

Assessing the Discriminatory Power of Biometric Verifiers

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Abstract

The task of establishing the distinctiveness of biometric data is important in many types of biometric applications. Earlier work had identified the concept of distance statistics as central to our approach to the individuality of a biometric, and the inferential statistical aspects had been considered crucial in evaluating the individuality of certain biometric data. Here we consider the geometrical aspects, and by using d -dimensional geometry we determine the upper limit on the number of subjects that can be distinguished by a given biometric verifier.

1. Introduction

Assessing the discriminatory power of biometric data is important in many biometric and forensic science applications, such as writer, face, fingerprint, speaker, or bite mark identification [1-7]. These and other biometrics have the problem of scientifically establishing individuality, which has been motivated by court rulings [7].

Earlier work identified the concept of distance statistics as central to an approach to biometric individuality [1-3]. It provided a methodology to establish a measure of discrimination that is statistically inferable. To establish the inherent distinctness of the classes – that is, to validate individuality – we transform the many-class problem into a dichotomy by using a "distance" between two samples of either the same person or of different people. A quantitative measure was associated with the discriminative power, and the proposed distance model seemed statistically inferable even if not all classes are observed.

Here, we take a look at the problem from a different angle. While previous work concerned the inferential statistical aspects and associated the False Accept Rate (FAR) and False Reject Rate (FRR) with the measure of individuality, we now claim that it was incomplete. We point out the limitations and pitfalls of the earlier work and present not only the statistical aspects of biometrics but also the geometrical aspects. Biometric samples, when represented by features, form a d -dimensional geometrical feature space. The size of the available biometric feature space is finite, and an arbitrary person's biometric sample occupies a part of the available space due to its intra-sample variation. If we divide the entire feasible space size by an arbitrary person's space size, one can easily estimate the upper limit number of individuals that can be distinguished by a given biometric verifier.

The remainder of the paper is organized as follows. Section 2 illustrates the biometric verification model which is recognized as a statistically inferable approach to establishing the individuality of a biometric. Section 3 introduces the geometrical aspects of biometric verification. Finally, section 4 draws some conclusions.

2. Biometric Models

For purposes of discussion, although any biometric verifier is amenable to this analysis, we will refer to the handwriting biometric. A quantitative assessment of the individuality of handwriting using computer-generated features of sample handwriting was previously considered [2, 3]. There are two basic kinds of biometric models: biometric identification and biometric verification models. The task at hand is to set up a methodology for validating the hypothesis that everybody writes differently.

Representative handwriting samples from over 1,000 subjects in U.S. population were collected. Several feature extractors were used to extract distinguishing writer attributes at several levels of document scrutiny: line spacing at the macro-level, which are numeric vectors, and character formation at the micro-level, which are binary vectors.

The discriminative power of handwriting was claimed to be established by using the handwriting samples and the features extracted from the samples. One possible approach to this is to view each handwriting sample as a point in a multi-dimensional feature space. Then, if all the samples of writer W_1 are close together and all the samples of writer W_2 are close together, but samples of W_1 and W_2 are far apart, we can say that W_1 and W_2 write differently and that samples of W_1 and W_2 belong to two different *classes* or *clusters* [7]. In order to validate individuality among n writers, we would have to determine whether the samples form n distinct clusters, where each cluster contains samples of the same writer and different clusters contain samples of different writers. A measure of the distinctness of the clusters would be a measure of confidence of the individuality hypothesis.

The task of determining the presence of distinct clusters can be approached by using the probability of correctly classifying samples of unknown writers as the criterion of clustering. In the identification model, given a handwriting sample x from an unknown writer and samples of handwriting from n known writers, we would like to identify the writer of x as one of the n writers.

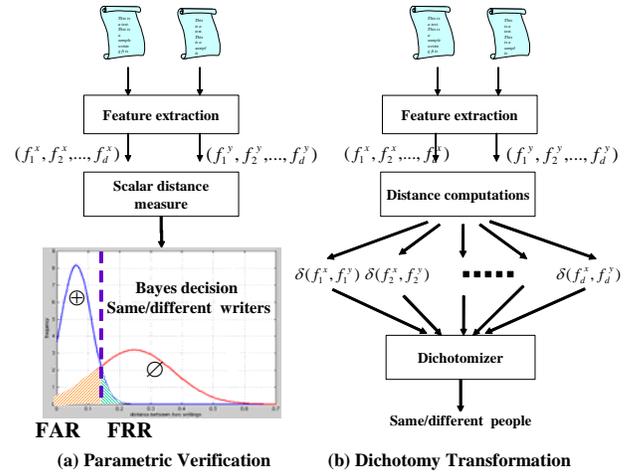


Figure 1: Biometric Verification Models

In the verification models shown in Figure 1, given two handwriting samples x_1 and x_2 and samples of handwriting from the n writers, we would like to determine whether x_1 and x_2 were written by the same person or by two different people from among the n writers. Both models involve classification, with the identification model leading to an n -class problem (or a polychotomy of the feature space) and the verification model leading to a 2-class problem (or a dichotomy of the feature distance space).

Each of these models can be regarded as tasks in machine learning. Handwriting samples are used to learn the discrimination task, and another set of samples is used to test the model for accuracy. Both models provide a probability of correct classification that can be used as a measure of confidence of the individuality hypothesis.

The question arises as to which model is better. The identification model has the advantage of being able to identify the writer directly. However, it is dependent on knowing all the writers in advance. The result with n writers does not generalize to $n+1$ writers. On the other hand, the verification model provides results that might be statistical inferable as depicted in Figure 2. The two different classification approaches would provide a measure of cross-checking our results.

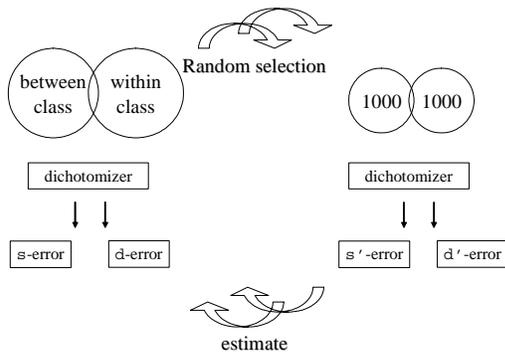


Figure 2: Statistical Inference in Biometric Verification.

Let x and y be handwriting samples represented by d features. In Figure 2, FAR is the probability of error that one classifies two biometric data as coming from the same person even though they belong to two different people, and FRR is the probability of error that one classifies two biometric samples as coming from different people even though they belong to a same person. Note that when a distance measure is used, the intra-distance distribution tends to be close to 0 whereas the inter-distance distribution tends to be far from 0. Thus, FAR is usually the left side area of the decision boundary. When a similarity measure is used, on the other hand, FAR is the right-side area of the decision boundary because the larger value means that the two biometric samples are similar, as defined in the following equations where T is the threshold value for the Bayesian decision.

$$FAR = \Pr (S(x, y) \geq T | c(x) \neq c(y))$$

$$FRR = \Pr (S(x, y) < T | c(x) = c(y))$$

The overall performance is the number of correctly classified instances divided by the total testing database size.

3. Geometrical Aspects of Biometric Verification

In the previous section, we saw that a biometric verifier could be represented as a statistically inferable model. Here we take a look at the biometric verifier from a geometrical point of view. Consider x a point in d -dimensional feature space

where x belongs to one of the writers. Consider also that a cluster of points in close proximity to x also belongs to the writer. Let x_m be the mean of the writer's biometric samples and every point within a sphere with center x_m and radius t belong to the writer. Now we can compute the number of writer clusters that can fit in the feature space.

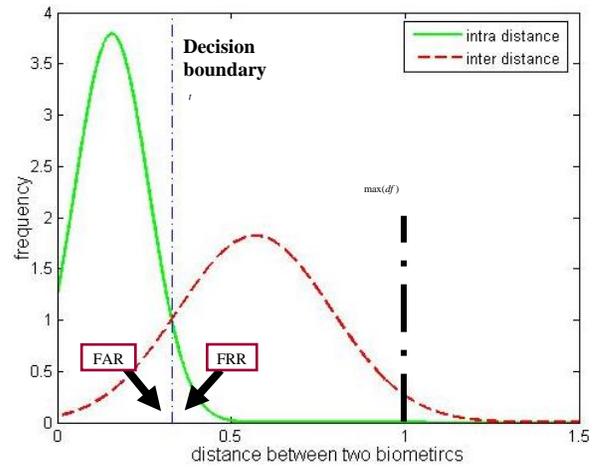
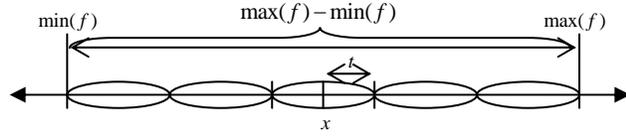


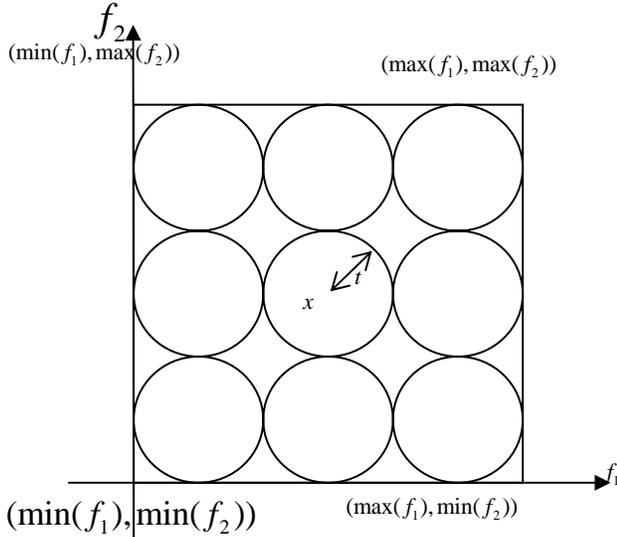
Figure 3: Two distributions.

Consider a biometric verification system based on people's heights. Each time one's height is measured, there are variations, called intra-variation, in the measurement. One can draw two distributions similar to those in Figure 3 and claim that FAR and FRR can be inferred to the entire population of a nation or world. However, this claim is incomplete.

Let's take a look at the geometrical aspects. One can find the threshold t , which is the decision boundary between the intra and inter-variation distributions. There are also maximum and minimum feasible height measurements. Then, as shown in Figure 4 (a), one can fit only a finite number of people, five, as shown in the figure, in this height biometric verifier. In other words, the height biometric verifier can distinguish up to five people.



(a) One dimensional space



(b) Two dimensional space

Figure 4: How many people can fit in the space?

If the feature space is two dimensional, one can apply the same logic to find the upper limit of people that can be uniquely distinguishable by a given biometric verifier.

We can utilize the hyper sphere to generalize the formula. If the dimension is 1, the number of distinguishable people is

$$m \leq \frac{\max(f) - \min(f)}{2t}$$

In two and three dimensional space,

$$m \leq \frac{(\max(f_1) - \min(f_1)) \times (\max(f_2) - \min(f_2))}{\pi t^2}$$

$$m \leq \frac{\prod_{i=1}^3 \max(f_i) - \min(f_i)}{\frac{4}{3} \pi t^3}$$

We can utilize $\max(df)$ to calculate the size of D as shown in Figure 5.

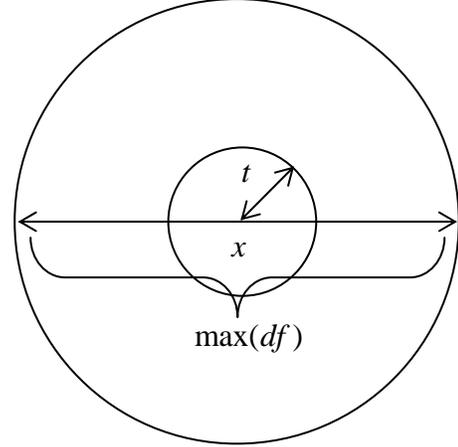


Figure 5: Hyper sphere model.

In 2 and 3 dimensions,

$$m \leq \frac{\pi (\max(dv))^2}{\pi t^2} = \frac{(\max(dv))^2}{t^2}$$

$$m \leq \frac{\frac{4}{3} \pi (\max(dv))^3}{\frac{4}{3} \pi t^3} = \frac{(\max(dv))^3}{t^3}$$

In general,

$$m \leq \frac{\max(df)^d}{t^d} = \left(\frac{\max(df)}{t} \right)^d$$

If one biometric verifier has 8 dimensions and every feature is normalized into number between 0 and 1 and the threshold is 0.3285, the system can only distinguish up to 7,377 people.

$$m \leq \frac{1^8}{0.3285^8} = 7,377$$

Clearly, a large m does not mean that it can distinguish m number of people. If feature axis are orthogonal, the above equation holds but it dramatically reduces if features are not independent from each other. Hence, we can utilize the geometrical aspects to reject a certain writer verification model when m is small.

4. Conclusion

In this paper, we considered the problem of establishing the individuality of a biometric. We showed that FRR and FAR from the biometric

verification model might be adequate measures that are inferable to the entire population. However, when including the geometric aspects of a biometric verifier, we showed that FRR and FAR are not sufficient to assess the discriminatory power. We also presented a formula that provides an upper limit on the number of people that a given biometric verifier can distinguish.

Furthermore, while the formula given here assumes that the feature axes are orthogonal, this may not be the case. Hence, the upper limit number of distinguishable people can be tightened by PCA and ICA.

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