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Matching of palmprints

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Abstract

This paper investigates the feasibility of person identification based on feature points extracted from palmprint images. Our approach first extracts a set of feature points along the prominent palm lines (and the associated line orientation) from a given palmprint image. Next we decide if two palmprints belong to the same hand by computing a matching score between the corresponding sets of feature points of the two palmprints. The two sets of feature points/orientations are matched using our previously developed point matching technique which takes into account the non-linear deformations as well as the outlier points present in the two sets. The estimates of the matching score distributions for the genuine and imposter sets of palm pairs showed that palmprints have a good discrimination power. The overlap between the genuine and imposter distributions was found to be about 5%. Our preliminary results indicate that adding palmprint information may improve the identity verification provided by fingerprints in cases where fingerprint images cannot be properly acquired (e.g., due to dry skin).

1. Introduction

Automatic human identification has become an important issue in today's information and network-based society (Gelsema and Veenland, 1999; Jain et al., 1999). The techniques for automatically identifying an individual based on his physical or behavioral characteristics are called biometrics. Biometric systems are already employed in a variety of domains that require some sort of user verification (e.g., for access control or welfare disbursement programs). Numerous distinguishing traits that have been used for personal identification include fingerprints, palmprints, face, voice, iris and hand geometry. It is generally accepted that fingerprint and iris patterns can uniquely define each member of an extremely large population which makes them suitable for large-scale recognition (establishing a subject's identity). However, in many applications, we only need to authenticate a person (confirm or deny the person's claimed identity). In these situations, one can also use different biometric traits such as voice, hand shape or palmprint.

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The science of fingerprints for identification is well established (Lee and Gaensslen, 1994). The work was pioneered by Galton (1892) who based his research on Herschel's data (Cherill, 1954). Herschel also kept a record of handprints at intervals ranging over long periods which were used to test the persistence of the ridge characteristics. Henry's classification was used in classifying fingerprints (Cherill, 1954) but for hand prints only a few systems have been advanced (Zhang and Shu, 1999; Alexander, 1973; Wilder and Wentworth, 1918). To our knowledge, none of these have been adopted in practice. While geometry of hands has been used in biometrics or identity verification, such systems are not very robust (Jain and Duta, 1999). Dermatoglyphics is another scientific area where palm patterns (ridge patterns, creases) are used to correlate them with medical disorders, e.g., genetic disorders and Downs syndrome.

This paper investigates to what extent the identity of a person can be verified based on feature points extracted from palmprints. Adding

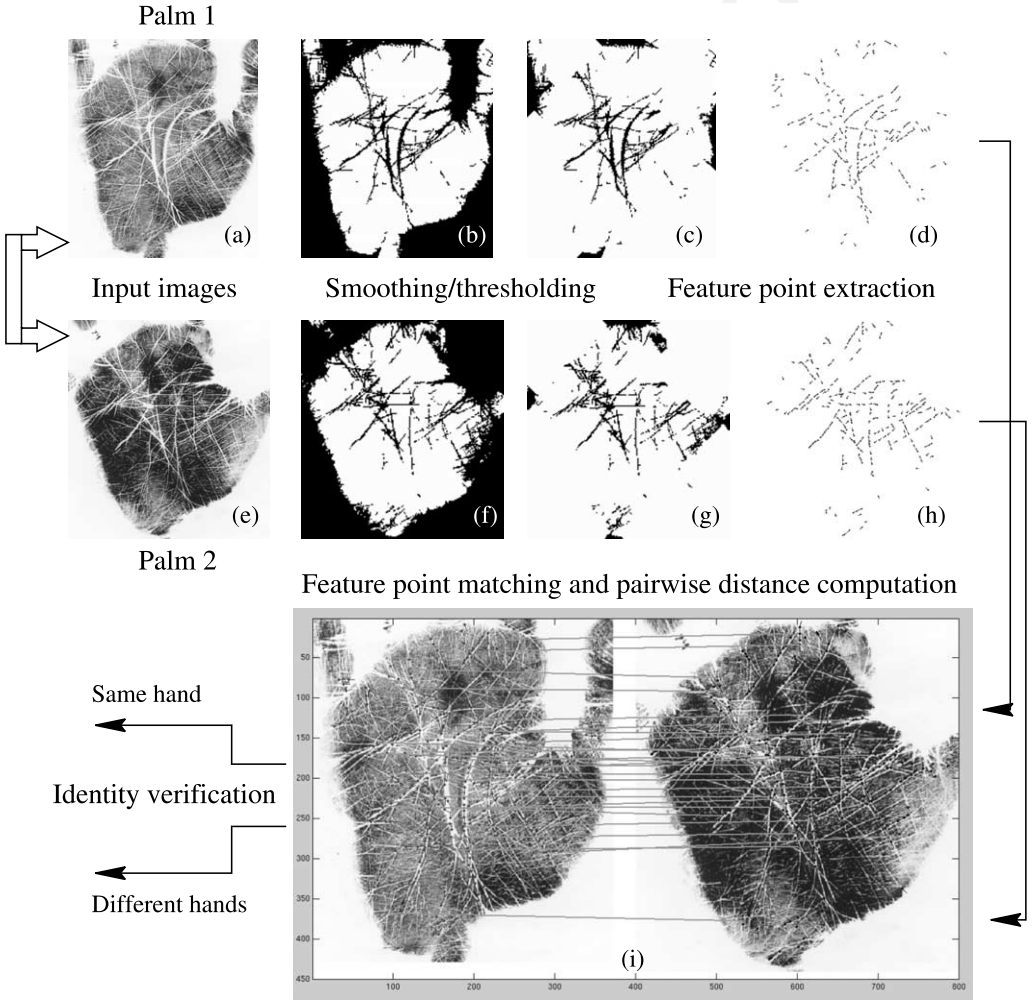

Fig. 1. Palmprint-based identity verification system: (a), (e) Original gray scale image of palms. (b), (f) Binarized palm images. (c), (g) Palm line pixels resulting from (b), (f) after morphological transformations. (d), (h) About 300 feature points/orientations computed by subsampling the feature points in (c), (g) along with their corresponding line orientation. (i) 25 out of the 153 point correspondences found between the feature points in (d) and (h). The matching score is (54%, 4.73).

palmprint information may improve the discrimination provided by fingerprints in cases where fingerprint information cannot be properly collected (a person's fingerprint may exhibit cuts or, sometimes, it may be even missing) (Jain et al., 1999).

2. Proposed method

Given a pair of palmprints, we propose the following palm matching paradigm (see also Fig. 1):

1. *Feature point extraction.* We define as feature points those points lying on the prominent palm lines. However, we do not explicitly extract palm lines as in (Zhang and Shu, 1999), but use only isolated points that lie along palm lines. We believe this is a faster way to extract features and that the feature point connectivity is not essential for matching purposes. For each such feature point, the orientation of its associated palm line is also computed. The feature points were extracted as follows:

   (i) The palm image is smoothed by replacing each pixel value with the average of its original value and the values of its four immediate

Fig. 2. Feature point matchings (both point positions and orientations are matched) corresponding to the palmprint pair in Fig. 1(i). The 153 point correspondences found are shown using light gray segments. The six main palm lines which have been matched are shown inside the solid gray areas. Due to a different position of the thumb in the two palm scans, the diagonal palm lines inside the ellipsoidal area differ by a non-linear transformation.

neighbors. Smoothing is aimed at removing local noise and very thin palm lines (the prominent palm lines are 6–10 pixels wide).

(ii) The smoothed image is binarized by applying an interactively chosen threshold T. All pixels whose values are greater than T are regarded as palm line pixels while the remaining ones are considered to be part of the background (Fig. 1(b), (f)).

(iii) A set of successive morphological erosions, dilations and subtractions are performed in order to remove the compact regions misclassified as palm lines (Fig. 1(c), (g)). The remaining foreground pixel locations are subsampled in order to obtain a set of 200–400 pixel locations which will be considered to be the feature points (Fig. 1(d), (h)).

(iv) Each feature point location is adjusted to be the pixel of maximum average gray value in a 4×4 neighborhood of its original location. This operation is an attempt to place the feature points along the medial axis (which is approximated by the set of maximum pixel values along a palm line) of its corresponding palm line.

(v) For each feature point, the orientation of its corresponding palm line is computed as the direction of the line segment of length 8 which has the maximum average contrast (absolute difference value) to its immediate surrounding (parallel segments placed 2 pixels above and below the given segment).

(vi) Since spurious feature points are still present, those points whose contrast (defined in step (v) above) is among the lowest 30% of all feature points are removed.

2. *Pairwise distance computation.* The two sets of feature points/orientations are matched (as explained in Section 3) and a matching score is computed. We define the matching score as a tuple (P, D), where P is the percentage of point correspondences with respect to the minimum number of feature points in the two sets, and D is the average distance (in pixels) between the corresponding points. The choice for this matching score was motivated by the two sources of variation present in different palm images of the same subject: (i) noise introduced by feature point extraction and (ii) non-linear palm deformations due to various finger positions.

The P component of the matching score attempts to model the amount of noise present in the feature point set. Consider for example that S is the set of "true" feature points along the main palm lines in Fig. 1(a). Due to image noise and limitations of the feature extraction procedure, we can only compute an estimate $\hat{S}$ of S which is the set of feature points actually shown in Fig. 1(d). Some of the "true" feature points could not be detected, while several spurious points were introduced. If we assume that only 80% of the points in S could be retrieved in $\hat{S}$ and the remaining points in $\hat{S}$ represent independent noise which are less likely to have matching points in a different instance of the same palm, then we might expect to find about $80\% \times 80\% = 64\%$ (with respect to the number of "true" feature points in S) point correspondences between two instances of the same palm. The D component of the matching score models the amount of non-linear deformation between two instances of the same palm. This is shown in Fig. 2 where, due to a different position of the thumb, the main diagonal palm line is somewhat rotated between the two images. Since the point matching only takes into account similarity transformations (composition of translation, rotation and scaling), non-linear deformations will increase the average distance between the corresponding points. Our approach does not attempt to model natural palm variations present in different subjects. This is a difficult task, and for palmprints, we do not believe that the three types of variation present (natural, noise and non-linear deformation) could be easily modeled separately.

3. *Identity verification.* Once the matching tuple (P, D) between two palmprints has been computed, the identity verification becomes a two-class (genuine vs. imposter) classification problem. The classification task can be treated as constructing a decision boundary in a $2D$ feature space (P and D are treated as two features), or some projection method can be applied in order to transform the data into a one-dimensional feature space. We chose to apply a discriminant analysis to the sets of intra-class and inter-class (genuine/imposter) matching scores in order to obtain a one-dimen-

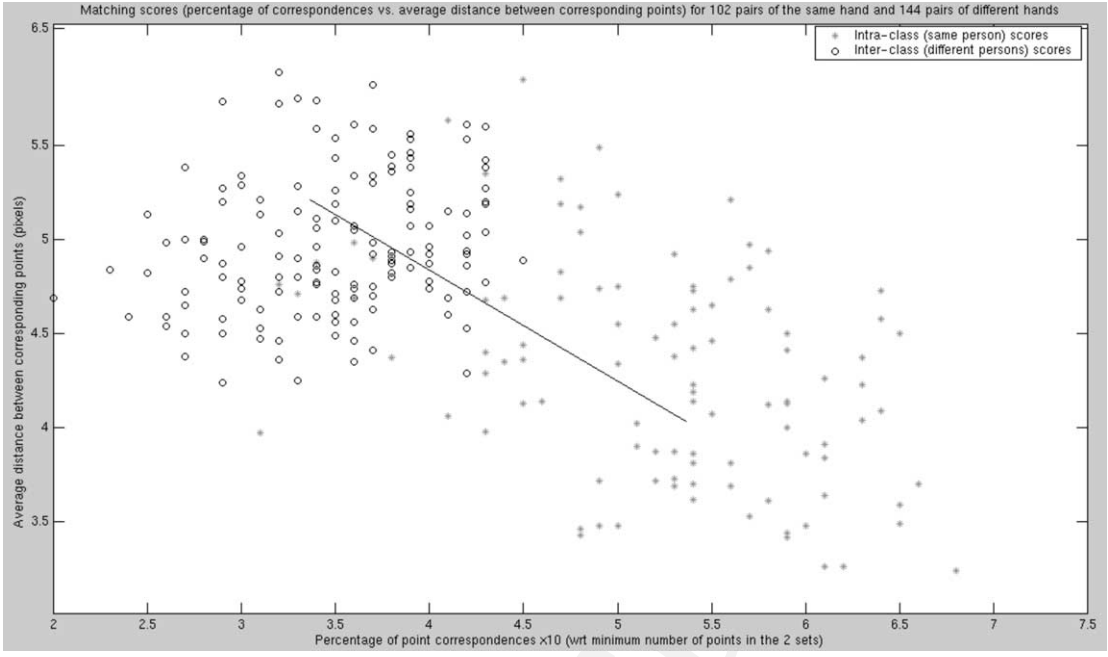

Fig. 3. Matching score tuples (percentage of correspondences vs. average distance between corresponding points) for the 102 intra-class pairs and 144 inter-class pairs. The line segment is the most discriminant axis (the projections of the points onto this line are most separable).

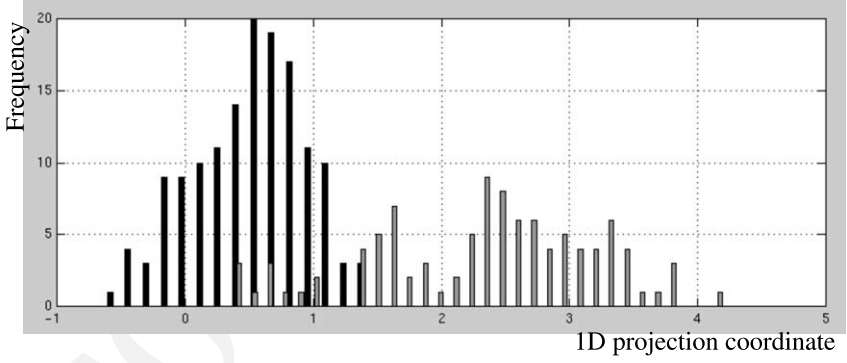

Fig. 4. Histograms of the 2D point projections on the most discriminant axis in Fig. 3. There is about 94% discrimination between the genuine and imposter distributions.

sional "similarity" score for the two palmprints (see Fig. 3). In this way, the decision rule reduces to a simple thresholding and the Neymann–Pearson rule that minimizes the false reject rate (FRR) for a fixed false accept rate (FAR) is employed to compute the "optimum" threshold (see Fig. 4).

3. Feature point matching

As mentioned in Section 2, we represent the features of a palmprint by a set of points in the Euclidean plane along with the palm line orientation at each feature point. Feature point matching

is the process of geometrically aligning two or more sets of points derived from images of the same object. Most studies dealing with point matching generally agree that if D is a "distance" function between two sets of points A and B, then the point set B is *aligned* to the point set A with respect to a transformation group G (e.g., rigid, similarity, linear, affine) if $D(A,B)$ cannot be decreased by applying to B a transformation from G. We use a least-squares type distance because there exists an analytical (exact) solution to the alignment problem once the point correspondences are known (Dryden and Mardia, 1998). However, in order to use a least-squares alignment method one should find point correspondences between the two sets. Most of the time, the point sets are automatically derived from images, so there are no known correspondences between them. Moreover, some points may have no correspondence so they should be rejected as outliers.

We have developed a registration procedure (Duta et al., 2001) based on a polynomial quasi-exhaustive exploration of the correspondence functions (match matrices) space. Its main novelty compared to techniques previously used in the literature (Besl and McKay, 1992; Gold et al., 1998; Feldmar and Ayache, 1996; Bookstein, 1997) is the way it resolves the *shrinking* effect (Feldmar and Ayache, 1996): an unconstrained linear registration of two sets of points tends to "shrink" one set with respect to the other since, theoretically, the "best" alignment is obtained when one point set is rescaled to become a single point. Our problem formulation requires a small *mean alignment error* [1] between the two chosen subsets, using as many point correspondences as possible. Unfortunately, if we have less than three correspondences, the MAE is 0 and this should be compensated for. Therefore, we want to explicitly specify in the search criterion that a q% increase in MAE with a p% increase in the number of correspondences is accepted as long as no individual distance between a pair of corresponding points exceeds a given threshold. One of the simplest functionals that captures this trade-off is the ratio between a compensated MAE and the number of correspondences:

$$f(M) = [\mathrm{MAE}(M) + K]/n, \tag{1}$$

where K is a constant depending on the percentages p, q and the scale of the object (see (Duta et al., 2001) for the properties of this functional and how to choose K). If we also impose the constraint that the mapping is one-to-one, we implicitly solve the shrinking problem. With a large number of one-to-one correspondences (and the assumption that the two shapes are not sampled at very different rates), there can be no shrinking of one shape with respect to the other. We denote by A and B the two sets of feature points to be matched. Following is a high level description of our registration algorithm.

1. Set $V_{\min} = \infty$.
2. For every pair of points $(a_{j1}, a_{j2}) \in A \times A$
   For every pair of points $(b_{k1}, b_{k2}) \in B \times B$, do steps (i)–(v)
   (i) Find the similarity transformation ψ that aligns the sets $\{a_{j1}, a_{j2}\}$ and $\{b_{k1}, b_{k2}\}$.
   (ii) Apply ψ to all the points in B to obtain B'.
   (iii) For every point b_k of B', find its nearest neighbor $\mathrm{NN}(b_k)$ in A. If the distance between b_k and $\mathrm{NN}(b_k)$ is smaller than a threshold T and the associated line orientations do not differ by more than 45° then set a correspondence between the two points. A match matrix M between A and B is constructed in this way. Since two points from B' can have the same nearest neighbor in A, we enforce the one-to-one correspondence requirement, that is, allow a point to be linked to its second to fifth nearest neighbor if the first one can be assigned to a closer point in B', and the length of the link does not exceed T. Recompute the transformation ψ that aligns the sets A and B according to the match matrix M.
   (iv) Compute $f(M)$.
   (v) If $f(M) < V_{\min}$ then $V_{\min} = f(M)$, $\psi_{\min} = \psi$.

[1] An *n-point* set $B = \{(x_i^B, y_i^B)\}_{i=1,\ldots,n}$ is said to be *aligned* to $A = \{(x_i^A, y_i^A)\}_{i=1,\ldots,n}$ if the *sum-of-squares* $\mathrm{SS}(A,B) = \sum_{i=1}^{n}[(x_i^A - x_i^B)^2 + (y_i^A - y_i^B)^2]$ cannot be decreased by scaling, rotating or translating B. In this case, $\mathrm{SS}(A,B)$ is called *Procrustes distance* between A and B (Dryden and Mardia, 1998), and the ratio $\mathrm{SS}(A,B)/n$ is called the *mean alignment error* ($\mathrm{MAE}(A,B)$).

3. Apply $\psi_{\min}$ to all the points in B to obtain B'.
4. For every point b_k of B', find its nearest neighbor in A. If the distance between b_k and its nearest neighbor is smaller than T and the associated line orientations do not differ by more than 45° then set a correspondence between the two. A match matrix M' between A and B is constructed in this way and enforced to correspond to one-to-one links.
5. Find the linear transformation ψ_{final} that aligns the corresponding sets $A_{M'}$ and $B_{M'}$.

4. Experimental results and discussion

A small data set of 30 (15 of each of the two hands) palmprint images of three persons was collected (12 prints of each of two persons, and 6 prints of the third one). There are various methods available to take palmprints as recently summarized by Reed and Meier (1990). However, since we wanted to study palmprints under different stretchings of palm, these methods did not seem to be suitable. The method for hand prints which we use depends on a specially designed handprint box which allows for differing hollowness of palm. Namely, the box contains a tough rubber pad framed on the top of which the subject's hand is placed but the rubber is elastic enough for the hand of the person taking the print to be placed inside and pressed firmly against the rubber, ensuring that the whole of the subject's handprint is clearly printed. The paper palmprints were scanned using a Hewlett Packard ScanJet 5200 flatbed scanner at a resolution of 200 dpi (image size 400×300 with 256 gray levels). The entire palm was preserved; fingers and thumb were omitted. Since no electronic sensors were used for the palmprint acquisition, the impression quality varied; some prints were very homogeneous while others missed the central palm region as well as other details. The data were acquired in two sessions separated by a week and three different finger positions for each hand were used per session.

From each palmprint, a set of approximately 300 feature points was extracted according to the algorithm presented in Section 2. Subsequently, for almost each palm pair that could be formed from the available data (a few pairs were omitted due to poor palm image quality) a matching score tuple was computed. As such, the density of the intra-class (respectively, inter-class) scores was estimated from 102 intra-class (respectively, 144) pairs. We show the alignment of a palmprint pair belonging to the same hand in Figs. 1(i) and 2 (for a detailed set of alignment results see http://web.cse.msu.edu/~dutanico). The different positions of the thumb in the two palmprints introduced non-linear deformations in the line structure (see the relative positions of the diagonal lines inside the ellipsoidal gray area in Fig. 2). For this reason, the average distance between the corresponding points associated with this palm pair (4.73) is larger than the average.

The resulting matching score tuples are plotted in Fig. 3; the intra-class (genuine) scores are denoted by "$*$" while the inter-class (imposter) scores are denoted by "$\circ$". One can notice that the genuine distribution resembles a 2D Gaussian centered at about 55% point correspondences and about 4 pixel distance between the corresponding points. This corresponds to about 25–30% independent noise in each feature point set as discussed in Section 2. The orientation of the ellipsoidal cloud is probably due to non-linear deformations, otherwise the average distance should not increase when the number of correspondences decreases. Also, the intra-class matching scores do not seem to depend on which hand pair (both left hands or both right hands) is matched. This shows that the two sources of variation discussed in Section 2 (noise and non-linear deformations) act consistently over the entire set of genuine palm pairs. However, the percentage of point correspondences between two palmprints is determined by the quality of the palm scan; for poor quality scans the "$*$" cloud in Fig. 3 is shifted to the left.

The inter-class (imposter) distribution also resembles a 2D Gaussian centered at about 35% point correspondences and about 5 pixel difference between the corresponding points. The orientation of the cloud is almost perpendicular to that of the genuine distribution cloud. This type of dependency between the percentage of point correspondences and the average distance between corresponding points is mostly encountered when

matching two sets of random points: the larger the number of point correspondences, the greater is the distance between the corresponding points, denoting that there is no clear good match between the two sets. The overlap between the genuine and the imposter distributions (the "$*$" points inside the "$\circ$" cloud) is primarily due to poor quality images in which the percentage of noise is about 40%.

The direction which best discriminates the genuine distribution from the imposter distribution is shown in Fig. 3 and is roughly parallel to the main axis of the genuine distribution. By projecting all 2D points onto this axis, one obtains the two 1D distributions shown in Fig. 4. One can notice that in this case discriminant analysis has almost the same discrimination power as the quadratic decision boundary applied to the original 2D data. By setting the decision boundary (threshold) at 1.25 there are 14 (12 genuine and 2 imposter) palm pairs which are misclassified. This corresponds to a $14/246 = 5.7\%$ total error rate.

Finally, we would like to mention that the point matching method described in Section 2 is not iterative (compared to previous methods as in (Bookstein, 1997)), that is, Step 2(iii) in our matching algorithm does not use a convergence criterion. Of course, if we perform Step 2(iii) several times, the resulting match matrix may be slightly different (up to about 5% of the feature points may have a different corresponding feature point or may be rejected as outliers). This is mostly due to thresholding the distance between corresponding points (e.g., a very small rotation of one point set can make the distance between several pairs of corresponding points exceed the threshold T and, as such, these points will be considered outliers by the new match matrix). The thresholding also makes our point matching method asymmetric (the final match matrix when matching a point set A to a point set B may be slightly different than the one obtained when matching B to A). However, since we use a large number of feature points, the influence of the asymmetry on the final (P, D) matching tuple is small (the estimations of the genuine and imposter distributions in Fig. 3 were computed based on ordered palm pairs and matching score asymmetry was within 5% and seemed to be random).

5. Conclusions

We have presented a preliminary study of a palmprint-based method for personal identity verification. Our approach first extracts a set of feature points along the main palm lines (and the associated line orientation) from each palmprint. Next we decide if two palmprints belong to the same hand by classifying the scores resulting from matching the feature sets of the two palmprints. The estimation of the matching score distributions for the genuine and imposter sets of palm pairs showed that palmprints have a good discrimination power. The overlap between the genuine and imposter distributions was found to be about 5%. However, these results may be biased by the small size of the data set which we have used. In this study the overlap is due exclusively to the noise present in the palm images or other non-linear deformation, but if more subjects are added, one should expect some overlap due to similar palms of different persons. To investigate this matter further, we plan to collect additional data and to re-estimate the genuine and imposter distributions.

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