

Fe-Fi-Fo-Thumb

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Abstract

Fingerprinting is one of the oldest techniques for identification, and it is still used by many agencies today. The primary motivation for this is that fingerprints are believed to be unique. This claim has been supported by empirical evidence, but there has been no scientific proof that it should be true. We provide a mathematical foundation to analyze the existence of such a phenomenon. This is accomplished by considering the physical limitations involved in recording a fingerprint, as well as the theoretical implications of defining a metric on the space of fingerprints. We pose a possible interpretation of fingerprint enumeration in terms of sphere packing. We also develop two concrete models to estimate the number of distinct fingerprints in existence and the likelihood that no two human beings in history have had the same fingerprint. The first model is a graph-theoretic approach based on the Voronoi diagram of minutiae distribution. This method is invariant under rotation, scaling, and translation. However, it appears to be too sensitive to perturbations caused by experimental error. As a result, it is unrealistic to consider this model for practical use. We produce an estimate of 1.11×10^{21} distinct fingerprints for a uniform distribution of 36 minutiae, and therefore find the probability that no two people in history have had the same fingerprint to be 0.00011. The second model we consider is based on correlating minutiae between two fingerprints that are sufficiently similar. We look at the probability that two independently generated thumbs will have a specified number of matching minutiae. We then consider the effect of perturbing each minutia by a normally distributed amount. By looking at the correlation between a given fingerprint and its perturbed counterpart, we are able to determine a reasonable number of matching minutiae to expect when comparing any two fingerprints. This allows us to estimate the probability that two randomly generated fingerprints will be identified as coming from the same person. With this model we find values of 1.95×10^{36} and $e^{-\frac{1}{2 \times 10^{15}}}$ for the number of distinct fingerprints with 36 minutiae and the probability that no two people have ever had the same fingerprint.

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1 Introduction

The process of identifying individuals based on various biometrics is a rapidly growing field. Having been studied for well over a century, the most traditional biometric used to for identification is the fingerprint. It is a common belief that fingerprints are unique to each human being; however, this biological occurrence has never been scientifically proven. To begin investigating the likelihood of this phenomenon, we state some rudimentary assumptions:

- By the term *fingerprint* we mean a 2-dimensional grayscale image representing the ridge structure of a person's finger.
- In deciding how many *unique* fingerprints exist, we acknowledge that multiple acquisitions of a particular fingerprint must not be counted more than once.

In order to decide what it means to *count* the number of possible fingerprints, we feel it is necessary to develop a brief mathematical framework for the theory of fingerprint matching.

1.1 A Mathematical Theory of Fingerprint Identification

The first concept we need is that of a *similarity metric*. This is a tool for measuring the apparent 'distance' between two fingerprints. Each similarity metric falls into one of two categories:

- **Continuous** – Associated with any two fingerprints is a real number representing the dissimilarity between them.
- **Discrete** – Any two fingerprints are considered *distinct* or *equivalent*.

We denote by $d(X, Y)$ the distance between two fingerprints X and Y .

Notice that the discrete metric may be derived from the continuous one by setting a *threshold*. That is, if $d(X, Y) \leq c$, for a specified constant c , then the fingerprints X and Y are determined to be equivalent.

Defining a similarity metric allows us to be more precise when discussing the error involved in repeat fingerprint acquisition. One can imagine taking many images of a particular person's finger and then determining the maximum distance between any two of these fingerprints. This gives us an estimate of how different two fingerprints must be so that they are *detectably* distinct. We are lead to the following definition:

Definition: Let X_1, \dots, X_n represent n fingerprints taken from the *same* finger. Then for a continuous similarity metric we define the **detectability radius** R_{detect} by

$$R_{detect} = \max\{d(X_i, X_j) \mid \text{for all } i \neq j\}$$

Note that the detectability radius is dependent on both the apparatus for acquiring fingerprints and the metric for comparing them.

1.2 Fingerprint Uniqueness via Spheres

One can interpret the question of fingerprint distinction in terms of *sphere packing*. The **sphere** of radius r about a fingerprint X is the set of all fingerprints Y whose distance to X is no greater than r :

$$S(X, r) = \{Y \mid d(X, Y) \leq r\}$$

Suppose one were to record the fingerprint of every individual on the planet. If the distance between any two of these fingerprints is less than the detectability radius (R_{detect}), then the fingerprints will be within the margin of experimental error and they must be considered equivalent. Therefore, if the union of all spheres centered around these fingerprints with radius $2R_{detect}$ forms a disjoint set, then we will have determined that no two people have the same fingerprint. Formally,

Let X_1, \dots, X_n represent the fingerprints of every individual in a given population. Then

$$\text{No two people have the same fingerprint} \iff \bigcap_{i=1}^n S(X_i, 2R_{detect}) = \emptyset$$

This suggests a method for determining the number of unique fingerprints:

1. Define a metric on the space of all fingerprints.
2. Determine a reasonable value for R_{detect} .
3. Estimate the number of non-overlapping spheres with radius R_{detect} that can be packed into the space of all possible fingerprints.

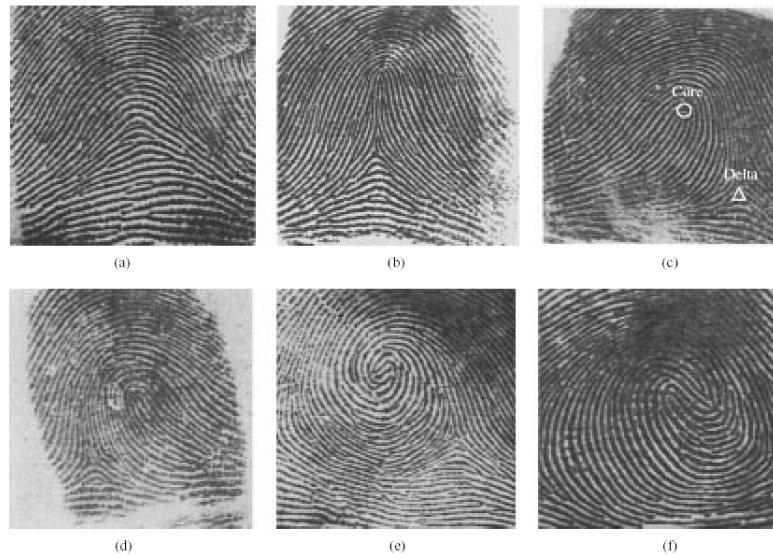
Unfortunately, as will be shown, this approach is not especially practical. However, the concepts underlying it will be useful for analyzing the models we develop in this paper.

2 Basic Information about Fingerprints and Thumbs

Throughout this paper we will be using some specific vocabulary to describe thumbprints. We provide the definitions here:

Pattern area – the primary region of a fingerprint.

Figure 1: The six basic types of fingerprints [1]: (a) arch, (b) tented arch, (c) right loop, (d) left loop, (e) whorl, and (f) twinloop.



Fingerprint type – The basic classification of a fingerprint: arch, tented arch, right loop, left loop, whorl, and twinloop. See **Figure 1**.

Ridge – A path of raised skin on the pad of a finger.

Core – The approximate center of a fingerprint.

Delta – A reference point on a fingerprint which, together with the core, is used to orient a fingerprint (see **Figure 1c**).

Bifurcation – A single ridge that divides into two ridges.

Ridge ending – A ridge that ends abruptly.

Minutia – A characteristic singularity in the ridge pattern of a finger.

Minutia type – A classification of minutiae. The most common types are bifurcations and ridge endings.

Minutia direction – A vector that characterizes the minutia's orientation.

2.1 The Information Contained in a Fingerprint

Human skin is fairly elastic. Accordingly, anomalies such as translation, rotation, scaling, and local perturbations sometimes occur while producing a fingerprint. The crucial features to consider when comparing fingerprints are those

which do not vary much between successive prints from the same source. There are other details discernable in fingerprints, such as skin pores, curvature of ridges, and spacing of ridges. However, these information sources are less reliable and ignored in many widely accepted fingerprint identification procedures.

2.2 Facts About Fingerprints

- The typical pattern area recorded in a fingerprint is 72mm^2 [3].
- The number of discernible minutiae in most fingerprints is between 20 and 70 [5]. In our models we assume an average of 36 minutiae, as done by [3].

One more fact [3] that we use extensively in our models is the followings:

Upon repeated printing of the same finger, there is a %97.5 chance that the minutiae will be within 0.69mm of the original location.

2.3 Assumptions about Fingerprints

To determine the number of unique fingerprints and the probability that no two people in history have had the same thumbprint we need to make a few general assumptions. Most of these have been supported by the literature available on fingerprinting.

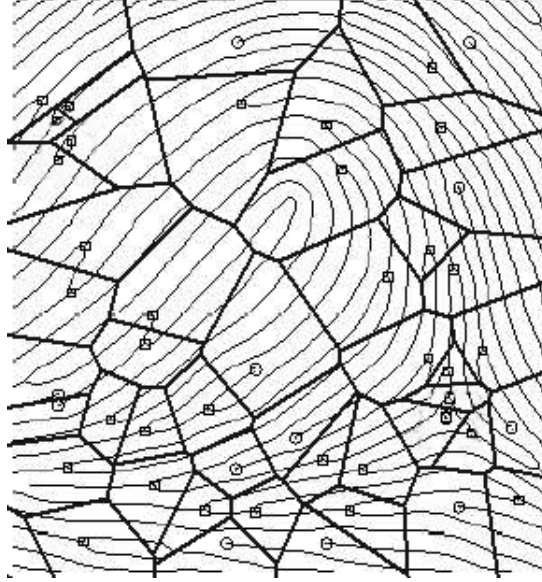
1. People's fingerprints do not change over time [3].
2. When comparing fingerprints it is sufficient to consider only overall print type and attributes pertaining to the minutiae [2].
3. The basic structure of the human fingerprint has not changed drastically throughout history [4].
4. Thumbprints exhibit the same characteristics as prints taken from other fingers of the hand.
5. Minutiae are uniformly distributed throughout the pattern area of the finger [9].

3 Model I: A Discrete Similarity Metric

One of the most desirable features of a fingerprint comparison algorithm is invariance under translation, rotation, and scaling. This seems to indicate that the problem of identifying fingerprints is of a *topological* nature, rather than *geometrical*. In this model we develop a **graph-theoretic** approach to analyze the process of fingerprint comparison and use it to produce a lower bound on the number of detectably distinct fingerprints.

We would like to understand the topology of a given minutiae distribution. For this reason we consider a spatial tessellation derived from the relative locations of the minutiae.

Figure 2: The minutiae Voronoi diagram of an image-enhanced fingerprint.



3.1 Minutiae and Voronoi Diagrams

A 2-dimensional tessellation, known as a *Voronoi diagram*, may be produced from any planar region by the following method [8]:

1. A finite collection of *seed points* is produced. These points may either be generated by a stochastic process, or acquired from a preexisting data source.
2. To each seed point is associated a planar sub-region known as a *cell*. Each cell consists of all points which are closer to the given seed point than any other seed point in the collection.

This tessellation is uniquely determined by the seed points.

Our model considers the Voronoi diagram obtained from the minutiae of a given thumbprint, which we refer to as a *minutiae Voronoi diagram*.

We produced a minutiae Voronoi diagram (using the Qhull [6] algorithm) for a real fingerprint. The result is pictured in **Figure 2**. The original fingerprint image with minutiae identified by small boxes is seen in **Figure 3**. The thumbprint data and minutiae extraction were provided by [7].

Figure 3: The original fingerprint from **Figure 2** with minutiae represented by small boxes.



3.2 The Role of Graph Theory in this Model

We are interested in enumerating the possible configurations of minutiae in fingerprints. However, there is a constraint that two fingerprints which are sufficiently similar (i.e. within R_{detect}) must be matched correctly. Therefore, we would like a way to compare Voronoi diagrams such that small perturbations in the position of seed points will not affect the comparison. To accomplish this, we consider the *graph* obtained from the minutiae Voronoi diagram.

*We refer to the graph obtained from the minutiae Voronoi diagram as the **minutiae graph**.*

This graph contains all the topological properties of the Voronoi diagram. It tells it which vertices are connected, but it does not contain any geometric measures, such as the lengths of the edges and the angles they form at each vertex.

We are now ready to define the fingerprint similarity metric for this model.

Definition:

We consider two fingerprints X and Y to be equivalent, $d(X, Y) = 0$, if their respective minutiae graphs are isomorphic, and distinct, $d(X, Y) = 1$, otherwise.

Since we are attempting to estimate the number of distinct fingerprints in existence, it is important to be able to determine the number of isomorphism classes of a large collection of graphs very quickly. We use the Nauty software package [10] to produce a standard representation of each graph, known as a *canonical label*. Having done so, the two graphs may be tested for isomorphism

by seeing if their canonical labels are equal.

Using isomorphism classes of minutiae graphs to compare fingerprints has the following advantages:

1. *Any unintentional rotation, translation, or scaling factor when recording a fingerprint will have absolutely no effect on the comparison.*
2. *A slight perturbation in the location of minutiae points will result in a topologically equivalent minutiae graph.*
3. *The complete graphic information in a Voronoi diagram generated by n points can usually be stored in $4n^2$ bits.*

The last assertion is based on the average number of vertices in a Voronoi diagram generated by n seed points [8].

3.3 Sensitivity of Minutiae Point Perturbation

In this section we investigate the sensitivity of this model to slight perturbations in the location of minutiae points. The similarity metric we are using here is the discrete one. Namely, graphs are either isomorphic or non-isomorphic. As a result, we are unable to directly measure R_{detect} . We know that minutiae graphs generated by sufficiently similar minutiae point distributions are isomorphic, but we would like to relate this vague statement to the more precise language of detectability radii. One possible interpretation is the following:

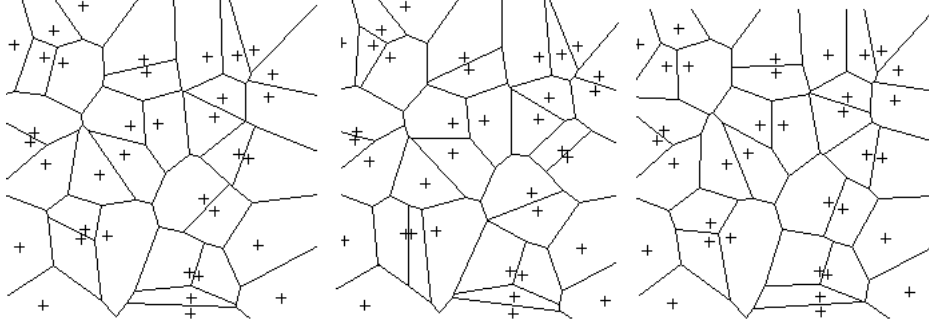
The inherent metric involved in this model is not really the discrete one, but rather a much more complicated metric which is then transformed into a discrete metric according to some sort of thresholding process.

In order to develop an understanding of how slight changes in the seed point distribution affect a Voronoi diagram, we perform the following experiment:

- Randomly distribute 36 minutiae.
- Generate the minutiae graph corresponding to that particular configuration of seed points.
- For each seed point, adjust its x and y coordinate by a random amount given by a normal distribution.
- Generate a new minutiae graph from these perturbed seed points.
- Determine if these two graphs are isomorphic.

In **Figure 4** we see the result of this experiment for two different perturbations of an initial minutiae point distribution. All three graphs look similar, but in fact have topological differences and are therefore *not* isomorphic.

Figure 4: Three similar but non-isomorphic minutiae graphs.



To estimate how much the minutiae can be perturbed before the graph changes topologically, we produce 10 initial minutiae distributions, perturb each one 100 times, record the number of isomorphism classes that occur, and then average this number over the 10 distributions. The result is depicted in **Figure 5**.

We see that for a standard deviation less than $0.005mm$, only 5 different isomorphism classes were observed. Recall there is a %97.5 chance that a given minutia will remain within $0.69mm$ of its initial location upon repeated fingerprinting. From this we can assume a normal distribution with standard deviation of $0.2mm$, which is 40 times greater than $0.005mm$. This shows that the similarity metric in this model is *hyper-sensitive*. Therefore, this algorithm would probably not work very well as a practical means of comparing fingerprints. However, it is still applicable to estimate the number of distinct fingerprints in the human race from a theoretical standpoint. The technology for acquiring fingerprints has been steadily increasing in recent years, so in the near future it is quite plausible that the location of minutiae will be determined with a much greater accuracy.

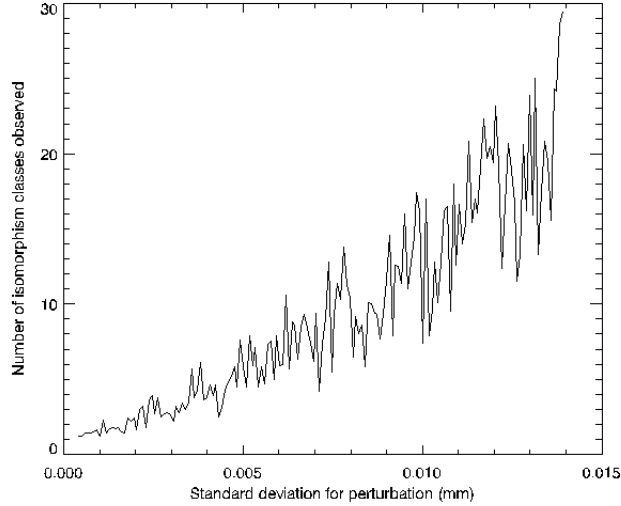
3.4 Estimating the Total Number of Distinct Fingerprints

Given n minutiae, we produced $m = 50,000$ uniformly distributed configurations of these points and their corresponding minutiae graphs. The number N of isomorphism classes that occurred is shown in **Figure 6** for values of n ranging between 1 and 20. This plot closely resembles the logistic equation:

$$\frac{dN}{dn} = N(a - bN),$$

where $\frac{a}{b} = m$ is the carrying capacity of the system. The explanation for this behavior is that the number of distinct graphs observed for a given number of minutiae is limited by the total number of graphs generated (50,000 in this case). This imposes an artificial bound on the population growth of isomorphism classes. By considering only small values of n , so that the growth is

Figure 5: The number of isomorphism classes observed when perturbing the seed point distribution according to a normal distribution $N(0, \sigma^2)$ for various values of sigma.



approximately exponential, we estimate the number N of isomorphism classes for a given value of n minutiae to be

$$N = 14e^{0.8(n-6)}$$

This extrapolates to a value of $N = 3.7 \times 10^{11}$ for $n = 36$ minutiae.

This value of N represents the number of distinct fingerprints possible based solely on a uniform distribution of 36 points. We can make this estimate more realistic by taking into account the various fingerprint types and distinguishing between bifurcations and ridge endings in minutiae. The approximate distribution of these traits is listed in **Table 1**.

From this data we see that each fingerprint of 36 minutiae contains on average 25 bifurcations and 11 ridge endings. Based on this we produce the following estimate:

$$\text{The number of distinct fingerprints with 36 minutiae is approximately } (3.7 \times 10^{11}) \binom{36}{11} (5) = 1.11 \times 10^{21}$$

4 Model II: A Continuous Similarity Metric

Given two fingerprints, we would like to determine the number of minutiae that lie in corresponding locations. To do this, we need a standardized coordinate

Figure 6: The number of isomorphism classes observed as a function of the number of minutiae considered.

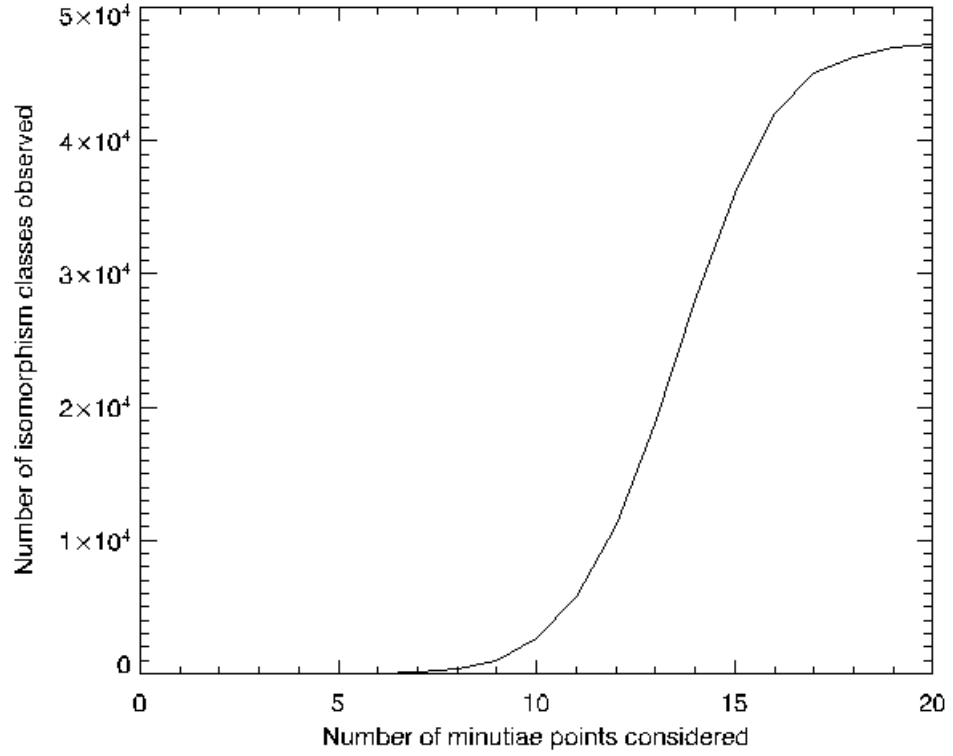


Table 1: Distribution of fingerprint and minutia types [11].

Fingerprint Type	Probability of occurrence
Left loop	0.338
Right loop	0.317
Whorl	0.279
Arch	0.037
Tented arch	0.029
Twin loop	rare
Minutia Type	Probability of occurrence
Bifurcation	0.7
Ridge ending	0.3

system. We must assume that the fingerprints we are working with have already been aligned. This is usually accomplished by locating the core and delta of the two fingerprints.

In this model we perform the following procedure:

1. Randomly select a fingerprint type from among the basic five according to their relative proportions (see **Table 1**).
2. Uniformly distribute 36 minutiae on a square region representing a finger's pattern area.
3. To each point, randomly associate a minutia type and direction (a real number between 0 and 360 degrees).
4. Repeat this process to create another fingerprint so that the two may be compared.

For any two minutiae from two different fingerprints, we say that they *match* if they are within $0.69mm$ of each other. We also stipulate that the minutiae directions must be within 22.5 degrees for them to be considered a match. This is based on empirical data of experimental error [3].

To determine the distribution for the number of minutiae matches from two randomly generated fingerprints, we first see if the fingerprints are of the same type. Next, we compare the type of each corresponding minutia in the two fingerprints. Finally, we see if the location and direction of each minutia is within the specified bounds.

We generate two independent fingerprints 50,000 times and produce a distribution for the number of minutiae matches. See **Figure 7**. We then reproduce the perturbation simulation from **Model I**, this time incorporating a perturbation in minutiae *direction*. We perform 50,000 repetitions of this experiment, producing the distribution for the number of matching minutiae seen in **Figure 8**.

4.1 Statistical Analysis

We want to find the probability that two independent fingerprints have at least 27 minutiae matches. This will be our estimate for the minimum number of minutiae matches required so that two fingerprints are considered equivalent. In other words, this is the *thresholding* number for our similarity metric. In order to estimate this probability, we need the complete probability distribution of matches from different prints. We only completed 50,000 repetitions, so we are forced to extrapolate from our data. There are two ways to do this.

The first approach is to approximate the number of matches with a normal distribution. By looking at a normal QQ plot, this seems like a reasonable approximation. To find the mean of this normal distribution, we first look at

Figure 7:
Distribution of Matches From Two Different Fingerprints

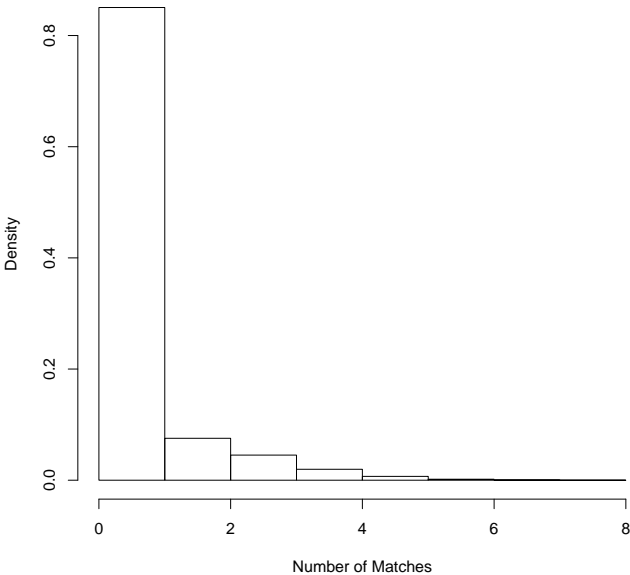
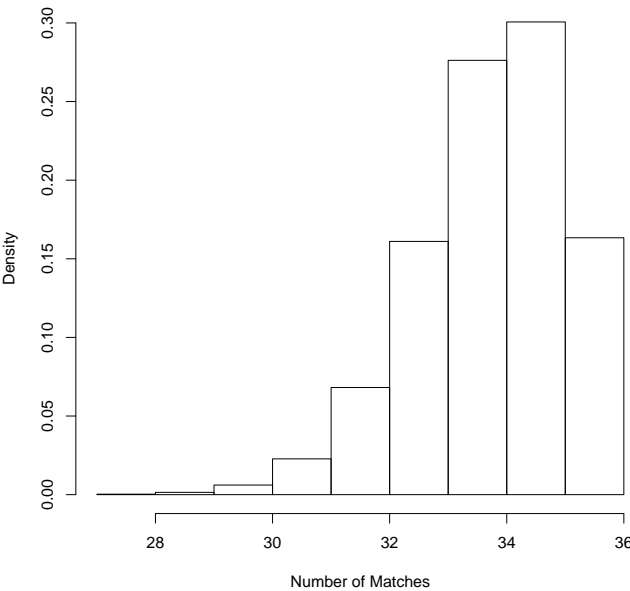


Figure 8:
Distribution of Matches From Repeated Finger Printing



the expected number of matches from the distribution in **Figure 7**, which we determine to be .504. To find the variance of this normal distribution, we look at the probability of seeing 4 or more matches.

$$P(\text{number of matches} \geq 4) = \frac{1449}{50000} = .029$$

We know that $\frac{x-\mu}{\sigma}$ is $N(0, 1)$, and that the Z value for .029 is 1.9. Hence we find that $\sigma = 1.83$.

To find the probability that 27 or more minutiae match, we look at the probability of seeing a Z-Score of $\frac{27-\mu}{\sigma} = 14.5$. Under the normal distribution, this probability is $2.03 \times e^{-46}$. However, we think a more appropriate approximation can be achieved with an alternate method.

The second approach for determining this probability is by looking at the Poisson distribution. We can assume that there is some rate at which matches occur. This rate is the number of matches divided by the number of trials simulated, which in this case equals .504. Using the Poisson approximation formula, we calculate that

$$P(27) = \frac{e^{-.504}(.504^{27})}{27!} = 5.12 \times 10^{-37}$$

This is an upper bound on the probability of seeing at least 27 minutiae matches, and hence matching two randomly generated fingerprints.

We can estimate the number of distinct fingerprints in existence simply by taking the inverse of this probability:

$$\text{The number of distinct fingerprints with 36 minutiae is approximately } \frac{1}{5.12 \times 10^{-37}} = 1.95 \times 10^{36}$$

4.2 Error Analysis and Sensitivity

This model was run with 36 uniformly distributed minutiae, an error-radius of $0.69mm$, and σ equal to $\frac{0.69}{\sqrt{2}Z_{.975}}$. We ran the same simulations with varied parameters to determine how much our overall results would be affected. We first tried doubling the error-radius. This resulted in more minutiae matches when comparing two random fingerprints. The histogram had upwards of 10 matching minutiae for the two random fingerprints. Of the times that there were matches, the average number was closer to 5. Since 10 matches are occurred approximately one ten-thousandth of the time, this model is no longer realistic. The FBI considers 10 matching features to be sufficient to identify the fingerprints [2].

Changing the number of minutiae resulted in a smaller proportion of minutiae matches between random fingerprints, whereas the proportion of matches in the same fingerprint stayed about the same. We looked at distributing 20 and 28 minutiae. The probability of two random minutiae matching when using

20 minutiae was 3.68×10^{-34} . This does not differ drastically from our previous estimate.

This leads us to our last two potentially influential parameters for this model. These are the distribution of minutiae over a fingerprint, and the $N(0, \sigma^2)$ error term. Beginning with σ , we look at what would happen if its value were doubled. That is, comparing two fingerprints from the same finger, we vary the minutiae coordinates by $N(0, (2\sigma)^2)$. This results in the average number of matches between fingerprints from the same finger going down from 34 to 29. The spread of this distribution is larger than before. This tells us that with more variation in the coordinates, the number of minutiae required for a match goes down.

Through our own observations we have noticed that the minutiae might not be distributed uniformly. We test the effect of clumping 6 to 10 minutiae on either side of the core. With this as our distribution we find that the number of matches between random prints goes down. This means that our assumption of a uniform distribution might be leading to a slight overestimate of the number of matches.

5 The Probability of Fingerprint Uniqueness

The total population of the human race is estimated to be about 100 billion [12]. Let M denote the number of distinct fingerprints and $N = 10^{11}$ the number of people who have ever lived. Then the probability that all fingerprints are unique is given by:

$$\frac{M}{M} \times \frac{M-1}{M} \times \cdots \times \frac{M-N}{M} = \frac{M!}{M^{N+1}(M-N-1)!}$$

This formulation is valid, but we do not have sufficient computing power to get a reasonable estimate from it. We can avoid this problem by making an estimate using the Poisson distribution. We do this under the assumption that two different fingers are matched to the same fingerprint at the rate λ . With this approximation we get that:

- **Model I:** $e^{-\lambda} = e^{-\frac{10^{22}}{1.1 \times 10^{21}}} = 0.00011$
- **Model II:** $e^{-\lambda} = e^{-\frac{10^{22}}{2 \times 10^{37}}} = e^{-\frac{1}{2 \times 10^{15}}}$

6 Conclusion

Either all human beings throughout history have had unique fingerprints or they have not. If we were to generate a population of 100 billion, the probability that it would have unique fingerprints, according to our first model, is 0.00011. According to our second model, this probability is $e^{-\frac{1}{2 \times 10^{15}}} \approx 1$. With either estimate, it seems quite conclusive that the fingerprint uniqueness is a reality, not just a myth.

6.1 Fingerprint vs DNA Evidence – A Final Test

According to the State of Wisconsin Department of Justice [13], the probability of DNA misidentification is of order one in a billion. Our second model, the probability of misidentification from fingerprinting is 10^{-37} . This indicates that fingerprinting is substantially more reliable than DNA testing.

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