

FEATURE AND COMPUTATIONAL TIME REDUCTION ON HAND BIOMETRIC SYSTEM

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Keywords: Principal Component Analysis, Pattern Recognition, Hand Biometric System, Parameterization, Feature reduction, Classification system.

Abstract: In real-time biometric systems, computational time is a critical and important parameter. In order to improve it, simpler systems are necessary but without losing classification rates. In this present work, we explore how to improve the characteristics of a hand biometric system by reducing the computational time. For this task, neural network-multi layer Perceptron (NN-MLP) are used instead of original Hidden Markov Model (HMM) system and classical Principal Component Analysis (PCA) procedure is combined with MLP in order to obtain better results. As showed in the experiments, the new proposed PCA+MLP system achieves same success rate while computational time is reduced from 247 seconds (HMM case) to 7.3 seconds.

1 INTRODUCTION

Biometrics is an emerging technology which is used to identify or verify people by their physical or behavioral characteristics. Amongst the physical characteristics which have been used in biometrics are the fingerprint, hand geometry, palm-print, face, iris, retina, ear, etc. (Jain et al., 2001).

While systems based on fingerprint and eyes features have, at least to date, achieved the best matching performance, human hand provides the source for a number of physiological biometric features. The most frequently used are fingerprint, palm-print, hand geometry, fingers geometry and hand edge. These human hand features are relatively stable and all the above mentioned characteristics can be easily extracted from one single image of the hand. Furthermore, these identification systems are very well accepted by users, as are simple and do not require to do anything special.


In this paper hand edge and its feature and time computational reduction have been studied as a first step for a real time application. We have worked on a new parameterization for the hand edge, and after the study of its behaviour, we have applied PCA

method in order to reduce the feature vector and computational load of the system.

2 DATABASE

Our database has been built based on 60 users, acquiring 10 samples per user. A scanner has been used in order to acquire each sample. The following table shows the most important characteristics of our database.

Table 1: Characteristics of our database.

Parameters	Data	Example
Number of classes	60	
Number of samples per classes	10	
Acquisition and Quantification	Gray Scale (8 bits, 256 levels)	
Resolution	150 dpi	
Size	1403 x 1021 pixels	
	reduced to 80%	

3 PARAMETERIZATION SYSTEM

We have considered just the hand perimeter. This image is considered without the wrist that has been extracted automatically from the shadow image. Hands are scanned placed more or less on the center, upward (wrist down).

Border determination as (x,y) positioning perimeter pixels of black intensity, has been achieved by processes of shadowing (black shape over white background), filtering of isolated points, and perimeter point to point continuous follow.

3.1 Perimeter Interpolation

Perimeter size variability induces us to consider a convenient perimeter point interpolation, in order to standardize perimeter vector description. For an interpolating process, in order to achieve reconstruction of the original shape, we may use any of the well known algorithms as mentioned in (Fu and Milios, 1994), (Loncaric, 1998), (Huang and Cohen, 1996), but a simple control point's choice criterion in 1-D analysis allows for an appropriate performance ratio on uniform control point's number and approximation error for all individuals of all varieties studied.

The general idea, for such choice, is to consider (x,y) positional perimeter points as $(x,F(x))$ graph points of a 1-D relation F .

Consideration of y coordinate as $y = F(x)$ is done, because of the way, hands images are presented in our study: hands have been scanned with maximum size placed over x ordinate.

For a relation G to be considered as a one-dimensional function, there is need to preserve a correct sequencing definition (monotonic behavior).

That is: A graph,

$$G = \{i = 1..n, (x_i, y_i) / y_i = f(x_i)\} \quad (1)$$

It is the description of a function f if ordinate points $x_i, i = 1..n$ must be such that: $x_i < x_{i+1}, i = 1..n - 1$.

We consider then the border relation F as a union of piece like curves (graphs) preserving the monotonic behavior criterion, i.e.

$$F = \bigcup_{j \in J} G_j \quad (2)$$

where: $G_j \subseteq F, \forall j \in J$ and

$$G_j = \{\alpha_j \in J_j, (x_{\alpha_j}, y_{\alpha_j}) / y_{\alpha_j} = f_j\},$$

For convenient sets of index J, J_j and restriction functions $f_j = f_{\{x_{\alpha_j} | \alpha_j \in J_j\}}$, such that the next point following the last of G_j is the first one of G_{j+1} . G_j graphs are correct f_j functions descriptions.

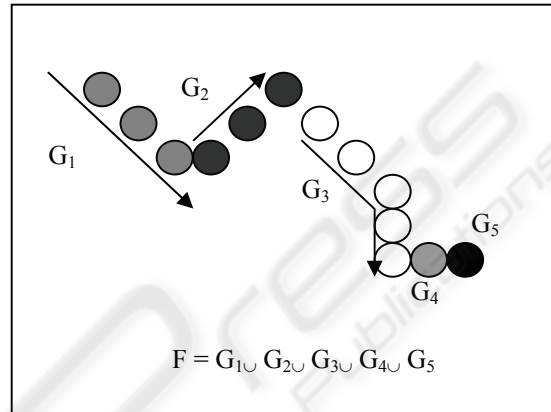


Figure 1: Example of an F relation decomposed in graphs with a correct function description.

Building the G_j sets is a very straightforward operation:

- Beginning with a first point we include the next one of F .
- As soon as this point doesn't preserve monotonic behaviour we begin with a new G_{j+1} .
- Processes stop when all F points are assigned.

In order to avoid building G_j reduced to singletons, as show in figure 1 (G_4 and G_5) the original F relation may be simplified to preserve only the first point of constant x ordinate series.

Afterwards, spreading of a constant number of points is done proportional to the length of the G_j and always setting in it is first one.

The point's choice criterion mentioned before allows, in two-dimensional interpolation, for taking account on points where reverse direction changes take place. Irregularity, of the surface curve, is taken into account with a sufficient number of interpolating points, as done in the uniform spreading way.

The 1-D interpolation has been perform using between 750 and 100 control points, with spline, lineal or closest interpolated point neighborhood, depending on the number of control points present

in the decomposed curve. As a reference at 300 dpi a crayon free hand trace is about 5 to 6 points wide.

Due to perimeter size variability inside a class, coding of (x,y) control perimeter points have been transformed taking account for size independence.

Considering the following definitions:

Γ the set of n , a fixed number, of control points, $\Gamma = \{X_{i=1..n} / X_i = (x_i, y_i)\}$ Where (x_i, y_i) are point coordinates of control perimeter points.

C_0 the central point of the Γ set:

$$C_0 = (1/n) \left(\sum_{i=1..n} x_i, \sum_{i=1..n} y_i \right),$$

$$(x_i, y_i)_{i=1..n} \in \Gamma,$$

$\beta_i = \text{angle}(C_0 X_i X_{i+1})$, $\alpha_i = \text{angle}(X_i C_0 X_{i+1})$ angles defined for each interpolating points of Γ .

Sequences of (x_i, y_i) positional points are then transformed in sequence of (φ_i, β_i) angular points.

The choice of a starting and a central point accounts for scale and leaf orientation. Placement of both points sets the scale: its distance separation. Relative point positioning sets the orientation of the interpolating shape. Given a sequence of such angles α_i and β_i , it's then possible to reconstruct the interpolating shape of a leaf. Geometrical properties of triangle similarities make such sequence size and orientation free.

4 REDUCTION PARAMETERS

Principal Components Analysis (PCA) is a way of identifying patterns in data, and expressing the data in such a way as to highlight their similarities and differences (Jolliffe, 2002). Since patterns in data can be hard to find in data of high dimension, where the luxury of graphical representation is not available, PCA is a powerful tool for analyzing data. The other main advantage of PCA is that once you have found these patterns in the data, and you compress the data, i.e. by reducing the number of dimensions, without much loss of information.

PCA is an orthogonal linear transformation that transforms the data to a new coordinate system such that the greatest variance by any projection of the data comes to lie on the first coordinate (called the first principal component), the second greatest variance on the second coordinate, and so on. PCA is theoretically the optimum transform for a given data in least square terms.

In PCA, the basis vectors are obtained by solving the algebraic eigenvalue problem

$R^T (XX^T) R = \Lambda$ where X is a data matrix whose columns are centered samples, R is a matrix of eigenvectors, and Λ Γ is the corresponding diagonal matrix of eigenvalues. The projection of data $C_n = R_n^T X$, from the original p dimensional space to a subspace spanned by n principal eigenvectors is optimal in the mean squared error sense.

Another possibility, not presented here, is to use Independent Component Analysis (ICA) (Jutten and Herault, 1991), (Hyvärinen et al. 2001) instead of PCA. In this case, we obtain independent coordinates and not only orthogonal as in previous case. ICA has been used for dimensional reduction and classification improvement with success (Sanchez-Poblador et al., 2004).

In our problem we have 60 different classes of hands, and for each class we have 10 different samples, where each one is a two column matrix between 750 and 100 points. First column corresponds to interior angles α_i and second column to exterior angles β_i , as explained before.

The procedure for applying PCA can be summarized as follows:

1. Subtract the mean from each of the data dimensions. This produces a data set whose mean is zero (X).
2. Calculate de covariance matrix (Covx)
3. Calculate the eigenvectors e_i and eigenvalues λ_i of Covx
4. Order the eigenvectors e_i by eigenvalue λ_i , highest to lowest. This gives us the components in order of significance.
5. Form a feature vector by taking the eigenvectors that we want to keep from the list of eigenvectors, and forming a matrix (R) with these eigenvectors in the columns.
6. Project the data to a subspace spanned by these n principal components.

5 CLASSIFICATION SYSTEM

As classification system, two different models have been used in this present work. Hidden Markov Models (HMM), and Neural Networks (NN).

5.1 Hidden Markov Models

An HMM is the representation of a system in which, for each value that takes a variable t , called time, it

is found in one and only one of N possible states and declares a certain value at the output. Furthermore, an HMM has two associated stochastic processes: one hidden associate with the probability of transition between states (non observable directly); and another observable one, an associate with the probability of obtaining each of the possible values at the output, and this depends on the state in which the system has been found (Rabiner and Juang, 1993). It has been used a Discrete HMM (DHMM), which is defined by (Rabiner and Juang, 1993) and (Rabiner, 1989); N is the number of states,

- M is the number of different observations,
- $A(N,N)$ is the transition probabilities matrix from one state to another,
- $\pi(N,1)$ is the vector of probabilities that the system begins in one state or another;
- and $B(N,M)$ is the probabilities matrix for each of the possible states of each of the possible observations being produced.

We have worked with an HMM called "left to right" or Bakis, which is particularly appropriate for sequences. These "left to right" HMM's turn out to be especially appropriate for signature edge because the transition through the states is produced in a single direction, and therefore, it always advances during the transition of its states. This provides for this type of model the ability to keep a certain order with respect to the observations produced where the temporary distance among the most representative changes. Finally, it has been worked from 40 to 80 states and 32 symbols per state.

In the DHMM approach, the conventional technique for quantifying features is applied. For each input vector, the quantifier takes the decision about which is the most convenient value from the information of the previous input vector. To avoid taking a software decision, a fixed decision on the value quantified is made. In order to expand the possible quantified values that the quantifier is going to acquire, multi-labelling is used, so that the possible quantified values are controlled by varying this parameter. The number of labels in the DHMM is related to values that can be taken from the number of symbols per state.

DHMM algorithms should be generalized to be adjusted to the output multi-labelling ($\{v_k\} k=1,..C$), to generate the output vector ($\{w(x_t, v_k)\} k=1,..,C$). Therefore, for a given state j of DHMM, the probability that a vector x_t is observed in the instant t , can be written as;

$$b_j(x_t) = \sum_{k=1}^C w(x_t, v_k) b_j(k) \quad (3)$$

where $b_j(k)$ is the output discrete probability, associated with the value v_k and the state j ; being C the size of the vector values codebook.

5.2 Neural Networks

In recent years several classification systems have been implemented using classifying techniques, such as Neural Networks. The widely used Neural Networks techniques are much known on applications of pattern recognition.

The Perceptron of a simple layer establishes its correspondence with a rule of discrimination between classes, based on the lineal discriminator. However, it is possible to define discriminations for not lineally separable classes using multilayer Perceptrons that are networks without refreshing (feed-forward) with one or more layers of nodes between the input layer and exit layer. These additional layers contain hidden neurons or nodes, are directly connected to the input and output layer (Bishop, 1995).

A neural network multilayer perceptron (NN-MLP) of three layers is shown on figure 2 and implemented, with two layers of hidden neurons. Each neuron is associated with weights and biases. These weights and biases are set to each connections of the network and, are obtained from training in order to make their values suitable for the classification task between the different classes. We have used a back-propagation algorithm in order to train the classification system.

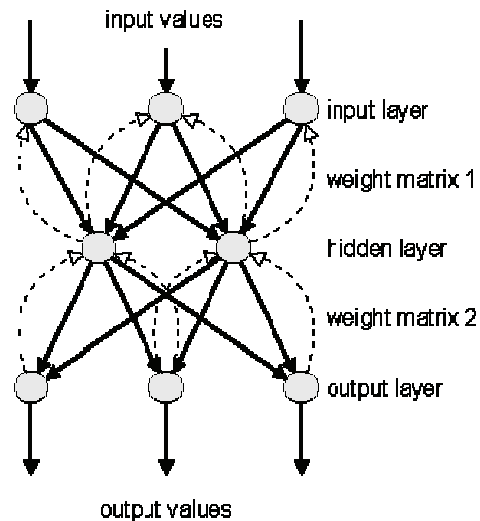


Figure 2: Multilayer Perceptron.

6 EXPERIMENTS AND RESULTS

All experiments have been repeated 5 times or more, therefore, the successes are showed by mean and standard deviation. The first experiment was to find the number of points more discriminate for the hand edge. From 750 to 100 edge points were used, and the best success was achieved with 200 points (see table 2).

After this experiment, we begin to study the feature reduction in order to keep the same success rate. PCA method was used for this task.

Different number of components is considered in the experiment, from 5 to 59 (as we have 60 different classes). As expected, the best classification result was achieved with the maximum number of principal components. Table 3 summarizes the success rates (only one experiment for each case) obtained with different number of principal components and using a multilayer perceptron (MLP) as a classification system. The neural network consisted of as many inputs as principal components in the first layer, a hidden layer of 60 nonlinear neurons (with $\tanh(\cdot)$ as activation function) and an output layer of 60 neurons. Scaled conjugate gradient was selected as optimization algorithm, with a maximum of 500 epochs. Half of the examples were used for training and the rest for test.

Table 2: Success rates for HMM classifier, using edge information.

Number of edge points	HMM states	Number of samples training	Success rates
750	60	4	46.61% ± 5.94
		3	38.09% ± 4.73
		2	32.41% ± 4.67
		1	23.55% ± 3.73
300	60	4	72.50% ± 4.77
		3	71.90% ± 4.36
		2	61.04% ± 6.48
		1	54.37% ± 5.71
200	60	4	84.17% ± 6.40
		3	82.33% ± 4.33
		2	79.79% ± 4.03
		1	73.92% ± 5.64
100	60	4	73.12% ± 6.21
		3	71.00% ± 7.84
		2	70.33% ± 2.33
		1	65.63% ± 5.63

Table 3: Success rates for MLP classifier, using edge information.

Number of Principal Components	Success rates
5	46.00%
10	68.33%
15	75.00%
20	79.33%
25	78.33%
30	76.33%
35	78.00%
40	78.33%
45	78.67%
50	79.33%
55	79.33%
59	83.33%

In order to explore the performances of the system, we repeat 20 times the classification algorithm with MLP, for 20, 40 and 59 principal components (see Table 4). Mean computational time of the algorithm was also calculated, and for the sake of comparison, we trained also a MLP with all the available parameters without any PCA reduction (corresponding to last line in Table 4).

Table 4: Success rates for MLP classifier, using edge information.

Number of Principal Components	Success rates	Mean time (seconds)
20	78.75% ± 0.81	7.30
40	80.93% ± 0.92	7.31
59	83.77% ± 1.34	7.30
398 features	83.60% ± 0.92	67.43

We can see that 59 components give us a success rate as well as the HMM model while reducing the standard deviation. On the other hand, if no PCA algorithm is used, the system works well but the computational time need for the system is higher (by a factor of 10). For the HMM case, computational time is much higher, about 247 seconds, and it can be a problem in some real-time applications.

Taking all the results in consideration, in table 4 is shown that MLP can obtain similar results as HMM (see table 2), and by using PCA, it has dramatically been reduced the computational time, as we deal with a much simpler classification system. This point is crucial in real-time operating systems and justifies the use of PCA+MLP architecture instead of HMM solution.

7 CONCLUSIONS

In this work we have presented a PCA+MLP architecture in order to classify 60 different classes of hands that keeps the success rate achieved by a HMM classification system, but with an important improvement on the computational time reduction. From HMM to MLP the computational time was reduced by a factor of 33, and by using PCA we have achieved to reduce 10 times more the computational time. This is the first step to get this application on real time, taking in account that the implementation has been done in MATLAB language.

Future work will include the study of Independent Component analysis (ICA) as a feature reduction dimension system in order to improve success rates. Too, a verification system and a fusion with geometry features will be implemented.

ACKNOWLEDGEMENTS

This work has been in part supported by “Programa José Castillejo 2008” from Spanish Government under the grant JC2008-00398; by the University of Vic under de grant R0904; by private funds from Spanish Company Telefónica, under “Cátedra Telefónica-ULPGC 2009”; and by funds from Research Action from Excellent Networks on Biomedicine and Environment belonging to ULPGC.

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