Genetic Programming for Multibiometrics

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Abstract

Biometric systems suffer from some drawbacks: a biometric system can provide in general good performances except with some individuals as its performance depends highly on the quality of the capture... One solution to solve some of these problems is to use multibiometrics where different biometric systems are combined together (multiple captures of the same biometric modality, multiple feature extraction algorithms, multiple biometric modalities...). In this paper, we are interested in score level fusion functions application (i.e., we use a multibiometric authentication scheme which accept or deny the claimant for using an application). In the state of the art, the weighted sum of scores (which is a linear classifier) and the use of an SVM (which is a non linear classifier) provided by different biometric systems provid one of the best performances. We present a new method based on the use of genetic programming giving similar or better performances (depending on the complexity of the database). We derive a score fusion function by assembling some classical primitives functions (+, *,-, ...). We have validated the proposed method on three significant biometric benchmark datasets from the state of the art. Keywords: Multibiometrics, Genetic Programming, Score fusion,

Authentication.

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1 1. Introduction

² 1.1. Objective

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Every day, new evolutions are brought in the biometric field of research. These evolutions include the proposition of new algorithms with better performances, new approaches (cancelable biometrics, soft biometrics, ...) and even new biometric modalities (like finger knuckle recognition [1], for example). There are many different biometric modalites, each classified among three main families (even if we can find a more precise topology in the literature) :

biological: recognition based on the analysis of biological data linked to an
individual (e.g., DNA analysis [2], the odor [3], the analysis of the blood
of different physiological signals, as well as heart beat or EEG [4]);

• *behavioural* : based on the analysis of an individual behaviour while he is performing a specific task (e.g., keystroke dynamics [5], online handwritten signature [6], the way of using the mouse of the computer [7], voice recognition [8], gait dynamics (way of walking) [9] or way of driving [10]);

morphological based on the recognition of different particular physical patterns, which are, for most people, permanent and unique (e.g., face recognition [11], fingerprint recognition [12], hand shape recognition [13], or
 blood vessel [14], ...).

Nevertheless, there will always be some users for which a biometric modality 20 (or method applied to this modality) gives bad results, whereas, they are better 21 in average. These low performances can be implied by different facts: the quality 22 of the capture, the instant of acquisition and the individual itself but they have 23 the same implication (impostors can be accepted or user need to authenticate 24 themselves several times on the system before being accepted). Multibiometrics 25 allow to solve this problem while obtaining better performances (i.e., better 26 security by accepting less impostors and better user acceptance by rejecting less 27 genuine users) and by expecting that errors of the different modalities are not 28

²⁹ correlated. In this paper, we propose a generic approach for multibiometric
³⁰ systems.

³¹ We can find different types of biometric multimodalites [15]. They use:

 different sensors of the same biometric modality (i.e., capacitive or resistive sensors for fingerprint acquisition);

2. several different representations for the same capture (i.e., use of points
 of interest or texture for face or fingerprint recognition);

³⁶ 3. different biometric modalities (i.e., face and fingerprint recognition);

4. different instances of the same modality (i.e., left and right eye for iris
recognition);

5. multiple captures (i.e., 25 images per second in a video used for face recognition);

6. an hybrid system composed of the association of the previous ones.

We are interested in the first four cases in this paper. Our objective is to automatically generate fusion functions which combine the scores provided by different biometric systems in order to obtain the most efficient multibiometrics authentication scheme.

46 1.2. Background

47 1.2.1. Performance Evaluation

In order to compare different multibiometrics systems, we need to present the how to evaluate them. Several works have already done on the evaluation of biometric systems [16, 17]. Evaluation is generally realized within three aspects:

performance: it has for objective to measure various statistical criteria
 on the performance of the system (*Capacity* [18], *EER*, *Failure To En- roll (FTE)*, *Failure To Acquire (FTA)*, computation time, *ROC* curves,
 etc [17]);

acceptability: it gives some information on the individuals' *perception*,
 opinions and *acceptance* regarding the system;

security: it quantifies how well a biometric system (algorithms and devices) can resist to several types of logical and physical attacks such as
 Denial of Service (DoS) attack.

In this paper, we are only interested in performance evaluation (because the fusion approach is not modality dependant and perception and security depend on the used modalities). The main performance metrics are the following ones:

- FAR (False Acceptance Rate) which represents the ratio of impostors accepted by the system;
- FRR (False Rejection Rate) which represents the ratio of genuine users rejected by the system;
- *EER (Error Equal Rate)* which is the error rate when the system is configured in order to obtain a *FAR* equal to the *FRR*;
- ROC (Receiver Operating Characteristic) curve which plots the FRR depending on the FAR and gives an overall overview of system performance;
- AUC (Area Under the Curve) which gives the area under the ROC curve.
 In our case, smaller is better. It is a way to globally compare performance
 of different biometric systems.

⁷⁴ We can also present the *HTER* (Half Total Error Rate) which is the mean ⁷⁵ between the *FAR* and *FRR* for a given threshold (this error rate is interesting ⁷⁶ when we cannot get the *EER*).

17 1.2.2. Biometric Fusion

There are several studies on multibiometrics. The fusion can be operated ondifferent points of the mechanism:

• template fusion: the templates captured by different biometric systems are merged together, then the learning process is realized on these new templates [19, 20]. Figure 1(a) presents this type of fusion. The fusion

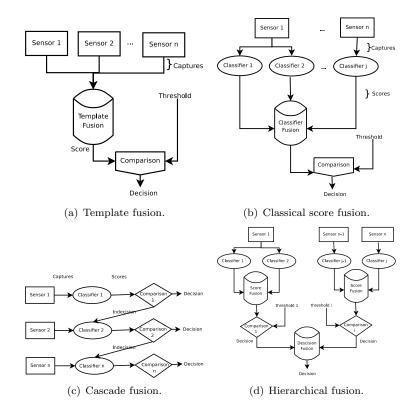
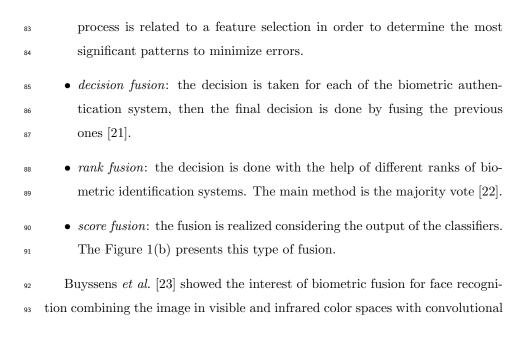


Figure 1: Illustration of different fusion mechanisms.



⁹⁴ neural networks. In [24], Mantalvao and Freire have combined keystroke dynam-⁹⁵ ics with voice recognition, it seems it is the first time that multibiometrics has ⁹⁶ been done with keystroke dynamics and another biometric modality. In [25], ⁹⁷ Hocquet *et al.* demonstrated the interest of fusion in keystroke dynamics in ⁹⁸ order to improve the recognition rates: three different keystroke dynamics func-⁹⁹ tions are used on the same capture. The sum operator (consisting in summing ¹⁰⁰ the different scores) seems to be the most powerful approach in the literature.

These fusion architectures are quite simple but powerful. Results can yet be 101 improved (in term of error rate or computation time) by using different archi-102 tectures. A cascade fusion [26] is another interesting approach. A first test is 103 done, if the user is correctly verified as the attended client or if it is detected 104 as an impostor, the algorithm stops. Otherwise, another biometric authentica-105 tion (with another capture from another modality) is proceeded until obtaining 106 a decision of acceptance or rejection, or reaching the end of the cascade. So, 107 instead of using one decision threshold, each test (except the last one) needs 108 two thresholds: one for rejection and one for acceptance. All scores between 109 these thresholds are considered in an indecision zone. This mechanism is pre-110 sented in Figure 1(c). Another advantage of this method is to decrease the 111 verification time by not using all the modalities, they are used only if necessary. 112 This method has been successfully applied on a multibiometric system using 113 face and fingerprint recognition in a mobile environment (where acquisition and 114 computation times are important) [26]. 115

Another kind of architecture has been proposed: it is a hierarchical fusion 116 scheme [27] (called multiple layers by their authors). Shen et al. have pre-117 sented this method with two different keystroke dynamics methods. The fusion 118 is done at different steps, and involves different mathematical operations on 119 scores (sum, weighted sum, product, min, max) and logical operations decision 120 (comparison to a threshold, or, and) on differents templates extracted from the 121 same capture. An extended version to any multibiometric system is presented 122 in Figure 1(d). We think our work can be seen as a generalization of this paper. 123

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It is also possible to model the distribution of the genuine and impostor matching scores, we talk about *Density-based score fusion*. In [28], scores are modelled with a Gaussian Mixture Model and have been tested on three multibiometric databases involving face, fingerprint, iris and speech modalities.

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Concerning non linear algorithms, Support Vector Machine (SVM) can also be used in a fusion process. Each score to combine is arranged in a vector and a training set is used to learn the SVM model. In [29], the SVM fusion to improve face recognition gives slightly better performances than weighted sum. Voice and online signature have been fused with SVM in [30]. In this experiment, arithmetic mean gives best results with noise free data, while SVM gives equivalent results with noisy data.

137 1.3. Discussion

In this paper, we are interested in biometric modality independent *transformationbased score fusion* [28] where the matching scores are first normalized and second combined. We have previously seen that in this case, arbitrary functions are often used. Our work is based on these various fusion architectures based on score fusion in order to produce a score fusion function automatically generated with genetic programming [31].

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¹⁴⁵ By the way, the definition of a fusion architecture is still an open issue ¹⁴⁶ in the multibiometrics research field [32], because the range of possible fusion ¹⁴⁷ configurations is very large. We think that using automatically generated fusion ¹⁴⁸ functions can bring a new solution to solve this kind of problems.

¹⁴⁹ 2. Material and Methods

In this section, we present all the required information in order to allow other researchers to reproduce our experiment.

152 2.1. Biometric databases

As it is well known that results can be highly related to the database, for this 153 study, we have used three different multibiometric databases: the first one is the 154 BSSR1 [33] distributed by the NIST [34] (referenced as BSSR1 in the paper), 155 the second one is a database we have created for this purpose (referenced as 156 PRIVATE in the paper) and the third one is a subset of scores computed with 157 the BANCA [35] database (referenced as BANCA in the text. In fact, BANCA 158 database is composed of templates. We have used the scores available in [36]). 159 As all these databases are multi-modal, the scores are presented with tuples: 160 the ith tuple of scores is represented as $s_i = (s_i^1, s_i^2, ..., s_i^n)$ for a database having 161 n modalities (in our case, $n \in \{4, 5\}$). 162

The three databases are presented in detail in the following subsections while
 Table 1 presents a summary of their description.

165 2.1.1. BSSR1 database

The BSSR1 [33] database consists of an ensemble of scores sets from different 166 biometric systems. In this study, we are interested in the subset containing 167 the scores of two facial recognition systems and the two scores of a fingerprint 168 recognition system applied to two different fingers for 512 users. We have 512 169 tuples of intra-scores (comparison of the capture of an individual with its model) 170 and 512 * 511 = 261,632 tuples of inter-scores (comparison of the capture of an 171 individual with the model of another individual). Each tuple is composed of 4 172 scores: $s = (s_{bssr1}^1, s_{bssr1}^2, s_{bssr1}^3, s_{bssr1}^4)$, they respectively represent the score of 173 the algorithm A of face recognition, the score of algorithm B of face recognition 174 (the same face image is used for the two algorithms), the score of the fingerprint 175 recognition with left index, the score of fingerprint recognition with right index. 176 This database has been used several times in the literature [28, 37]. 177

178 2.1.2. PRIVATE database

The second database is a chimeric one we have created by combining two public biometric template databases: the AR [38] for the facial recognition and ¹⁸¹ the GREYC keystroke [39] for keystroke dynamics.

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The AR database is composed of frontal facial images of 126 individuals 183 under different facial expression, illumination conditions or occlusions. This is 184 a quite difficult database in reason of these specificities. These images have 185 been taken during two different sessions with 13 captures per session. The 186 GREYC keystroke contains the captures on several session during a two months 187 period involving 133 individuals. Users were asked to type the password "greyc 188 laboratory" 6 times on a laptop and 6 times on an USB keyboard by interleaving 189 the typings. 190

We have selected the first 100 individual of the AR database and we have associated each of these individuals to another one in a subset of the GREYC keystroke database having 5 sessions of captures. We then used the 10 first captures to create the model of each user and the 16 remaining ones to compute the intra and inter scores.

These scores have been computed by using two different methods for the face recognition (the scores $s_{private}^1$ and $s_{private}^2$ and three different ones for the keystroke dynamics ($s_{private}^3$, $s_{private}^4$ and $s_{private}^5$ scores). The face recognition algorithms are based on eigenfaces [11] and SIFT keypoints [40] comparisons between images from the model and the capture [41]. Keystroke dynamics scores have been computed by using different methods [42] based on SVM, statistical information and rhythm measures.

203 2.1.3. BANCA database

The lastest used benchmark is a subset of scores produced by the help of 204 the BANCA database [36]. The selected scores correspond to the following 205 one labelled: IDIAP_voice_gmm_auto_scale_25_100_pca.scores for s_{banca}^1 , SUR-206 REY_face_nc_man_scale_100.scores for s_{banca}^2 , SURREY_face_svm_man_scale_0.13.scores 207 for s_{banca}^3 and 208 UC3M_voice_gmm_auto_scale_10_100.scores for s_{banca}^4 . 209 We have empirically chosen this subset. G1 set is used as the learning set, 210

Table 1: Summary of the different databases used to validate the proposed method

Nb of	BSSR1	PRIVATE	BANCA
users	512	100	208
intra tuple	512	1600	467
inter tuple	261632	158400	624
items/tuples	4	5	4

- while G2 set is used as the validation set. Users from G1 are different than users from G2.
- 213 2.1.4. Discussion

²¹⁴ The main differences between these three benchmarks are:

- the biometric modalities used in BSSR1 and BANCA have better performances than the ones in PRIVATE;
- the quantity of intra-scores is more important in PRIVATE (only one tuple
 of intra-score per user in BSSR1 instead of several in PRIVATE);
- BSSR1 and BANCA are databases of scores (by the way, we do not know the biometric systems having generated them) whereas PRIVATE is a database of templates (we had to compute the scores);
- BSSR1 and BANCA are more adapted to physical access control applications (i.e., a building is protected by a multi-modal biometric system), while PRIVATE is more adapted to logical access control (i.e., the authentication to a Web service is protected by a multi-modal biometric system).

In the following subsections, we describe the proposed methodology to automatically generate a score fusion function with genetic programming. We adopt the classical score fusion context described in Figure 1(b). Before using the scores provided by different biometric systems, we need to normalize them.

231 2.2. Score Normalization

It is necessary to normalize the various scores before operating the fusion process: indeed, these scores come from different classifiers and their values do not

necessarily evolve within the same interval. We have chosen to use the tanh [43] 234 operator to normalize the scores of each modality. Equation (1) presents the 235 normalization method, where μ^m_{gen} and σ^m_{gen} respectively represents the average 236 and standard deviation of the genuine scores of the modality m. The genuine 237 scores are obtained by comparing the model and the capture of the same user: 238 they are also called the *intra scores*. In opposition, the *inter scores* are obtained 239 by comparing the model of a user with the capture of other users. score' and 240 score respectively represents the scores after and before normalisation. 241

$$score' = \frac{1}{2} \left\{ tanh\left(\frac{1}{100} \left(\frac{score - \mu_{gen}^m}{\sigma_{gen}^m}\right) + 1 \right\}$$
(1)

We have selected this normalization procedure from the state of the art because it is known to be stable [44] and does not use impostors patterns which can be hard or impossible to obtain in a real application. The aim of this paper is not to analyse the performance of biometric systems depending on the normalization procedure, but to present a new multibiometrics fusion procedure. The scores of each modality have been normalized using this procedure.

248 2.3. Fusion Procedure

In this study, we have chosen to use genetic programming [31] in order to 249 generate score fusion functions. Genetic programming belongs to the family of 250 evolutionary algorithms and its scheme is quite similar to the one of genetic 251 algorithms [45]: a population of computer programs (possibly represented by a 252 tree) evolves during several generations; different genetic operators are used to 253 create the new population. Programs are evaluated by using a fitness function 254 which produces a value that is used for their comparisons and gives a probability 255 of selection during the tournaments. In a system where the computer programs 256 are represented by trees, their leaves mainly represent the entries of the problem, 257 the root gives the solution to the problem and the other nodes are the various 258 functions taking into arguments the values of their children nodes. 259

The leaves are called terminals and can be of several kinds: (a) pseudovariables containing the real entries of the problem (in our case, the list of scores of each modality), (b) some constants possibly randomly generated, (c)
functions without any arguments having any side effect, or (d) some ordinary
variables.

The different genetic operators usually used during the evolution are (a) the crossover, where randomly choose sub-trees have two different trees are exchanged, (b) the mutation, where a sub-tree is destroyed and replaced by another one randomly generated, or (c) the copy, where the tree is conserved in the next generation. The different steps of a genetic programming engine are presented as following:

An initial population is randomly generated. This population is composed
 of computer programs using the available functions and terminals. The
 trees are built using a recursive procedure.

274 2. The following steps are repeated until the termination criterion is satis275 fied (the fitness function has reached the right value, or we reached the
276 maximum number of generations).

(a) Computation of the fitness measure of each program (the programming is evaluated according to its input data).

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- (b) Selection of programs with a probability based on their fitness to apply them the genetic operations.
- (c) Creation of the new generation of programs by applying the follow ing genetic operations (depending on their probabilities) to the pre viously selected programs:
 - Reproduction: the individual is copied to the new population.
 - Crossover: A new offspring program is created by recombining randomly chosen parts from two select programs. An example is provided in Figure 2.
 - Mutation: A new offspring program is created by mutating one node of the selected program at a randomly chosen place. An example is provided in Figure 3.
- 3. the single best program of the whole population is designated as the winner. This can be the solution or an approximate solution to the problem.

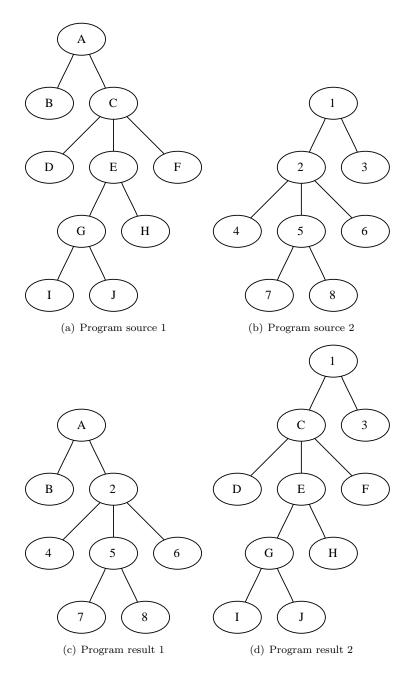


Figure 2: Crossover in genetic programming: node C from tree 1 is exchanged with node 2 from tree 2. Program result 1 is the new individual to add to the new generation.

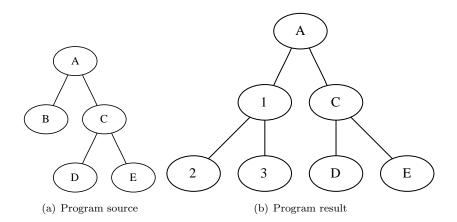


Figure 3: Mutation in genetic programming: node B is replaced by another sub-tree.

Different applications to genetic programming are presented in [46] as well 294 as their bibliographic references. The fields of these applications can be listed 295 in curve fitting, data modelling, symbolic regression, image and signal process-296 ing, economics, industrial process control, medicine, biology, bioinformatics, 297 compression... but, it seems, so far of our knowledge, that it has not been 298 yet applied to multibiometrics. We only found one reference on genetic pro-200 gramming in the biometrics field. In this paper [47], authors have used genetic 300 programming to learn speaker recognition programs. They have used an island 301 model where different islands operate their genetic programming evolution, and, 302 after each generation some individuals are able to leave to another island. The 303 obtained performance was similar to the state of the art in speaker recognition 304 in normal conditions, but, the generated systems performed better in degraded 305 conditions. 306

More information about the configuration of the genetic programming system is presented in the next section.

³⁰⁹ 2.4. Parameters of the Genetic Programming

We want to use a score fusion function that returns a score related to the performance of a multibiometric system. This score has to be compared with a threshold in order to make the decision of acceptance or rejection of the user. In this case, none logical operation is required in the generated programs and different information can be extracted from the result of the fusion function (we can compute the ROC curve, the EER, ...).

316 2.4.1. Fitness Function

The EER (Error Equal Rate) is usually used to compare the performance of different biometric systems together. A low EER means that FAR and FRR are both low and the system has a good performance if its threshold is configured accordingly to obtain this value. For this reason, we have chosen to use this running point to evaluate the performance of the generated score fusion functions.

To compute the EER, we consider the highest and lowest values in the final 323 scores generated by the genetic programming. Then, we set a threshold at the 324 lowest score and linearly increment it until obtaining the highest score value in 325 1000 steps. For each of these steps, we compute the FAR (comparison between 326 the threshold and the inter scores) and FRR (comparison between the threshold 327 and the intra scores). The ROC curve can be obtained by plotting all these 328 couples of (FAR, FRR), while the EER is the mean of FAR and FRR for the 329 couple having the lowest absolute difference. So, the fitness function is fitness =330 $(FAR_i + FRR_i)/2$, where i is the threshold for which $abs(FAR_i - FRR_i)$ is 331 minimal. 332

333 2.4.2. Genetic Programming Parameters

In this section, we present the various parameters used in the genetic programming algorithm. Table 2 presents the various parameters of the evolutionary algorithm.

To achieve this experiment, we used the PySTEP [48] library. The generated programs contain basic functions (+, -, *, /, min, max, avg). The terminals are the scores of the biometric systems and random constants between 0 and 1. The whole fitness cases are completed with a single tree evaluation, thanks to the numpy [49] library. Each fitness case is a tuple of scores (where each score

Table 2: Summary of the configuration of the genetic programming iterations. Numbers used in function set can be scores or constants.

Configuration	Values
Objective	Generates a function producing a multibiometrics score.
Functions set	 +: addition of two numbers, -: subtraction of two numbers, *: multiplication of two numbers, /: division of two numbers, min: returns the minimum of two numbers, avg: returns the mean of two numbers
Fitness function	Computes the EER of the multibiometric system
Terminal set	BSSR1PRIVATEBANCA• a: scores from s_{bssr1}^1 , • c: scores from s_{bssr1}^2 , • d: scores from s_{bssr1}^3 , • d: scores from s_{bssr1}^4 , • 50 constants lin- early distributed between 0 and 1.• a, b, c: keystroke dynamics scores $(s_{private}^3, s_{private}^4), s_{private}^4)$, • d, e: face recognition scores $(s_{private}^1, s_{private}^2), s_{banca}^3$, • d, e: face recognition scores $(s_{private}^1, s_{private}^2), s_{banca}^4$, • 50 constants lin- early distributed between 0 and 1.• a: scores from s_{banca}^1 , • b: scores from s_{banca}^4 , • 50 constants lin- early distributed between 0 and 1.
Initial popula-	500 random trees with a depth between 2 and 8 built with the ramped half and
tion Evolution pa- rameters	 half method. Number of individuals: 500, Maximal number of generations: 50, Depth limited to: 8, Probability of crossover: 45%, Probability of mutation: 50% Probability of mutation: 50% Probability of mutation: 50%
Termination cri- terion	Best individual has a fitness inferior at 0.001 (by the way, this value would never be met) or maximal number of generations reached.
Learning set	First half of the intra-scores tuples and first half of the inter-scores tuples.
Validating set	Second half of the intra-scores tuples and second half of the inter-scores tuples.

³⁴² comes from a different biometric modality) and its result value is the score
³⁴³ returned by the generated multimodal system. The global fitness value of a tree
³⁴⁴ is the EER value computed with the previously generated scores (computation
³⁴⁵ of the ROC curve, then reading of the EER value from it).

PySTEP is a strongly typed genetic programming engine, but, in our case, we do not use any particular constraints: the root node can only have a function as child (no terminal in order to avoid an unimodal system, and any function of the set), while the other function nodes can have any of the functions as children as well as any of the terminals.

The maximal depth of the generated trees is set to 8. In order to avoid 351 to stay in a local minimal solution, the mutation probability is set to 50%. 352 500 individuals evolve during 50 generations. We have set this few quantities, 353 because during our investigations, using a population of 5000 individuals on 354 100 generations did not give so much better results (gain not interesting in 355 comparison to the computation time). Each database has been splitted in two 356 sets of equal size: the first half is the learning set and the second half is the 357 validation set. 358

The mutation rate is set to 50%, the cross-over rate to 45% and the reproduction rate to 5%. For mutation and cross-over the individuals are selected with a tournament of size 10 with a probability of 80% to select the best individual. The same individual can be selected several times. For the reproduction, the individuals are selected with an elitism scheme: the 5% best individuals are copied from generation n - 1 to generation n. During a crossover, only the first offspring (of the two generated ones) is kept.

366 3. Results

In this section, we present the results of the generated fusion programs on the three benchmark data sets.

The results are compared to other functions from the state of the art: (a) the *min* rule which returns the minimum score value, (b) the *mul* rule which returns the product of all the scores, (c) the *sum* rule which returns the sum of the scores, (c) the *weight* rule which returns a weighted sum, and (d) an SVM implementation. The weighs of the weighted sum have been configured by using genetic algorithm on the training sets [50, 51] (in order to give the best results as possible). The fitness function is the value of the EER and the genetic algorithm engine must lower this value. Table 3 presents the configuration of the genetic algorithm.

Parameter	Value
Population	5000
Generations	500
Chromosome signification	weights of the fu-
	sion functions
Chromosome values interval	[-10; 10]
Fitness	EER on the gen-
	erated function
Selection	normalized ge-
	metric selection
	(probability of
	0.9)
Elitism	True

Table 3: Configuration of the genetic algorithm to set the weights of the weighted sum

For the SVM, we have computed the best parameters (i.e., search the Cand γ parameter giving the lowest error rate) using the learning database on a 5-fold cross validation scheme. We have used the *easy.py* script provided with libSVM [52] for this purpose. We have then tested the performance on the validation set. We only obtain on functional point (and not a curve) when using an SVM. That's why we have used the HTER instead of the EER.

Table 4 presents the performances, for the three databases, of each biometric systems, fusion mechanisms from the sate of the art, and our contribution.

Concerning the state of the art performances, can see that the simple fusion functions *sum* and *mul* tend to give better performances compared to the best biometric method of each database, but they are outperform by the *weight* rule. The *min* operator gives quite bad results (it does not improve the best biometric system). The SVM method gives good results but is outperform by the weight
method.

Table 5 presents the gain of performance against the *weight* operator (which gives the best results in Table 4) in term of EER and AUC.

This gain is computed as following:

$$gain = 100 \frac{(EER_{weight} - EER_{gpfunc})}{EER_{weight}}$$
(2)

where EER_{weight} and EER_{qpfunc} are respectively the EER values of the weighted 394 fusion and the generated score fusion function (the same procedure is used for 395 the AUC). Better values than the weighted sum are represented in **bold**. The 396 EER gives a local performance for one running point (system configured in or-397 der to obtain an FAR equal to the FRR), while the AUC gives a gives a global 398 performance of the whole system. These two information are really interesting 399 to use when comparing biometric systems. Figure 4 presents the ROC curves 400 of the generated programs against the weighted sum. Performance of the initial 401 biometric systems are not represented, because we have already seen that they 402 are worst than the weighted sum (same remark for the other fusion functions). 403 Logarithmic scales are used, because error rates are quite small. 404

We can see from Table 5 and Figure 4 that most of the time, the automati-405 cally generated functions with genetic programming give slightly better results 406 than the weighted sum. These improvements can be local and global and vary 407 between 16% and 59% for the EER and 0.05% and 76% for the area under 408 the curve. When there is no improvement, the results are equal or (in one 409 case) slightly inferior. Even if there is some difference between training (not 410 represented in this paper) and validating sets, we cannot observe overfitting 411 problem. The BSSR1 dataset presents the largest difference of performance 412 between training and validation sets, but, the results are still better than the 413 ones from the state of the art (and the same problem can be observe with the 414 weighted sum). By the way, the fitness criterion has never been met, we did 415 not achieve to obtain fusion functions doing no error. So, the evolution always 416

Table 4: Performance (HTER in %) of the initial methods $(s_*^1, s_*^2, s_*^3, s_*^4, s_*^5)$, the state of the art fusion functions (sum, min, mul, weight) and our proposal on the three databases. Bold values represent better performance than the initial biometric systems, and * represents fusion results better than state of the art.

(a) BSSR1			
Method		HTER	
		BSSR1	
Biometric systems	s_{bssr1}^1	04.30%	
	s^2_{bssr1}	06.19%	
	s^3_{bssr1}	08.41%	
	$s^1_{bssr1}\ s^2_{bssr1}\ s^3_{bssr1}\ s^3_{bssr1}\ s^4_{bssr1}$	04.54%	
Fusion functions	sum	00.70%	
	min	05.04%	
	mul	00.70%	
	weight	00.38%	
	SVM	0.77% (FAR=1.16%, FRR=0.39%)	
Proposal	$_{\rm gpI}$	0.40%	

(b) PRIVATE

Method		HTER	
PRIVATE			
Biometric systems	$s^1_{private}$	8.92%	
	$s^2_{private}$	11.53%	
	$s^3_{private}$	15.69%	
		06.21%	
	$s^{\star}_{private} \ s^{5}_{private}$	31.43%	
	sum	02.70%	
	min	13.72%	
Fusion functions	mul	02.67%	
	weight	02.26%	
	SVM	05.47% (FAR=10.87, FRR= 0.07%)	
Proposal	gpA	$01.57\%^{*}$	

(c) BANCA

Method		HTER	
BANCA			
Biometric systems	s^1_{banca}	04.38%	
	$s^2_{banca}\ s^3_{banca}$	11.54%	
	s^3_{banca}	08.97%	
	s^4_{banca}	07.32%	
Fusion functions	sum	01.28%	
	min	04.38%	
	mul	01.28%	
	weight	00.91%	
	SVM	01.01% (FAR= 1.71 %, FRR=0.32%)	
Proposal	$\mathrm{gp}\Phi$	$00.75\%^{*}$	

Table 5: Performance gain betwain our proposal and the weighted sum (which gives the best results in the methods of the state of the art).

Database	EER	AUC
BSSR1	-5.26%	0.05%
PRIVATE	34.85%	23.85%
BANCA	17.58%	76.74%

417 ended when reaching the 50^{th} generation.

Figure 5 represents the fitness evolution during all the generations of one 418 genetic programming run on the BSSR1 database. A logarithmic scale has been 419 used to give more importance to the low values and track easier the fitness 420 evolution of the best individual of each generation. We can observe the same 421 kind of results with the other databases. The fitness convergence appears several 422 generations before the end of the computation. The worst program of each 423 generation is always very bad which implies that the standard deviation of the 424 fitness is also always quite huge. This can be explained by the high quantity of 425 mutation probability and the low quantity of good programs kept for the next 426 generation. When running the experiment several times, we obtain the same 427 convergence value. We can say that we reach the maximum performance of the 428 system. 429

430 4. Discussion

The score fusion functions generated by the proposed approach give a slightly 431 better performance than the fusion functions used in the state of the art in multi-432 biometrics. We can argue that genetic programming is adapted to automatically 433 define score fusion functions returning a score. The tradeoff of this performance 434 gain is the need of training patterns which are not necessary for sum, mul or 435 min (but this requirement is already present for the weighted sum or the use 436 of an SVM). By the way, this is not really a problem, because we already need 437 training patterns to configure the threshold of decision (if we do not want to do 438 it empirically) or if we need to normalize the scores before doing the fusion. 439

440 Another problem inherent to genetic programming is the complexity of the

generated programs. It is probable that some subtrees could be pruned or sim-441 plified without loosing performance. Another trail would be to add regulariza-442 tion parameter to the fitness function (for example, the number of nodes or the 443 depth of the tree). Generated programs would be more readable by an human 444 and quicker to interpret. Figure 6 presents a simple generated tree (depend-445 ing on the database, they can be more or less complex). Even if the program 446 is quite short (comparing to the other generated functions), it includes useless 447 code (e.g., the subtree avg(a, a - 1/12) could be simplified by a - 1/24). Some 448 generated trees include preprocessing steps by not using all the modalities in 449 the terminal set. 450

Genetic programming generated score fusion functions give performance slightly equal or better than genetic algorithm configured weighted sum. Even if computation time is more important than for genetic algorithm, we can think that the gain is not really important between the two methods, but, to obtain these results, genetic programming needed a population ten times smaller and ten times less of generations.

457 5. Conclusion

We propose in this paper a new approach for multibiometrics based on the automatic generation of score fusion functions. We have seen interesting approaches in the state of the art and decided to improve them by automatically generated score fusion programs by the help of genetic programming.

Our contribution concerns the designing of multibiometric systems while 462 using a generic approach based on genetic programming (and is inspired from the 463 state of the art architectures). The proposed method returns a multibiometrics 464 score to be compared with a defined threshold. The proposed multibiometric 465 system has been heavily tested on three different multibiometric databases. We 466 obtained great improvements compared to classical fusion functions used in the 467 state of the art. We hope to have opened a new path in the fusion of biometric 468 systems thanks to genetic programming. 469

Results could surely be improved by using different parameters in the genetic
programming engine (i.e., more individuals and generations, different range of
constants, different functions, ...). It could be interesting to test other performance metrics could be improved by adding quality measures of the capture,
and if genetic programming could produce template fusion programs.

475 6. Acknowledgment

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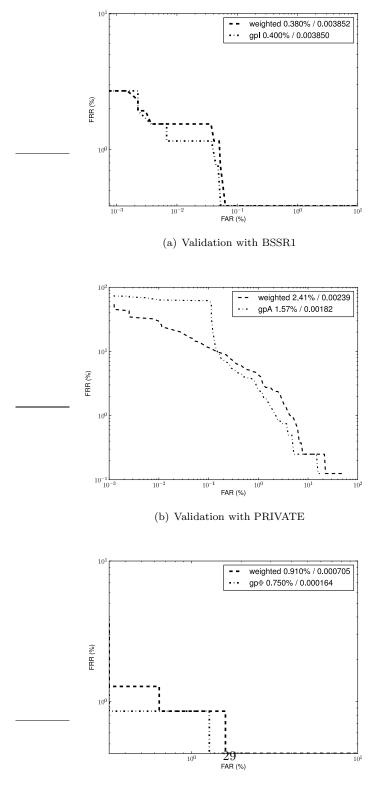
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(c) Validation with BANCA

Figure 4: ROC curves of the fusion systems from the state of the art and with genetic programming. The EER of each fusion function is presented in the legend. Note the use of a logarithmic scale.

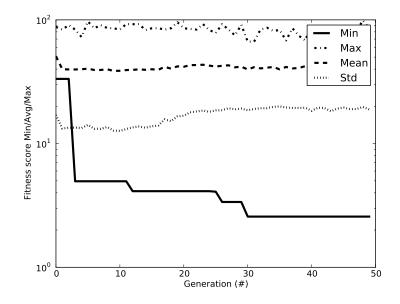


Figure 5: Fitness evolution of one run of the genetic programming evolution. The max, min, mean and std values of the fitness are represented. We want to minimize the fitness value, so lower is better.

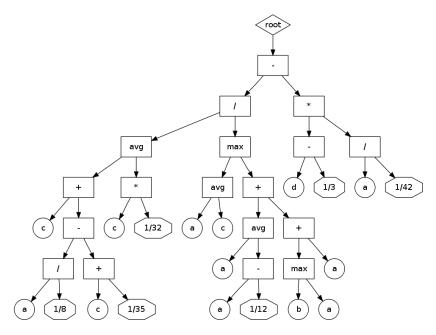


Figure 6: Sample of a "simple" generated program. We can observe the complexity of the generated fusion function.