03% ± 0.02%</td>
<td>-</td>
</tr>
<tr>
<td>Exp5</td>
<td>-</td>
<td>-</td>
<td>1.15% ± 0.33%</td>
</tr>
<tr>
<td>Exp6</td>
<td>0.41% ± 0.2%</td>
<td>0.08% ± 0.03%</td>
<td>4.48% ± 0.65%</td>
</tr>
</tbody>
</table>

Table 8: Evaluation of score level fusion approaches using different minutiae types and comparison strategies (in EER ± 90% confidence interval). Experiment description in Sec. 4.3.4.
the simple direct correlation comparison. Since no dedicated comparison strategies can be used in case of a helper data based template protection system, this results is valuable for the selection of features.

5 Conclusions

The paper has extended the work on spectral minutiae representations for vein [11]. The complex spectral minutiae are introduced which utilize the orientation in addition to the minutiae location, therefore a minutiae orientation extraction algorithm based on a fast convolution approach is proposed. Furthermore, the mutual information as a comparison method is investigated regarding the biometric performance in case of the SFIR-GT database using the location based spectral minutiae.

Two different approaches for the normalization of the spectra are investigated: the complex magnitude approach and the proposed real-valued method. An evaluation revealed: the latter method performs better in terms of equal error rates for the selected databases. Since this representation is not translation and rotation invariant the following assumptions can be made: 1) the samples of the datasets are only slightly translated and rotated, and 2) the real-valued part of the spectra has higher capabilities for classification.

The fast rotation comparison improves the performance compared to the direct correlation measure utilizing the SNIR and the UC3M datasets, though not statistically significant. In SFIR-GT the direct comparison yields in a superior performance, thus it can be assumed that the samples are less rotated.

Statistics about the computation time for the spectra generation and the comparisons are provided, proving its applicability.

The reliability is further increased using algorithm fusion. Analyzing the performance of different vein minutiae type sets (bifurcation and endpoints) show diverse results, bifurcations seem to be more stable than endpoints. Fusion at feature level of the two type sets leads to significantly better performance results for the SNIR dataset.

Score level fusion between location and complex spectral minutiae seems to increase recognition performance slightly. Fusing scores from the two best performing
algorithms is not improving accuracy significantly.

Summarizing it can be stated, that the proposed solution yields in most cases a significantly improved performance in comparison with other point-to-point based approaches. In addition it produces fixed-length and structure feature vectors, that are compatible with state-of-the-art template protection systems. Depending on the normalization of the spectra, a trade-off between an improved biometric performance (outperforming all other presented point-to-point based approaches) and the property of translation invariance can be made.

Future work focuses on combining the advantages of the normalization approaches – high classification performance and translation invariant representation – into a single one.

The next step is to combine the proposed approach for vein recognition, where the sensitive information is hidden inside the body, with the Helper Data Scheme – as a privacy enhancing technology – resulting in a secure system fulfilling strict legislative requirements and user expectations regarding privacy.

6 Acknowledgments

The authors would like to thank the Nanyang Technological University and University Carlos III of Madrid for making their vein pattern data sets available to the research community.

References


Figure 1: Overview biometric pipeline. Bold: newly proposed algorithms with regard to [11]. Corresponding sections given in curly brackets.
Figure 2: Overview spectral comparison strategies. Bold: newly proposed algorithms with regard to [11]. Corresponding sections given in curly brackets.

Figure 3: Sample dorsal hand vein (SNIR) after different stages of the pre-processing pipeline of the proposed system: (a) raw, cropped vein image; (b) contrast enhanced image; (c) segmentation of an optimized vein pattern image; (d) skeletonization of segmented image; (e) overlay of extracted minutiae points and skeleton. Red circles: endpoints, blue stars: branch points.
Figure 4: Sample far-infrared dorsal hand vein image (SFIR-GT)[18], description as in figure 3.

Figure 5: Sample wrist vein image (UC3M)[18], description as in figure 3.

Figure 6: Filter mask used for orientation detection. Left side: kernel, right side: as applied on binary image.
Figure 7: Endpoint patterns and their corresponding filter response.

Figure 8: Bifurcation patterns and their corresponding filter response.
Figure 9: Illustration of the SML representation procedure. (a) vein pattern and its minutiae points; (b) representing minutiae points as isotropic two-dimensional Gaussian functions. (c) the Fourier spectrum in a Cartesian coordinate and a polar-logarithmic sampling grid. (d) the Fourier spectrum sampled on a polar-logarithmic grid.

Figure 10: Sample SML spectra as described in 3.3. (a) complex modulus; (b) real-valued spectrum.
Figure 11: Sample SMC spectra as described in 3.3. (a) complex modulus; (b) real-valued spectrum.

Figure 12: Receiver Operation Characteristics from the databases: (a) SNIR, (b) SFIR, (c) SFIR-GT, (d) UC3M.
Figure 13: Statistics on the average time (in milliseconds) for computing one spectral minutiae representations for the different datasets.

Figure 14: Statistics on the average comparison time (in milliseconds) for the location and complex minutiae (SML/SMC) using comparison based on correlation (C), correlation fast rotation (C-FR), the mutual information (MI) as well as MI in combination with the fast rotation (MI-FR) for the different datasets. Details in Sec. 4.3.2.