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IMAGE & SIGNAL PROCESSING

Feature Selection Using Multi-Objective Modified Genetic Algorithm in Multimodal Biometric System

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Abstract
Today the multimodal biometric system has become a major area of study that is identified with applications of a large size in a recognition system. The feature selection is probably found to be the best factor to be optimized and is an on-going challenge in the midst of the optimization problems in the human recognition system. The feature selection aspires to bring down the number of the features, remove all types of redundant data and noise which result in a very high rate of recognition. The step further effects on the human recognition system and its performance. The work further presents a newer biometric system of verification that was multimodal and based on three different features which are the face, the hand vein, and the ear. This has today emerged as an extensively researched topic which spans various disciplines like signal processing, pattern recognition, and also computer vision. The features have been extracted by making use of the Incremental Principal Component Analysis (IPCA). Further, the work presented another novel algorithm of feature selection which was based on the Multi-Objective Modified Genetic Algorithm (MOM-GA). The Genetic Algorithm (GA) had been modified by means of introducing a levy search as opposed to a process of mutation. The algorithm has also proved to be an effective method of computation in which the search space is found to be highly dimensional. A classifier that makes use of the K-Nearest Neighbour (KNN) for classifying all accurate features is used. There were some investigations that were carried out and these results proved that this MOM-GA feature selection algorithm had been found as that which can generate certain excellent results using a minimal set of chosen features.

Keywords Multimodal biometric system · Feature selection · Incremental principal component analysis (IPCA) · Genetic algorithm (GA) · Multi-objective modified using genetic algorithm (MOM-GA) · Levy search and K-nearest neighbor (KNN)

Introduction

The Biometric techniques have been used to a great extent to be a hedge against theft of identity. A method that was used to either identify or verify the individual's identity was based on their physiological or their behavioural traits. The physiological biometrics was based on the data that was derived from that of a direct dimension of one part of the human body. It includes the iris-scan, retina scan, facial recognition, hand geometry, fingerprint or the DNA. The biometrics of behaviour has been based on the data which is derived from any action that is taken by individuals in their behavioural traits. The characteristics of behavioural biometrics include voice recognition, signature scan, and keystroke-scan. A physiological or a behavioural trait of any human is used to be a biometric trait until such time it remains unique, permanent, collectible and universal. The premise to this is that the biometric can be a measurable feature or a behavioural trait which is a good indicator of the identity compared to the bequest system like a password or a PIN. The biometrics was first introduced in the year 1879 at the time Alphonse Bertillon (1853–1914), who was a French Criminologist, brought about an anthropometrical signalment also called the Bertillonage system to identify criminals. There was a method used for identification that was based on the anthropometry of various parts of the body that include the head, the fingers or the ear for which there is no change in size once it attains full growth. But

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there is a need for robustness and better accuracy for a biometric identification [1].

Today, multimodal biometrics has been gaining a lot of importance and is getting to be a very hot topic of research. The system of personal identity authentication which is based on the unimodal biometric is not widely acceptable to a certain user group or a particular situation. Thus, the technology of biometrics technology has been developed for alleviating all problems that are intrinsic to the unimodal systems. The multimodal biometric systems will be expected as being even more reliable owing to various pieces of evidences that are present for meeting the stringent performance along with their needs that have been imposed by these applications [2].

There are multimodal systems that can address all problems of the non-universality and they can provide the measures of anti-spoofing by making this challenging for the intruders to be able to spoof the biometric traits. One of the approaches to avoid the intruders to spoof the system is requesting the user to present one more random subset so that the systems further ensure that there is a live-user interacting at the point of acquisition. But, there is also a scheme of integration that is needed for fusing any information that is presented by their individual modalities. In addition to this, a multimodal biometric system can take more than a single feature into consideration. This can help in the identification and also the verification of the person having more accuracy even in case there are less matching scores.

A biometric fusion refers to a technique used for integrating the results of classification from every channel of biometrics. This multimodal fusion is a combination of various features of biometrics for improving strengths and reducing the limitations of all individual aspects. The scheme of fusion is efficient which influences to a great extent the accuracy of this biometric system. A multimodal biometric system with its fusion has a total of five modules [3]:

> **The Feature-level fusion**: Here, the signals will be processed initially and all feature vectors will be extracted from every single biometric trait. After this is done, feature vectors will be combined in order to form another composite feature vector that is classified again.
>
> **The Matching score level fusion**: for this level, as opposed to creating a combination of the feature vectors, they also get processed and the individual matching score will be identified and is combined in order to make a new classification. There are several techniques of statistical learning that are used for combining the match scores. This type of a match score-level fusion is known as the confidence-level fusion.
>
> **The Decision-level fusion**: here, each decision level fusion along with its modality is independently pre-classified and the features duly extracted from such a captured trait which is based on the features are extracted. The last and final classification based on a fusion of the outputs of various other modalities [4].
>
> **The Rank-level fusion**: this fusion was the usage of subsets that are sorted into various matches from their individual modalities for making a final decision. As all outputs in the biometric modalities were expressed as performance ranking, there may not be any compatibility found among these fusion features.
>
> **The Sensor-level fusion**: a direct fusion at the level of the sensor is through a concatenation of the information used for fusion. This has further been conditioned based on the compatibility found among that of the raw sources of data.

A feature extraction is a very critical stage in processing for the identification of biometrics. But the actual usefulness of the features which have been extracted may further include some redundant or irrelevant features that can result in a decrease in the performance of the biometric systems [5]. An objective of this feature selection was the identification of relevant and the suitable feature subsets for various datasets to represent all domains of the application without compromising on the prediction accuracy.

But owing to the problem of the curse of dimensionality, there were several features that can occupy the feature space and the system also suffers from certain limitations. A search space has been explored by means of using the algorithms of feature selection for identifying an optimal and discriminatory subset of all features. The algorithms of feature selection may get grouped into the filters and the wrappers and their approaches that were identified based on the option of a metric of evaluation and also identify some better performance measures.

Feature selection [6] contains finding relevant features that permit an objective function that needs to be optimized. A common approach that is used in a feature selection are: The Sequential Forward Selection (SFS), the Sequential Backward Selection (SBS) and finally the Sequential Floating Forward Selection (SFFS). All approaches will begin with a new initial subset and then sequentially either add or remove features which can locally optimize an objective function. Contrastingly, all exhaustive searches are quite expensive, algorithmically complex and time-consuming. Thus, there are some new approaches that make use of the artificial intelligence which has been proposed for solving problems in feature selection.

The meta-heuristics are now a recent generation in the methods of optimization that has been proposed in order to solve problems which are complex [7]. The GA has been inspired by Darwin's theory of biological evolutions. The Particle Swarm Optimization (PSO) will further simulate the social interaction and its behaviour of the fish schooling and bird flocking. The Ant Colony Optimization (ACO) further imitates the manner in which the colonies of ants can identify the route that is the shortest between its food and nest. The Harmony Search (HS) algorithm had been conceptualized by using the process of searching for one such perfect state of harmony. The Charged System Search (CSS) makes use of the electric laws of Physics and the Newtonian laws of mechanics for guiding Charged Particles (CP). For this work, the MOM-GA (the face, the ear, and the hand vein features) are used for the multimodal biometric system. The rest of the investigation has been organized thus. Section 2 has discussed the work related to literature. The various methods employed in this work are described in Section 3. Section 4 explains the results of the experiment and Section 5 concludes the work.

Related works

Karthiga and Mangai [8] have proposed a high and robust multimodal biometric system based person multimodal biometric that makes use of the method known Covariance Matrix Incremental Principal Component Analysis (CMIPCA). The primary goal of the method of CMI-PCA was to work with three main steps and further attain a fusion integration of fusion level, faces, ears and, the hand dorsal vein. Firstly, the multimodal biometric features of a person will be sensed and the extraction of features had been performed by using an IPCA that was a Gabor-based filter for improving the level of robustness of the IPCA. The next step was the matching of the features extracted along with storing the test image from its database and this matching is based on the CMI-PCA. This score matching that is based on the CMI-PCA for maintenance of the scale of the extracted features and then computes a mean score value for matching test images without having a covariance matrix range. Lastly, the CMI-PCA will include a combination of various ranks of biometric identification to make a final decision.

Liu et al., [9] had proposed another rank-level framework that is used for a robust fusion. Firstly, the work will define the rank distance for measuring the image relevance at the level of a rank. On the basis of this, the Bayes similarity was introduced for evaluating the quality of retrieval of the individual features by which all true matchings will obtain a higher weight compared to the outliers. After this, the work further constructs a new directed Image Graph for encoding the actual relationship between the images. Every image has been connected to the KNN using an edge and this edge will be weighted by using the Bayes similarity. There are multiple rank lists from the various methods that have been merged through the Image Graph. Also, a fused Image Graph with a local ranking has been performed for re-ordering all initial rank lists. This will aim at a local optimization and is more robust to the global outliers.

Paul and Gavrilova [10] had further presented a method known as the multi-level of the random projection made on the face and the ear based biometric traits. The templates that were privacy preserved had been used for this system. The primary idea behind this computation of privacy preserve will be an algorithm of random projection. There are multiple matrixes of random projection that have been used for the generation of various templates for a biometric authentication. The method that is a random fusion has been used in this method proposed and so it can provide a better security to the template, quality of feature and privacy. There are multiple templates that are randomly fused which have been used for the purpose of recognition and a decision fusion is finally applied for generating the final results of classification. This works in a way that is similar to human cognition for the works of face recognition and this will preserve the privacy and the system's multimodality which was a detailed validation of the analysis of performance in various sets of the virtual and multimodal face or ear databases.

Haghighat et al., [11] had presented a Discriminant Correlation Analysis (DCA), which was a new technique of feature level fusion which incorporates class associations in the analysis of correlation of the feature sets. The DCA further performs another effective fusion of feature by means of a maximization of the pair-wise correlation which is across two of the feature sets and also all between-class correlations along with restricting the correlation among classes. This method proposed may be used for pattern recognition which was for ensuring fusion of features that are extracted from various modalities or also combining various feature vectors extracted from one single modality. It has to be noted that the DCA has been the very first technique giving consideration to a class structure that is in the feature fusion. Furthermore, it can have a computational complexity that is low and this may be employed in applications that are real-time.

In this area of research, the issues were to increase the accuracy in feature extraction for the methodology of the recognition system of the ear biometrics. Soni et al., [12] further presented a technique known as the Gabor filter feature selection, where the Gabor equation had been projected on a digital image that makes use of various angles and a scale but this can generate a Gabor coefficient matrix that is of a higher dimension. There is also an increase in the confusion and reduction in the Correct Recognition Rate (CRR) for the system. In order to increase the CCR, all feature redundancy will have to be reduced by making use of the process of filtering. This Gabor DWT filter technique proposed for the system of ear biometrics recognition, the redundant features are reduced and the optimized features will get chosen.

Farmanbar and Toygar [13] had further employed various schemes of fusion that were based on the feature-level and match-score level in order to provide a system of recognition that was robust. This method further presented another new multimodal approach that was based on either a face or a palm-print system of biometrics by deploying the technique of match score-level fusion. The local binary patterns were performed to be a local feature extractor obtaining an efficient descriptor of the texture. The feature selection was performed by making use of a backtracking search algorithm for choosing another optimal subset of the face and the palm print and features extracted from them. Thus, the time or the feature dimensions had been reduced to a considerable extent. After this, the match score-level fusion was performed.

Ghoualmi et al., [14] had proposed another new architecture for the ear biometrics aiming at solving problems in acquisition in the 2D ear images. This system makes use of another new image of the ear which is in contrast to the enhancement approach which is based on the grey-level mapping using the Artificial Bee Colony (ABC) algorithm to be its optimizer. The technique further permits a better-contrasted 2D images of the ear. In the stage of feature extraction, a Scale Invariant Feature Transform (SIFT) has been used. In the matching phase, three ear image databases were used for testing which are: the IIT Delhi, the USTB 1 and the USTB 2, and this had been compared to the traditional ear image and the approaches to contrast enhancement, the Histogram Equalization (HE) and the Contrast Limited Adaptive Histogram Equalization (CLAHE).

Eskandari and Toygar [15] had proposed Particle Swarm Optimization (PSO) along with the Backtracking Search Algorithm (BSA) for the purpose of choosing optimized features with weights for achieving a robust system of recognition by means of reducing the actual number of features in a feature level fusion of multimodal biometric systems along with an optimization of the weights that are assigned to a face-iris based multimodal biometric system and their scores found in the score level fusion step. In addition to this, for ensuring an improvement in both the face and the iris recognition, followed by the recognition of the multimodal face-iris system of biometrics. This way the methods proposed will attempt correction and alignment of the location of eyes by means of measuring the angle of iris rotation.

Kumar and Singh [16] further proposed another new and unique Bacterial Foraging Optimization (BFO) along with a PSO approach to identify the individual recognition and its accuracy. This hybrid approach can mitigate all irrelevant facial found within the feature subsets. The results prove that the identification was accurate and superior compared to other approaches found in the literature.

Gopal and Selvakumar [17] further proposed some multimodal biometrics systems for both the face, and the fingerprint recognition by employing a weighted sum and score level fusion. Additionally, this Hybrid Bacterial Foraging along with a parameter-free PSO (BF-pfPSO) algorithm had been used for the optimization that is assigned to both modalities of the face and the fingerprint. The extraction of features of the face was made by making use of the Principal Component Analysis (PCA) and in the feature extraction of fingerprints, this has been done by means of a minutiae matching. Matching scores of the modalities will be fused once the normalization that uses the technique of weighted sum score level fusion is used and this result is compared to that of the Equal error rate and the Receiving Operating Characteristics (ROC) curve in order to measure its performance.

Methodology

Here in this section, a dataset has been used from the Olivetti Research Laboratory (ORL) database for the face, the University of Science and Technology Beijing (USTB) databases that are considered for the ear and the North China University of Technology (NCUT) database that is for the hand vein. The face, the ear and the hand vein features have been extracted by means of employing the technique of the IPCA, the feature fusion that has used the rank level, the proposed method of the MOM-GA is used for feature selection and finally the KNN classifier have been discussed.

Dataset

The Olivetti Research Laboratory (ORL) face database [18] consists of a set of images of the face that had been taken at the AT&T lab between the period of April 1992 and April 1994. This was utilized for a project of face recognition that was conducted collaborating with the Speech, Vision and the Robotics Group belonging to the Engineering Department of the Cambridge University. There were ten images of 40 subjects taken during different times, changing their lighting, the facial details (either with or without glasses) and facial expressions (eyes open or closed, smiling or not smiling. All images were taken where the subject was against either a dark or a homogeneous background in an upright and frontal position (with a tolerance for side movement).

The University of Science and Technology Beijing (USTB) Ear databases [19] were available for the purpose of academic research. An IMAGE DATABASE I consists of about 150 images with 60 volunteers. There were some ear images found in the USTB database has 17 vertically aligned roll ψ for rotation. This refers to the dataset as an USTB containing 60 subjects with 3 images for each subject. This has been set to tune parameters of the Local Binary Pattern (LBP) and for the training of the Eigen-Ear technique, and is called a train set.

The hand veins are imaged using a Far-Infrared (FIR) or a Near-Infrared (NIR) technique of imaging providing contactless and the data acquisition which was non-invasive. For this 150 images of the hand vein had been acquired in a natural lighting (indoor environment). This was called the North China University of Technology that was based on hand-dorsa vein database (NCUT) dataset (the hand vein) [20]. In yet another detailed method, about 10 right and about 10 left vein images of the back of the hand had been captured from 102 subjects falling under the age bracket of 18 and 29, among which there were 50 men and 52 women. This has made this dataset a much more important one in the hand vein biometrics. The pattern is well-defined when the skin behind the hand is taut and so subjects had to clench their fists for acquiring the patterns. There had been no other variations to illumination but there were certain changes owing to the time.

Feature extraction using incremental principal component analysis (IPCA)

There are several techniques through statistical methods that were unsupervised. Ideally, these methods had to find a newer set of images to represent the face, the ears, and the hand veins. There was a traditional PCA algorithm had further computed all the eigenvectors and the eigenvalues for the purpose of a covariance matrix. This algorithm will further require an image data matrix for solving this problem (the batch method). Another new method for this work, known as the incremental principal component based method will now update the eigenvectors every time there is a new image that is coming in [21].

The eigenvector x along with the eigenvalue λ of C a covariance matrix C is as in (1):

$$\lambda.x = C.x \tag{1}$$

By means of duly replacing (1) an unknown C along with a sample covariance matrix $\frac{1}{n}\sum_{i=1}^{n} u(i).u^T(i)$ and with v = λ. x, the equation below has been obtained as in (2):

$$v(n) = \frac{1}{n}\sum_{i=1}^{n} u(i).u^T(i).x(i) \tag{2}$$

In which the v (n) denotes the nth step belonging to v after entering n images. The observations from the given image are denoted by u(i) and are given as vectors of d dimension [u(1), u(2)…].

As the λ = ||v|| and x = v/||v||, x (i) has been set to v (i-1)/||v (i-1)|| (by estimating x(i) based on the previous value of the v). Equation (2) results in a new equation as in (3):

$$v(n) = \frac{1}{n}\sum_{i=1}^{n} u(i).u^T(i).\frac{v(i-1)}{\|v(i-1)\|} \tag{3}$$

The eq. (3) may also be presented in a method which is a recursive one as in (4):

$$v(n) = \frac{n-1}{n}v(n-1) + \frac{1}{n}u(n)u^T(n)\frac{v(n-1)}{\|v(n-1)\|} \tag{4}$$

In which the $\frac{n-1}{n}$ denotes the actual weight of the earlier estimate and $\frac{1}{n}$ the new data's weight.

To start, set v (0) = u (1), and the very first direction for the data spread [22]. This IPCA algorithm provides an initial estimate of its principal component v (1) corresponding to a new and maximum eigenvalue as per (5):

$$v(1) = \frac{1}{n}u(1).u^T(1).\frac{v(0)}{\|v(0)\|} \tag{5}$$

Every time a new image which is found is introduced, eigenvectors get updated. They are then presented in an order that is decreasing, along with its corresponding eigenvalue. All the other vectors of higher order are estimated using the Stochastic Gradient Ascent (SGA): Start using a new set of ortho-normalized vectors and update them with the iteration step recovering orthogonality by using the Gram-Schmidt Ortho-normalization (GSO). In the case of a real-time online computation, the GSO has to be completely avoided since it is time-consuming. All further vectors will have to be orthogonal to one and other for ensuring their independency. Thus it helps in the generation of "observations" within a space that is complementary for computing eigenvectors of a higher order. For instance, in order to be able to compute a new vector of a second order, the data has to be subtracted from the projection on its estimated first order eigenvector v_1 (n), as per (6):

$$u_2(n) = u_1(n) - u_1^T(n)\frac{v_1(n)}{\|v_1(n)\|}\frac{v_2(n)}{\|v_2(n)\|} \tag{6}$$

In which the u_1 (n) = u (n). The residual obtained, u_2 (n), in a complementary space of the v_1 (n), will serve as an input data to an iteration step.

This way, it is possible to enforce orthogonality while a convergence is arrived at. So the sample that is available can be employed to avoid the GSO which is quite time-consuming. Once the convergence is complete, the vectors will get enforced as orthogonal as they have been estimated in the spaces that are complementary.

Feature fusion using rank level

The rank-level fusion has been a new approach and has not been investigated well. At the time each biometric matcher becoming a subset of the matches that are sorted in the order of decreased confidence a fusion can happen at a rank level. A goal of the rank-level fusion was for the purpose of consolidating a rank output by the various individual biometric subsystems (the matchers) for arriving at a consensus rank for every identity.

Ross et al. had described three different methods for combining the ranks which were assigned by the matchers. These are the methods of the Highest rank, Borda count along with the Logistic Regression. The highest rank method has every possible match that is assigned to that of the highest (the minimum) rank that was computed using different matchers. There are broken ties in order to arrive at a ranking order which was strict and its final decision made based on ranks combined [23].

Alternatively, the Borda Count method makes use of the ranks that are assigned to users by the matchers along with their performance of modules are equally good. Finally, the method of the logistic regression makes use of a weighted sum of individual ranks and the weights are assigned to various matchers using a logistic regression. This method is an extremely efficient one at the time there are matching modules with significant differences in accuracy and also needs a phase of training for the determination of these weights.

But the method does have a drawback. For the systems that are multi-biometric, there may be either four or sometimes even five identities that show the initial three identities. This only means that there could be certain identities may appear for one matcher and there may also be chances of wrong results on completion of a rank-level fusion. For dealing with such critical issues, there are modified methods in rank-level fusion. The work further proposed using all the three matchers, the face, the ear, and the vein. These identities appear in at least two matchers and if they appear only in one, they are not considered [24].

A good example of the method of Borda count and logistic regression is the rank-level fusion. The lower the rank, the more accurate its result. In this, the ranks for the "Person 1" will be 3, 2, and 1 that is from the face, the ear, and the hand vein matchers. So, for the method of the Borda Count, the ranks are later divided by 3 (the number of matchers). It now gets two where this is its second rank (since 1.33 was found for a "Person 2"). In the method of logistic regression 0.3, 0.4, and 0.3 are assigned as weights for the face, the ear, and hand vein. The higher the weight the lower the performance. The ear matcher has less accurate results compared to the face of the matchers of the hand vein. So, if it is "Person 1," it will have 3, 2, and 1 from the face, the ear, and the hand vein. In the case of a rank calculation which is reordered, initial ranks that get multiplied using their weights (3 by 0.3, 2 by 0.4, and finally 1 by 0.1). Once this is done, three newer ranks of the "Person 1" will be added and then is divided by 3 (the number of matchers) and another new rank 0.67 is arrived at which is now considered as the rank 2 (the second from that of the lowest) in its final rank. After this, the "Person 5" will appear in the results of the ear matcher and not considered to be the final one.

Proposed multi-objective modified genetic algorithm (MOM-GA) feature selection

Once there is an extraction for both parents and children image in pairs, features are concatenated for achieving a feature vector which is combined to record the parents-children image pairs. A feature vector for a parent and child is called the centromere. This is exactly in the centre of a combined feature vector. The feature vector that comes out is high-dimensional. The aim here was to remove all useless features and this can result in the reduction of dimensions for a feature vector. For the purpose of this work, the MOM-GA that is based on the GA had been proposed [25].

The GA had been used originally for choosing the binary strings. One major trait of the GA was that it was evolved in a method used for exploring the manner in which the interdependency among the bits found in a string is and so it is well-suited for this problem and can improve performance. For most of these cases, the performance is better compared to the forward and the backward algorithms in connection to the number of evolutions needed for reaching the minimum [26].

The chances of identifying an optimal subset for a classification is quite high at the time the GA has been employed for a feature selection that has suitable functions of fitness along with some possible considerations. Taking advantage of these, there was a method of feature selection known as the GA that was proposed. This method of wrapper-based feature selection further took advantage of the algorithm of supervised learning for evaluating the actual significance of that of the feature subset and this employs the GA for optimizing the actual searching of features found in the process of selection. This method has a performance that has been tested on a medical dataset along with several other classifiers.

The GA has been a method that moves to a newer population from its existing one. It normally has two different operators called the crossover and the mutation. The former exchanges the subparts of two of the chromosomes or else it will perform a recombination among two other chromosomes. The latter will now change the allele values of certain locations in a chromosome. The GA further evaluates every individual's fitness and this denotes the superiority of results that are achieved by means of a fitness function. A chromosome that is suitable at the time there was a higher chance of being able to choose for the formation of the subsequent generation. In case the fittest among the chromosomes in the population is not able to meet this need, both the crossover and the mutation functions are carried out. Their functions were carried out again and again until such time acceptable results were obtained.

The proposed algorithm has some operational steps which are [27] initialization of population, the performance of both crossover and mutation, evaluation of fitness and the stopping criteria. The algorithm will initially assign a search space that was binary since the chromosomes were bit strings and every bit had represented every feature in the training dataset. The initial population was created in a random manner along with the assumption that a feature value '1' has been representing a certain feature which has to be chosen for the evaluation that will continue to maintain a similar position in the feature value (the same index) and in case it is '0', there is no feature chosen to maintain the feature value position. The selection of the parents is random where their length remains the same compared to their total features.

The next step performs a crossover operation. There are two parents or two individuals (the chromosomes) that have been combined in order to form a child (a new chromosome). The third step now performs a mutation operation which can randomly change allele values from that of a crossover child (C) for producing the subsequent generation. In its fourth step, there is a fitness value calculated from a feature subset from that of step 3. The accuracy of classification will be considered to be the fitness value and then will validate its subset. In case the accuracy of classification has been taken to be its fitness value that can validate a new subset generated. In case the classification and its accuracy (the fitness value) is able to satisfy completely a termination condition, the feature subset is taken to the be selected one or else follow step 2 to step 4 in a manner which is iterative until such time the termination condition has been arrived at.

The Multi-Objective GA (MOGA) mechanism is used in this work which is based on the Pareto-optimality. This solution further dominates the other at the time the former is able to achieve either a better or an equal value compared to the latter. Thus, the Pareto has been composed of all of the solutions that are non-dominated for the problem. The MOGA has assigned a similar probability of selection to the solutions that are non-dominated in its current population. This method also includes the dividing of the population in various classes based on the actual number of individuals that dominate the members of every class. So, the scheme of selection for the MOGA includes the five steps mentioned below [28]:

1. Every individual has been assigned a rank that is equal to the actual number of individuals that dominate it including one (the chromosomes that encode the non-dominated solutions will receive a rank 1).
2. The population will be sorted increasingly in accordance with the rank.
3. Every individual will be assigned a probability of selection that is based on the ranking since a lower ranking will receive lower probabilities.
4. A selection probability for every class of equivalence (chromosomes with a similar rank that are non-dominated) has been averaged.
5. There is a new population that is created by means of following the stochastic universal sampling of Baker.

A crossover works in two different parts of the chromosome simultaneously. So there is another standard operator that is applied over the C1 and the C2. The operator performs this as below: p, a crossover point will be generated randomly in the Cl and two parents gets crossed at its p-th variable in the C1. A crossover is also developed in two parts of the chromosome, the C1 and C2, producing some meaningful descendants.

There are two different operators that are employed and each one among them acts on different parts of the chromosome. There is a brief description that is given below: The Mutation on the C1: since this is a critical part of the chromosome that is binary coded, there is a very simple binary mutation which is developed that can flip the value of a gene. The mutation on the C2: This mutation operator chosen for the C2 can be similar to that which is proposed by the Thrift. There is a local modification that has been developed by means of bringing about a change in the actual numbers of the labels for the variable to the upper or the lower value (for which there needs to be decision made randomly). At the time the value is changed to its lowest (1) or its highest, there is only one change that is possible. The GA was modified by means of using a levy search as opposed to a process of mutation. In order to be able to identify an optimal solution to this problem, there is an optimization technique that needs to be used correctly. Generally, a technique of global optimization is ideal only if it has some of the traits mentioned below [29]:

This method also has to be simple and easy to implement.
There has to be a proper balance existing between exploration and its exploitation.
A true global optimum will have to be found for every run.
Convergence will have to be fast.
The algorithm must have a minimum number of parameters used for tuning.
The algorithm will also need a minimal power of computation to be able to run well.

This approach that is proposed was population-based and makes use of solutions for proceeding to its global solution. Its initial population is generated randomly to ensure that its initial solution has been duly distributed in the entire solution space. The run of this algorithm will not change and for every such generation, the population undergoes a crossover and also a mutation. Once each operation is complete, there is a new elitism that is applied for choosing ideal solutions. Before every generation ends, its best solution found within the current population and this performs a Lévy flight for the purpose of increasing the solution space exploration of that of the solution space for its next generation. For every generation, there is a new aim of the algorithm to ensure a new population is created by means of replacing the points in its current population using better points through its genetic principles. By means of ensuring a repeated reproduction process (the crossover and the mutation), this population gets guided to the global optimum.

In an original Cuckoo Search (CS), one single cuckoo will lay only one egg at one time by means of a Lévy flight. In a hybrid approach, each of the two parent cuckoos reproduces two eggs. The female cuckoo tends to mimic the eggs of host birds. In order to account for such a behaviour, the mutation operator had been added to this algorithm. This reflects the actual behaviour of mutation of eggs and the genes for increasing productivity. Even with having this type of mutation of genes, there is a chance that the alien egg is discovered by the host and this will be determined by the egg quality. Thus, a strategy of elitism will be used for keeping all eggs of all the high quality and the eggs with a poor quality will be discarded.

There is now a new review as to how this kind of distribution is performed by employing a Levy flight. By means of using a Levy flight [30], the new state of a particle has been calculated as in (7):

$$X^{t+1} = X^t + \alpha \oplus Levy(\beta) \tag{7}$$

In which the α denotes the catula size of the step that is related to the scales of the problem. In this method, the α denotes the random number for the dimensions of the particles as in (8).

$$X^{t+1} = X^t + random(size(D)) \oplus Levy(\beta) \tag{8}$$

The product $\oplus$ will now denote entry-wise multiplications. A scheme which is non-trivial to generate a new step size s, and have samples and re-summarized as in (9):

$$s = random(size(D)) \oplus Levy(\beta) \sim 0.01 \frac{u}{|v|^{1/\beta}} \left(x_j^t - x_i^t\right) \tag{9}$$

In which u and the v tend to get drawn from their normal distributions (10 and 11):

$$u \sim N\left(0, \sigma_u^2\right) \quad v \sim N\left(0, \sigma_v^2\right) \tag{10}$$

With the

$$\sigma_u = \left\{ \frac{\Gamma(1+\beta)\sin(\pi\beta/2)}{\Gamma[(1+\beta)/2]\beta 2^{(\beta-1)/2}} \right\}^{1/\beta}, \sigma_v = 1 \tag{11}$$

For which Γ denotes the standard Gamma function.

Table 1 FAR % with GA Feature Selection

GAR %	Face, ear & hand vein	Face & ear	Face & hand vein
0.001	65.82	64.53	61.89
	69.37	66.17	63.08
	69.38	66.17	62.66
	71.48	67.48	63.89
	72.92	68.58	66.79
	74.58	72.66	67.44
0.01	75.18	75.42	69.81
	78.23	75.04	71.3
	82.24	81.11	77.31
	87.54	84.13	79.8
	94.1	91.76	84.92
	95.4	92.19	87.51
0.1	95.01	92.84	89.6
	98.41	93.38	88.64
	98.41	93.23	90.14
	98.41	93	90.03
	98.41	94.72	89.45
1	98.41	96.59	91.28

K-nearest neighbor (KNN) classifier

The KNN classifier is found to be well-suited for the classification of the persons that are based on images owing to a lower time taken for the execution and a better accuracy compared to the other methods used including the Hidden Markov

Table 2 FAR % with Multi Objective Modified GA (MOM-GA) Feature Selection

GAR %	Face, ear & hand vein	Face & ear	Face & hand vein
0.001	72.88	72.8	70.18
	75.89	76.98	73.18
	75.59	76.28	73.22
	77.15	78.19	74.33
	80.47	80.73	74.49
	81.77	81.54	77.32
0.01	80.37	79.52	83.49
	84.63	86.03	82.78
	90.41	91.31	90.78
	94.74	95.51	94.12
	97.9	96.42	94.12
	96.69	97.17	94.12
0.1	97.86	97.17	94.12
	98.45	97.17	94.12
	99.78	97.17	94.12
	99.78	97.17	94.12
	99.78	97.17	94.12
1	99.78	97.17	94.12

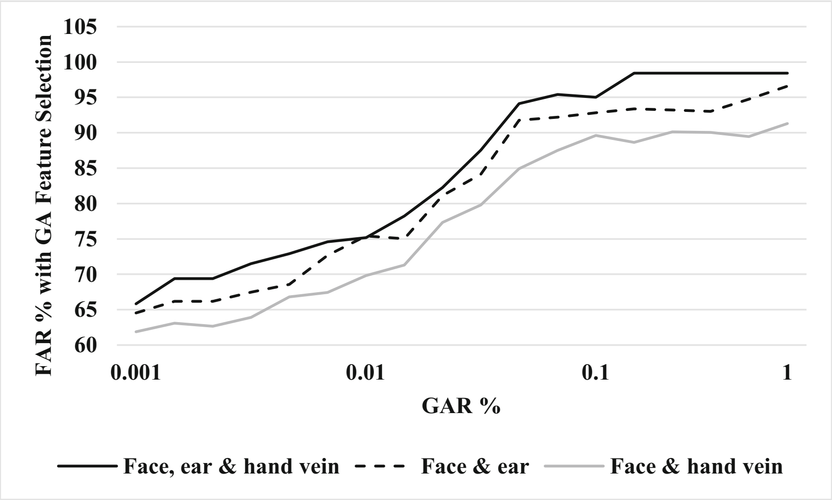

Fig. 1 FAR % with GA Feature Selection

Model (HMM) and the kernel method. Even though there are some methods such as the Support Vector Machine (SVM) and the Ada Boost are more accurate compared to the KNN classifier, the latter does have a much faster time of execution and is more dominant compared to the SVM. In this simple scheme of classification, there is a new image space and a test set will be recognized through assigning it to a label of its closest point in this set in which the distance will be measured in the image space [31].

The metric of the Euclidean distance is selected for determining the proximity between data point in the KNN. There is also some distance that is assigned between the pixels within the dataset. The distance is also called the Euclidean distance that exists between two of the pixels. This Euclidean distance is given by (12):

$$d(x,y)=\sqrt{(x_1-y_1)^2\dots\dots\dots(x_n-y_n)^2} \tag{12}$$

The Euclidean distance will be the default as a classifier of the KNN. The distance between both features is measured on the basis of the distance cosine and its correlation.

The KNN was a method that classifies objects and is an instance-based method of learning also known as lazy learning. This k-nearest neighbour algorithm has been identified as a simple one among all other algorithms and the objects here are classified by their majority vote among neighbours and are assigned to a certain class among the k nearest neighbours (the k being a positive integer, is typically small). In case k = 1, then an object will be assigned to this nearest neighbour class [32].

1. Every data pixel value that is within a data set will have a class label in the same set, Class = {c1,...,cn}.
2. Data points', the k-closest neighbours (where k is the number of neighbours) will be found by a new analysis of its distance matrix.

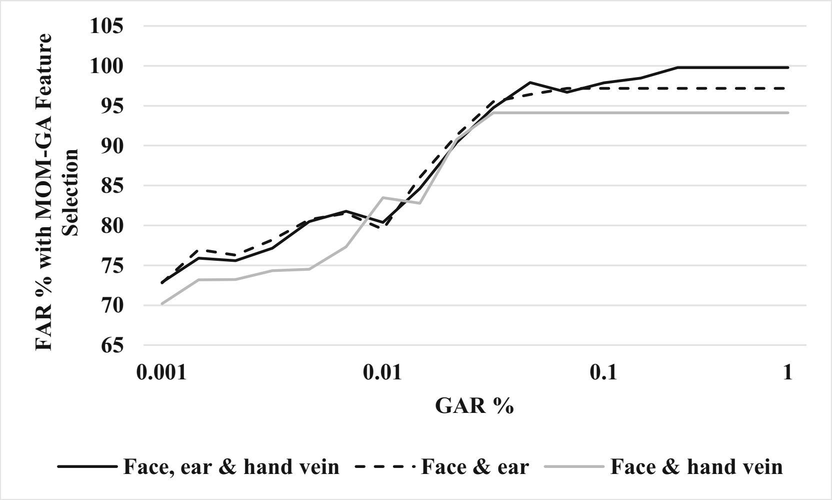

Fig. 2 FAR % with Multi Objective Modified GA (MOM-GA) Feature Selection

3. The data points that are k-closest will be analysed for the determining the class label that is very common in this set.
4. The commonest class label is assigned to a data point which is analysed.

Results and discussion

In this section, the face, ear & hand vein, face & ear and face & hand vein features are used. The False acceptance Rate (FAR) is defined as the fraction of fraud score greater than the predefined threshold. The Genuine Acceptance Rate (GAR) is defined as the fraction of genuine score greater than the predefined threshold. The FAR % with GA feature selection and FAR % with MOM-GA feature selection as shown in Tables 1 and 2 and Figs. 1 and 2.

From the Fig. 1, it can be observed that face, ear & hand vein has higher FAR % with GA feature selection by 3.62% for face & ear and by 8.75% for face & hand vein.

From the Fig. 2, it can be observed that face, ear & hand vein has higher FAR % with MOM-GA feature selection by 0.52% for face & ear and by 3.62% for face & hand vein.

Conclusion

The multimodal biometric systems are used for improving identification systems to a great extent for the purpose of improving the population coverage. The extraction of feature by using the IPCA algorithm will compute all principal components for a sequence of image vectors in an incremental manner to improve the performance of the system recognition and also improve coverage. This feature extraction through using the IPCA algorithm will compute all principal components in the image sequence in an incremental manner. This does not include a covariance matrix (so is covariance-free). This process identifies and also removes all redundant and irrelevant information and reduces the dimensionality of data. In order to identify an optimal feature set, from that of a large set which is challenging, the MOM-GA has been proposed. The GA is a heuristic search algorithm based on ideas that are evolutionary in natural selection or genetics that were invented by Holland. They represent an exploitation of random search for solving problems in optimization. The GA was a powerful metaheuristic that is used for solving the binary problems. Using the GA with multi-objective can successfully perform a search for solutions that are guided by simultaneously optimizing multiple goals or criteria. The results have shown that the face, the ear, and the hand vein which has a higher percentage of FAR with the GA feature selection that was by about 3.62% for the face and ear and by about 8.75% for the face, and hand vein. For the face, the ear and the hand vein the percentage of FAR was higher with the MOM-GA feature selection which was by about 0.52% for the face and the ear and further by about 3.62% for the face and the hand vein.

Compliance with ethical standards

Conflict of interest R. Karthiga declares that she has no conflict of interest. Dr. S. Mangai declares that she has no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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