Consensus fingerprint matching with genetically optimised approach

W. Sheng[a,*], G. Howells[b], M.C. Fairhurst[b], F. Deravi[b], K. Harmer[b]

[a]School of Engineering and Design, Brunel University, Uxbridge, London UB8 3PH, UK
[b]Department of Electronics, University of Kent, Canterbury, Kent CT2 7NT, UK

ARTICLE INFO

ABSTRACT

Fingerprint matching has been approached using various criteria based on different extracted features. However, robust and accurate fingerprint matching is still a challenging problem. In this paper, we propose an improved integrated method which operates by first suggesting a *consensus matching function*, which combines different matching criteria based on heterogeneous features. We then devise a genetically guided approach to optimise the consensus matching function for simultaneous fingerprint alignment and verification. Since different features usually offer complementary information about the matching task, the consensus function is expected to improve the reliability of fingerprint matching. A related motivation for proposing such a function is to build a robust criterion that can perform well over a variety of different fingerprint matching instances. Additionally, by employing the global search functionality of a genetic algorithm along with a local matching operation for population initialisation, we aim to identify the optimal or near optimal global alignment between two fingerprints. The proposed algorithm is evaluated by means of a series of experiments conducted on public domain collections of fingerprint images and compared with previous work. Experimental results show that the consensus function can lead to a substantial improvement in performance while the local matching operation helps to identify promising initial alignment configurations, thereby speeding up the verification process. The resulting algorithm is more accurate than several other proposed methods which have been implemented for comparison.

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1. Introduction

Fingerprints are the manifestation of graphical ridge and valley patterns on the tips of human fingers. Owing to their uniqueness and permanence, the use of fingerprints is considered to be one of the most effective methods of personal verification, and thus the fingerprint is currently among the most popularly used biometric modality in automatic biometric systems. The continuing needs of law enforcement agencies and opportunities arising for the developers of civilian applications mean that automated fingerprint matching systems are becoming increasingly widespread. Considering the nature of most applications (both civil and criminal), the reliability of fingerprint matching systems is particularity important since the consequences of false matching can often lead to damage while false rejection can be very annoying. However, although significant progress in automating the matching process has been made,

reliable automatic fingerprint verification is still a challenging problem [5].

As is the case with most widely researched pattern recognition problems, there are many different approaches to fingerprint matching. Minutiae-based techniques, which use minutia points such as ridge endings or bifurcations as features for matching, represent the most popular approach [12,13,16,33]. Despite the relative simplicity and efficiency in storage of this approach, however, minutiae-based fingerprint matching has its drawbacks. First, it is not always easy to extract minutia points accurately, especially for poor-quality images. Second, minutiae do not necessarily embody the most significant component of the rich discriminatory information available in the fingerprints. In addition, there are difficulties related to aligning the minutia point patterns from the query and template fingerprints due to the lack of knowledge about the correspondence between two point sets. Generally, finding the best alignment between two minutiae sets is an extremely difficult problem [12].

Recently, there has been some interest in using texture features such as orientation fields [15] and ridge patterns (shape and density) [11,23] for fingerprint matching. In comparison with minutiae, texture features can be more robust with respect to the extraction process and less sensitive to noise contamination. However, these features may not provide very good discrimination

* Corresponding author. Tel.: +44 1227 823701; fax: +44 1227 456084.
E-mail addresses: weiguo.sheng@brunel.ac.uk (W. Sheng),
w.g.j.howells@kent.ac.uk (G. Howells), m.c.fairhurst@kent.ac.uk (M.C. Fairhurst),
f.deravi@kent.ac.uk (F. Deravi), k.harmer@kent.ac.uk (K. Harmer).

information since fingerprints from different fingers may share similar orientation fields and/or ridge patterns. Typically, also, matching two fingerprints using such features requires a proper alignment of the query and template fingerprints. However, as with the case of aligning minutia point patterns, finding the correct alignment between two orientation fields or ridge patterns is not a trivial problem. In [11,23], the ridge patterns are aligned based on a single reference point, and are therefore not robust with respect to errors in the location of the reference point. In [15], orientation fields are aligned by a steepest descent algorithm, which is, however, sensitive to the initial alignment configurations and susceptible to local optima.

There is a growing belief that combining different features available in fingerprint images can improve the performance of fingerprint matching systems. Several combination schemes [8,26,29] have been proposed in the literature, in which features are usually incorporated at the verification stage in the processing chain. The scheme presented in Ross et al. [26], designated a hybrid matcher, combines minutiae with ridge flow information to verify fingerprints. In this matcher, fingerprint images are first aligned based on minutiae information by the elastic string matching technique [12]. The verification is then carried out based on the minutiae set along with ridge feature map matching. Gu et al. [8] and Wan et al. [29] describe similar schemes in which fingerprint images are first aligned based on minutiae points by the generalised Hough transform (GHT) method [25] and then verification is performed by combining minutiae with text feature matching. These schemes are essentially minutiae-based matching and their performance depends heavily on the quality of minutiae information. Mistakes which inevitably occur during the minutiae extraction stage will be propagated to the alignment stage in the algorithms and may cause the final match scores to be meaningless, fundamentally constraining their performance.

In this paper, we propose a new approach based on the general combination technique. We first suggest a function—the *consensus matching function*—which integrates different matching criteria based on heterogeneous features. Then we invoke a genetically guided process which can be used to optimise the consensus matching function for aligning fingerprints while simultaneously implementing the verification task. In contrast to previously adopted combination schemes, for example [8,26,29], in our method different features are implicitly harnessed at the fingerprint alignment stage for fingerprint verification. Hence, the process can be more robust to possible erroneous outcomes of the minutia detection algorithm. Additionally, our proposed method employs the global search functionality of a genetic algorithm (GA) [9] along with a local matching operation for population initialisation in order to identify the optimal or near optimal alignment between two fingerprints. Experimental results show that the use of the proposed consensus matching function in combination with the genetically guided optimisation process can significantly improve the robustness and accuracy of fingerprint verification.

The rest of the paper is organised as follows. In Section 2, we formulate the fingerprint matching problem in detail. In Section 3, we first introduce several matching criteria based on different features and then define the consensus function. Section 4 presents the details of the genetically guided fingerprint matching based on the optimisation of the consensus function. Section 5 describes the data sets used here, and this is followed by an explanation of the parameter settings of the proposed method. Experimental results are reported in Section 6, with a summary and a discussion of future work provided in Section 7.

2. Problem formulation

Fingerprint images or their representations often suffer from translation, rotation, and minor scale variation transformation due to different pressures applied by the finger on the sensor device. Let us denote the transformation parameters as $G(t_x, t_y, \theta, s)$ composed of four individual parameters: t_x, t_y, θ, and s, where t_x and t_y are the translations along the x and y directions, respectively, θ is the rotation angle and s is the scaling factor. The transformation $F(q_i) = (x_i', y_i', \alpha_i')$ of a point $q_i = (x_i, y_i, \alpha_i)$ can be written as follows:

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = s \begin{bmatrix} \cos\theta & -\sin\theta \\ \sin\theta & \cos\theta \end{bmatrix} \begin{bmatrix} x_i \\ y_i \end{bmatrix} + \begin{bmatrix} t_x \\ t_y \end{bmatrix}$$

and

$$\alpha_i' = \alpha_i + \theta,$$

where (x_i, y_i) are the pixel coordinates of the point with respect to the image frame and α_i is the orientation. Fingerprint alignment is thus a process of finding the transformation parameters which can optimise the correlation information between the compared fingerprint representations. After alignment, the verification process is subsequently performed by examining the fingerprints for corresponding features in the aligned representations. Since particular fingerprint features can be used for both alignment and verification, the problems are inter-related and can potentially be solved simultaneously.

3. Consensus matching function

A number of fingerprint representations for fingerprint matching algorithms have been proposed in the literature. Different representations are often related to different features of the fingerprints in determining appropriate matching criteria. In a minutiae-based representation, for example, the number of corresponding minutia pairs is typically used to define the matching criterion. In the orientation field based representation, the matching criteria can be developed by comparing the orientation angles, while in the ridge-based representation, the difference of average distance between ridges in local areas has often been used as the basis for defining a matching condition. Since different fingerprint features usually offer complementary information about the matching task [19], incorporation of various criteria based on different features can offer a viable strategy by means of which the performance of fingerprint matching systems can be improved. In this section, we propose a function for this purpose by integrating several criteria by means of a weighted sum rule for alignment, which can be optimised to solve the corresponding verification problem simultaneously. A related motivation for proposing such a function is to build a robust criterion that can perform well across a range of typically encountered situations in fingerprint matching instances (e.g., matching fingerprints with low-quality images or with small regions of overlap). We designate the proposed function the *consensus matching function*, as it provides a criterion to represent the consensus across criteria based on heterogeneous fingerprint features to determine whether an acceptable match has occurred. Three criteria, namely: a minutiae-based criterion, an orientation field based criterion, and a ridge density map based criterion have been selected to design the consensus matching function. These criteria are based on substantially different features of fingerprints and thus should serve as a sound basis for our purposes. However, the choice of the criteria for the consensus matching function is flexible; by incorporating more criteria based on other features or using other more effective combinations of the matching criteria could result in even better performance. In the following sections, we first introduce the three criteria chosen to design the consensus matching function. This is followed by an explanation of the proposed consensus matching function.

3.1. Minutiae-based criterion

Minutiae are local ridge characteristics that occur at either a ridge bifurcation or a ridge ending. The basic principle underpinning minutiae-based matching is that corresponding minutia pairs of the correctly aligned fingerprints should be close to each other. Therefore, the matching is commonly determined by the ratio of corresponding minutia pairs to the total number of minutiae in the region of overlap. A criterion for the matching operation can be written as

$$S(M_q, M_t) = 2 * n/(q + t),\tag{1}$$

where t and q are the number of minutiae located inside the intersection of the template fingerprint (M_t) and query fingerprint (M_q), respectively. The number of matched pairs, n, is identified using a tolerance zone. Two minutiae correspond if a minutia from the query set is located within a tolerance zone around a minutia from the template set. This criterion produces a value from 0 to 1, the value representing the degree of agreement between the two minutiae sets. The value is expected to be large for correct alignments.

3.2. Orientation field based criterion

The orientation field, which describes the global structure of the fingerprint ridge pattern, is a collection of the directions of ridge flows. As with the minutiae information, orientation fields can be used as a basis for fingerprint matching [8]. The rationale is that, after two orientation fields have been properly aligned, corresponding elements should have roughly the same orientation. Let $O_q(x, y)$ and $O_t(x, y)$ denote two orientation angles at the sample point (x, y) in the query orientation field O_q and template orientation field O_t, respectively. The relative orientation of $O_q(x, y)$ with respect to $O_t(x, y)$, denoted by $\lambda(O_q(x, y), O_t(x, y))$, can be formulated as the minimum angle required to rotate a line of orientation $O_t(x, y)$ in the counter clockwise sense such as to make it parallel with a line of orientation $O_q(x, y)$. To evaluate the difference between two orientation angles, a dissimilarity metric can be written as

$$d(O_q(x, y), O_t(x, y)) = (2/\pi) \min\{\lambda(O_q(x, y), O_t(x, y)), \lambda(O_t(x, y), O_q(x, y))\},$$

which takes values between 0 and 1, representing the two extrema for parallel and orthogonal orientations, respectively. Then, a matching criterion between the orientation fields of O_q and O_t can be defined as

$$S(O_q, O_t) = (1/|\Omega|) \sum_{(x,y) \in \Omega} \exp(-\mu * d(O_q(x, y), O_t(x, y))),\tag{2}$$

where μ is set to be 10, which has been empirically established in [8], and $|\Omega|$ is the region of overlap of the effective areas where the fingerprint ridge pattern is to be found. A large value of $S(O_q, O_t)$ indicates there is a high degree of correspondence between the aligned orientation fields.

3.3. Ridge density map based criterion

The ridge density of a fingerprint is the average distance between ridges in the local area (in the direction perpendicular to the local orientation). Thus, the density map describes the ridges' denseness or sparseness within a given fingerprint. Given two density maps R_q (query) and R_t (template) to be matched, we calculate the dissimilarity score as

$$d(R_q(x, y), R_t(x, y)) = |1/R_q(x, y) - 1/R_t(x, y)|,$$

where $1/R_q(x, y)$ and $1/R_t(x, y)$ measure the ridge frequencies at the sample point (x, y) in the query density map R_q and template density

map R_t, respectively. By normalising the score, a matching criterion can be defined as

$$S(R_q, R_t) = (1/|\Omega|) \sum_{(x,y) \in \Omega} \exp(-(1/2) * d(R_q(x, y), R_t(x, y))).\tag{3}$$

This criterion is expected to give values within the range of 0–1 and maximising $S(R_q, R_t)$ will, therefore, maximise the agreement between the two density maps.

3.4. Consensus matching function

The three matching criteria described above naturally have relative strengths and weakness, and none of them in isolation is likely to provide consistently robust results across all possible fingerprint matching instances. Here, we suggest a consensus matching function derived through a combination process based on a weighted sum rule. More formally, the consensus matching function consists of adding together the above three matching criteria using a weighting coefficient for each. This means that the fingerprint matching operation can be transformed to a combinational optimisation problem of the form

$$\max CMF = \sum_{i=1}^{m} w_i f_i(x),\tag{4}$$

where m is the number of component criteria (specifically, $m = 3$ in the scenario considered here), w_i are the non-negative weighting coefficients representing the relative importance of the criteria such that $\sum_{i=1}^{m} w_i = 1$, and $f_i(x)$ are component criteria corresponding to the $S(M_t, M_q)$, $S(O_q, O_t)$, and $S(R_q, R_t)$, respectively.

4. Genetically guided consensus fingerprint matching

The large number of possible translations, rotations, and scalings means that optimising the consensus matching function for simultaneous fingerprint alignment and verification can be an extremely difficult problem. We propose a genetically guided optimisation algorithm to approach a solution to this problem. The proposed algorithm can be divided into two stages: population initialisation and GA-based evolution. The initialisation stage aims efficiently to produce an initial population of alignment configurations by examining the local features of fingerprints. Using this initial population, GA-based evolution is then launched and tries to identify the optimal or near optimal global alignment by examining the global features of fingerprints while solving the verification simultaneously. The GA-based evolutionary procedure consists of selecting parents for reproduction, performing a modified arithmetic crossover with the parents, applying mutation to the offspring, and carrying out competition replacement. The evolution is terminated when one of the following two stopping criteria is met: (1) the fitness value of the best population individual has not changed for N generations or (2) the fitness value of the best population individual exceeds a certain threshold value, which means the two fingerprints are verified as belonging to the same finger. The output of the algorithm is the best solution encountered during the evolution. The flow of the algorithm is shown in Fig. 1.

In the following sections, we describe in more detail how the solutions are initially created and how they evolve during the optimisation process.

4.1. Local matching for population initialisation

Within the domain of GAs, a population is a collection of solution strings which encode the parameters of the search space. Our representation for each individual solution string $i = (t_{x,i}, t_{y,i}, \theta_i, s_i)$ consists

Step 1. Apply a local matching operation (see Section 4.1) to initialise *P* sets of solution strings, which encode alignment configurations, based on a real-parameter representation.

Step 2. Calculate the fitness value according to equation (4) for each individual solution string in the initial population.

Step 3. Repeat the following sub-steps (a) to (d) until a stopping criterion is met.

    a) Select the pairing individuals based on the *k*-fold tournament selection method [7]. This procedure is repeated until *P*/2 parent pairs are selected.

    b) Generate intermediate offspring by applying a modified arithmetic crossover and then perform Gaussian mutation on the offspring (see Section 4.2).

    c) Calculate the fitness value for each of the offspring according to equation (4).

    d) Create a new generation of size *P* from the individuals of the previous generation and their offspring.

Step 4. Provide the fitness value and alignment configuration of the best individual from the terminal population.

Fig. 1. A genetically guided consensus fingerprint matching.

of a vector of four real numbers, where the first two positions represent translations along the *x* and *y* directions, respectively, the next position represents the rotation angle, and the last position represents the scaling factor. To produce an initial population, here we introduce a local matching operator by examining local features of minutiae. Here the local feature describes the characteristics of the minutia in its neighbourhood. This information can be used to find potential matches in another minutiae set when the local feature is distinctive. The resulting initial population can help to reduce the search space for recovering the optimal or near optimal global alignment.

The minutiae local feature representation proposed by Tico and Kuosmanen [28] has been used for designing the local matching operator. In this representation, each minutia defines a local structure, which is called a *minutia descriptor*, comprising information about the orientation field sampled in a circular pattern in a broad region around the minutia point. The circular pattern consists of *L* concentric circles of radii r_l, $(1 \leqslant l \leqslant L)$, each circle comprising K_l sampling points $p_{k,l}$, $(1 \leqslant k \leqslant K_l)$, equally distributed along its circumference. The minutia descriptor is invariant to rotation and translation [28] and, hence, it can characterise the minutia location with respect to the fingerprint pattern regardless of the position and orientation of the finger on the acquisition sensor. Let $a = \{\alpha_{k,l}\}$ and $b = \{\beta_{k,l}\}$ be two minutia descriptors. The dissimilarity between *a* and *b* can be computed as

$$D(a,b) = (1/K) \sum_{l=1}^{L} \sum_{k=1}^{K_l} d(\alpha_{k,l}, \beta_{k,l}),$$

where $K = \sum_{l=1}^{L} K_l$, $\alpha_{k,l}$ and $\beta_{k,l}$ are two orientation angles estimated at $p_{k,l}$ for descriptors *a* and *b*, respectively, and $d(\alpha_{k,l}, \beta_{k,l})$ is the orientation distance between angles.

Based on the minutia descriptor, we introduce a local matching operator to produce an initial population, as follows. If *Q* and *T* denote the query and template fingerprint to be matched, the operator selects a random minutia descriptor from the fingerprint *Q* and compares it to each minutia descriptor in fingerprint *T*. The magnitude of the dissimilarity measured between the two minutia descriptors serves as the basis for identifying a potential corresponding pair. The minutia pair which generates the smallest dissimilarity value is considered to be *correspondent*. The transformation is calculated by translating and rotating the query fingerprint to align this correspondence and then used to initialise one individual solution within the population. The scaling factor is constructed by random assignment of a real number to the last attribute. The initial value is constrained to be in the predefined range, *δs*, but is otherwise random. Each individual in the population is constructed in this way, but by selecting

a minutia descriptor that has not been considered before. Where the number of minutia descriptors in *Q* is less than the number of individuals within the population to be initialised, translation and rotation parameters of the remaining individuals are constructed within the predefined ranges of δt_x, δt_y, and $\delta\theta$, respectively, in the same way as the scaling factor. All the ranges are determined empirically from the experimental data sets. Their values, however, are not critical for the initialisation since the population is usually dominated by the solutions that are constructed by the local matching operator.

After each individual has been initialised, a population of local alignment parameters is obtained. Note that this population does not contain all correct local transformations. However, even if a population contains many wrong local transformations this is not expected to have a detrimental effect on the proposed evolutionary based algorithm, because the wrong local transformations are unlikely to be selected for reproduction in the next generation. It should also be noted that correct local transformations in the population can only guarantee accurate alignment of regions adjacent to the reference minutia descriptors. However, they may lead to poor alignments in regions distant to the reference minutia descriptors since the local matching phase for initialisation does not consider global feature information. Based on this initial population, a GA-based evolutionary procedure is then launched by further examining the global features.

4.2. GA-based evolution

The evolution process proceeds through a series of evolving generations. During each successive generation, we first select parent pairs from the existing population by means of the *k*-fold tournament selection mechanism [7]. These pairs are then recombined via crossover and mutation operators to generate offspring.

The crossover operator exchanges information between a pair of parents. The arithmetic crossover technique [7] has been used as the reproduction operator. Traditional arithmetic crossover linearly combines two parent solutions producing two new offspring according to the following equations:

Offspring $1 = a * Parent\ 1 + (1 - a) * Parent\ 2,$

Offspring $2 = (1 - a) * Parent\ 1 + a * Parent\ 2,$

where $a \in [0, 1)$ is a random weighting factor. In the context of our experiments, sometimes the traditional arithmetic crossover may result in two similar offspring. Since processing the other similar offspring may give no additional benefit but double the computational time, in our algorithm, we apply either of the above equations randomly to produce only one single offspring, therefore avoiding such a situation. The crossover is performed on each paired parent.

After every crossover, a low probability of Gaussian mutation is applied to the attributes of offspring as follows:

$$a_i^* = a_i + \sigma N(0,1)a_i,$$

where $\boldsymbol{a}_i$ is the attribute value of offspring before the mutation, a_i^* is the attribute value of offspring after the mutation, $\boldsymbol{N}(0,1)$ is a random Gaussian number (mean 0, standard deviation 1), and $\sigma \in [0.1, 0.2]$ is a random mutation step size. The new attribute value is clipped if it falls outside of the lower or upper bounds of that attribute.

Each selected pair sequentially undergoes crossover and mutation to generate its offspring. The population used in the next generation of the evolution is formed by selecting the best individuals in terms of fitness values from the previous population and their offspring. The fitness of each individual solution is calculated by first extracting the transformation encoded within it and then applying the transformation to the minutiae set M_q, orientation field O_q, and ridge density map R_q of the query fingerprint to obtain the M_q', O_q', and R_q' comprising the transformed minutiae set, orientation field, and ridge density map, respectively. Given the M_q', O_q', and R_q' and the corresponding M_t, O_t, and R_t of the template fingerprint, the values of matching criteria (1), (2), and (3) are subsequently calculated. The fitness of the individual is finally computed according to Eq. (4). The evolution ultimately tries to optimise the fitness to identify the optimal or near optimal global alignment between the fingerprints while solving the verification problem simultaneously.

5. Data sets and parameter settings

In this section, we provide a description of the data sets used in our experiments. This is followed by a description of the implementation parameter settings for the proposed algorithm. Four public domain collections of fingerprint images, labelled DB_{1a}, DB_{3a}, DB_{1b}, and DB_{3b} proposed in [18] as part of the Fingerprint Verification Competition (FVC2002) have been used in the experiments. These fingerprint images were collected using different scanners with a resolution of 500 dpi and contain a wide variety of image qualities. DB_{1a} and DB_{3a} each comprise 8×100 fingerprints while DB_{1b} and DB_{3b} each contain 8×10 fingerprints (eight impressions per finger). The details of the fingerprint image data collection process can be found in [18].

The minutiae information for the images in the data sets is derived using the method described in [6]. Fig. 2 lists the functional steps of this method. After performing image enhancement to improve the

contrast of ridges against valleys, it first generates the quality maps by detecting regions of low contrast, low ridge flow, and high curvature in the image. Then, a binary representation of the fingerprint is constructed by applying a rotated grid on the ridge flows of the fingerprint. Next, minutiae are generated by comparing each pixel neighbourhood with a family of minutia templates. Finally, a series of heuristic rules are used to merge and filter out the spurious minutiae. The orientation field is extracted using the technique outlined by Ratha et al. [24] and smoothed by applying the approach presented in Wang et al. [30]. Based on the resultant orientation field, the ridge density map is estimated using the x-signature algorithm proposed by Hong et al. [10].

The proposed algorithm requires a number of parameters to be set. These include the GA parameters, the weighting coefficients for the consensus matching function, the sampling point selection for calculating the orientation field and ridge density map based matching, the ranges for population initialisation, and the geometric constraints for minutiae matching. The values of GA parameters, weighting coefficients and sampling point selection are determined experimentally using the union of data sets DB_{1b} and DB_{3b}. To establish these values, firstly, all other variables are held constant with only the one to be established changing, and three runs are completed for a wide range of values in each case. The results from each of the three runs are averaged and the best average is selected. Both the matching accuracy and efficiency are used in determining the values of parameters. This process is expected to produce a set of appropriate initial values of the variables. To make sure that these values are properly chosen, we then repeat the above process by varying each variable again with all others being held constant using the established initial values. The mutation probability is found to be 0.02. Generally, we have found that a mutation rate of 0.01–0.05 offers the best results. The order of tournament selection controls how quickly a population is "taken over" by dominant individuals in the population [2]. We use a tournament order of three. The number of generations, N, used to terminate the evolution and the population size, p, are set to be 10 and 20, respectively. A larger value of either N or p may lead to a longer running time, but with no significant improvement of the matching performance. The weighting coefficients for the consensus matching function are found to perform well with values of 0.50, 0.35, and 0.15 for minutiae, orientation field, and ridge density map based matching, respectively. For the sampling point selection, there is a trade-off between matching accuracy and computational efficiency. More sample points will generally result in a higher matching accuracy, but also in a more expensive fitness computation. We have found that points which are sampled from the region of overlap of effective areas, spaced 16 pixels apart, offer an adequate trade-off between accuracy and efficiency. The ranges of δt_x, δt_y, $\delta\theta$, and δs for population initialisation are set to be $[-150, 150]$, $[-150, 150]$, $[-0.6, 0.6]$, and $[0.9, 1.1]$, respectively, but these values are not critical. The geometric constraints Δd and $\Delta\theta$ for minutiae matching are set as 15 and 0.195, respectively, which were established in [21] for fingerprint images scanned at 500 dpi resolution.

6. Experiments

We next report a series of experiments performed over the remaining two data sets DB_{1a} and DB_{3a}. We initially examine the significance of the local matching operation for population initialisation within the proposed algorithm. Then, the proposed consensus matching function is evaluated by comparing it with its three component criteria for fitness computation. Next, we compare the performance of the proposed algorithm with some previous fingerprint matching methods. Finally, the effectiveness of the GA to optimise the consensus criterion is assessed. All the results reported in
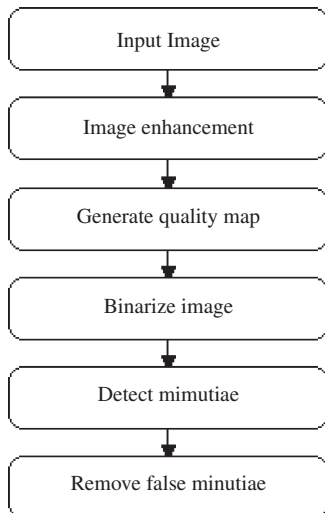


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Input Image
    ↓
Image enhancement
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Generate quality map
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Binarize image
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Detect mimutiae
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Remove false minutiae
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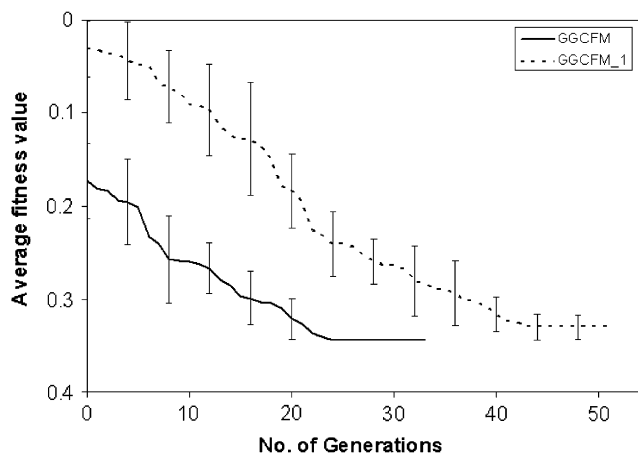**Fig. 2.** Minutiae detection process described in [6].

Fig. 3. Average fitness values of the best individual versus number of generations of the two algorithms corresponding to 10 trials of a typical genuine matching.

this paper were obtained with simulations on a PC with an Intel[TM] Pentium[TM] 4 processor at 3.4 GHz running under WindowsXP Professional. Unless otherwise stated, matching performance indicators shown in this paper have been estimated using the experimental protocol proposed in [17]. According to the protocol, a set of 2800 genuine matching pairs and 4950 non-matching pairs are selected from each of the data sets for performance evaluation.

First, experiments were conducted to examine the significance of the local matching operation for population initialisation within the proposed algorithm. For this purpose, we examined and compared the proposed genetically guided consensus fingerprint matching algorithm (GGCFM) with the same algorithm without the local matching operation (GGCFM_1). In the case of GGCFM_1, individuals of the initial population are randomly initialised using the method described in Section 4.1. Both algorithms are compared based on the same parameter settings. In order to investigate the convergence properties, the terminal condition for both algorithms is that the fitness value of the best population individual has not changed for 10 generations. Fig. 3 shows the average fitness scores over generations corresponding to ten trials of a typical genuine matching. The GGCFM shows that, compared with GGCFM_1 (i.e., with no local matching), the local matching operation helps to identify promising transformations. As a result, it speeds up the evolution by reducing the number of generations needed for the GGCFM to converge. In fact, this is the main justification for introducing the operation into the GGCFM.

Then, we evaluate the proposed consensus matching function by comparing it with its three component criteria, both used individually and in pair-wise combinations, for fitness computation. Before reporting the experimental results, we will examine the independence of the three component criteria used individually for fingerprint matching since this can play an important role in performance improvement [22]. As shown in [14], the correlation coefficient, ρ, between the matching scores can be used as a measure of diversity between a pair of matchers. A low value of ρ reflects a strong independence between two matchers and a large improvement can be gained by combining these two matchers. Our experiments on DB_{1a} show that the correlation coefficient for the three possible pairings of the matchers, i.e., between minutiae set matching and orientation field matching, between minutiae set matching and ridge density map matching, and between orientation field matching and ridge density map matching, are found to be 0.37, 0.34, and 0.42, respectively. These values are all less than 0.5, suggesting that the minutiae, orientation field, and ridge density map are mutually independent features for fingerprint matching.

Fig. 4 shows the receiver operating characteristic (ROC) curves obtained over the two data sets when using different matching

criteria for fitness computation. In the case of three pair-wise combinations, the weighting coefficients were determined following the same procedure described in Section 5.2. Looking first at the ROCs of the three criteria used individually for fitness computation, we can see that the orientation field and ridge density map based criteria generally do not perform as well as the minutiae-based criterion. This is mainly because orientation fields are not enough to differentiate those fingerprints which are similar globally (e.g., fingerprints of the same type) but different in local details, while ridge density maps suffer from a lack of discrimination information. Looking next at the criteria used in pair-wise combinations for fitness computation, the ROCs show that the matching accuracy is improved for all the pair-wise combinations compared with their individual component criteria, demonstrating that the three criteria can complement each other to improve the matching performance. By combining all the three criteria, the results show that the consensus function is able to achieve the best matching accuracy.

Next, we report a set of experiments to compare our algorithm with previously reported work, two minutiae-based matching methods [27,25] and a hybrid matching method [8]. Before discussing the comparative results, we first briefly describe the methods to be compared and their implementation details. The two minutiae-based methods [27,25] have been selected for comparison, each of which uses a different strategy to align fingerprints. In [27], we formulated fingerprint verification as a minutiae point pattern matching problem and proposed to align the minutiae sets through the use of a GA. To improve the computational efficiency, a local improvement operator based on a single iteration of the classical point matching method, ICP [4], was integrated into the genetic search. The matching score is calculated based on the number of matched minutia pairs and the result of the minutiae's local feature similarity. In [25], the minutiae sets are first aligned by means of the GHT and the matching score is subsequently determined by counting the matched minutia pairs and normalising by the total number of minutiae in the area of overlap. We refer to this method as GHT-based matching. The GHT for alignment works by discretising the space of all possible transformations into a finite set of values. For each pair of potentially matching minutiae the transformation necessary to align them is calculated and evidence for this transformation is accumulated in the voting space. After testing all possible minutiae correspondences, the optimal candidate in the voting space is selected as the estimation of the alignment parameters. The hybrid matching method is recently proposed by Gu et al. [8]. In this method, fingerprints are first aligned by a minutiae-based GHT approach and the verification is then performed by combining the minutia set with the orientation field based matching.

For experiments on the two data sets described, parameter values of the three algorithms are specified or chosen to optimise performance, according to settings specified in the original source papers. To make the comparisons more meaningful, the minutiae and orientation field information used in the tested algorithms are extracted using the same method as described in Section 5.2. The estimated ROC curve results (averaged over 10 trials) of the four methods on the two data sets are shown in Fig. 5. Table 1 lists a performance level based on equal error rate (EER), a measure which is commonly used to summarise the accuracy of a matching system, and which is defined as the error rate where the system's false match rate equals its false non-match rate.

These results show that, in comparison with the three previously proposed methods, the GGCFM is able to achieve more accurate matching results in both data sets. For our previous method, the EERs of the ROCs turned out to be 1.0% and 3.7% on the two data sets, respectively. By comparison, in the GGCFM, the EER values are around 0.8% and 3.1%, respectively. The performance improvement of the GGCFM over our previous method is mainly due to the use of
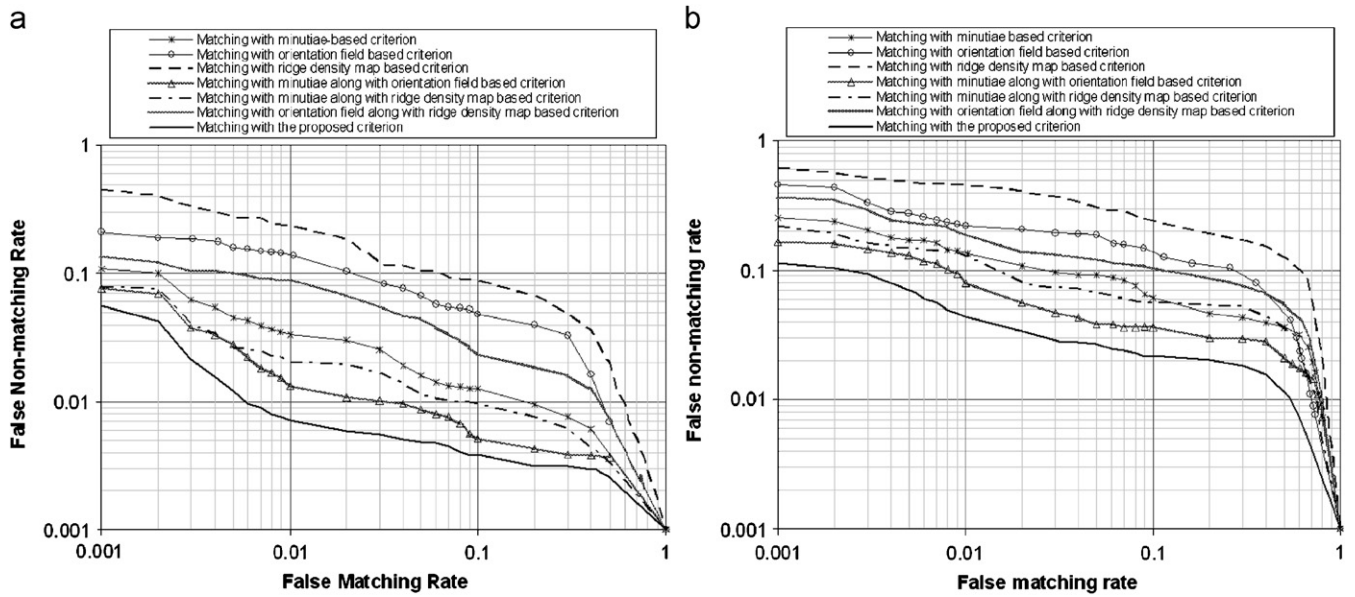
Fig. 4. ROC curves estimated on (a) DB$_{1a}$ and (b) DB$_{3a}$ when different matching criteria are used for fitness computation.
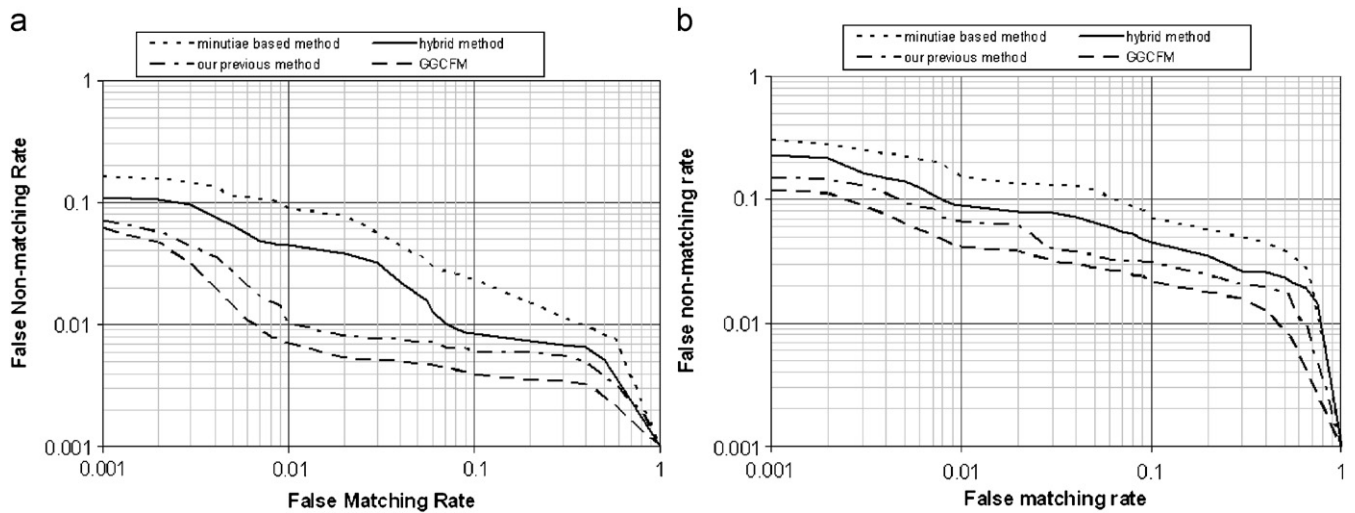

Fig. 5. ROC curves (averaged over 10 trials) estimated on (a) DB$_{1a}$ and (b) DB$_{3a}$ for our previous method, the minutiae-based method, hybrid method and our proposed GGCFM.

Table 1
EERs estimated on the two data sets.

Methods	EER (%)	
	DB$_{1a}$	DB$_{3a}$
GGCFM	0.8 (0.06)	3.1 (0.14)
Our previous method [27]	1.0 (0.06)	3.7 (0.12)
Minutiae-based method [25]	4.1 (±0.0)	8.6 (±0.0)
Hybrid method [8]	3.1 (±0.0)	5.8 (±0.0)
Consensus function with the hill-climbing search	2.5 (0.42)	5.9 (0.69)

The entries in the table (averaged over 10 trials) give the means in the form *mean* (±*standard deviation*).

the consensus matching function, which enhances the robustness of the fingerprint matching. In comparison with the GHT-based matching and hybrid matching, the GGCFM significantly improves the fingerprint matching accuracy, which can be observed from the ROC curves in Fig. 5 and EER values in Table 1. The EERs, for example, on DB$_{3a}$ of the GHT-based matching and hybrid matching are measured to be 8.6% and 5.8%, respectively, while our algorithm returns about 3.1%. The poorer performance of the GHT-based matching and hybrid matching is mostly because these methods depend heavily on the quality of extracted minutiae information as well as on the accuracy of the GHT based alignment. The presence of spurious minutiae and absence of genuine minutiae, which often occurs during the process of extraction minutiae, can cause many false votes in the Hough voting space and lead to the wrong transformation estimations. Additionally, the GHT based alignment has difficulty in identifying highly accurate transformations since only the set of the discretised parameter values are tested. Another fact worthy of note is that both GA-based methods (GGCFM and our previously reported method) show improved performance in terms of matching accuracy. This result is an indication that the genetically guided search mechanism helps in recovering more accurate transformation between two fingerprint impressions, hence leading to more accurate matching. For

completeness of comparison, it should be noted that, in the context of FVC2002 [18], there are fingerprint verification systems (e.g., algorithms denoted as PA15, PA27, and PA02 in FVC2002) which have better matching performance than the GGCFM. However, these systems are either commercial or created by independent developers who usually do not publish details of their algorithms. This means that very little information about the most successful fingerprint verification systems is available to academic researchers working in this area, and it is difficult to review and compare with such systems.

It is of interest to investigate the effectiveness of the proposed method further by examining the transformation parameters determined during the verification process. The corresponding minutiae between fingerprints captured from the same finger can be established by visually inspecting the fingerprints and good transformations should accurately identify the corresponding minutiae, thus enabling the validation of transformations corresponding to different parameter values. We therefore select 50 pairs (each pair from the same finger) randomly from DB_{3a}, and evaluate the transformations obtained by each of three algorithms (GGCFM, GHT-based matching, and hybrid matching) by mean of visually inspecting the identified minutia correspondences between each pair. The results reveal that 73.2%, 65.4%, and 68.7% of corresponding minutia pairs identified by the GGCFM, GHT-based matching, and hybrid matching, respectively, are correct. For the GHT-based matching and hybrid matching methods, the poorer performance is largely due to the local reference based alignments, which can correctly align the regions adjacent to the reference local structures. However, these are usually not appropriate for aligning regions far away from the reference structures and therefore leading to false minutia pairs considering a lot of spurious minutiae presented, especially in the poor-quality images.

Finally, we report experiments to assess the effectiveness of the genetic search mechanism by comparing it with a hill-climbing search to optimise the consensus criterion for fingerprint verification. The following hill-climbing search procedure was compared. Let us denote t and q to be the template and query fingerprints, respectively. The initial transformation parameters $G_0(t_x, t_y, \theta, s)$ are set randomly such that the effective areas of t and q are overlapping by at least 30% with $\theta = 0$ and $s = 1.0$. The procedure starts by applying the transformation parameters G_0 to the query fingerprint to obtain q_0. The consensus function is then computed for G_0 and for a selection of neighbouring points on the cost surface. The transformation that leads to the greatest increase in the function is selected as G_1 and this process is repeated until the value of the consensus function ceases to increase. To make the comparison more meaningful, we repeat the hill-climbing search with different initial transformation parameters for each verification task for a period comparable to the amount of time our proposed algorithm spends, and the best transformation is selected. Table 1 lists the results in terms of EER of the hill-climbing search for fingerprint verification. The results indicate that the genetic search mechanism outperforms the hill-climber. One of the important reasons for poor performance of the hill-climbing search is that it may converge to less promising locally optimal transformations, thus degrading the verification performance.

7. Summary and future work

In this paper, we have presented a consensus fingerprint matching algorithm based around a genetically optimised approach. A GA-based evolution with a consensus matching function for fitness computation and a local matching operation for population initialisation is at the heart of the proposed method. The effectiveness of the local matching operation, the consensus matching function and the genetic search mechanism has been clearly demonstrated in the experimental results presented, which also confirm that the

proposed method is a robust and accurate matching algorithm. The method can achieve more accurate matching results than those reported in our previous work and the conventional minutiae-based method, and outperform another recently proposed approach which also uses complementary criteria for matching.

The consensus function, in combination with the genetically guided optimisation for fingerprint matching, is thus seen to be both viable and easily extendable by incorporating further criteria based on other features available in the fingerprints, such as gray-level information [3] and curvature maps [32]. Since heterogeneous features usually play a complementary role for matching, the robustness of the proposed method is expected to be improved further by using a consensus function which harnesses criteria based on a more comprehensive set of complementary features. However, it should be noted that the use of the proposed consensus function (based on the three heterogeneous features) is already more expensive than the use of its component criteria for fingerprint verification in the proposed method. For example, on DB_{1a}, the minutiae, orientation field and ridge density map based criteria need ~ 2.96, ~ 2.04, and ~ 2.13 s, respectively, in terms of the average matching time (which is defined as the average CPU time for a single match operation between a template and a query image), while the consensus function takes about 3.72 s. Also, integrating criteria based on additional features would make further demands in relation to computational costs. It should also be recognised that the current implementation of the proposed method is relatively expensive compared to the minutiae-based method [25] (~ 1.37 s on DB_{1a}) and the hybrid method [8] (~ 1.46 s on DB_{1a}). We expect to significantly reduce the matching cost by investigating the following research directions. First, GAs are extremely easy to adapt to parallel computing and clustering environments [7]. As massively parallel computers become more common, parallel implementations of the proposed algorithm can be exploited. Each processor can be devoted to a pair of solutions since the algorithm's operations focus on them. As a result, the matching efficiency can be significantly improved as the entire population is processed in parallel. Additionally, GAs are not well suited for fine-tuning solutions which are close to optimal ones [7], and this results in a large execution time being incurred. To improve this situation, incorporation of local searches into the regeneration step of the GAs has been shown to be very effective for many combinatorial optimisation problems [1,20,31]. In this regard, local improvement operations can be developed and hybridised with the proposed method to improve its computational efficiency.

Acknowledgement

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About the Author—WEIGUO SHENG received his M.Sc. in Information Technology from the University of Nottingham, UK, in 2002 and his Ph.D. in Computer Science from Brunel University, UK, in 2005. He is currently a Research Fellow in the School of Engineering and Design at Brunel University, UK. His research interests include evolutionary computation, heuristic search, and data clustering with particular focus in biometrics and bioinformatics.

About the Author—GARETH HOWELLS is a Senior Lecturer in Electronic Engineering at the University of Kent, U.K. He received his Ph.D. degree in Computer Science in 1991 specialising in the investigation of the practical difficulties present in the efficient exploitation of various aspects of Theoretical Computer Science in the large. He was subsequently involved in substantial research into the formal verification of digital systems and the practical development and application of artificial neural systems. This work resulted in the development of a wholly declarative theorem proving tool for digital system verification and the development of a generic formal mathematical model describing the behaviour of artificial neural systems. His research interests have also involved the practical application of formal mathematical logic to the design both of artificial neural networks and more general pattern classification techniques. Over the last decade, his research interests have moved into the biometric security field and he has been responsible for the design of a generalised document security system and substantial work on the investigation of techniques for the direct generation of encryption keys from biometric samples removing the need for any form of biometric template storage.

About the Author—MICHAEL FAIRHURST is the Head of the Department of Electronics at the University of Kent in the UK. His research interests focus on computational architectures and algorithms for image analysis and classification, and applications including handwritten text reading, and document processing, medical image analysis and, especially, security and biometrics.
Current projects include work on multimodal biometrics, on assessing the vulnerability of biometric identification techniques and on the analysis of handwriting, both for identification purposes and to improve the effectiveness of automated processing for forensic applications. Biometric processing also underpins work which is investigating document encryption linked to biometric data. In related work, he is further developing work he pioneered at Kent which has established novel techniques for the assessment and monitoring of neurological conditions through the analysis of patients' writing and drawing abilities.
Professor Fairhurst sits on numerous Conference, Workshop, Government-sponsored Committees, and on the Editorial Boards of several International Journals. He has published some 350 papers in the scientific literature, and is an elected Fellow of the International Association for Pattern Recognition (IAPR) in recognition of his contributions to the field.

About the Author—FARZIN DERAVI obtained his first degree in Engineering and Economics from the University of Oxford in 1981 and his M.Sc. in Electronic Engineering from Imperial College, University of London in 1982. From 1983 to 1987 he worked as a research assistant at the University of Wales, Swansea where he obtained his Ph.D. In 1987 he joined the academic staff at Swansea where he was active in teaching and research in the Department of Electrical and Electronic Engineering. In 1998 he joined the Department of Electronics at the University of Kent where he is a Reader in Information Engineering. His current research interests include texture recognition, fractal coding, integrated audio–visual processing, and biometric systems.
Dr. Deravi is a Member of the Institute of Electrical and Electronic Engineers, the Institution of Engineering and Technology, and the British Machine Vision Association. He was the founding chair of the IET Professional Network on Visual Information Engineering and is currently Editor-in-Chief of the IET Image Processing Journal. He also serves on BSI, CEN, and ISO committees on Biometric Standardisation.

About the Author—KARL HARMER received his M.Eng in Electronic and Computer Systems Engineering from Loughborough University in 2003. After working as a controls/software engineer for the power distribution industry, he has returned to academia and is now undertaking a Ph.D in Electronic Engineering at the University of Kent. His current research interests include image and signal processing, pattern recognition, data clustering and biometrics.