Continuous Distribution Approximation and Thresholds Optimization in Serial Multi-Modal Biometric Systems

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Abstract: Multi-modal biometric verification systems use information from several biometric modalities to verify an identity of a person. The false acceptance rate (FAR) and false rejection rate (FRR) are metrics generally used to measure the performance of such systems.

In this paper, we first approximate the score distributions of both genuine users and impostors by continuous distributions. Then we incorporate the exact expressions of the distributions in the formulas for the expected values of both FAR and FRR for each matcher. In order to determine the upper and lower acceptance thresholds in the sequential multi-modal biometric matching, we further minimize the expected values of FAR and FRR for the entire processing chain. We propose a non-linear bi-objective programming problem whose objective functions are the two error probabilities. We analyze the efficient set of the bi-objective problem, and derive an efficient solution as a best compromise between the error probabilities. Replacing the least squares approximation of the score distributions by a continuous distribution approximation, this approach modifies the method presented in Stanojević et al. [15] (doi: 10.1109/ICCCC.2016.7496752)[a].

The results of our experiments showed a good performance of the sequential multiple biometric matching system based on continuous distribution approximation and optimized thresholds.

Keywords: multi-modal biometrics, sequential fusion, multi-criteria optimization, continuous distribution approximation.

1 Introduction

This paper is an extension of [15] (doi: 10.1109/ICCCC.2016.7496752). The mathematical model introduced in [15], that derives optimized thresholds for bi-modal biometric systems, is here formulated generally, for N-modal biometric systems. In addition, the linear approximation of the biometric scores, based on the least squares method, is here replaced by a non-linear continuous distribution approximation. We report our new computation results and compare them with previous results.

Biometrics is the automated recognition of individuals based on their behavioral and biological characteristics [11]. Biometric recognition is used for many purposes including criminal

identification, secure access control, forensics and so forth. It was intensively researched and widely applied in the last decade [18]. A number of biometric technologies have been developed and several of them are being used in a variety of applications [7]. The most commonly used modalities are fingerprints, face, iris, speech, and hand geometry. Due to their strengths and weaknesses, the choice of one or another modality is strictly dependent on the application requirements.

In his book [5], Kaklauskas presented different methods for analyzing the body language (movement, position, use of personal space, silences, pauses and tone, the eyes, pupil dilation or constriction, smiles, body temperature and the like) for better understanding people's needs and actions, including biometric data gathering and reading. Filip [3], briefly reviewed the book, and emphasized that it addressed two modern research domains: intelligent and integrated decision support systems and biometrics-based human-computer interface.

An analysis of a multi-modal biometric system based on level of fusion was presented in [10]. The authors discussed the biometric systems, the limitations of individual biometric, and various fusion levels and methods of multi-modal systems.

The parallel fusion mode was first introduced in 1998 [4]. Fingerprint and face modalities were simultaneously used for identification. Serial fusion of multiple matchers is a good trade-off between the widely adopted parallel fusion and the use of a mono-modal verification system [12]. An alternative to parallel fusion of biometric data is the use of serial fusion.

Kumar and Kumar [6] presented a new approach for the adaptive management of multi-modal biometrics. They employed the ant colony optimization for the selection of the key parameters like decision threshold and fusion rule, to ensure the optimal performance in meeting varying security requirements during the deployment of multi-modal biometrics systems.

Zhang et al. [18] proposed a novel framework for serial multi-modal biometric systems based on semi-supervised learning techniques. They have promoted the discriminating power of the weaker but more user convenient traits over the use of the stronger but less user convenient traits. In this way, they proposed an alternative to other existing serial multi-modal biometric systems that suggest optimized orderings of the traits deployed and parameterizations of the corresponding matchers but ignore the most important requirements of common applications. Their experiments on two prototype systems demonstrated the advantages of their methodology.

Marcialis et al. [8] proposed a theoretical framework for the assessment of performance of serial fusion multi-modal systems, theoretically evaluated the benefits in terms of performance, and estimated the errors in the model parameters computation. They analyzed the model from the point of view of its pros and cons, and performed preliminary experiments on a benchmark found in the literature.

The importance of the use of multi-modal biometrics in the area of secure person authentication is highlighted in a recent study [13]. That study provided a different perception on how to use biometrics on the highest level of the network security with the fusion of multiple biometric modalities.

Snelick et al. [14] studied the performance of the multi-modal biometric authentication systems using the state-of-the-art commercial off-the-shelf (COTS) fingerprint and face biometric systems on a large-scale population. They also proposed new methods of normalization and fusion that improved the accuracy of the biometric systems.

The remainder of the paper is organized as follows. In Section 2 we formulate the problem that we wish to solve. Two solving methods are presented in Section 3: the linear approximation method is briefly presented in Section 3.1, and our novel approach is introduced in Section 3.2. Our computational results on random generated instances are given in Section 4.1, and the numerical results on NIST-BSSR1 and NIST-BSSR2 databases are reported in Section 4.2. The conclusions and some directions for future work are included in Section 5.

2   The Formulation of the Problem

Multi-modal biometric verification systems use information from several biometric modalities to verify an identity of a person. The false acceptance rate (FAR) and false rejection rate (FRR) are metrics generally used to measure the performance of such systems. The FAR is the probability that the system incorrectly matches the input pattern to a non-matching template in the database. It measures the percent of invalid inputs which are incorrectly accepted. In case of similarity scale, if the person is an impostor in reality, but the matching score is higher than the threshold, then he is treated as genuine. The FAR depends on the threshold value: the FAR increases as the threshold decreases. The FRR is the probability that the system fails to detect a match between the input pattern and a matching template in the database. It measures the percent of valid inputs which are incorrectly rejected. It also depends on the threshold value: the FRR increases as the threshold value increases. The visual characterization of the trade-off between the FAR and FRR is generally given by a graphic representation of the genuine acceptance rate (GAR=1-FRR) with respect to the false acceptance rate.

In general, a matching algorithm performs a decision based on a threshold. The threshold determines how close to a template the input needs to be for it to be considered a match. If the threshold is reduced, there will be fewer false non-matches but more false accepts. Conversely, a higher threshold will reduce the FAR but increase the FRR. Our goal is to find the system's thresholds that assure a good compromise between the minimizations of the false acceptance rate and false rejection rate.

Pato and Millett, in their book [11], emphasized that the biometric recognition systems are inherently probabilistic. In their opinion, the biometric recognition involves matching, within a tolerance of approximation, of observed biometric traits against previously collected data for a subject. The approximate matching is required due to the variations in biological attributes and behaviors both within and between persons.

Let us assume that the multi-modal biometric system consists of N matchings. After any of the first $N-1$ matchings (indexed in the formulas from 2 to N), one of the following three decisions will be made: accept the person as genuine, reject the person as impostor, or demand another matching. Naturally, after the last matching (that uses the index 1 in formulas), only two decisions will be possible: to accept, or to reject the person.

For each modality in the system, we collect data from n persons. For each person we take m samples, and construct an $m \times n$ matrix M of input information. For real-life databases the components of matrix M are vectors derived by using classic protocols, that extract biometric features from the real data collected (images, videos, speeches).

In the beginning we restrict our attention to one of the first $N-1$ matchings. Using the matrix M we compute the distances between each two collected samples, and derive the distributions for the genuine users and impostors. The distribution of the genuine users is constructed using the distances between each two components of the same column of the matrix M. The distribution of the impostors uses the distances between each component of matrix M and each component of matrix M that lies on different columns. Two samples obtained from the same person are highly expected to have a small distance between them. Thus, the genuine distribution will generally have a range of smaller values than the impostor distribution. A graphical representation of such distributions is shown in Figure 2 (top) using normalized histograms.

Since the number of distances computed for the genuine distribution is significantly less then the number of distances computed for the impostor distribution, and the number of intervals used to construct the histograms is the same for both distributions, the height of the genuine distribution is significantly greater than the height of the impostor distribution.

Let A_k and B_k denote the minimal distance in the impostors distribution and the maximal
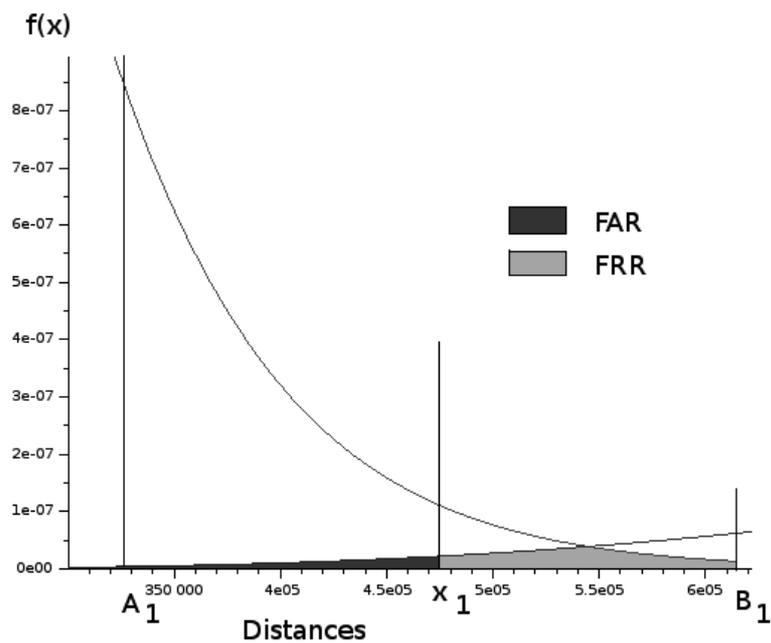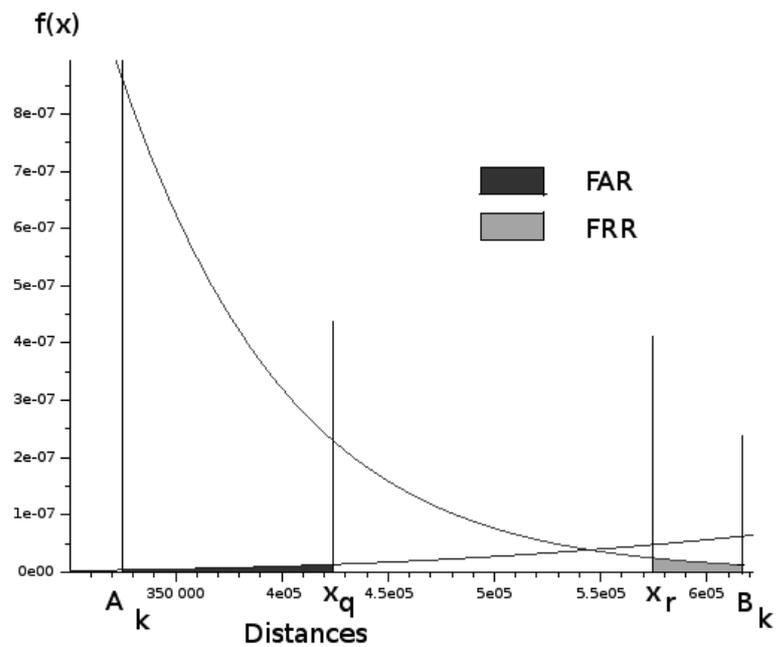
Figure 1: The areas involved in computing the FAR and FRR on the first $N-1$ match levels (top), and on the last match (bottom)

distance in the genuine distribution, respectively, for the k-th matching (we assume that $A_k < B_k$, otherwise the decision is trivial, and the system is error-free). When one of the first $N - 1$ matchings of the biometric system is used to verify a person, a decision is made according to two thresholds $x_q, x_r \in [A_k, B_k]$, $q = 2k - 2$, $r = 2k - 1$ as follows: if the distance between the given sample and the sample in the database is less than x_q the person is accepted as genuine; if it is greater than x_r the person is rejected as impostor; but if the distance belongs to the uncertainty region $[x_q, x_r]$, the verification process demands another matching (see Figure 1, top).

For the last matching in the sequence, the distributions of both genuine users and impostors are constructed in the same way; two values A_1 and B_1 are specified, with the same meaning as A_k and B_k, $k = 2, \ldots, N$ from the first matchings; but the decision is based on a single threshold denoted by x_1, that lies between A_1 and B_1 as follows: if the distance is less than x_1 the identity of the verified person is accepted as a genuine user, otherwise it is rejected as impostor (see Figure 1, bottom).

The main problem is to find proper values for the thresholds involved in the given sequence of matchings. Our goal is to provide optimized values for these thresholds, in sense of minimizing both false acceptance and false rejection errors, FAR and FRR, respectively.

3   Solving Methods

We first have to evaluate the false acceptance and false rejection errors with respect to the thresholds x_k, $k = 1, \ldots, 2N - 1$. Having a graphical representation of the score distributions of both genuine users and impostors, let $a_k(x_q)$, $q = k - 2$ denote the area under the impostor distribution bounded to the right by the vertical line that passes through x_q; and let $b_k(x_r)$, $r = 2k - 1$ denote the area under the genuine distribution bounded to the left by the vertical line that passes through x_r – for the k-th matching (see Figure 1, top). Similarly, let $a_1(x_1)$ denote the area under the impostor distribution bounded to the right by the vertical line that passes through x_1; and $b_1(x_1)$ denote the area under the genuine distribution bounded to the left by the vertical line that passes through x_1 – for the last matching (see Figure 1, bottom).

The probability of a false match error based on the k-th matching is $a_k(x_q)$, and it is $a_1(x_1)$ for the last matching. Similarly, the probability of a false non-match error based on the k-th matching is $b_k(x_r)$, and it is $b_1(x_1)$ for the last matching.

The function FAR_N, that describes the probability of a false match error in the general case of a biometric system with N modalities is computed using the recurrent formula

$$FAR_k(x_1, \ldots, x_{2k-1}) = a_k(x_q) + [a_k(x_r) - a_k(x_q)] FAR_{k-1}(x_1, \ldots, x_{2k-3}), \tag{1}$$

where $q = 2k - 2$, $r = 2k - 1$, $FAR_1(x_1) = a_1(x_1)$.

Similarly, the function FRR_N, that describes the probability of a false non-match error in the general case of a biometric system with N modalities is computed using the recurrent formula

$$FRR_k(x_1, \ldots, x_{2k-1}) = b_k(x_q) + [b_k(x_q) - b_k(x_r)] FRR_{k-1}(x_1, \ldots, x_{2k-3}), \tag{2}$$

where $q = 2k - 2$, $r = 2k - 1$, $FRR_1(x_1) = b_1(x_1)$.

In order to find proper bounds to the uncertainty regions involved in the verification process, we minimize both probabilities of error. Since a low false match error means a high false non-match error and reverse, we have to search for a good compromise between the two errors. Such

compromise is achieved by solving the bi-objective programming problem

$$
\begin{aligned}
\min \quad & FAR_N(x_1, ..., x_{2N-1}), \\
\min \quad & FRR_N(x_1, ..., x_{2N-1}), \\
\text{s.t.} \quad & A_k \le x_{2k-2} \le x_{2k-1} \le B_k, k = 2, \ldots, N \\
& A_1 \le x_1 \le B_1.
\end{aligned}
\tag{3}
$$

Model (3) is the generalization of Model (2) given in [15].

3.1　Local Linearization Approximation

In this section we briefly present the local linearization approach used in [15] to approximate the areas involved in Formulas (1) and (2). The discrete score distributions of both genuine users and impostors were approximated using the least squares method. A graphical representation of the discrete distributions (points) and their linear approximations (the straight lines) may be seen in Figure 4. The scores for genuine users are on the left, and the scores for the impostors are on the right. The representation is restricted to the region significant to the decision, i.e. to the intersection of the distributions.

In [15] the theoretical presentation of the approach was restricted to bi-modal systems, and quadratic expressions with respect to the thresholds x_1, x_2 and x_3, were derived. Combining them, a polynomial expressions of degree 4 were obtained, for the objective functions of the optimization model. The bi-objective optimization problem formulated in [15] is a particular case of Model (3), obtained for $N = 2$. For a general multi-modal matching system with N modalities, the expressions of the objective functions obtained by the linear approximation are polynomials of degree $2N$.

3.2　Continuous Distribution Approximation

In this section we propose a new way to approximate the discrete score distributions of both genuine users and impostors. In the previous approach, the discrete data collected from the users was grouped in intervals, relative frequencies were computed, and the discrete set of pairs *(frequency, midpoints of the intervals)* was continuously and linearly approximated using the least squares method.

We now propose to use a continuous distribution that approximate the initial discrete collection of data. We need to compute the mean and the variance of the data, separately for each modality, genuine users and impostors, and try to identify a continuous distributions that best fit the distance frequencies.

Figure 2 shows how the continuous distributions approximate the original score distributions for both genuine users and impostors, for one modality. In this representation the Gamma distribution was used for the genuine scores and the normal distribution for the impostors. For the same data set – representing the genuine users scores distribution – we performed a fit distribution test, that identified as best fit distributions the Gamma, Generalized Gamma (4P), and Johnson SB. The goodness of fit was performed for 61 well-known distributions. Among those distributions, the Kolmogorov-Smirnov test identified the Generalized Gamma (4P) distribution as the best fit, the Anderson-Darling test identified Johnson SB distribution as the best fit, while the Chi-squared test identified the Gamma distribution as the best fit.

Figure 3 graphically shows how the input data (with all values grouped in a histogram) may be approximated by Gamma, Normal, and Beta probability density functions. We were restricted to choose among Gamma, Normal, Beta, Erlang, and Chi-square distributions due
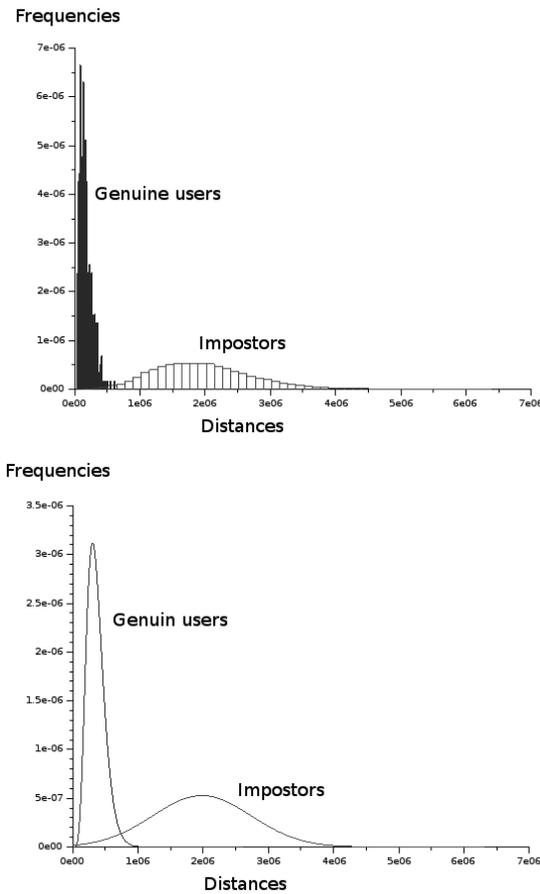
Figure 2: The approximation based on Gamma distribution for the genuine scores, and on normal distribution for the impostors scores versus the original (discrete) score distributions
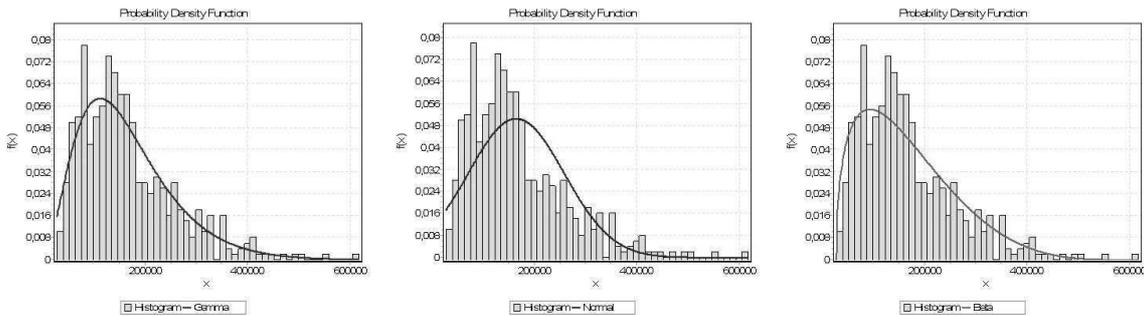
Figure 3: Probability density functions for the continuous approximations using Gamma, Normal, and Beta distributions. The characteristics of the distributions are given in Table 1

Table 1: Fitting results for the probability density functions of the Gamma, Normal, and Beta distributions presented in Figure 3

Distribution	Parameters
Gamma	$\alpha = 3.1919; \beta = 52049$
Normal	$\sigma = 92990; \mu = 166130$
Beta	$\alpha_1 = 1.4696; \alpha_2 = 4.7366; a = 29877; b = 616440$

Table 2: The goodness of fit for the Gamma, Normal, and Beta distributions (presented in Figure 3), using Kolmogorov-Smirnov, Anderson-Darling and Chi-squared statistics tests. The rank is given out of 61

Distribution	Kolmogorov-Smirnov statistic / rank	Anderson-Darling statistic / rank	Chi-squared statistic / rank
Gamma	0.04247 / 15	1.26490 / 19	6.4661 / 1
Normal	0.11578 / 37	11.63 / 36	50.698 / 38
Beta	0.06484 / 25	4.3973 / 27	22.072 / 25

to the toolbox of the programming language we used for the optimization. Despite the fact that these distributions are not the best fit, they behave well during experiments since they approximate relatively well the initial score distributions in along the intervals relevant to the optimization. We used *EasyFit 5.6 Standard* software (http://www.mathwave.com) for goodness fitting distribution.

Table 1 reports the parameters that describe the fitting results. These parameters were computed with respect to the mean and variance of the original score distribution. Table 2 shows the results for the statistic tests Kolmogorov-Smirnov, Anderson-Darling and Chi-squared applied to the data graphically represented in Figure 3. It also includes the ranks of the chosen distributions in the ranking list of 61 well-known distributions.

Figure 4 shows that the probability density function of the continuous distribution (the non-linear graph) better approximates the original set of data than the linear function (the straight line) obtained by the least squares method presented in the previous section. On the top side of the figure the approximations for the genuine users scores is given. For the impostors scores the approximations are given on the bottom side.

According to the new proposed approximation method, we use the cumulative density functions (cdf) to express the probabilities a_k and b_k, $k = 1, \ldots, N$, in Model (3). Thus, $a_k(x) = cdf_k^I(x)$, $k = 1, \ldots, N$ in FAR (1) for impostors, and $b_k(x) = 1 - cdf_k^G(x)$, $k = 1, \ldots, N$ in FRR (2) for genuine users. Model (3) is a nonlinear bi-objective problem independent on the approximation used. One way to solve Problem (3) is to aggregate the two objective functions, and optimize the obtained function. We propose the weighted sum method, with the initial weights $(1, 1)$, to aggregate the objectives. In this way we optimize the total error rate (TER), that is one parameter used in analyzing the performance of an biometric system.

By changing the set of weights, we favor one or another type of error. In order to chose certain weights to aggregate the FAR and FRR, the analyst must know/model the cost functions for false rejections and false acceptances. There are more system specific factors that may influence the priorities in favoring one or another of the error rates. Analyzing such characteristics is beyond the scope of this work. Our approach provides optimized thresholds from the point of view of minimizing the total error rate.

We solved the single objective optimization problem

$$
\begin{aligned}
\min \quad & FAR_N(x_1, ..., x_{2N-1}) + FRR_N(x_1, ..., x_{2N-1}), \\
\text{s.t.} \quad & A_k \leq x_{2k-2} \leq x_{2k-1} \leq B_k, k = 2, \ldots, N \\
& A_1 \leq x_1 \leq B_1.
\end{aligned}
\tag{4}
$$

numerically. A starting point was chosen by taking the midpoint of the feasible interval for the threshold x_1, the point that is at one third from the left bound of the feasible interval for the x_{2k-2}, and the point that is at one third from the right bound of the feasible interval for the threshold x_{2k-1}, $k = 2, \ldots, N$. We optimized one variable at a time, fixing others to either their
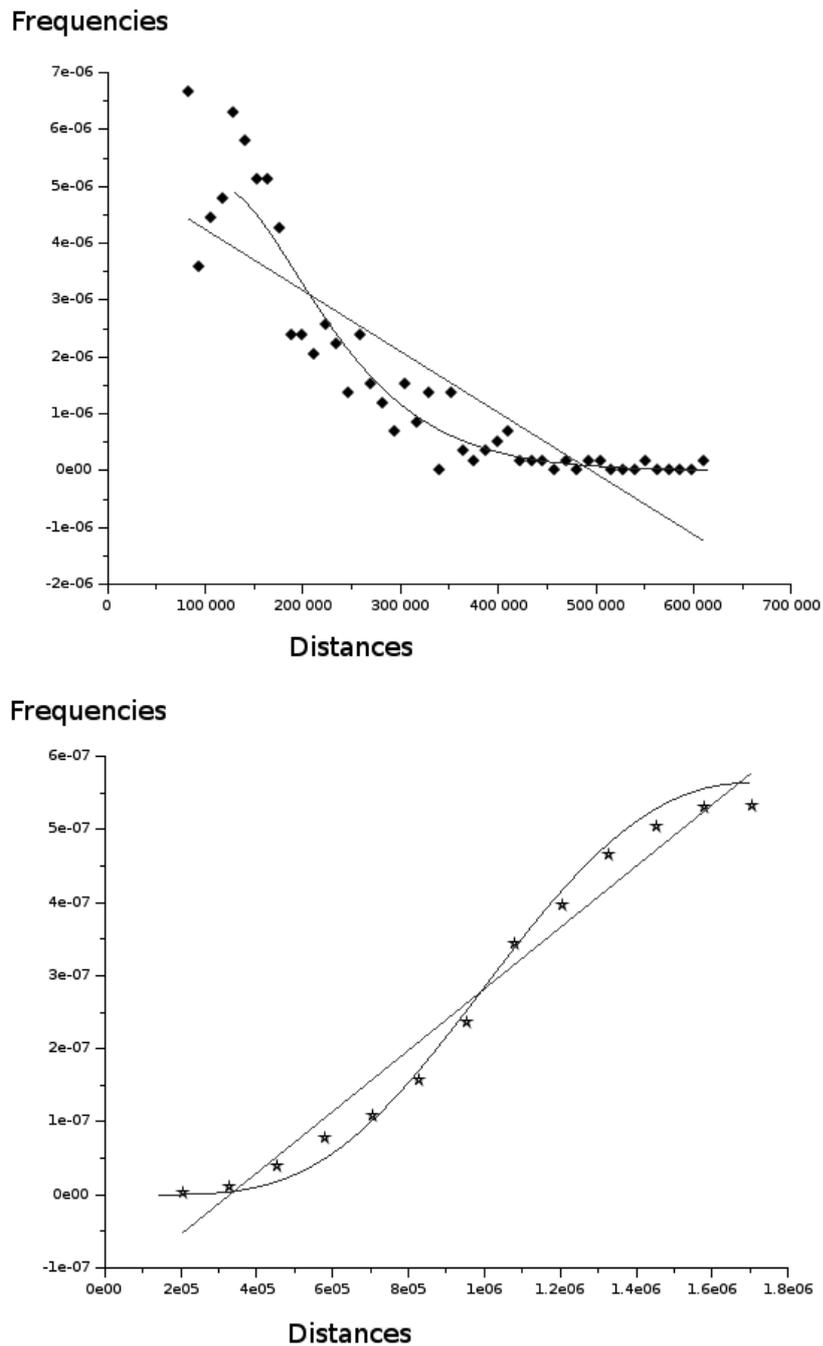
Figure 4: The approximation based on the least square method versus the approximation based on continuous distributions for both genuine users and impostors

initial values or previously obtained optimal values. The optimization process was stopped when the distance between two consecutive solutions dropped under a given threshold.

The advantage of finding optimized thresholds, to be used by the decision-maker in constructing the sequential multi-modal system, resides in yielding the needed information in the a priori stage of the decision. Generally, the trade-off between two conflicting objectives, and particularly the trade-off between FAR and FRR, may be a subject of a wider discussion. The usefulness of a priori, a posteriori, and interactive methods in multiple objective optimization are highly emphasized in the literature (see for instance [1]). A visualization technique for accessing the solution pool in the interactive methods of multiple objective optimization can be found in [2].

We used *GNU-Octave* (https://www.gnu.org/software/octave/) for the optimization step.

4   Computation Results

4.1   Experiments Using Random Generated Instances

In order to test the performance of our method we organized the experiments, as in [15].

First, the input data, necessary to construct the score distributions, were randomly generated according to the rules that made them proper data for biometric tests. More precisely, we have generated a set of vectors with l real positive components. Each of these vectors simulates the essential information that in real situations is extracted from the taken pictures of a person during a biometric measurement. The first sample of each user is generated as a vector of uniformly distributed random numbers. The mean and standard deviation were varied through instances. Each subsequent sample of the same user is generated as a vector of random numbers with normal distribution, keeping the same mean and variance as for its corresponding first sample. In this way we provided that the samples of one person are more similar to each other than when compared to samples of another person.

We computed the Euclidean distances between each two generated vectors, and split them in two categories to be used for the construction of the genuine and impostor distributions. For the continuous distribution approximations we used the Gamma distribution for the genuine users and the Normal distribution for the impostors. We computed the bounds A_k, B_k, $k = 1, 2$; used the approximations to evaluate the errors of false acceptance and false rejection; and constructed the bi-objective optimization model. In order to find the optimized thresholds we added the two error functions, and minimized the total error.

Each triple (x_1, x_2, x_3), including the triple of optimized thresholds, defines a bi-modal biometric system, whose performance will be evaluated.

In order to estimate the FAR and FRR of each system using the same data as in constructing the genuine and impostor distributions, we successively collected the answers of the system, obtained when each person $i = 1, \ldots, n$ claims that he/she is the person $k = 1, \ldots, n$, and he/she is verified with all samples $j = 1, \ldots, m$ of the person k, according to the specific thresholds of the system. Each time when the system accepts a person i as being the person k, the numerator of the ratio FAR increases with 1 unit. Similarly, each time when the system rejects a person i when he/she claims that he/she is person i the numerator of the ratio FRR increases with 1 unit. The nominator of FAR is $n(n-1)m^2$, while the nominator of FRR is $m(m-1)n/2$. Finally, we compute the genuine acceptance rate (GAR) as 1-FRR. When biometric samples of a control group are available, we collect the system's answers obtained by checking the control samples instead of the initial samples.

The numerical results are grouped in two tables. Table 3 contains the results obtained by both methods LS (based on least square approximation), and CD (based on continuous distribution approximation). Comparing the two methods we note that, considering the total error rate, CD

Table 3: Comparison of LS and CD for certain instances with given characteristics

Instances characteristics	FAR		GAR		TER	
	LS	CD	LS	CD	LS	CD
$n = 100, \quad m = 5, \quad l = 3$	9.4%	0.52%	99.6%	98.5%	9.80%	2.03%
$n = 100, \quad m = 5, \quad l = 5$	2.2%	0.77%	100%	99.5%	2.20%	1.26%
$n = 100, \quad m = 5, \quad l = 10$	0.05%	0.19%	99.2%	99.8%	0.85%	0.35%
$n = 200, \quad m = 5, \quad l = 10$	0.001%	0.05%	99.5%	99.9%	0.50%	0.15%

Table 4: The numerical results obtained by running CD on more instances with given characteristics

Instances characteristics	FAR		GAR		TER	
	$l = 5$	$l = 10$	$l = 5$	$l = 10$	$l = 5$	$l = 10$
$n = 100, \quad m = 10$	0.91%	0.08%	99.6%	99.94%	1.31%	0.14%
$n = 200, \quad m = 10$	0.96%	0.08%	99.7%	99.97%	1.31%	0.11%
$n = 500, \quad m = 10$	0.92%	0.08%	99.6%	99.98%	1.34%	0.10%

performs better than LS in all cases. Analyzing separately the values of the false acceptance rate and genuine acceptance rate, CD is better for two sets of instances, and LS is better for other two sets of data.

The results reported in Table 4 were obtained by running the CD method on instances with 100, 200 and 500 users. For each user 10 different samples were available. The samples were described by vectors of length 5 and of length 10. It is obvious that the number of genuine users used to train the system does not influence the error rates. Contrary, the length of the vectors used to describe the individuals is very important, as expected, since the error rates are much smaller in the case of $l = 10$ than in the case of $l = 5$. More precisely, when the length of the vectors is greater, more biometric information is enclosed in them, thus a more clear separation between individuals exists. Consequently, the score distributions of genuine users and impostors are less overlapped, the uncertain regions are smaller, and the total error rate is smaller. Contrary, a small vector length correspond to a wide overlapping of the score distribution, and to a biometric system with greater error rates.

4.2   Experiments Using the NIST-BSSR Matching Score Sets

The NIST BSSR1 multi-modal database contains scores from 517 users. For each user, the database contains one score set from the comparison of two right index fingerprints, one score set from the comparison of two left index fingerprints, and two score sets (from two separate matchers) from the comparison of two frontal faces. The score sets from the left (right) indexes are referred as "Li" ("Ri"). Each matching set contains 517 genuine scores and $266,772$ (i.e. 516×517) impostor scores. We transformed the given scores into distances, i.e. a great (small) score representing a similarity (non-similarity) between two collected samples is transformed to a small (great) distance between the same two samples. As a part of our experiments we derived the optimized thresholds for the bi-modal systems developed from the BSSR1 database; and considered the Li-Ri and Ri-Li 2-matcher combinations.

The NIST BSSR2 multi-modal database contains scores from 6000 users. For each user, the database contains one score set from the comparison of two right index fingerprints, and one score

Table 5: Computation results for NIST-BSSR1 instances

match		LS			CD Gamma-Normal			CD Gamma-Gamma		
1st	2nd	FAR	GAR	TER	FAR	GAR	TER	FAR	GAR	TER
Li	Ri	0.15%	94.59%	5.57%	0.62%	94.39%	6.23%	0.69%	95.36%	5.33%
Ri	Li	0.11%	93.82%	6.30%	0.35%	94.78%	5.58%	0.73%	95.30%	5.37%

Table 6: Computation results for NIST-BSSR2 instances

match		LS			CD Gamma-Normal			CD Gamma-Gamma		
1st	2nd	FAR	GAR	TER	FAR	GAR	TER	FAR	GAR	TER
Li	Ri	0.96%	95.87%	5.09%	1.03%	94.59%	6.46%	0.61%	95.42%	5.19%
Ri	Li	1.55%	96.12%	5.4%	0.75%	94.44%	6.40%	0.62%	95.44%	5.19%

set from the comparison of two left index fingerprints. The score set from the left (right) indexes are referred as "Li" ("Ri"). Each matching set contains 6000 genuine scores and 35,994,000 (i.e 5999×6000) impostor scores. As for the BSSR1 dataset, we transformed the similarity scores into distances; derived the optimized thresholds; and considered both possible combinations.

Tables 5 and 6 report the numerical results obtained by running CD on NIST-BSSR1 and NIST-BSSR2. In these tables we include the results obtained by running LS in order to compare the performances, and the results obtained by two versions of the CD. The first version used Gamma distribution for both genuine users and impostors, while the second version used Gamma distribution for the genuine users and the Normal distribution for the impostors. According to these experiments, it is better to choose the continuous distribution Gamma for both genuine users and impostors. For BSSR1 instances, the total error rate for CD Gamma-Gamma is considerably smaller than the total error rate obtained by LS method. For BSSR2 instances the total error rate obtained with CD Gamma-Gamma is better then the one obtained by LS, in the case when checking the left fingerprint is the first modality, and checking the right fingerprint is the second modality in the biometric system.

Many papers referred to the same matching score dataset (see for instance [6], [9], [16], and [17]). Searching for papers that report experimental results to compare with, we faced two main issues. First issue is related to the fact that there is no consistent way to deal with this database. For example, some authors randomly selected the scores for the system training, and used the rest for evaluation, thus making impossible to repeat their experiments; and/or discarded some scores due to apparent template acquisition errors, but without explaining which scores were discarded [16]. The second one is related to the fact that we propose a set of thresholds to be used in the multi-modal system; but we do not generate a ROC curve, thus the Equal Error Rate (EER) cannot be employed straightforward to validate our approach.

5   Conclusions and Future Works

In this paper we proposed a novel approach to determine the upper and lower acceptance thresholds in sequential multi-modal biometric matching systems. The new approach uses continuous distribution for the score distributions approximations of both genuine users and impostors. It improved the results obtained by the least square approximation approach. In the present paper we introduced the general mathematical model that may be used to minimize the total error function, and derive the thresholds in a general multi-modal system with N modalities. We solved the non-linear optimization problem numerically. The paper is an extension of [15], where the linear approximation of the biometric scores based on the least squares method was

introduced, and the optimization model was given biometric systems with 2 modalities.

One of the advantages of the new approach is the fact that it relays on less input parameters than the previous method. The method based on the least square approximation included the computation of the frequencies needed for constructing the histograms for the score distributions. The number of the intervals for the histogram is theoretically uncertain for guaranteeing the best results.

Generally, the optimization of the thresholds for a serial multi-modal system serves the a priori need of the decision maker when building a convenient multi-modal biometric system. Our method that provides optimized thresholds for a multi-modal biometric system is fast, and relatively simple to implement. For a biometric system that works in real time, the existence of multiple matchings, and the possibility that the unproblematic genuine users pass the system after the first match with a low false rejection rate, offers the advantage of an increased speed of the matching process. Moreover, if the first match is based on a face image, or a video record that may be taken even without user's will, then the process is even faster.

The numerical results of our experiments were reported in the paper. For the majority of our experiments on random generated instances, the pair (FAR, GAR), obtained by our method, dominates at least one pair (FAR, GAR) from the set of the final results obtained by the fusion based method. The experiments showed a good performance of the sequential bi-modal biometric matching system based on optimized thresholds and continuous approximation of the distribution scores.

Our numerical results on real life datasets were also included in the paper. We referred to the NIST-BSSR1 and BSSR2 data sets, and intend to extend our experiments to more benchmark data from the literature. We performed some experiments with multi-modal biometric systems with more than two matchings, but the instances were not yet statistically relevant. The research may advance by refining the approximation step needed for obtaining the expressions for the false acceptance and false rejection rates to be used for finding the optimized thresholds. One direction is to search for the fitting distributions that approximate well the initial score distributions just along the uncertain region. It is also possible to involve other metrics, instead of the Euclidean distance, to compare the samples vectors.

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