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Automated Authentication using Information Fusion and Score Normalization in Multimodal Biometric Systems

[1]Sasidhar Kothuru,[2]Kailasarao. K
[1]*Department of Information Technology, SNIST, Andhra Pradesh, India*
[2]*Department of Computer Sci.& Engineering, MRCET, Andhra Pradesh, India*

***Abstract*-Multimodal biometric system combines the evidence obtained from multiple modalities. By using an effective fusion scheme and normalization techniques we can significantly improve the over all accuracy and performance of biometric systems. In this paper we have presented information fusion and score normalization approaches that performs better in identification process based on biological features.**
***Keywords:* Multimodal biometrics, information fusion, Score Normalization**

INTRODUCTION

Unimodal biometric systems often affected by several problems like noisy sensor data, non- universality, lack of individuality, lack of invariant representations and spoofing traits. Multimodal biometric systems overcome these limitations by consolidating the evidence obtained from different sources. These sources may be (1) multiple sensors for the same biometric (2) multiple instances of the same biometric, (3) multiple representations and Matching algorithms for the same biometric, (4) multiple units of the same biometric or (5) multiple biometric traits. A multimodal biometric system can reduce the FTE (Failure to Enroll) rate and provides more resistance against spoofing. Multimodal biometric systems can also provide the capability to search a large database in an efficient and fast manner.

LEVELS OF FUSION

Fusion in multimodal biometric systems is four levels. They are Sensor Level, Feature Level, Score Level and Decision Level. These levels can be broadly categorized into fusion prior to matching and fusion after matching

Fusion Prior to Matching

Prior to matching, information can take place either at the sensor level or at the feature level. The raw data from the sensor(s) are combined in sensor level fusion. In sensor level fusion, the multiple cues must be compatible and the correspondences between points in the data must be known in advance. Future level fusion refers to combing different feature vectors that are obtained from one of the following sources; →Multiple sensors for the same biometric trait, →Multiple instances of the same biometric trait, →Multiple units of the same biometric trait or Multiple biometric traits. When the future vectors are homogeneous, a single resultant feature vector can be calculated as a weighted average of the individual feature vectors. When the feature vectors are non-homogeneous, we can concatenate them to form a single feature vector. Biometric systems that integrate information at an early stage of processing are believed to be more effective than those systems which perform integration at a later stage. Integration at the feature level is difficult due to several reasons [1].

Fusion after Matching

Schemes for integration of information after the classification/ matcher stage can be divided into four categories:
→Dynamic classifier selection
→Fusion at the decision level,
→Fusion at the rank level
→Fusion at the matching score level

A dynamic classifier selection scheme chooses the results of that classifier which is most likely to give the correct decision for the specific input pattern.

Integration of information at the decision level could occur when each biometric matcher individually decides on the best match based on the input presented to it.

When the output of each biometric matcher is a subset of possible matches sorted in decreasing order of confidence, the fusion can be done at rank level.

When the biometric matchers output a set of possible matches along with the quality of each match (matching score), integration can be done at the matching score level.

Fusion at Matching Score Level

There are two approaches for consolidating the scores obtained from different matchers. One is to formulate it as a classification approach, and the other approach is to treat it as a combination approach.

CLASSIFICATION APPROACH:

A feature vector is constructed using the matching scores output by the individual matchers and then classified as Accept or Reject.

We can use several classifiers to consolidate the matching scores and can take a decision. Consider the matching scores resulting from face and iris recognition modules as a two-dimensional feature vector. Fisher's discriminant analysis and a neural network classifier with radial basis function are then used for classification. Ross and Jain [2] use decision tree and linear discriminant classifiers for combining the scores of face, fingerprint and hand- geometry modalities.

Combination Approach to Score Level Fusion:

In combination approach, the individual matching scores are combined to generate a single scalar score which is then used to make the final decision. To ensure a meaningful combination of the scores from the different modalities, the scores must be first transformed to a common domain.

Kilter et al. [3] have developed a theoretical frame work for consolidating the evidence obtained from multiple classifiers using schemes like sum rule, product rule, max rule, min rule, median rule and majority voting. In order to employ these schemes, the matching scores must be converted into posteriori probabilities conforming to a genuine user and an impostor. They consider the problem of classifying an input pattern X into one of m possible classes (in a verification system m = 2) based on the evidence provided by R different classifiers or matchers. Let $\vec{xi}$ be the feature Vector (derived from the input pattern X) presented to the i^{th} matcher. Let the outputs of the individual matchers be $P(\omega_j \mid \vec{x_i})$ i.e. the posterior probability of the class ω_j given the feature vector $\vec{xi}$. Let $c \in \{\omega_1, \omega_2, \ldots, \omega m\}$ be the class to which the input pattern X is finally assigned. The following rules can be used to estimate c:

Product Rule:
This rule is based on the assumption of statistical independence of the representations $\vec{x_1}$, $\vec{x_2}$, $\vec{x}_R$. The input pattern is assigned to class c such that

$C = \mathrm{argmax}_j \prod_{i=1}^{R} P(\omega_j | \vec{x_i})$.

In general, different biometric traits of an individual are mutually independent. This allows us to make use of the product rule in a multimodal biometric system based on independence assumption.

Sum Rule: The sum rule is more effective than the product rule when there is a high level of noise leading to ambiguity in the classification problem. The sum rule assigns the input pattern to class c such that

$C= \mathrm{argmax}_j \sum_{i=1}^{R} P(\omega_j \mid \vec{x_i})$

Max Rule: The max rule approximates the mean of the posteriori probabilities by the maximum value. In this case, we assign the input pattern to class c such that

$C= \mathrm{argmax}_j \max_i P(\omega_j \mid \vec{x_i})$

Min Rule: The min rule is derived by bounding the product of posteriori probabilities. Here, the input pattern is assigned to class c such that

$C= \mathrm{argmax}_j \min_i P(\omega_j \mid \vec{x_i})$

Information fusion approaches are shown in below figure

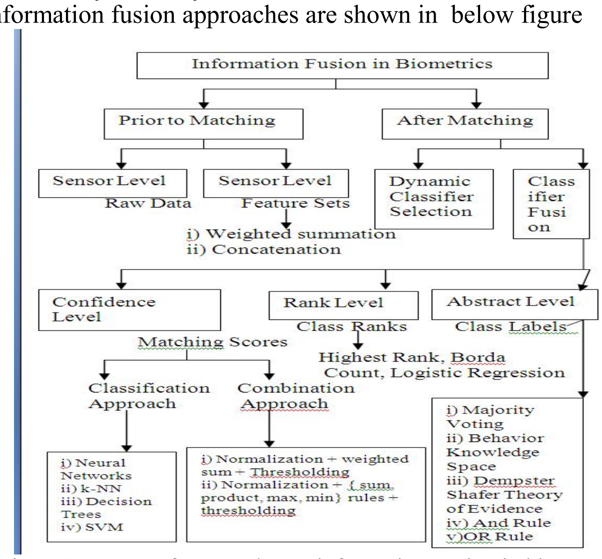


Fig 1: Summary of approaches to information Fusion in bio metric Systems

SCORE NORMALIZATION TECHNIQUE

Consider a multimodal biometric system that follows the combination approach to fusion at the fusion level. The theoretical framework developed by kittler et al. [3] can be applied to this system only if the output of each modality is of the form P (genuine | X) i.e. the posteriori probability of user being "genuine" given the input biometric sample X. In practice, most biometric systems output a matching score s. verlinde et al. [4] has proposed that the matching score s is related to P (genuine | X) as follows:

$$S= f(P(\text{genuine} \mid X)) + \eta(X) \rightarrow 1$$

Where f is a monotonic function and η is error made by the biometric system that depends on the input biometric sample X. This error could be due to the noise introduced by the sensor during the acquisition of the biometric signal and the errors made by the feature extraction and matching process. If we assume η is zero, it is reasonable to approximate P (genuine | X) by P (genuine | s). In this case problem reduces to computing P (genuine| s) and this requires estimating the conditional densities P (s|genuine) and P (s| impostor). Snelick et al. [5] assumed a normal distribution for the conditional densities of the matching scores ($p(s| \text{genuine}) \sim N(\mu_g, \sigma_g)$ and $p(s|\text{impostor}) \sim N(\mu_i, \sigma_i)$, and used the training data to estimate the parameters μ_g, σ_g, μ_i, and σ_i. The posteriori probability of the score being that of a genuine user was then computed as,

$$P(\text{genuine} |s) = \frac{p(s| \text{genuine})}{P(s| \text{genuine}) + p(s| \text{impostor})}$$

This approach has two drawbacks

1) The assumption of a normal distribution for the scores may not be true in many cases.

2) The approach does not make use of prior probabilities of the genuine and impostor users that may be available to the system. Due to these reasons we have proposed the use of a non-parametric technique i.e. Parzen window density estimation method [6] to estimate the actual conditional density of the genuine and impostor scores. After estimating the conditional densities, the Bayes formula can be applied to calculate the posteriori probability of the score being that of a genuine user. Thus,

$$P(\text{genuine} |s) = \frac{p(s| \text{genuine}) * p(g)}{p(s)}$$

Where $p(s) = (p(s| \text{genuine}) * p(g) + P(s| \text{impostor}) * p(i))$

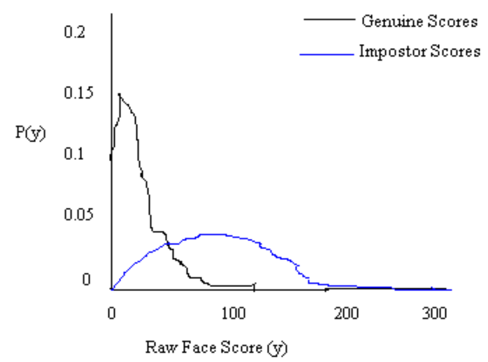
and p(g) and p(i) are the prior probabilities of a genuine user and an impostor.

Although the parzen window density estimation technique significantly reduces the error in the estimation of P(genuine | s), the density estimation still has inaccuracies non-zero due to the finite training set and the problems in choosing the optimum window width during the density estimation process. Further, the assumption that the value of η in equation 1is zero is not valid in most practical biometric systems. Since η depends on the input biometric sample X, it is possible to estimate η only if the biometric system outputs a confidence measure on the matching score along with the matching score itself. In the absence of this confidence measure, the calculated value of P (genuine | s) is not a good estimate of P (genuine | X) and this can lead to poor recognition performance of the multimodal system.

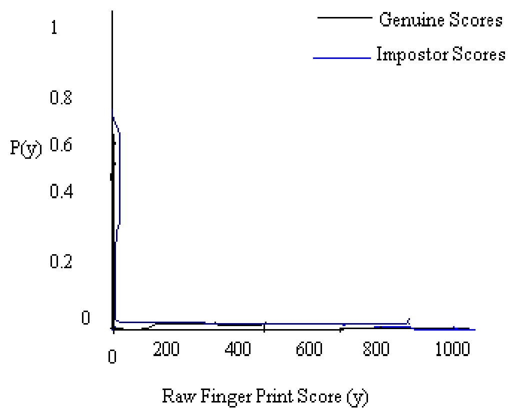
Need for Score Normalization

The following issues needed to be considered prior to combining the scores of the matchers into a single score. The matching scores at the output of the individual matchers may not be homogeneous. For ex: one matcher may output a distance (dissimilarity) measure while another may output a proximity (similarity) measure. Further, the outputs of the individual matchers need not be on the same numerical scale (range). Finally, the matching scores at the output of the matchers may follow different statistical distributions. Due to these reasons, score normalization is essential to transform the scores of the individual matchers into a common domain prior to combining them. Score normalization is a critical part in the design of a combination scheme for matching score level fusion.

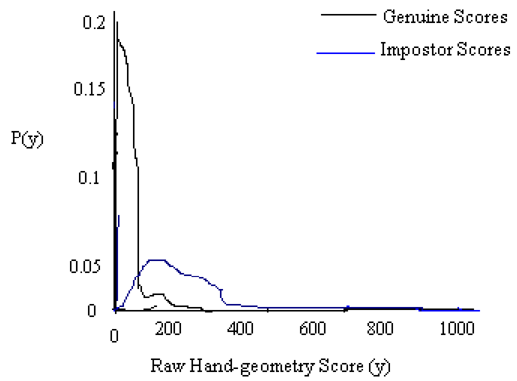
The following figure shows the conditional distributions of the face, fingerprint and hand – geometry matching scores used in our experiments.



a) Face (distance score)



b) **Finger Print (Similarity Code)**



c) Hand- geometry (distance Score)

CONCLUSION

In this paper we have presented various approaches for integrating evidence obtained from multiple cues in a biometric system. Fig 1 presents a high-level summary of information fusion techniques. The combination approach to score level fusion has received considerable attention. Most of the score level fusion techniques can be applied only when the individual modalities can provide a reasonably good recognition performance. These techniques cannot handle less reliable (soft) biometric identifiers that can provide some amount of discriminatory information, but are not sufficient for recognition of individuals.

In this paper we also presented score normalization, which refers to changing the location and scale parameters of the matching score distributions at the outputs of the individual matchers, so that the matching scores of different matchers are transformed into a common domain. For a good normalization scheme, the estimates of the location and scale parameters of the matching score distribution must be robust and efficient.

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AUTHORS

K.Sasidhar, is currently working as Associate Professor in the department of IT, SNIST Hyderabad, A.P, INDIA. He has 13 years of experience in reputed engineering colleges. He has published three International Journals and Participated in 7 international, national conferences and Seminars.

K.Kailasarao is currently working as Professor and Head of CSE Department, MRCET, Hyderabad He has 20 years of experience. To his credit he has 6 renewed publications. He involved in conducting various Conferences as a coordinator at MRCET, Hyderabad.