A Study on the Iris Biometric Authentication

by

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We hereby certify that this dissertation, submitted by Seung-Seok Choi, satisfies the dissertation requirements for the Master degree in Computer Science and has been approved.

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Abstract

This paper presents a methodology for quantitatively establishing the discriminative power of iris biometric data. It is difficult, however, to establish that any biometric modality is capable of distinguishing every person because the classification task has an extremely large and unspecified number of classes. The purpose of this study is to investigate various combinations of features, distance measures, and classifiers to find the best combination for determining the individuality of the iris biometric. Based on this review, a proposed methodology is used to establish a measure of discrimination that is statistically inferable. To establish the inherent distinctness of the classes, i.e., to validate individuality, we transform the many class problem into a dichotomy by using a distance measure between two samples of the same class and between those of two different classes. Various features, distance measures, and classifiers are reviewed and evaluated. For feature extraction I compare simple binary and multi-level dimensional wavelet features. For distance measures I examine scalar distances, feature vector distances, and histogram distances. Especially, I compare conventional binary feature distance measures and evaluate their performance. Finally, for the classifiers I compare Bayes decision rule, nearest neighbor, artificial neural network, and support vector machines. The experiment of the eleven different combinations is performed. The best one uses multi-level 2D wavelet features, the histogram distance, and a support vector machine classifier.

Table of Contents

List of Figures

List of Tables

Chapter 1

Introduction

I consider the task of establishing the distinctiveness of each individual in a population when there is a set of measurements that have an inherent variability for each individual. This task of establishing individuality can be thought of as showing the distinctiveness of the individual classes with a very small error rate in discrimination. The problem is important in many biometric and forensic science applications such as writer, face, fingerprint, speaker, or bite mark identification. All these applications face the problem of scientifically establishing individuality, which is motivated by court rulings [1].

Establishing a measure of uniqueness for a particular biometric is a challenging problem. A very small error rate of a certain performance evaluation of a biometric model can be a candidate for a measure of individuality. There are two important models in biometrics: identification (polychotomy, one-of-many decision) and verification (dichotomy, binary decision) [2~5]. It has been argued that the verification model is clearly more suitable than the identification model for establishing the individuality of a biometric [3]. Consider the many-class problem where the number of classes (individuals) is too large to be completely observed, such as the population of a country. Most biometric identification problems fall under the aegis of the many-class problem. Although classification techniques that assume a fixed number of classes are not particularly useful for establishing individuality in many class problems, some studies nevertheless use the identification model and present a confusion matrix [6~12].

To establish the inherent distinctness of the classes, i.e., to validate individuality, we transform the many class problem into a dichotomy by using a distance measure between two samples of the same class and between samples of two different classes. This model allows the inferential classification of patterns without having to observe all the classes. It is a method for measuring the reliability of classification of all classes based on information obtained from a small sample of classes drawn from the class population. In this model, two patterns are categorized into one of only two classes; they are either from the same class or from the two different classes. Given two biometric data samples, the distance between the two samples is first computed. This distance measure is used as data to be classified as positive (intra-variation, within person or identity) or negative (inter-variation, between different people or non-identity). In [3, 4], the individuality of handwriting using the distance statistics was shown. In this paper, I generalize the results to the iris biometric domain. Pankanti, et al., also showed this model to establish the individuality of fingerprints [13].

Hence, the problem of iris biometric individuality is as follows. Given two iris samples, the feature distance between the two samples is classified as intra-person (identity) or inter-person (non-identity). We use the terms intra-person distance and inter-person distance. Two types of errors, False Accept Rate (FAR) and False Reject Rate (FRR), are inferable to testing sets and even to the entire population.

The proposed model has the additional advantage that it allows the use of multiple heterogeneous features, whereas most pattern recognition techniques require that the features be homogeneous [14]. Both continuous and non-continuous features have been studied widely in the areas of pattern recognition [14], machine learning [15], and feature selection [16]. In Liu and Motoda's version of the hierarchy of feature types [16], only elementary feature types were considered: discrete ordinal and nominal, continuous, and complex. Features observed in real applications, however, often have more complicated feature types such as histograms, strings, etc. By taking distance measures, we are able to integrate various types of features into one useful for many forensic science and biometric authentication problems. Thus, the proposed dichotomy model integrates multiple features types into feature distance scalar values [17].

The purpose of this paper is to investigate various combinations of features, distance measures, and classifiers to find the best combination for determining the individuality of the iris biometric. For feature extractions, I compare simple binary and multi-level 2D wavelet features. For distance measures, I examine scalar distances (such as Hamming and Euclidean), feature vector distances, and histogram distances. Finally, for the classifiers, I compare Bayes decision rule, nearest neighbor, artificial neural network, and support vector machines. Among the eleven different combinations tested, the best model uses the multi-level 2D wavelet feature, histogram distance, and a support vector machine classifier.

The remainder of the paper is organized as follows: Chapter 2 illustrates the dichotomy model which is a statistically inferable approach to establishing the individuality of a biometric. Chapter 3 compares this model with the polychotomy model in terms of statistical inferability. Chapter 4 explains the general procedures for the experiment. Chapter 5 presents the various features and distance measures explored for iris authentication. Chapter 6 examines the definitions of conventional binary feature distance measures and evaluates their performance. Chapter 7 compares the experimental results of various classifiers using different combinations of features and distance measures. Finally, Chapter 8 draws some conclusions [18].

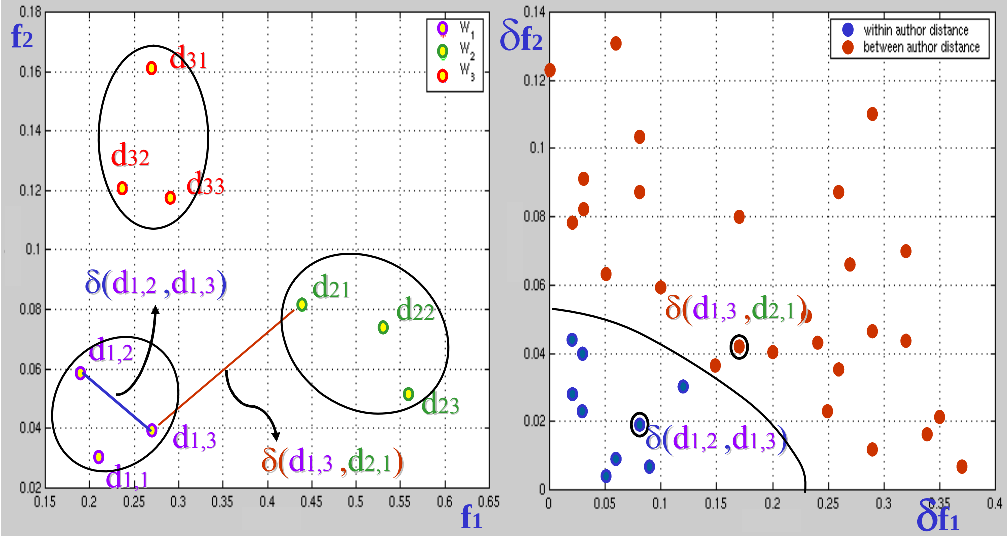
Chapter 2

Dichotomy Model

The multi-category classification problem, or *Polychotomizer*, is stated as follows. There are *m* exemplars of each of *n* people (*n* = very large). Given a biometric exemplar, *x*, of an unknown person, the task is to determine whether *x* belongs to any of the *n* subjects and if so, to identify the person. As the number of classes is enormously large and almost infinite, I shall demonstrate that this problem is seemingly insurmountable. To circumvent this problem, I propose a *dichotomy model* that can handle the *many class problem*. I show how to transform a large *polychotomy* problem into a simple *dichotomy* problem, a classification problem that places a pattern in one of only two categories.

2.1. Dichotomy Transformation

To illustrate the transformation process, suppose there are three people, $\{P_1, P_2, P_3\}$. Each person provides three biometric data samples with two features extracted per sample. Figure 1 (a) plots the biometric samples for the three people, where the features are real-values. To transform this feature space into a distance vector space for real valued features, I take the vector of distances of every feature between samples by the same person and categorize it as an *intra-person distance* denoted by $\vec{x}_{\oplus}$. Similarly, *inter-person distance* distances are obtained by measuring the distances between two different persons' biometric samples, denoted by $\vec{x}_{\ominus}$.



(a) Feature space
(Polychotomy)

(b) Feature Distance space
(Dichotomy)

Figure 1. Transformation from (a) Feature domain to (b) Feature distance domain

I use subscripts of the positive ⊕ and negative ∅ symbols as the nomenclature for all variables of intra-person distance and inter-person distance, respectively. Let $\vec{d}_{ij}$ denote a feature vector corresponding to the i^{th} person's j^{th} biometric sample, then $\vec{x}_{\oplus}$ and $\vec{x}_{\Theta}$ are obtained as follows:

$$\vec{x}_{\oplus} = |\vec{d}_{ij} - \vec{d}_{ik}| \quad \text{where } i = 1 \text{ to } n, \text{ and } j,k = 1 \text{ to } m,\ j \neq k \qquad (1)$$

$$\vec{x}_{\Theta} = |\vec{d}_{ij} - \vec{d}_{kl}| \quad \text{where } i,k = 1 \text{ to } n,\ i \neq k \text{ and } j,l = 1 \text{ to } m \qquad (2)$$

where *n* is the number of people, and *m* is the number of biometric samples per person. Note that the result of the dichotomy transformation is not a scalar value but a vector of distances. Figure 1 (b) represents the transformed plot. The original feature space is transformed to a feature distance space. For example, an *intra-person distance*, *W* (within), and an *inter-person distance*, *B* (between), in Figure 1 (a), correspond to the points *W* and *B* in the feature distance space in Figure 1 (b), respectively. Thus, there are only two categories: *intra-person distance* and *inter-person distance* in the feature distance space.

Let $n_\oplus = |\vec{x}_\oplus|$ and $n_\ominus = |\vec{x}_\ominus|$, the sizes of inter- and intra-person distance classes, accordingly.

Fact 1 If *n* people provide *m* biometric samples each, there are $n_\oplus = \binom{m}{2} \times n$ positive data samples, $n_\ominus = m \times m \times \frac{n(n-1)}{2}$ negative samples, and $\binom{mn}{2}$ samples in total.

Proof: $n_\oplus = \binom{m}{2} \times n$ is straight-forward. To count the *inter-person distance* data, we can enumerate them as $m \times (m \times (n-1)) + m \times (m \times (n-2)) + \cdots m \times (m \times 1)$. For the first person, there are $(m \times (n-1))$ number of other people's biometric data and he or she has *m* data. For the second person, there are $(m \times (n-2))$ number of other people's biometric data that are not counted yet. Therefore, $n_\ominus = m \times m \times \sum_{i=1}^{n-1} i = m \times m \times \frac{n(n-1)}{2}$. Now, $n_\oplus + n_\ominus = \binom{mn}{2} = \frac{(mn)!}{(mn-2)!2} = \frac{(mn)(mn-1)}{2}$

$$= \frac{m(m-1)}{2} n + m^2 \frac{n(n-1)}{2} = n_\oplus + n_\ominus$$ ∎

For example, for the handwriting data collection of [4, 5] 1000 people (statistically representative of the U.S. population) provided exactly three samples each. Hence, $n_\oplus = 3000$, $n_\ominus = 4{,}495{,}500$, and there are 4,498,500 in total.

Most statistical testing requires that the observed data be statistically independent. The distance data is, however, not statistically independent: one obvious reason being the triangle inequality of three distance samples of the same person. This caveat should not be ignored. One immediate solution is to choose randomly a smaller sample from a large sample obviating the triangle inequality. One can, for example, partition $n_{\oplus} = 3000$ samples into disjoint subsets of 500 each to guarantee no triangle inequality problem.

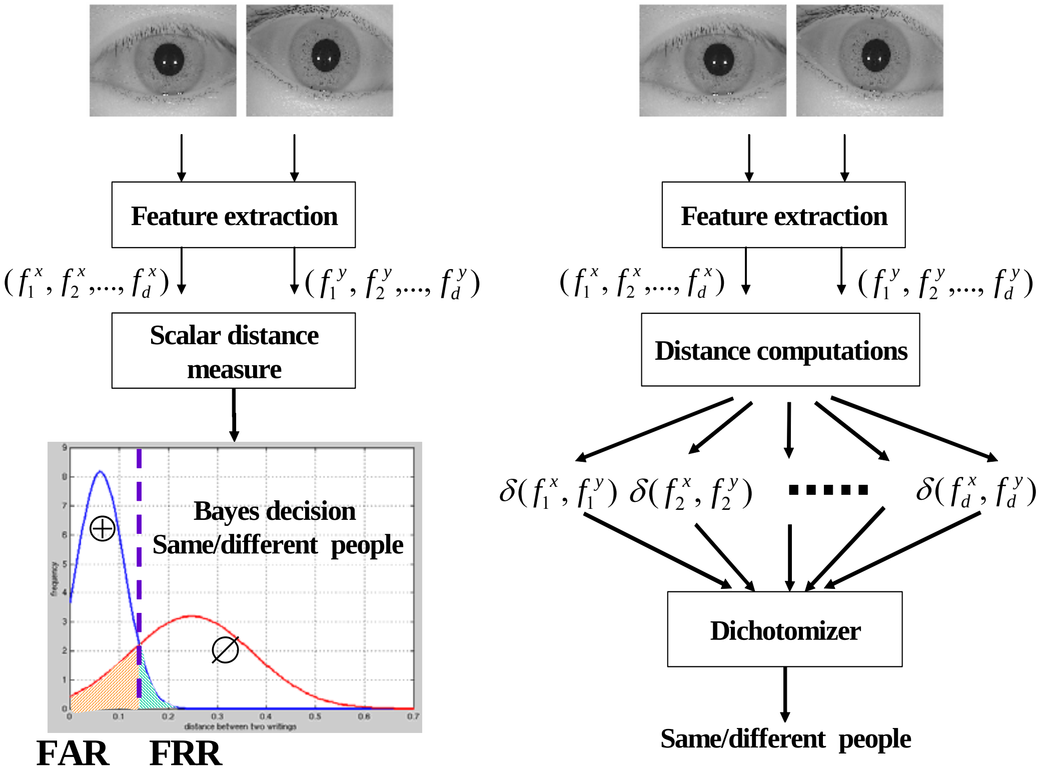
In the *dichotomy* model, we formally state the problem as follows: given two randomly selected biometric samples, the problem is to determine whether the two exemplars belong to the same person. Figure 2 depicts the whole process using the *dichotomy transformation*. Let f_i^j be the i^{th} feature of j^{th} biometric data.

First, features are extracted from both biometric data *x* and *y*: $\{f_1^x, f_2^x, \cdots, f_d^x\}$ and $\{f_1^y, f_2^y, \cdots, f_d^y\}$. Then, each feature distance is computed: $\{\delta(f_1^x, f_1^y), \delta(f_2^x, f_2^y) \cdots, \delta(f_d^x, f_d^y)\}$. In equations (1) and (2), δ is the absolute difference between two real values. However, the features need not be real valued and could be any form such as nominal, strings, histograms, etc. Depending on the feature type, suitable distance measures are associated, e.g., approximate string matching distance for string type features. Thus, the previous equations can be rewritten as follows:

$$\vec{x}_{\oplus} = \delta(\vec{d}_{ij} - \vec{d}_{ik}) \text{ where } i = 1 \text{ to } n, \text{ and } j, k = 1 \text{ to } m, \ \ j \neq k \quad (3)$$

$$\vec{x}_{\Theta} = \delta(\vec{d}_{ij} - \vec{d}_{kl}) \text{ where } i, k = 1 \text{ to } n, \ i \neq k \text{ and } j, l = 1 \text{ to } m \quad (4)$$

where δ varies depending on feature types [17]. In all, the *dichotomizer* takes this feature distance vector as the input, and outputs the decision, i.e., “same person” or “different people.”



(a) Parametric Verification (b) Dichotomy Transformation

Figure 2. dichotomy transformation process

A good descriptive way to represent the relationship between two populations (classes) is to calculate the overlap between the two distributions. Figure 3 illustrates the two distributions assuming that they are normal. Although this assumption is invalid, we can use it to describe the behavior of two populations figuratively without loss of generality. Assuming that we are using a *Bayes optimal classifier* with equal prior probabilities, *type I error* (FRR) occurs when the same person's biometric data are identified as coming from different people, and *type II error* (FAR) occurs when the biometric data provided by two different people are identified as coming from the same person as shown in Figure 3 (a).

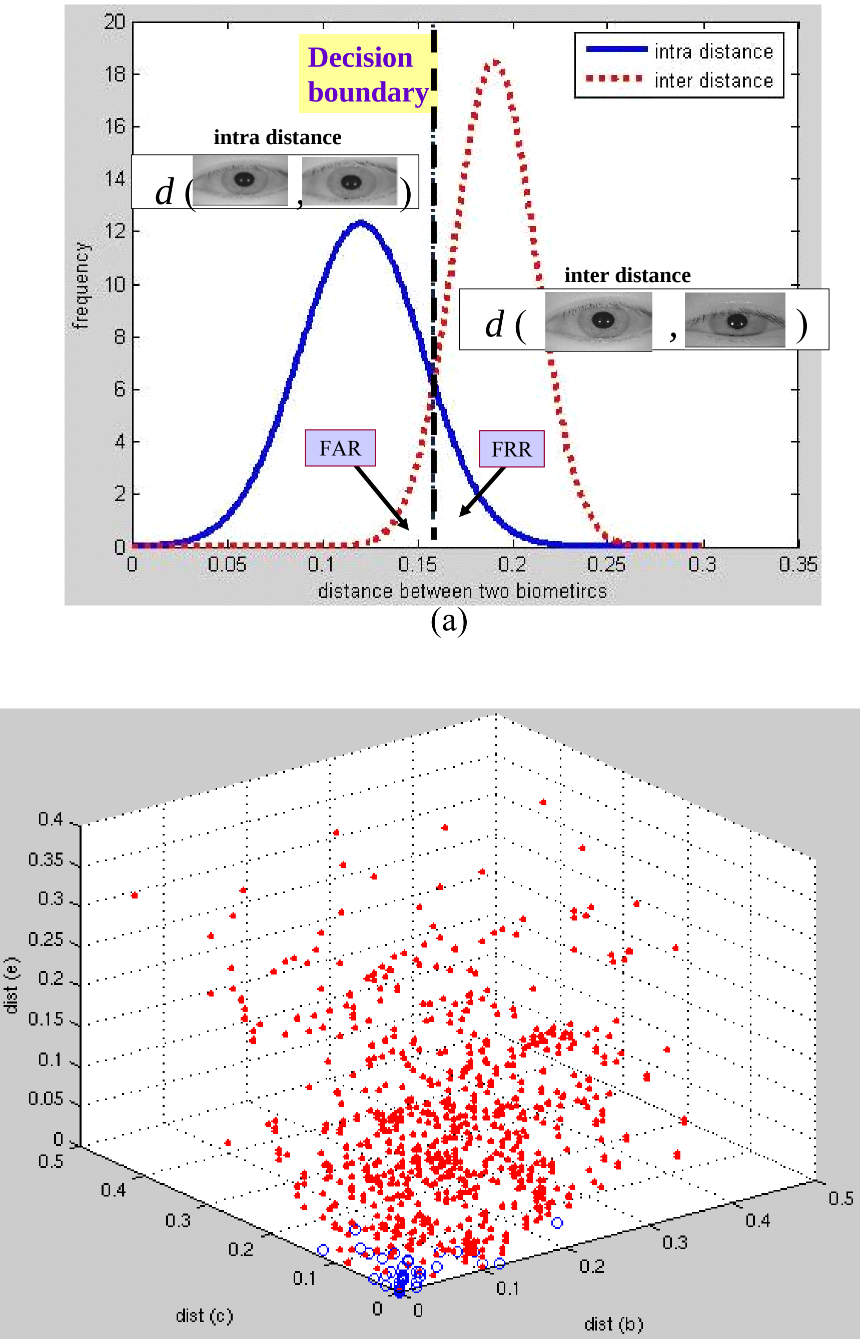
$$FRR = \Pr\ (dichotomizer(\vec{d}_{ij} - \vec{d}_{kl}) \geq T \mid i = k) \qquad (5)$$

$$FAR = \Pr\ (dichotomizer(\vec{d}_{ij} - \vec{d}_{kl}) < T \mid i \neq k) \qquad (6)$$

Let $\hat{x}$ denote the distance x position where two distributions intersect. As shown in Figure 3 (a), *FRR* is the right-side area of the positive distributions where the decision bound is $T = \hat{x}$.

Suppose one must make a crisp decision and choose the intersection as a classification boundary. Then, FRR is the probability of error that one classifies two biometric data as different people even though they belong to a same person. *FAR* is the left-side area of the negative distributions, i.e., the probability of error that one classifies two biometric data as coming from the same person even though they belong to two different people.

As is apparent from Figure 3, the intra-person distance distribution is clustered toward the origin, whereas the inter-person distance distribution is scattered and away from the origin. Utilizing the fact that the intra-person distance is smaller, I design the *dichotomizer* to establish the decision boundary between the intra and inter-person distances.



(a)

(b)

Figure 3. (a) Type I and II errors (b) 3-D Space Distribution.

Chapter 3

Comparison: Polychotomy vs. Dichotomy

I now compare the *dichotomy model* with the *polychotomy model* in terms of accuracy and statistical inference. Consider the multiple-class problem where the number of classes is small, and one can observe many instances of each class. To show the individuality of the classes statistically, one can cluster the instances into classes and infer the separation to the entire population. It is an easy and valid method to establish the individuality as long as a substantial number of instances for each class are observable. Now, consider the *many class problem* where the number of classes is too large to be observed, such as the population of a country. Many pattern identification problems, and most of the forensic science applications mentioned above, fall under the aegis of many class problems. Although classification techniques that assume a fixed number of classes are not appropriate for establishing individuality in many class problems, most of the existing studies use the *identification* model and present the confusion matrix [6~12].

The definition of *inferential statistics* is to measure the reliability of individuality for the entire population based on information obtained from a sample drawn from the population. I claim that the identification model is not statistically inferable for many class problems. In this model, to draw valid conclusions, one must observe samples from every single person, which is clearly impossible. For instance, consider handwritten alphabets and the task of validating the individuality of alphabet shapes. If one observes instances of only the alphabet characters {A, B, C} and draws the conclusion that all alphabet characters are distinct, this is invalid because not all classes have been observed, and, for example, there maybe indistinguishable version of italic *I* and l. Without knowing the geometrical distributions of the unseen classes (populations), one cannot draw the statistical inference; true error of the entire population cannot be inferred from the error estimate of the sample population because there are unseen classes (the rest of the population, e.g. U.S. or other country populations).

One immediate and obvious drawback of the *dichotomy* model is that it may fail to detect the difference between, for example, P_1 and P_2 that do not differ greatly in feature distance space even though they are different geometrically in the original feature space as shown in Figure 4.

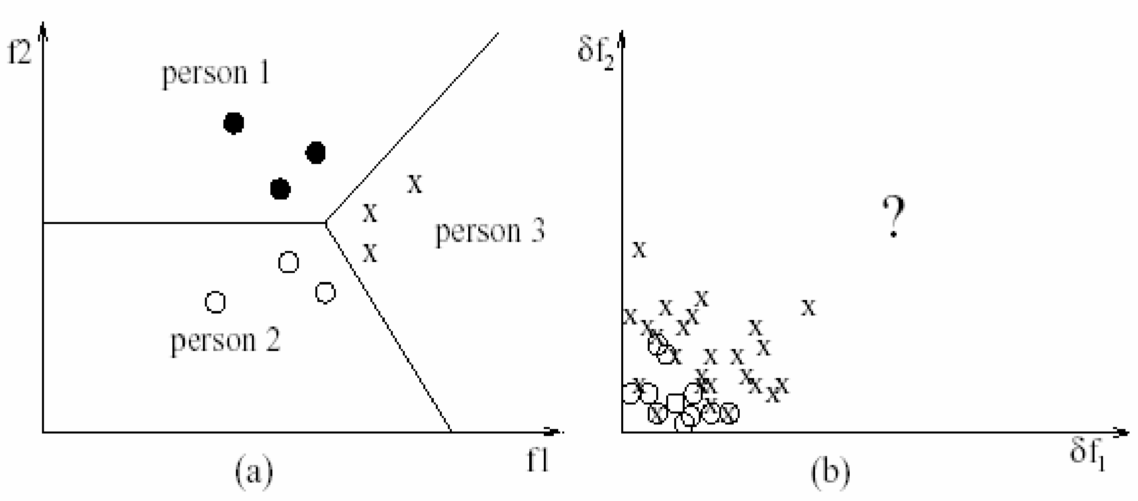
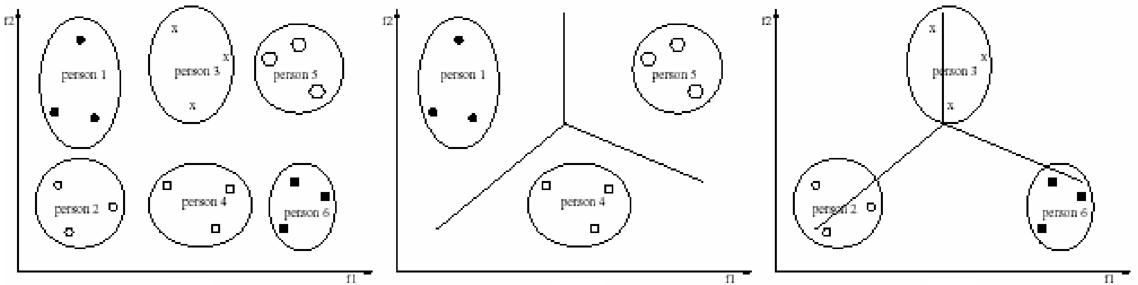


Figure 4. Comparison between (a) feature domain (*polychotomy)* perfectly classifiable and (b) feature distance domain (*dichotomy)* possibly not dichotomizable.

It is desirable if all the distances between data of the same class (person) in the feature domain belong to the within-class-distance class in the feature distance domain. Similarly, we would like all distances between two different classes in the feature domain to belong to the between-class-distance class in the feature distance domain. Unfortunately, this is not always the case; perfectly clustered class in the original feature domain may not be perfectly dichotomized in the feature distance domain. The comparison in the *dichotomy* model is relative to a population and is crucially affected by the choice and diversity of the population. The broader the spread of the feature distributions among members of the population, the less we learn about detecting real differences between individuals who do not differ greatly. However, our experimental results show that these extreme cases are rare.

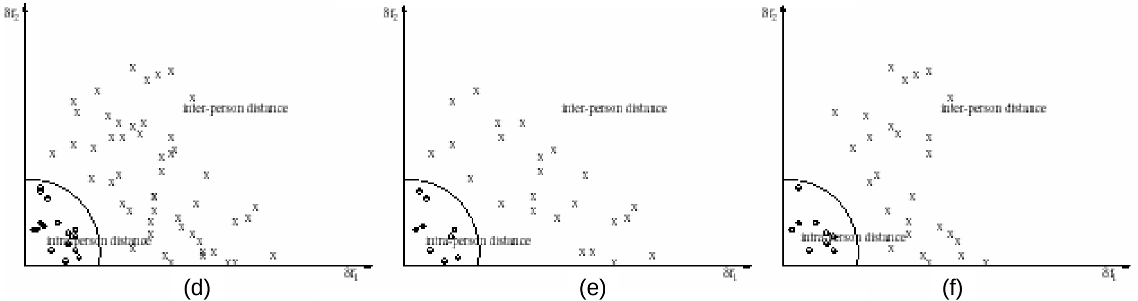
The objective is to validate the individuality of biometric data statistically, but not to detect the difference of particular instances. I are attempting to infer the individuality of the entire population based on the individuality of a sample of *n* people, where *n* is much less than the population. I claim that the *dichotomy* model is a sound and valid *inferential statistics* approach.

By definition, *inferential statistics* measures the reliability of individuality of the entire population based on information obtained from a sample drawn from the population. I explain the justification of the dichotomy model using *inferential statistics*.



(a) (b) (c)

Feature Domain (Polychotomy)



(d) (e) (f)

Feature Distance Domain (Dichotomy)

Figure 5. Statistical Inference in Polychotomy and Dichotomy: (a) all classes in feature domain, (b) partial classes and a classifier in feature domain, (c) the other classes, (d) entire population in feature distance domain, (e) a sample representative to the population in feature distance domain, (f) another sample representative to the population in feature distance domain.

Suppose that we use the polychotomy model to validate the individuality of biometric data. In this model, a population consists of the biometric data of every person in the population. To draw a valid conclusion, therefore, one must observe samples from every single person, which is impossible. If we observe only 1,000 people (classes/populations), drawing a statistically inferential conclusion is invalid because there are unseen classes. One cannot draw the statistical inference; true error of the entire population cannot be inferred from the error estimate of the sample population of 1000 because there are unseen classes (the rest of the population).

Figure 5 (a)-(c) illustrates this issue. Suppose there are only 6 people in the universe (a), and we observe the biometric data of three people (1, 4, and 5) (b) because we assume that observing all people is difficult. Although one can successfully discriminate among the three people using a pattern classification or machine learning technique, the learned polychotomizer is not suitable for the other classes, as shown in (c). Clearly, the polychotomy model is not statistically inferable.

Transforming the US population class-classification problem into a two class problem helps us overcome this issue, as shown in Figure 5 (d)-(f), where (d) and (e) are the dichotomy transformed plots of (b) and (c), respectively. There are only two populations, and we can acquire sufficient instances of each class or population. Since every new instance also maps onto these two classes, the distribution of the sample population can be used to infer the distribution of the entire population. Although we might do better by detecting real differences between individuals who do not differ greatly in the polychotomy model, the statistical inference is of primary interest and the dichotomy model is a sound and valid inferential statistical model whereas the polychotomy one is not. As we shall see later in section 5, as borne out by our training and testing results, only 3% of the data was misclassified. Since misclassification error can be attributed to a number of factors such as feature selection in addition to "masking". "Masking" likely occurred in an even smaller percentage. In all, inferring the error probability of the entire population through the dichotomizer model is more useful than detecting real differences between individuals who do not differ greatly from the sample population in the polychotomy model.

I further support our claim that the polychotomy (identification) model is not statistically inferable one. When the number of classes increases, the error rate increases. In other words, the error rate counted in the polychotomy model based on only *n* people (classes), increases dramatically as the entire population increases, as shown in Figure 6, and therefore, it is not possible to make inferences regarding the entire population [19].

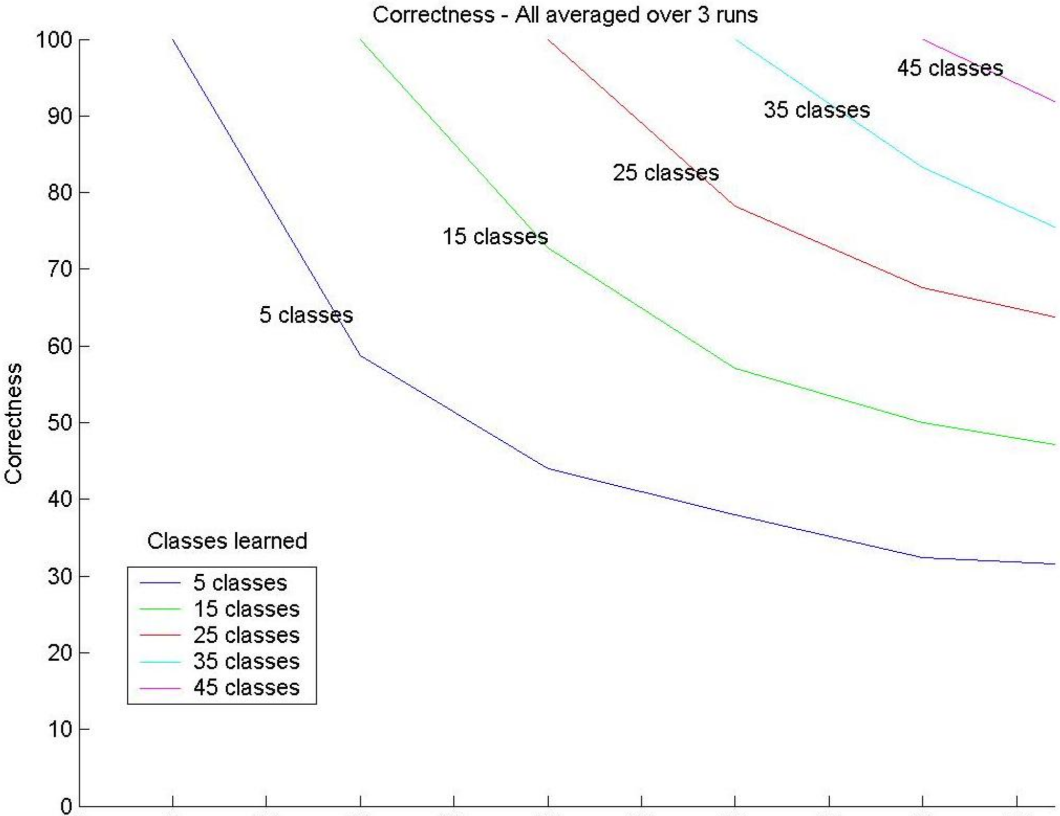


Figure 6. Generalizability of Iris identification

We have a trade-off between tractability and accuracy. Since sampling a sufficiently large sample from each individual person is intractable, we transform the feature domain into the feature-distance domain where we can obtain large samples for both classes. By using this transformation, the problem becomes a tractable inferential statistics problem, although we might get lower accuracy. However, if the number of classes is sufficiently small that it is possible to obtain samples for each class, then one may use the polychotomizer to validate the individuality of classes.

Nevertheless, one cannot exclude the dichotomizer even in small, multiple-class classification problems. On one hand, the polychotomizer may be better if the features are in a vector form of homogeneous scalar values since techniques in *pattern recognition* typically require that features be homogeneous. On the other hand, however, the solution proposed overcomes the non-homogeneity of features since feature distances are nothing but scalar values. Various heterogeneous features and distance measures used are discussed in [17] and in the following section. Hence, the proposed dichotomy model provides two advantages: it is statistically inferable and it allows non-homogeneous features.

Chapter 4

Experimental Procedures

In order to extend the proposed method to establish the discriminative power of biometric modalities, I first give an outline of the procedure and describe each step.

The procedure to establish the discriminative power of a given biometric measure is as follows:

1 Data acquisition
  1.1 Recruit a sufficient number of subjects to represent the population
  1.2 Collect multiple biometric data from each subject
2 Feature extraction and Dichotomy Transformation
  2.1 Extract features using image or signal processing techniques
  2.2 Apply suitable distance measures for features
3 Hypothesis testing
  3.1 Design pattern classification (dichotomy)
  3.2 Validate the results

The first step 1.1, recruiting a sufficient number of subjects to represent the population is crucial in order to infer the results to the entire population. The basis for collecting samples from the population to represent a certain nation or universe comes from the sampling strategy suggested in the field of experimental design [20-21]. The two populations of interest are the intra and inter person variations. In order to obtain the representative samples of these two populations, we perform sampling based on standard properties: randomness, sample size, and representation. Randomly selecting a large number of subjects from the representative population provides representative samples of the two populations: intra and inter person classes.

Step 1.2, collecting multiple biometric data from each subject, is necessary to obtain the intra person distance data. At least three samples per subject are recommended.

In step 2, the proposed dichotomy transformation model requires first the extraction of features and then the application of suitable distance measures. Various image or signal processing techniques can be used to extract features from a given modality. Depending on the feature measurement type, suitable distance measures, e.g., *Euclidean, dot-product, string matching, histogram matching*, etc, can be used to transform the feature space into the feature-distance space.

The final step 3 is hypothesis testing. Once the two-class data, i.e., intra and inter person distances, are computed, various pattern classifiers may be used to perform the dichotomy. Separate intra and inter person distance data are used to validate the results. The two-class error rate is used as the measure of individuality. Estimating the error probability is one of the simplest problems in statistical inference [21-22] and performance evaluation [15].
The error probability estimation for the *forensic* and *biometric* data individuality problem is depicted in Figure 7.

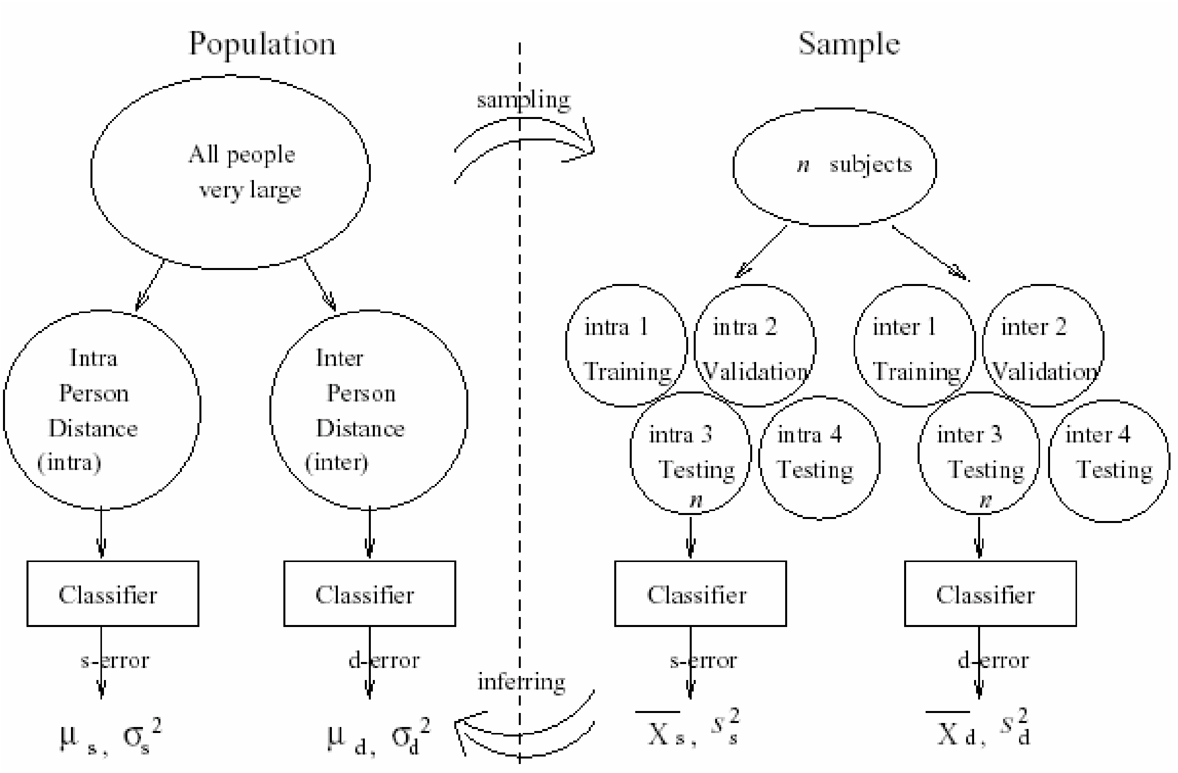


Figure 7. Error Evaluation Experimental Setup.

A large number of subjects, *n*, are chosen for the experiment and they provide *m* biometric data each. There are two populations of interest and they are the *intra person distance* (or simply *intra*) and *inter person distance* (or simply *inter*). A sample of *intra* is obtained from pairing two biometric data samples provided by a same person. A sample of *inter* is obtained from pairing biometric samples provided by two different subjects. A dichotomy classifier is designed using the training and validation sample sets. The error probability is measured using the testing sample sets. There are two errors for each population as discussed earlier. The *s-error* is the error probability that the system classifies the two samples as a member of *intra* although they were provided by two different subjects, while the *d-error* is the error probability that the system classifies the two samples as a member of *inter* even though they were provided by one subject. Sample error means are denoted as $\overline{X_s}$ and $\overline{X_d}$ for *s-error* and *d-error*, respectively. They are often known as point estimates of the population error means, μ_s and μ_d.

A classification system is trained using training sets *intra 1* and *inter 1* with two validation sets *intra 2* and *inter 2*. The system is tested using the remaining multiple testing sets.

In addition to the point estimates, we are interested in confidence intervals for μ_s and μ_d. They are intervals within which we have reason to believe that the true population means, μ_s and μ_d, lie assuming they are normal. The formula for the $1-\alpha$ level confidence interval for μ_s is:

$$\text{confidence interval for } \mu_s \approx \overline{X_s} \pm t[1-\alpha/2; n-1]\sqrt{s_s^2/n} \tag{7}$$

$$\approx \overline{X_s} \pm z[1-\alpha/2; n-1]\sqrt{\frac{\overline{X_s}(1-\overline{X_s})}{n}} \tag{8}$$

Because *n* is quite large, one can use either *Student's t* distribution or the normal table to compute the confidence interval. Although the population variance σ_s^2 is unknown [18], one can assume that $\sigma_s^2 \approx s_s^2$ for a large *n*. Thus, the normal table is often used in evaluating performance [15]. I use both, and choose the one that gives the tighter bound for the sake of higher precision. In both cases, $np(1-p) > 5$ and thus one can use either the normal table or the t-table.

The normality assumption on the error distribution is a sine-qua-non in the analysis. The error probability follows a binomial distribution. A *Binomial distribution* gives the probability of observing *r* errors in a sample of *n* independent instances. A discrete binomial distribution function is then

$$P(r) = \frac{n!}{r!(n-r)!} p^r (1-p)^{n-4} \tag{9}$$

The expected, or mean value of *X* is

$$E[X] = np \tag{10}$$

The variance of X is

$$Var(X) = np(1-p) \tag{11}$$

For sufficiently large values of n the binomial distribution is closely approximated by a Normal distribution with the same mean and variance.

$$\text{s - error ND}(\mu_s, \frac{\sigma_s^2}{n}) \quad \text{and} \quad \text{d - error ND}(\mu_d, \frac{\sigma_d^2}{n})$$

Most statisticians recommend using the Normal approximation only when $np(1-p) \geq 5$ [15].

In the final step for the hypothesis testing, claim that $\mu_s = \overline{X_s}$ and $\mu_d = \overline{X_d}$ where $\overline{X_s}$ and $\overline{X_d}$ are error estimates using *intra 3* and *inter 3* sample sets. Given the results, we can perform the hypotheses test on the means.

$$\mathrm{H}_0^1 : \mu_s = \overline{X_s} \qquad \mathrm{H}_\mathrm{A}^1 : \mu_s \neq \overline{X_s} \tag{12}$$

$$\mathrm{H}_0^2 : \mu_d = \overline{X_d} \qquad \mathrm{H}_\mathrm{A}^2 : \mu_d \neq \overline{X_d} \tag{13}$$

I would like to validate the hypotheses using the other test sets. From *intra 4* and *inter 4*, we obtain new sample means, $\overline{X_s}'$ and $\overline{X_d}'$. From the equation (8), we obtain the critical regions for the means. If $\overline{X_s}'$ falls within the acceptance regions, accept the null hypothesis H_0^1 and similarly, if $\overline{X_d}'$ falls under the acceptance regions, accept the null hypothesis H_0^2. Otherwise, reject them.

Chapter 5

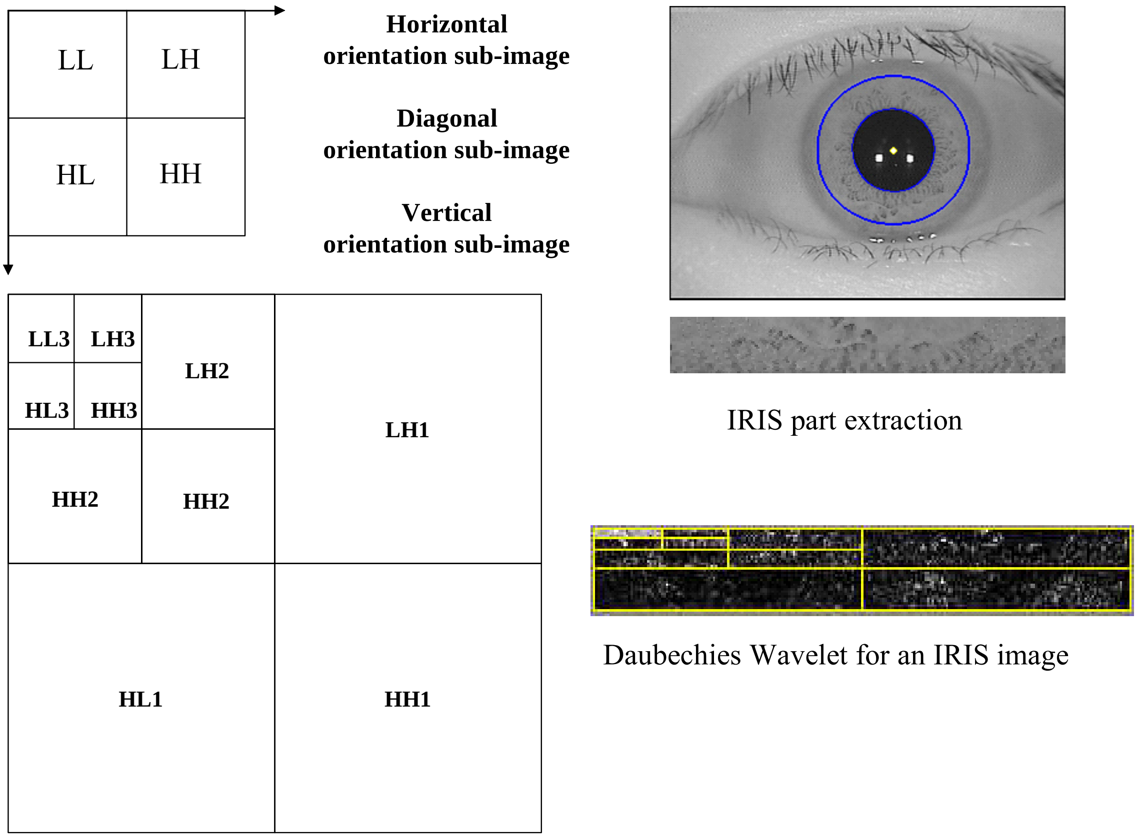
Feature Extraction and Distance Measures

The dichotomy model requires the extraction of features and the use of suitable distance measures. In this section, I review the features and distance measures previously used for iris authentication, a subset of which I investigate and compare in this study.

First, I consider the *iriscode* [20], which is a 256 binary feature extracted by applying a 2D Gabor wavelet filter. In [23], the *Hamming* distance in eqn (14) was used for the model in Figure 1 (a).

$$\partial(f^x, f^y) = f^x \bullet f^{y'} + f^{x'} \bullet f^y \qquad (14)$$

Second, multi-level 2D wavelet features have been widely used [24-27]. The hierarchical wavelet transform decomposes the original iris image into a set of frequency windows having narrower bandwidths in the lower frequency region [24]. Decomposing images with the wavelet transform yields a multi-resolution from detailed images to approximation images in each level. As shown in Figure 8, LH, HL, and HH represent detailed images for horizontal, vertical, and diagonal orientation, respectively, in one-level. Sub-image LL corresponds to an approximation image that is further decomposed, resulting in a two-level wavelet decomposition. The result of a three-level decomposition is shown in the lower-left portion of Figure 8.



IRIS part extraction

Daubechies Wavelet for an IRIS image

Figure 8. Three-level wavelet transform.

L. Ma et al. tried to extract more distinctive statistical features by using a filtering process [24]. G. Kee et al. presented a tree-structured wavelet transform in order to obtain means and standard deviations, which are used as iris feature sets [25]. Mallat suggested that statistics obtained from wavelet decomposition are sufficient for presenting texture difference [26].

I use the 2D Daubechies wavelet transform technique to extract features from an iris image as folows. Each iris image is decomposed into 3 levels and each sub-image is divided into 2x2 windows, which results in 12 different sub-images. For each-sub image, mean and variance values are calculated. As a result, 24 numeric feature values are extracted. One can use the Euclidean distance between two vectors in eqn (15) for the Figure 1 (a) model. One can also use the absolute vector difference measure in eqn (16) for the Figure 1 (b) model.

Note that the result of the eqn (15) is a scalar value whereas that of the eqn (16) is a d-dimensional feature distance vector.

$$\partial(f^x, f^y) = \sqrt{\sum_{i=1}^{d}(f_i^x - f_i^y)^2} \qquad (15)$$

$$\begin{aligned}\partial(f^x, f^y) &= | f^x - f^y | \\ &= (| f_1^x - f_1^y |, | f_2^x - f_2^y |, \cdots, | f_d^x - f_d^y |)\end{aligned} \qquad (16)$$

Third, instead of extracting mean and variance values for each sub-image, I utilize 12 linear type histograms as feature sets as previously proposed [27]. For each sub-image, the linear type of histogram is obtained as a feature from each decomposed sub image. f_i^x and f_i^y are ordinal histograms not simple numeric scalar values. There are numerous histogram distance measures [29] and I consider the two popular ones: eqn (17) shows the Euclidean distance and eqn (18) the histogram edit distance [28, 29]. Note that the histogram distance measure is applied to each of the 12 histogram features per iris image, resulting in a 12 dimensional feature distance vector.

$$\partial_i(f_i^x, f_i^y) = \sqrt{\sum_{j=1}^{b}(f_{i,j}^x - f_{i,j}^y)^2} \qquad (17)$$

$$\partial_i(f_i^x, f_i^y) = \sum_{j=1}^{b}\left|\sum_{k=1}^{j}(f_{i,k}^x - f_{i,k}^y)\right| \qquad (18)$$

Chapter 6

Binary Feature Distance Measures

In this section, I extend my study on distance measures for the binary features. I present definitions of conventional binary feature distance measures and evaluate their performance with proposed classificatiosn model [31].

6.1. Basic Binary Similarity Measures

Let x, y, and z be binary feature vectors of fixed length d, and let x_i denote the ith feature value which is either 0 or 1. One of the most popular measures in comparing two fixed-length bit patterns is the Hamming distance in eqn (19), which is the count of the bits that differ in the two patterns [33]. It is a simple geometrical L_1 distance, also known as Manhattan or city block distance, applied to d-dimensional binary space.

$$\begin{aligned}
&D_{\text{Hamming}}(x,y) = x^t\overline{y} + \overline{x}^t y \qquad (19)\\
&D_{\text{Hamming}}(x,y) = \sum_{i=1}^{d}|x_i - y_i|\\
&S_{\text{Hamming}}(x,y) = d - D_{\text{Hamming}}(x,y) = x^t y + \overline{x}^t\overline{y}\\
&S_{\text{Hamming}}(x,y) = \sum_{i=1}^{d} s_i\\
&\quad \text{where } s_i = \begin{cases} 1 & \text{if } x_i = y_i \\ 0 & \text{otherwise} \end{cases}
\end{aligned}$$

The term $x^t y$ denotes the positive matches, i.e., the number of 1 bits that match between x and y. The term $\overline{x}^t\overline{y}$ is the negative matches, i.e., the number of 0 matching bits. The terms $x^t\overline{y}$ and $\overline{x}^t y$ denote the number of bit mismatches – the first where pattern x has 1 and pattern y has 0, and the second where pattern x has 0 and pattern y has 1.

Fact 1. The Hamming distance has been shown to be metric [14].

While the Hamming distance is the number of bits differing in the two patterns, the Hamming similarity is the number of identical bits in the two patterns. Sokal and Michener normalized the Hamming similarity as in eqn (20) [34], and an alternative normalized Hamming similarity is given by Rogers and Tanimoto in eqn (21) [35].

$$s_{\text{Sokal-Michener}}(x,y) = \frac{x^t y + \overline{x}^t \overline{y}}{d} \tag{20}$$

$$s_{\text{Rogers-Tanimoto}}(x,y) = \frac{x^t y + \overline{x}^t \overline{y}}{x^t y + \overline{x}^t \overline{y} + 2x^t \overline{y} + 2\overline{x}^t y} \tag{21}$$

The term $x^t y$ is the inner product of two vectors, which yields a scalar, and it is sometimes called the scalar product or dot product. It can be converted to a distance by subtracting it from d, and this distance is clearly non-metric because of the reflexivity violation; $D_{\text{inner-product}}(x,y) = 0$ if $x = y$ and $|x| = |y| = d$ and $D_{\text{inner-product}}(x,y) > 0$, otherwise.

Fact 2. Nonnegativity, symmetry, and triangle inequality are trivial and preserved in the inner product [36].

$$\begin{gathered} s_{\text{inner-product}}(x,y) = x^t y \\ s_{\text{inner-product}}(x,y) = \sum_{i=1}^{d} s_i \\ \text{where } s_i = \begin{cases} 1 & \text{if } x_i = y_i = 1 \\ 0 & \text{otherwise} \end{cases} \end{gathered} \tag{22}$$

A normalized inner product is given in eqn (23) [14] and various alternative normalizations in eqns (24~27) [37-39, 42].

$$S_{\text{normalized-inner-product}}(x,y) = \frac{x^t y}{\|x\|\|y\|} = \frac{x^t y}{\sqrt{x^t x y^t y}} \tag{23}$$

$$S_{\text{Russell-Rao}}(x,y) = \frac{x^t y}{d} \tag{24}$$

$$S_{\text{Jaccard-Needham}}(x,y) = \frac{x^t y}{x^t y + x^t \overline{y} + \overline{x}^t y} \tag{25}$$

$$S_{\text{Dice}}(x,y) = \frac{x^t y}{2x^t y + x^t \overline{y} + \overline{x}^t y} \tag{26}$$

$$S_{\text{Kulzinsky}}(x,y) = \frac{x^t y}{x^t \overline{y} + \overline{x}^t y} \tag{27}$$

The Jaccard, Dice, and Kulzinsky similarity measures differ in their ranges: the Jaccard measure ranges from 0 to 1, the Dice measure from 0 to ½, and the Kulzinsky measure from 0 to ∞. Eqns (25~27) can be generalized to eqn (28) which for $\sigma = 0$ becomes the Kulzinsky coefficient, for $\sigma = 1$ the Jaccard coefficient, and for $\sigma = 2$ the Dice coefficient.

$$S_{\text{Generalized Jaccard}}(x,y) = \frac{x^t y}{\sigma x^t y + x^t \overline{y} + \overline{x}^t y} \tag{28}$$

Another popular distance measure between binary feature vectors is the Tanimoto metric defined in eqn (29) [14] where n_x and n_y are the numbers of 1 bits in x and y, respectively, and $n_{x,y}$ is $x^t y$.

$$D_{Tanimoto}(x,y)=\frac{n_x+n_y-2n_{x,y}}{n_x+n_y-n_{x,y}}=\frac{x^t\overline{y}+\overline{x}^t y}{x^t\overline{y}+\overline{x}^t y+x^t y} \qquad (29)$$

The Tanimoto coefficient [14], defined in eqn (30), is another variation of the normalized inner product which is frequently encountered in the fields of information retrieval and biological taxonomy.

$$S_{Tanimoto}(x,y)=\frac{x^t y}{x^t x+y^t y-x^t y} \qquad (30)$$

Most similarity measures are variations either of Hamming or of the inner-product. Generally, the former ones treat the presence, $x^t y$, and the absence, $\overline{x}^t\overline{y}$, of features equally while the later take only the presence, $x^t y$, into account and exclude $\overline{x}^t\overline{y}$. The decision to include or exclude the $\overline{x}^t\overline{y}$ term is a difficult and contentious one [42, 43]. Prior to 1950 when the *Hamming* distance was introduced, the use of inner-product based similarity coefficients flourished. Sokal and Michener made a good argument to include the negative matches [34, 42, 43] but they used equal weights for both positive and negative matches.

Hence, we propose a new measure with variable credit for the $\overline{x}^t\overline{y}$ term, eqn (31), where σ is the contribution factor, and $0 \le \sigma \ll \infty$. We call it the *azzoo* similarity measure because we can alter the credit for the zero-zero matches relative to that for the one-one matches (azzoo = **a**lter **z**ero **z**ero **o**ne **o**ne).s

$$
\begin{aligned}
S_{azzoo}(x,y) &= x^t y + \sigma \overline{x}^t \overline{y} \\
&= \sum_{i=1}^{d} x_i y_i + \sigma \sum_{i=1}^{d} (1-x_i)(1-y_i) \\
S_{azzoo}(x,y) &= \sum_{i=1}^{d} s_i \\
\text{where } s_i &= \begin{cases} 1 & \text{if } x_i = y_i = 1 \\ \sigma & \text{if } x_i = y_i = 0 \\ 0 & \text{otherwise} \end{cases}
\end{aligned} \tag{31}
$$

Note that for $\sigma = 0$, S_{azzoo} becomes the inner product, and for $\sigma = 1$, the Hamming similarity measure. Although S_{azzoo} requires finding the optimal σ factor, the experimental results in later sections show that it outperforms both the Hamming and inner-product similarity measures.

Originally, the half-credit similarity, S_{00-11} was used in an offline handwriting recognition system [44] and it is the same as S_{azzoo} with $\sigma = 0.5$. It gives full credit to features present in both patterns, $x^t y$, half credit to those not present in either pattern, $\overline{x}^t \overline{y}$, and no credit to those present in only one of the patterns, $x^t \overline{y}$ and $\overline{x}^t y$, as defined in eqn (32) [44, 45, 46] and here we generalized the half-credit similarity to S_{azzoo}.

$$S_{00-11}(x,y) = x^t y + \frac{\overline{x}^t \overline{y}}{2} \tag{32}$$

The range of S_{azzoo} is $\left[0,d\right]$ if $0 \le \sigma \le 1$ and $\left[0,\sigma d\right]$ if $\sigma > 1$. Assuming $0 \le \sigma \le 1$, S_{azzoo} can be converted to a distance measure for metric property testing, eqn (33).

$$D_{azzoo}(x,y) = d - S_{azzoo}(x,y) = d - \left(x^t y + \sigma \overline{x}^t \overline{y}\right) \tag{33}$$

Nonnegativity and symmetry are trivial and preserved. Reflexivity is violated, however, because $D_{azzoo}(x,y)=0$ iff $x=y$ and $|x|=|y|=d$ and $D_{azzoo}(x,y)\neq 0$ otherwise. Similarly, $S_{azzoo}(x,y)=d$ if $x=y$ and $|x|=|y|=d$ and $\sigma d \le S_{00-11}(x,y) < d$ if $x=y$ and $|x|<d$.

Theorem 1. The triangle inequality property is valid for $D_{azzoo}(x,y)$, i.e.,

$D_{azzoo}(x,y)+\ D_{azzoo}(y,z)\ge D_{azzoo}(x,z)$.

Proof

$\overline{x}^t\overline{y}+\overline{y}^t\overline{z}\ge\overline{x}^t\overline{z}$ by Fact 1 line 1

$d-(x^ty+\overline{x}^t\overline{y})+d-(y^tz+\overline{y}^t\overline{z})\ge d-(x^tz+\overline{x}^t\overline{z})$ by Fact 2 line 2

Now, evaluate $D_{azzoo}(x,y)+\ D_{azzoo}(y,z)\ge D_{azzoo}(x,z)$.

$$d-(x^ty+\sigma\overline{x}^t\overline{y})+d-(y^tz+\sigma\overline{y}^t\overline{z})\ge d-(x^tz+\sigma\overline{x}^t\overline{z})$$

$$\begin{aligned}d-(x^ty+\overline{x}^t\overline{y})+d-(y^tz+\overline{y}^t\overline{z})+(1-\sigma)\overline{x}^t\overline{y}+(1-\sigma)\overline{y}^t\overline{z}\\ \ge d-(x^tz+\overline{x}^t\overline{z})+(1-\sigma)\overline{x}^t\overline{z}\end{aligned}$$

Hence, the theorem is true by line 1 and line 2 □

Similarly, since $S_{azzoo}(x,y)=x^ty+\sigma\overline{x}^t\overline{y}=S_{\text{inner-product}}(x,y)+\sigma S_{\text{inner-product}}(\overline{x},\overline{y})$, the properties of the azzoo similarity measure are similar to those of the inner-product measure.

Other popular similarity measures utilize coefficients of correlation and have been used frequently in both psychology and ecology studies [42]. The correlation similarity measure is given in eqn (34) and Yule and Kendall [40] suggested a similar coefficient given in eqn (35).

$$S_{\text{correlation}}=\frac{x^ty\times\overline{x}^t\overline{y}-x^t\overline{y}\times\overline{x}^ty}{\sqrt{(x^t\overline{y}+x^ty)(\overline{x}^ty+\overline{x}^t\overline{y})(x^ty+\overline{x}^ty)(\overline{x}^t\overline{y}+x^t\overline{y})}}\qquad(34)$$

$$S_{\text{Yule}}=\frac{x^ty\times\overline{x}^t\overline{y}-x^t\overline{y}\times\overline{x}^ty}{x^ty\times\overline{x}^t\overline{y}+x^t\overline{y}\times\overline{x}^ty}\qquad(35)$$

While Hamming based similarity measures are additive forms of the positive and negative matches, the correlation based measures are multiplicative forms. Nonetheless, contribution factors of positive and negative matches are considered equally important in correlation based similarity measures as well as Hamming based ones.

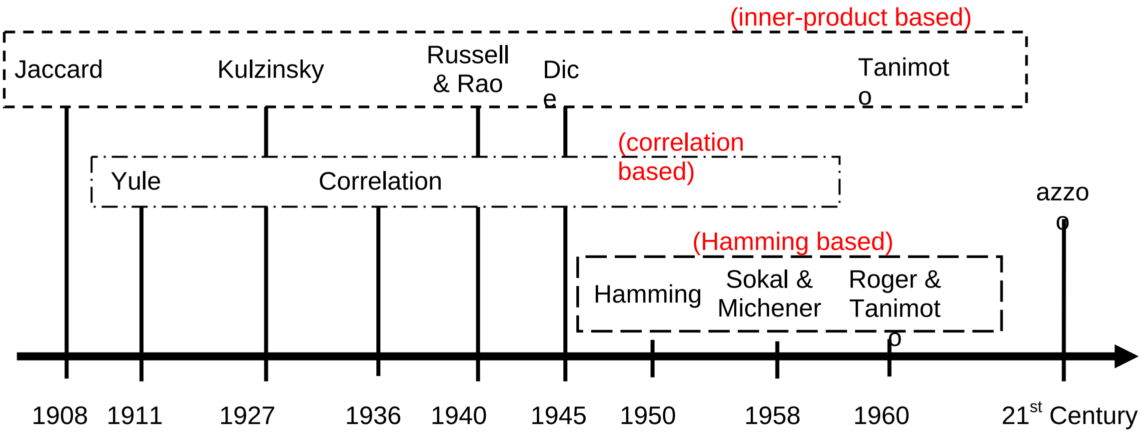


Figure 9. A chronological table for binary vector similarity measures.

Historically, all the measures enumerated above have had great value in their respective fields. Figure 9 shows a chronological table for binary feature vector similarity measures in which these conventional measures are categorized into three major groups: inner-product, Hamming, and correlation based groups.

6.2. Binary Similarity Measures with Weights

To further improve their discrimination capability, weights can be applied to distance or similarity measures [44] and optimized using techniques such as genetic algorithms [47, 48]. When features have numeric values, a scaling problem arises. In order to mitigate this problem, one can combine the nonlinear accuracy weighting with the Minkowski distance concept as shown in eqn (36) where $P(C/i)$ is the probability of being correct when only feature i is used [41, 42].

$$D_{\text{weighted Minkowski}} = \sum_{i=1}^{d} \left[P(C/i)^{a} \left| x_i - y_i \right|^{r} \right] \tag{36}$$

When features are binary, one can still generalize eqn (36) to eqn (37) by setting $r = 1$ and $P(C/i)^{a} = w_i$.

$$\begin{aligned} D_{\text{weighted-Hamming}}(x, y) &= \sum_{i=1}^{d} w_i \left| x_i - y_i \right| \\ S_{\text{weighted-Hamming}}(x, y) &= \sum_{i=1}^{d} w_i (x_i y_i + \bar{x}_i \bar{y}_i) \end{aligned} \tag{37}$$

The weighted Hamming distance has been applied to numerous applications such as image template matching [49, 50] and object recognition [50]. The weighted Hamming distance provides an improvement over the simple Hamming distance for discriminating between similar images [49, 50]. This distance measure gives greater importance to error pixels which appear in close proximity to other error pixels. Error pixels which appear close together tend to correspond to structurally meaningful features. In [51], a slightly different weighted Hamming distance was introduced to optimize the distance measure for object detection by adding a null weight, w_0. Similarly, the inner product similarity measure can be optimized by applying weights as shown in eqn (38).

$$S_{\text{weighted-inner-product}}(x, y) = \sum_{i=1}^{d} w_i x_i y_i \tag{38}$$

Here, we claim that the performance can be further improved by optimizing the similarity measure rather than distance measure. Since the Hamming distance is the number of mismatches, the weights are applied to the mismatched bits, whereas in a similarity measure the weights are applied to the matching bits. As discussed in the earlier section, there are two kinds of matches: positive and negative matches. Although the Hamming similarity can be improved by applying the equal weights are applied to both positive and negative matches, we claim that if different weights are applied, the performance is further improved, and the proposed weighted 00-11 similarity measure is given in eqn (39).

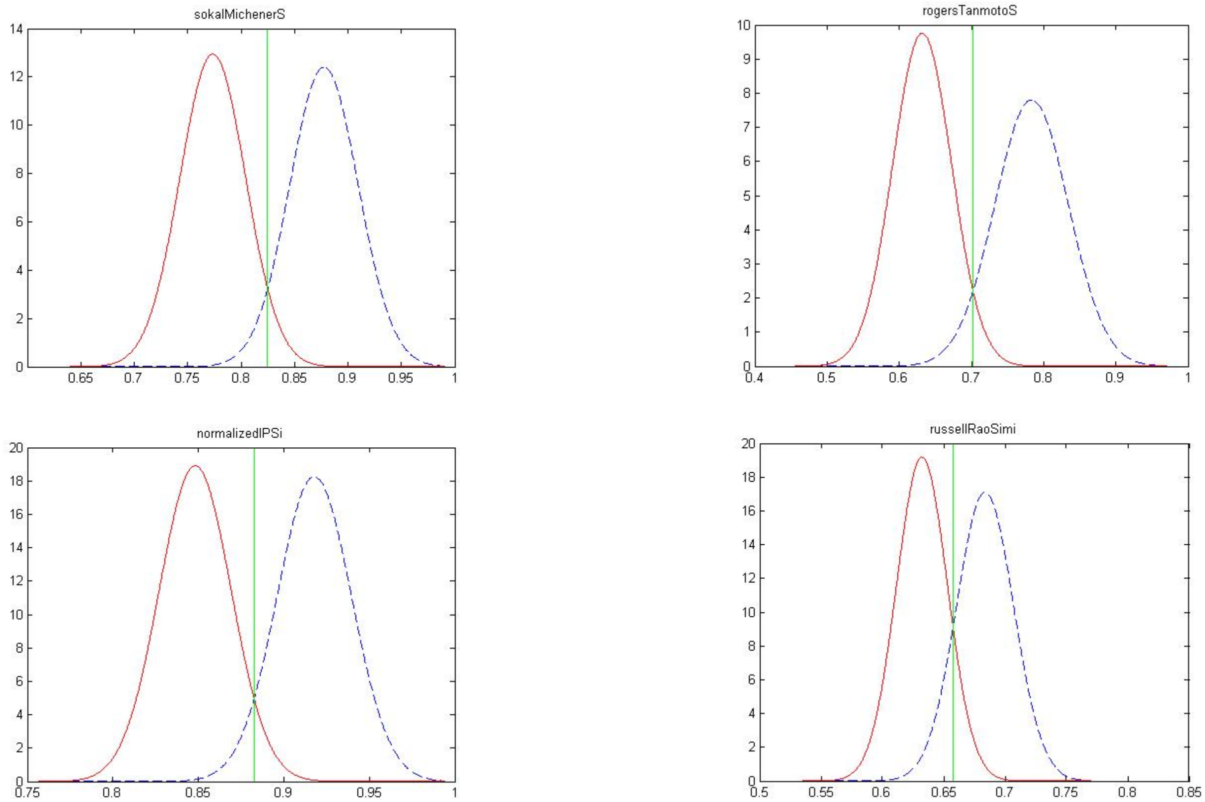
$$S_{weighed-00-11}(x,y)=\sum_{i=1}^{d} w_{\oplus i}x_i y_i+\sum_{i=1}^{d} w_{\Theta i}\overline{x}_i\overline{y}_i \tag{39}$$

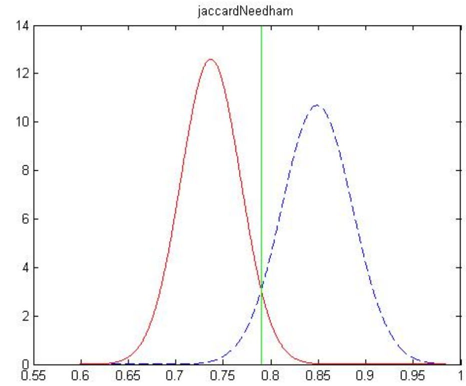
Note that if $w_\oplus$ and w_Θ are identical, $S_{weighed-00-11}=S_{\text{weighted-hamming}}$ and if $w_\Theta=0$, $S_{weighed-00-11}=S_{\text{weighted-inner-product}}$.

There are twice as many coefficients to optimize in this new similarity measure than in the weighted Hamming or inner product similarity measures. This is a multi-dimensional, space optimization problem, and one can use a genetic algorithm to determine the weights from training data. A genetic algorithm can be a general optimization method that searches a large space of candidate objects to find one that performs near optimal according to the fitness function [46, 47]. Genetic algorithms offer a number of advantages: they search from a set of solutions rather than from a single one, they are not derivative-based, and they explore and exploit the parameter space. For the weight adaptive model, we create a numerical optimization model that depends on a set of weights.

6.3. Evaluation for the Binary Feature Distance Measures

The iris biometric verification models were trained on 500 distance or similarity values obtained from the intra- and inter-class sets. These scalar values form distributions and the mean and variance can be computed for each distribution. Assuming normal distributions, one can easily find the Bayes decision threshold. For testing, each scalar distance value is classified into the intra or inter person class by comparing to the threshold value. Figure 10 depicts the intra and inter similarity distributions using various similarity measures and Table 1 shows the comparative results of the overall performances. Finally, Figure 11 shows the performance as a function of the contribution factor, σ, and highlights the relative performance of the inner product, Hamming, and azzoo measures. The S_{azzoo} with $\sigma = 1.175$ yields the best performance.




jaccardNeedham
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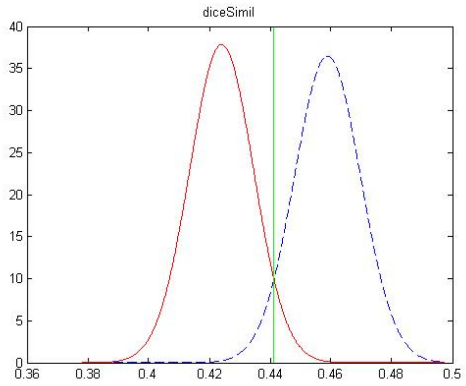
1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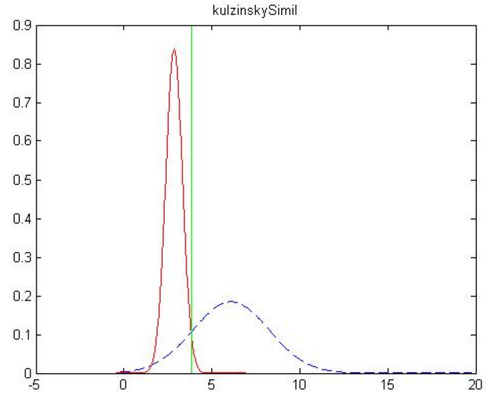
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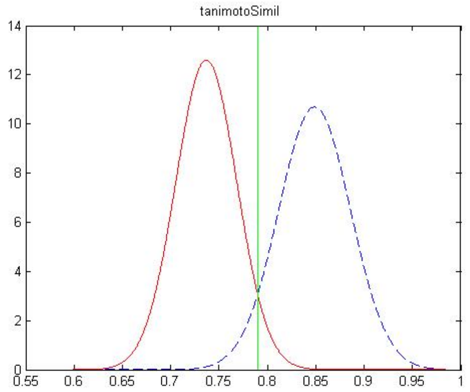
tanimotoSimil
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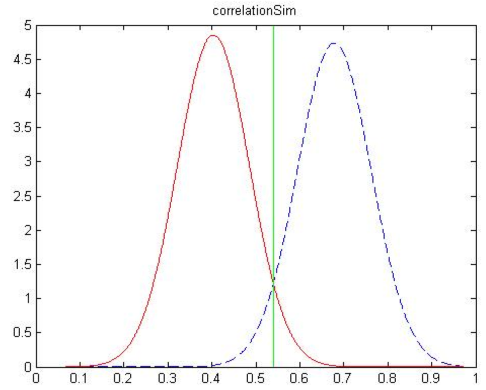
1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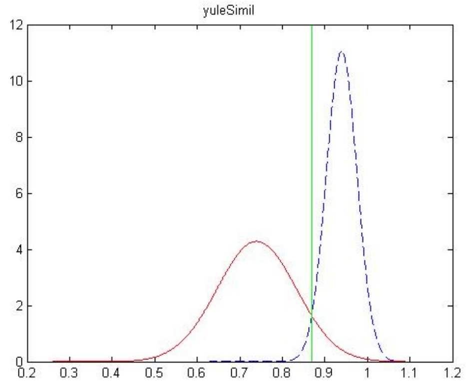
yuleSimil
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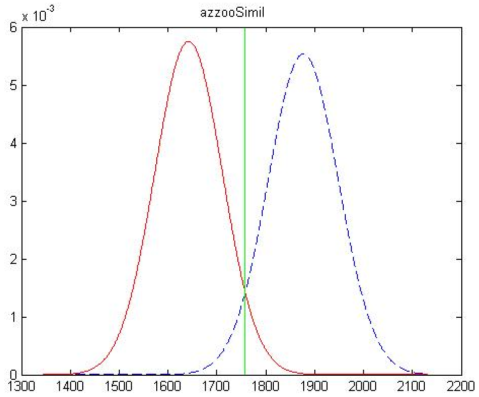
azzooSimil
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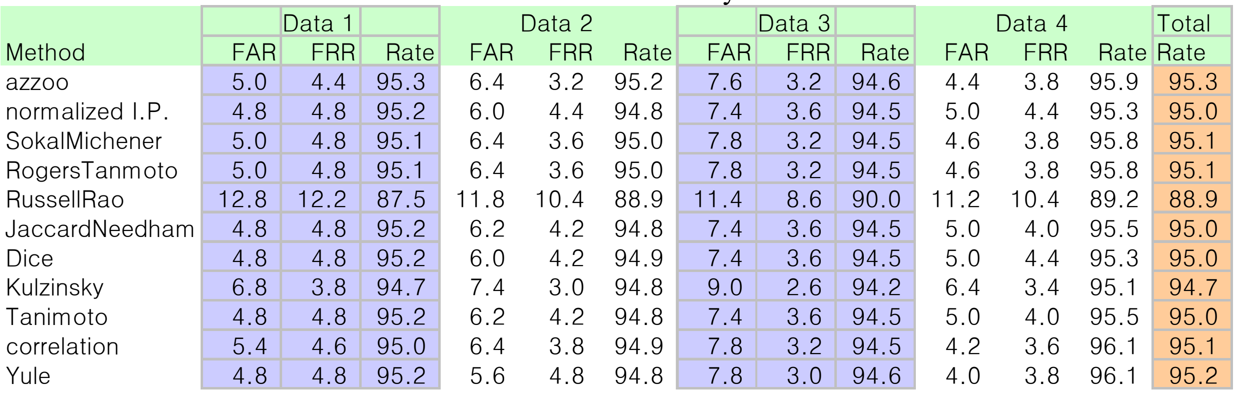
Figure 10. Intra and inter distance distributions for the various similarity measures.

Table 1. Performance evaluation of the similarity measures on the iris database.



	Data 1			Data 2			Data 3			Data 4			Total
Method	FAR	FRR	Rate	FAR	FRR	Rate	FAR	FRR	Rate	FAR	FRR	Rate	Rate
azzoo	5.0	4.4	95.3	6.4	3.2	95.2	7.6	3.2	94.6	4.4	3.8	95.9	95.3
normalized I.P.	4.8	4.8	95.2	6.0	4.4	94.8	7.4	3.6	94.5	5.0	4.4	95.3	95.0
SokalMichener	5.0	4.8	95.1	6.4	3.6	95.0	7.8	3.2	94.5	4.6	3.8	95.8	95.1
RogersTanmoto	5.0	4.8	95.1	6.4	3.6	95.0	7.8	3.2	94.5	4.6	3.8	95.8	95.1
RussellRao	12.8	12.2	87.5	11.8	10.4	88.9	11.4	8.6	90.0	11.2	10.4	89.2	88.9
JaccardNeedham	4.8	4.8	95.2	6.2	4.2	94.8	7.4	3.6	94.5	5.0	4.0	95.5	95.0
Dice	4.8	4.8	95.2	6.0	4.2	94.9	7.4	3.6	94.5	5.0	4.4	95.3	95.0
Kulzinsky	6.8	3.8	94.7	7.4	3.0	94.8	9.0	2.6	94.2	6.4	3.4	95.1	94.7
Tanimoto	4.8	4.8	95.2	6.2	4.2	94.8	7.4	3.6	94.5	5.0	4.0	95.5	95.0
correlation	5.4	4.6	95.0	6.4	3.8	94.9	7.8	3.2	94.5	4.2	3.6	96.1	95.1
Yule	4.8	4.8	95.2	5.6	4.8	94.8	7.8	3.0	94.6	4.0	3.8	96.1	95.2

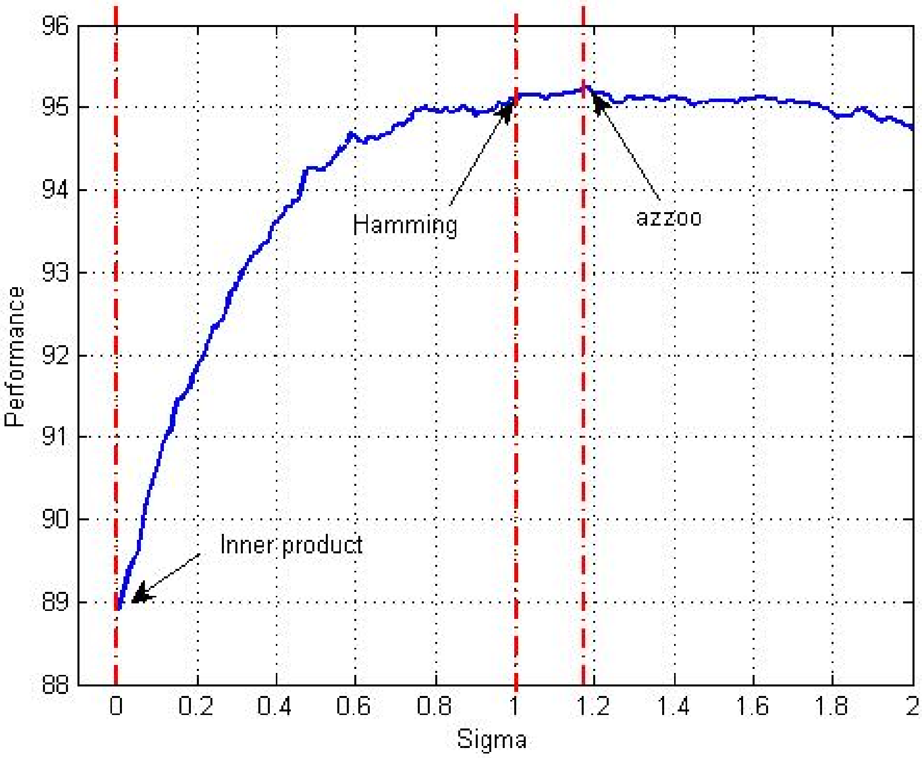


Figure 11. Performance vs. the contribution factor σ .

Chapter 7

Comparative Experimental Results

In this section, I compare the experimental results obtained by using several classifiers with a variety of different features and distance measures. From the iris biometric image database [25], I selected 10 left bare eye samples of 52 subjects.

IRIS database[25] consists of subject demographic data and features obtained from an IRIS sample. . From 60 subjects, 800 IRIS images are taken. Each subject provided 10 exemplars. Thus, the IRIS database consists of two entities: subject data and IRIS feature data. Figure 12. shows a few exemplars from the IRIS database. Age range is from 19 to 36. Iris images distinguish left or right eyes and whether the subject wears glasses or lens. For the experiment, 10 left bare eye samples of 52 subjects are used [27].

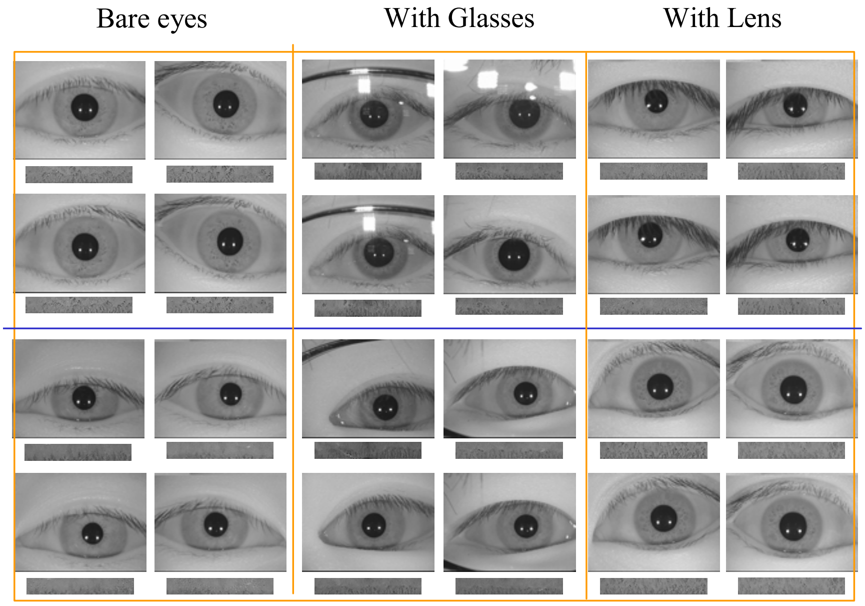


Figure 12. Samples from the IRIS database.

In order to test the described models, two sets of samples are required: intra-class distance and inter-class distance sets. The intra-class distance sample is acquired by randomly selecting two iris data from the same subject while the inter-class distance sample is obtained by randomly selecting two iris data from two different subjects. I prepared three sets of inter and intra distance data for training and three independent ones for testing, each of size 1000 (500 intra-class and 500 inter-class pairs).

Table 2. Eleven different models

	Features	**Distance**	**Classifier**
1	Iriscode (Binary)	Hamming eq (7)	Bayes decision
2	Wavelet means & variances	Euclidean eq (8)	Bayes decision
3	Wavelet means & variances	Vector difference eq (9)	Nearest Neighbor
4	Wavelet means & variances	Vector difference eq (9)	ANN
5	Wavelet means & variances	Vector difference eq (9)	SVM
6	Wavelet histo	Euclid eq (10)	Nearest Neighbor
7	Wavelet histo	Euclid eq (10)	ANN
8	Wavelet histo	Euclid eq (10)	SVM
9	Wavelet histo	Edit dist eq (11)	Nearest Neighbor
10	Wavelet histo	Edit dist eq (11)	ANN
11	Wavelet histo	Edit dist eq (11)	SVM

As shown in Table 2, I examined eleven different models. Models 1 and 2 use the parametric verification model of Figure 1 (a), and the remaining models use the dichotomy transformation model of Figure 1 (b).

The parametric method models 1 and 2 were trained on 500 scalar distance values obtained from the intra- and inter-class sets. These scalar distance values form distributions and the mean and variance can be computed for each distribution. Assuming normal distributions, one can easily find the Bayes decision threshold. For testing, each scalar distance value is classified into the intra- or inter-distance class by comparing to the threshold value as depicted in Figure 3 (a).

Table 3. Parametric model evaluation results:
1000 sample pairs per test.

Model	**Sets**	**FRR**	**FAR**	**Performance**
1 iriscode + Hamming eqn (7)	Training	19.0%	21.5%	79.8%
	Test 1	10.2%	4.6%	92.6%
	Test 2	12.0%	3.2%	92.4%
	Test 3	10.4%	3.2%	93.2%
2 Wavelet means & variances + Euclidean eqn (8)	Training	13.5%	23.2%	81.7%
	Test 1	4.2%	25.6%	85.1%
	Test 2	5.6%	23%	85.7%
	Test 3	4.6%	24.2%	85.6%

Table 3 shows the error rates and overall performance values for models 1 and 2. Two observations can be drawn from these results. First, the results of the traditional parametric model using the scalar distance measure in Figure 2 (a) are disappointing compared to those of the other model in Figure 2 (b). The reason is that multivariate distance analysis is clearly better than a single scalar distance analysis. The other observation is that the FRR in the testing sets are much smaller than those in the training set, suggesting that the two distributions are not normal.

Models 3-11 used the dichotomy transformation to obtain 500 samples of d-dimensional feature distance vectors for intra- and inter-class sets. Regardless of the types of features, the feature distance vectors are all numeric values when proper distance measures are applied. Thus, the feature distance vectors become inputs to the dichotomizer as shown in Figure 1 (b).

I tested three well-known classifiers [14] as the dichotomizer: nearest neighbor, artificial neural network (ANN), and support vector machine (SVM).

I selected the artificial neural network for a dichotomizer because it is equivalent to multivariate statistical analysis. There is a wealth of literature regarding a close relationship between neural networks and the techniques of statistical analysis, especially multivariate statistical analysis, which involves many variables [14, 30]. I selected the support vector machine because it has gained considerable popularity recently and has become state-of-the-art [32].

Table 4. Dichotomy model performance results:

1000 independent sample pairs per test.

		Wavelet means & variances (Models 3-5)	Wavelet histogram + eqn (10) (Models 6-8)	Wavelet histograms + eqn (11) (Models 9-11)
Nearest Neighbor	Test 1	90.5	81.0	89.9
	Test 2	90.8	80.6	92.6
	Test 3	91.0	81.3	92.0
Artificial Neural Network	Training	95.8	90.9	99.2
	Test 1	94.8	82.4	96.1
	Test 2	96.7	83.8	96.9
	Test 3	95.6	82.5	96.7
Support Vector Machine	Training	97.6	88.9	**98.8**
	Test 1	96.2	85.7	**97.9**
	Test 2	97.5	86.3	**98.5**
	Test 3	96.7	86.8	**97.9**

Table 4 shows performances of models 3-11. In general, support vector machines outperform artificial neural networks which, in turn, outperform nearest neighbor classifiers. The best performing SVM model was the one using the 2D three-level wavelet histogram features with the histogram edit distance in eqn (11).

Chapter 8
Conclusions

In this paper, I considered the problem of establishing iris individuality. I first argued that the quantitative error rate measure for the biometric identification model is not appropriate for the measure of establishing biometric individuality since the error rate cannot be inferable to the entire population. I also argued that FRR and FAR from the biometric verification model are adequate measures that are inferable to the entire population. I performed the evaluation of conventional binary feature distance measures. I examined eleven biometric verification models for the problem of establishing iris individuality.

To establish the discriminative power of the individuality of the iris biometric, I used a 52-subject iris image database. I transformed the many-class problem into a dichotomy problem by using distances between two samples of the same class and between two samples of different classes. I examined eleven ways of implementing a dichotomy model by selecting different combinations of features, distance measures, and classifiers. Of these eleven models, I found that the combination of multi-level 2D wavelet features, histogram distances, and a support vector machine classifier yielded the best overall correctness of 98%.

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