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INTERPRETATION OF PARTIAL
FINGERMARKS USING AN
AUTOMATED FINGERPRINT
IDENTIFICATION SYSTEM

THESE DE DOCTORAT

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IMPRIMATUR

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Abstract

In the subject of fingerprints, the rise of computers tools made it possible to create powerful automated search algorithms. These algorithms allow, inter alia, to compare a fingermark to a fingerprint database and therefore to establish a link between the mark and a known source. With the growth of the capacities of these systems and of data storage, as well as increasing collaboration between police services on the international level, the size of these databases increases. The current challenge for the field of fingerprint identification consists of the growth of these databases, which makes it possible to find impressions that are very similar but coming from distinct fingers. However and simultaneously, this data and these systems allow a description of the variability between different impressions from a same finger and between impressions from different fingers. This statistical description of the within- and between-finger variabilities computed on the basis of minutiae and their relative positions can then be utilized in a statistical approach to interpretation. The computation of a likelihood ratio, employing simultaneously the comparison between the mark and the print of the case, the within-variability of the suspects' finger and the between-variability of the mark with respect to a database, can then be based on representative data. Thus, these data allow an evaluation which may be more detailed than that obtained by the application of rules established long before the advent of these large databases or by the specialists experience.

The goal of the present thesis is to evaluate likelihood ratios, computed based on the scores of an automated fingerprint identification system when the source of the tested and compared marks is known. These ratios must support the hypothesis which it is known to be true. Moreover, they should support this hypothesis more and more strongly with the addition of information in the form of additional minutiae. For the modeling of within- and between-variability, the necessary data were defined, and acquired for one finger of a first donor, and two fingers of a second donor. The database used for between-variability includes approximately 600000 inked prints. The minimal number of observations necessary for a robust estimation was determined for the two distributions used. Factors which influence these distributions were also analyzed: the number of minutiae included in the configuration and the configuration as such for both distributions, as well as the finger number and the general pattern for between-variability, and the orientation of the minutiae for within-variability. In the present study, the only factor for which no influence has been shown is the orientation of minutiae

The results show that the likelihood ratios resulting from the use of the scores of an AFIS can be used for evaluation. Relatively low rates of likelihood ratios

supporting the hypothesis known to be false have been obtained. The maximum rate of likelihood ratios supporting the hypothesis that the two impressions were left by the same finger when the impressions came from different fingers obtained is of 5.2 %, for a configuration of 6 minutiae. When a 7th then an 8th minutia are added, this rate lowers to 3.2 %, then to 0.8 %. In parallel, for these same configurations, the likelihood ratios obtained are on average of the order of 100,1000, and 10000 for 6,7 and 8 minutiae when the two impressions come from the same finger. These likelihood ratios can therefore be an important aid for decision making. Both positive evolutions linked to the addition of minutiae (a drop in the rates of likelihood ratios which can lead to an erroneous decision and an increase in the value of the likelihood ratio) were observed in a systematic way within the framework of the study. Approximations based on 3 scores for within-variability and on 10 scores for between-variability were found, and showed satisfactory results.

Résumé

Dans le domaine des empreintes digitales, l'essor des outils informatisés a permis de créer de puissants algorithmes de recherche automatique. Ces algorithmes permettent, entre autres, de comparer une trace à une banque de données d'empreintes digitales de source connue. Ainsi, le lien entre la trace et l'une de ces sources peut être établi. Avec la croissance des capacités de ces systèmes, des potentiels de stockage de données, ainsi qu'avec une collaboration accrue au niveau international entre les services de police, la taille des banques de données augmente. Le défi actuel pour le domaine de l'identification par empreintes digitales consiste en la croissance de ces banques de données, qui peut permettre de trouver des impressions très similaires mais provenant de doigts distincts. Toutefois et simultanément, ces données et ces systèmes permettent une description des variabilités entre différentes appositions d'un même doigt, et entre les appositions de différents doigts, basées sur des larges quantités de données. Cette description statistique de l'intra- et de l'intervariabilité calculée à partir des minuties et de leurs positions relatives va s'insérer dans une approche d'interprétation probabiliste. Le calcul d'un rapport de vraisemblance, qui fait intervenir simultanément la comparaison entre la trace et l'empreinte du cas, ainsi que l'intravariabilité du doigt du suspect et l'intervariabilité de la trace par rapport à une banque de données, peut alors se baser sur des jeux de données représentatifs. Ainsi, ces données permettent d'aboutir à une évaluation beaucoup plus fine que celle obtenue par l'application de règles établies bien avant l'avènement de ces grandes banques ou par la seule expérience du spécialiste.

L'objectif de la présente thèse est d'évaluer des rapports de vraisemblance calculés à partir des scores d'un système automatique lorsqu'on connaît la source des traces testées et comparées. Ces rapports doivent soutenir l'hypothèse dont il est connu qu'elle est vraie. De plus, ils devraient soutenir de plus en plus fortement cette hypothèse avec l'ajout d'information sous la forme de minuties additionnelles. Pour la modélisation de l'intra- et l'intervariabilité, les données nécessaires ont été définies, et acquises pour un doigt d'un premier donneur, et deux doigts d'un second donneur. La banque de données utilisée pour l'intervariabilité inclut environ 600000 empreintes encrées. Le nombre minimal d'observations nécessaire pour une estimation robuste a été déterminé pour les deux distributions utilisées. Des facteurs qui influencent ces distributions ont, par la suite, été analysés: le nombre de minuties inclus dans la configuration et la configuration en tant que telle pour les deux distributions, ainsi que le numéro du doigt et le dessin général pour l'intervariabilité, et la orientation des minuties pour l'intravariabilité. Parmi tous ces facteurs, l'orientation

des minuties est le seul dont une influence n'a pas été démontrée dans la présente étude.

Les résultats montrent que les rapports de vraisemblance issus de l'utilisation des scores de l'AFIS peuvent être utilisés à des fins évaluatifs. Des taux de rapports de vraisemblance relativement bas soutiennent l'hypothèse que l'on sait fausse. Le taux maximal de rapports de vraisemblance soutenant l'hypothèse que les deux impressions aient été laissées par le même doigt alors qu'en réalité les impressions viennent de doigts différents obtenu est de 5.2%, pour une configuration de 6 minuties. Lorsqu'une 7ème puis une 8ème minutie sont ajoutées, ce taux baisse d'abord à 3.2%, puis à 0.8%. Parallèlement, pour ces mêmes configurations, les rapports de vraisemblance sont en moyenne de l'ordre de 100, 1000, et 10000 pour 6, 7 et 8 minuties lorsque les deux impressions proviennent du même doigt. Ces rapports de vraisemblance peuvent donc apporter un soutien important à la prise de décision. Les deux évolutions positives liées à l'ajout de minuties (baisse des taux qui peuvent amener à une décision erronée et augmentation de la valeur du rapport de vraisemblance) ont été observées de façon systématique dans le cadre de l'étude. Des approximations basées sur 3 scores pour l'intravariabilité et sur 10 scores pour l'intervariabilité ont été trouvées, et ont montré des résultats satisfaisants.

Contents

Remerciements	i
Abstract	v
Résumé	ix
Contents	xiii
1 Introduction	1
2 Theoretical Foundations	7
2.1 History of fingerprint identification	7
2.2 The morphological development of fingerprints	8
2.2.1 Morphogenesis	10
2.2.2 Studies on heredity and factors influencing ridge development	11
2.3 The Identification process	13
2.3.1 Analysis	14
2.3.2 Comparison	14
2.3.3 Evaluation	16
2.4 Automated Fingerprint Identification Systems	28
2.4.1 History	28
2.4.2 How it works	29
2.4.3 Concluding remarks on AFIS	30
3 Methodology	33
3.1 Probabilistic approach	33
3.1.1 Considerations for within- and between-finger variability . .	35
3.2 The AFIS used	36
3.3 The Hypotheses	37
3.3.1 Hypothesis 1: Within Variability can be modelled using a generally applicable probability density function	37
3.3.2 Hypothesis 2: Between finger variability can be modelled by a generally applicable probability density function	41

4	Within-Finger Variability	43
4.1	Introduction	43
4.2	Evaluation of sample size	43
	4.2.1 Material and Methods	43
	4.2.2 Results	49
4.3	Comparison between marks, livescan images and rolled inked prints	57
	4.3.1 Material and Methods	58
	4.3.2 Results	62
4.4	Influence of the number of minutiae included in the configuration .	87
	4.4.1 Material and methods	87
	4.4.2 Results	87
4.5	Comparison between two minutiae configurations on the same finger	90
	4.5.1 Introduction	90
	4.5.2 Material and Methods	90
	4.5.3 Results	92
4.6	Influence of the orientation of the minutiae	96
	4.6.1 Material and Methods	96
	4.6.2 Results	97
4.7	Estimation of the parameters from the highest score possible for a given configuration	98
	4.7.1 Material and Methods	98
	4.7.2 Results	98
5	Between-Finger Variability	113
5.1	Introduction	113
5.2	Description of the general patterns present in the database	114
	5.2.1 Material and methods	114
5.3	Evaluation of sample size	117
	5.3.1 Material and Methods	117
	5.3.2 Results	118
5.4	Dependence of between finger variability on finger number and gen- eral pattern	121
	5.4.1 Introduction	121
	5.4.2 Material and Methods	121
	5.4.3 Results	122
5.5	Dependence of between finger variability on the number and place- ment of minutiae	136
	5.5.1 Introduction	136
	5.5.2 Material and methods	136
	5.5.3 Results for increasing number of minutiae	137
	5.5.4 Results for differing minutiae configurations	138
	5.5.5 Approximation of parameters	140
	5.5.6 Conclusions on between-finger variability	143

6	Testing of the different approximations using Likelihood ratios	145
6.1	Introduction	145
6.2	Material and methods	146
6.3	Results on likelihood ratios	148
6.4	Discussion of the results on the testing of LR _s	172
7	Discussion	175
7.1	General approach	175
7.2	Within- finger variability	177
7.3	Between-finger variability	181
7.4	Likelihood ratios	183
7.4.1	Case example & application of the model to cases	186
7.5	Outlook	189
8	Conclusion	195
	Bibliography	199
	Appendices	207
A	Application of the parameter estimation to a new donor	211
A.1	Material and Methods	211
A.2	Results	214
B	Commands for score extraction	229
B.1	Data acquisition in the system	229
B.2	Command lines for the extraction of marks or tenprints, the extraction of scores, and that of general patterns	229
C	Matlab functions for the computations of Likelihood ratios and Tippett plots	231
C.1	Function importing the data from the different text-files	231
C.2	Function for putting data into a vector format	232
C.3	The global function for the Tippett plots	233
C.4	The function for computing LR _s using different options	239
C.5	The function for actually plotting the Tippett plots	242
C.6	Computing the approximated parameters for the between-finger variability	244

Chapter 1

Introduction

Fingerprints as a means of identifying an individual from a latent print have been used for more than a century. They were the forensic evidence which was perceived as the most reliable, proving identity without doubt. This reference as a unique feature even lead to expressions including the word "fingerprint" being used to describe techniques that allowed the identification of individuals or compounds (DNA fingerprinting, fingerprint region of infrared spectra). In more recent years, approximately since the 1990s, scrutiny on this type of evidence has increased. This is due to overall increased scrutiny in United States courts on specialist and in particular scientific evidence due to a change in jurisprudence based on, in particular, *Daubert v. Merrell Dow Pharmaceuticals, Inc.* (1993), as well as two related court decisions, *General Electric Co. v. Joiner* (1993) and *Kumho Tire Co. v. Carmichael* (1999). While *Daubert v. Merrel Dow* and *General Electric Co. v. Joiner* deal with scientific evidence, in *Kumho Tire Co. v. Carmichael*, the court extends the criteria established in the first two decisions to non-scientific expert testimony (Berger, 2000). Jointly with this first reason, the forensic identification sciences (fingerprints, handwriting, tool marks, etc.) have also come under critical examination due to the perceived gold standard set by DNA evidence (Saks and Koehler, 2005) that, in order to be admitted by the courts, had to be researched very thoroughly.

Also, wrongful identifications of fingerprints have been detected and published; most recently, the wrongful identification of Brandon Mayfield in relation with the Madrid bombings of 2004. The Spanish police found, on a bag containing explosives and detonators, a latent fingerprint. They launched an international search of this fingerprint through Interpol. The FBI searched this latent in their database and found a match with Brandon Mayfield, a lawyer. An identification was carried out, and verified by 2 other examiners and, at a later point, by a third independent examiner. The identification was communicated to the Spanish police, who did not agree with the FBI's identification. Finally, the Spanish police identified the latent with the finger of another person, communicated this identification to the FBI, and the FBI withdrew its identification of Brandon Mayfield (Office of the Inspector General, 2006).

The identification of Brandon Mayfield is particularly interesting because of the

number of verifications carried out (3) and the individuals having made these verifications. The examiners involved in this error are all well trained and highly experienced; also, the fact that an independent expert also agreed with the original identification may be thought of as putting in question the usefulness of verification.

This wrongful identification (as well as others exposed) casts doubt on fingerprint identification as it is practiced today. Once the fact that the identification was wrong was exposed (in the Mayfield case, as well as in other cases), differences between the mark and the non-matching print have been found and highlighted. In some instances, these differences were the reason for the exposure of the fact that the identification was not valid. It remains that these differences were, in the wrongful identification, 'explained away'. This is one of the reasons for the wrongful identification highlighted in a report reviewing the FBI's identification of Brandon Mayfield (Office of the Inspector General, 2006). This report, especially the reasons for the wrongful identification exposed in it, is enlightening. Reasons for this wrongful identification mentioned in the report are:

- The unusual similarity of the prints. The report mentions that this case illustrates a particular hazard of the large databases of fingerprints and the powerful search algorithms, that jointly allow to find very similar fingerprints.
- Bias from the known prints of Mayfield. Here, the report highlights that examiners were using backward reasoning from the known print in order to infer on characteristics of the latent.
- Faulty reliance on extremely tiny (Level 3) details. In particular the report remarks negatively on the practice of using similarities while dismissing or discounting dissimilarities.
- Failure to assess the poor quality of similarities. The features used in the identification were quite unclear, and, according to the report, the quality of the agreement was inadequate to support the conclusion of identification.
- Failure to reexamine the latent print following a report by the Spanish police that did not identify the mark to Mayfield's fingerprint. Again, according to the report, the FBI did not adequately examine the possibility of having erred in identifying Mayfield after learning the negative result from the Spanish national police.

Some of these points, e.g. the unusual similarity of the prints, bias from the known prints, and the failure to assess the poor quality of similarities, are extremely important. Arguably, the most alarming point here is the link between the use of AFIS (Automated Fingerprint Identification System) and the risk of finding very similar prints to the partial marks submitted. This problem, which will very certainly resurface, is an evident one. Also, databases are presently increasing, due to political decisions and increased international collaboration (Schengen agreement in

Europe, where a centralized database of fingerprints of non citizens is in operation). Since in some jurisdictions (see also chapter 2.3.3), the decision of identification is based on the experience of the examiner, that is on his or her ability to recognize the sufficiency of features to identify, this is troublesome. In fact, the personal experience of any human cannot even approach the numbers of fingerprints which are included in these databases (even admitting all of the prints seen are remembered), and the closest matches are found and extracted from these databases. Such a system may pose demands on the characteristic used, which is undoubtedly extremely discriminating, that surpass the possibilities of latent to fingerprint comparisons as carried out presently.

Among these points mentioned is the bias introduced by using backward reasoning from the print, leading to the inference (or recognition) of characteristics on the mark. This is bad practice, and has been recognized as such for a long time (Ashbaugh, 1991). This bad practice does not seem to be quite as rarely used as good practice would have it. Ashbaugh (1991) even goes so far as to say that it is a common comparison procedural error to examine the clear image before the unclear one.

'Explaining away' differences is mentioned among the reasons for this false identification, and this could possibly be a recurrent observation in wrongful identifications. This interpretation (and active search) of differences is arguably one of the most difficult parts in fingerprint comparison and evaluation. It is indeed far from trivial to distinguish dissimilarities from discrepancies in some cases.

The failure to assess the poor quality of similarities seems linked to the failure to assess the dissimilarities correctly. Both, from the author's point of view, stem again from the individuals lack of experience; not the particular examiners' experience, which is, in the Mayfield case at least, impressive and undisputed, but the fact that no human can properly assess the rarity of the configuration of features observed when the two impressions have been matched in a database of millions of fingerprints. Then, when more similarities than have ever been observed previously between non-matching prints are observed in a case, this will lead to an identification, even when in reality the mark and print are from different sources.

The reliance on extremely small details, that were only visible on one out of ten of the ten print cards of the individual used for the identification, is also a cause for concern. It is indeed more than questionable to use characteristics for the demonstration of similitude, when at the same time, lack of correspondence will be automatically explained away. Differences are explained because they are deemed to be due to differences in apposition and the characteristics used are not expected to reproduce reliably. These are therefore characteristics that can be considered to be used only for demonstrating identity of source and not for demonstrating difference of source. This confers an inherently prejudicial quality to such features: the point of view taken in the present thesis is that any feature, characteristic, or mark used to support the proposition that a mark originated from a given source should also

have the capacity of supporting the converse view.

Furthermore, these small characteristics can be confused with artifacts (eg. background, matter on the latent) quite easily, particularly on a latent print which is unclear. The author also thinks that these characteristics need research, in order to investigate if truly they show enough variability between individuals to counter the undisputedly high within source variability.

The present thesis may help to address some of these issues. On one hand, a probabilistic approach is chosen. This means that the result of the evaluation of a comparison between a mark and a print will be a measurement of the likelihood of the correspondence of the features observed if both impressions come from the same finger put in relation with the likelihood of observing this correspondence if the two impressions come from different fingers. These measurements are hoped to aid in the proper assessment of the meaning of similarities as well as some of the dissimilarities that are observed in a given comparison. Also, the fact that not an absolute identification (or exclusion) will result from these measurements presents potential advantages. The result thus obtained clearly needs to be inserted into a given case and used simultaneously with other elements as well as prior probabilities (or only prior probabilities, that may have been updated by other elements) by the trier of fact. This may aid to avoid some of the ill effects that may result from the use of large databases.

The goal of this thesis is thus to use a pre-existing interpretational canvas for the evaluation of forensic evidence including partial fingermarks, the likelihood ratio. The evidence is, in this study, considered to be the comparison between a partial mark and a (potentially) matching print. The probabilistic tool developed here is foreseen to be employed only once a possible match has been found; normal exclusions based on clear differences are still considered to be carried out by examiners before this step. The tool can nevertheless help the assessment of dissimilarities that have not, in this first step, led to exclusion; indeed, a probability distribution of the within-finger variability is fitted to data obtained from comparisons between impressions known to come from the same finger. This distribution is then used for the attribution of a probability to dissimilarities observed in a given comparison (by way of the score value obtained). The evaluation of such dissimilarities is therefore no longer binary in this step; it is an assessment of whether the dissimilarities are reasonable under the hypothesis of both impressions coming from the same source. The tool therefore only aids the examiners final decision concerning the value that can be attributed to the comparison under evaluation, once the characteristics used in the comparison have been noted. A proximity measure is then used in order to quantify the 'similarity' between two minutiae configurations, originating from the mark and the print, respectively. This proximity measure is the score such as it is output by a particular AFIS. This system, and consequently the score, is used as a 'black box': how the score is computed is largely unknown and remains so after the research. It is known that AFIS distinguish well between same source and different

source impressions, even when one of these impressions is partial. The originality of the present study resides therefore not in the interpretational canvas as such, but in the measure used to assess the proximity of two minutiae configurations; here, the scores issued from an AFIS are employed. AFIS are not, at the present time, used for inference purposes, but only as tools for searching. The interest of using these scores for inference is, first of all, the quality of this measure: scores have been conceived and optimised with the precise goal of obtaining large numbers when comparing a given configuration on a mark to an inked print from the same finger, and obtaining low numbers when the mark is confronted to an inked print from a different finger. These systems have been used and improved for over 20 years; and performance tests show regularly that some of these systems (such as the system used here) fulfill this task of distinguishing similar from different impressions remarkably well (Wilson et al., 2003). This score can therefore be expected to be extremely useful in an evaluative setting, quite probably it is even the overall best measure that can be found at the present point in time. Secondly, the use of such systems is quite widespread, and the score obtained between the mark and the inked print retained is therefore widely accessible. This signifies that a tool based on such scores may find widespread use without the need of, on the side of interested parties, investment in new computer programs or the need of end-users to learn the use of such new programs.

Since this direct use is only possible for identical systems, the present thesis can also be used to guide the implementation of the use of scores from other systems in the same canvas. The proper way of integrating the output of such systems in a likelihood ratio, the data needed to properly model within- and between-finger variabilities as well as the entire data-acquisition and treatment processes are made as transparent as possible. Consequently, the establishment of such models on other systems is straightforward and quick.

Some historical notes on the uses of fingerprints will, in the following, precede a brief introduction concerning the reasons for the undertaking of this research as well as some notions on the characteristics of fingerprints and a general description of Automated Fingerprint Identification Systems (AFIS). The working hypotheses will be presented, and the remainder of the document is ordered by hypotheses concerned with first within- and then between-finger variability, where under each heading both the data used and the results obtained are presented and discussed. This separation is intended to give a clear picture of which part of the data a particular conclusion is based on. A general discussion and conclusion of the overall results follow and end the present thesis.

Chapter 2

Theoretical Foundations

2.1 History of fingerprint identification

Man has taken an interest in fingerprints since prehistoric times. This is shown by representations of hands or papillary patterns on the walls of caves of quaternary men, as well as on potteries from the neolithic era (Locard, 1931). Texts by Cummins and Midlo (1943) and Berry (1991) also establish early uses of fingerprints, which may indicate consciousness of the individuality of the patterns on the fingers or hands.

The first description of the ridges and furrows of friction ridge skin is due to Nehemiah Grew (Berry and Stoney, 2001). A description and a classification of general patterns into 9 classes was established by Purkinje (1823) in his thesis, which also discusses the functions of ridges, furrows and pores. None of these authors has carried out any research on the possibility to identify using these characteristics, nor on their permanence. Permanence has been shown later by Hermann Welker, who made two inked prints of his palms in 1856 and in 1897, and who published the two figures (Welcker, 1898), as well as by Herschel, who took his prints in 1860 and in 1890 (Berry and Stoney, 2001). Herschel also proposed to the Inspector of Jails in Bengal, India, to take fingerprints of all persons committed to prison to confirm their identities in 1877 (in what is called the “Hooghly letter”) (Berry and Stoney, 2001). Herschel did not propose the use of fingerprints found on crime scenes, but only the use of inked prints for the identification of persons.

According to Berry and Stoney (2001) as well as Cole (2004), it is Thomas Taylor who first proposes the use of fingerprints found on crime scenes for identification purposes (Taylor, 1877), and not, as is generally accepted, Faulds (1880) (Cummins and Midlo, 1943). Note that the possibility of identifying criminals on the basis of the marks left on crime scenes precedes the demonstrations of permanence.

Classification systems, allowing the identification of recidivists even when, for example, the recidivist gives a false name, have been proposed by several researchers. A first system was presented by Galton in 1893 to a committee that was considering the Bertillon anthropometric system and its possible replacement (Berry and Stoney, 2001). This first classification system was only a foundation. Two people

developed fingerprint classification systems that were used for decades afterwards (notwithstanding slight modifications in some countries): Ivan Vucetich and Sir Edward Henry (Berry and Stoney, 2001). The Galton-Henry system was the more widely spread of the two, and was used in most countries both in Europe and North America, while the Vucetich system was mostly used in South America.

From the beginning of the 20th century, therefore, fingerprints started being used for both the identification of recidivists and the identification of criminals on the basis of latent prints found on crime scenes.

2.2 The morphological development of fingerprints

There are three premises classically referred to in order to support fingerprint identification:

1. Each fingerprint is unique
2. Fingerprints are permanent
3. Fingerprints are inalterable.

The last two premises mean that fingerprints do not change (by themselves) and cannot be changed voluntarily.

Since the decisions in *Daubert* (*Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 1993) and *Kumho* (*Kumho Tire Co. v. Carmichael*, 1999), the examiner's capacity to determine a common and unique source for a distorted and partial mark and an inked print has been questioned more frequently. Since such a determination is only possible if fingerprints are unique, much effort has been focussed on the confirmation of fingerprint unicity. Research on much data has been called for in order to prove the individuality of fingerprints. In the present thesis, fingerprint individuality is considered to be a point demonstrated not by the examination of many prints but by morphogenesis. Individuality is furthermore not considered to be particularly relevant: indeed, when considering what is sometimes put forward, that each fingerprint is different when considered in sufficient detail, the point becomes eventually tautological. A second problem is that too detailed an analysis does not permit repeatability anymore: the individuality of reproducible (or permanent) and partial information of the fingerprint has not been proven, nor has any assessment allowed to establish how much information would be truly unique as well as still being permanent. This also shows the interrelatedness of the three premises above: if in order to be unique, the fingerprint needs to be examined in too much detail, then this detail cannot be permanent, since it is known that cells for example are replaced periodically (Wertheim, 2000). Inalterability, i.e. that fingerprints cannot be changed voluntarily, is not strictly true, and this premise should therefore be abandoned: microsurgical intervention now indeed allows the replacement of fingerprints (using, for example, the volar skin of toes). Another

concept, observable uniqueness, would be much more helpful than the postulates that 'nature never repeats itself' or that fingerprints are unique when observed in sufficient detail, including the molecular level. Also, as Stoney (1991) highlights, it is impossible to prove individuality using statistics; the result of statistical analysis will be a probability of finding two (partial) fingerprints that are not distinguishable. Broeders (2003) states the crux of the matter very clearly:

There are two major principles underpinning classical forensic identification science. The first is the principle of uniqueness, summed up in the phrase 'Nature never repeats itself', which is [...] echoed in claims like 'All fingerprints/ears/voices are unique'. The second is the principle of individualization, which says that every trace can be related to a unique source.

The main problem here lies in the second of these assumptions. While the first principle, that every object is unique, is an unproved assumption which - in a philosophical but forensically trivial sense - is both necessarily logically true and impossible to prove, it is the second principle that is largely responsible for methodological problems surrounding forensic identification science. The real question is not if all physical traces are unique and therefore theoretically capable of being uniquely identified with a particular source but whether they can always be so identified in the forensic context and using the methods and procedures employed by the forensic scientist. That is also, or rather should be, the central question in the currently raging fingerprint debate.

Leaving aside the discussion of uniqueness: what has been shown satisfactorily is that reproducible fingerprint features are extremely varied between different fingers. This is shown by morphogenesis, factors influencing this process, as well as regular use and investigation of fingerprints, including studies on twins (Jain et al., 2001; Srihari et al., 2008).

As mentioned before, permanence, the second basis of fingerprint identification, is linked to the features examined; it has been shown for minutiae and pores by the description of the morphology of the skin, and has been furthermore empirically shown on true handprints. However, even for these features, permanence is linked to the method used for comparison. What has been shown is that two minutiae will always have the same ridge count between them (and of course excluding scarring), and will be positioned in the same way on the finger over time. However, whether the distance between them is constant or not is another matter entirely. Again, variation over time should be measured with the same metric used to describe the variation between fingerprints in order to determine whether or not fingerprints from a same finger are more similar to each other, even when they have been taken at large time intervals, than fingerprints of different fingers are.

In conclusion, therefore, individuality and permanence of fingerprints are linked concepts, both depending on the level of detail examined. Also, as the amount of

information taken into account on a given impression increases, while individuality will increase, permanence will decrease to the point where an impression is identical only to itself and no other (not even to another impression from the same finger).

Since the individuality as well as the permanence and immutability are based in the morphogenesis, more particularly in the factors influencing the development of ridge skin and the structure of friction ridge skin, these elements will be presented here, although briefly.

2.2.1 Morphogenesis

The formation of papillary ridges in the fetus is described by Babler (1991) as well as by Wertheim and Maceo (2002) and summarised in Champod et al. (2004). Furthermore, an excellent literature review is found in Kücken (2004). This section is based on those sources.

During the 5th and 6th week of gestation, the hands of the fetus start to develop. During the 6th week, formations corresponding to the fingers are observed, and interdigital notches appear. During the 7th week, fingers start to differentiate in the form of cartilage, the exterior morphology of the hand shows finger formation and the tissue between these fingers disappears. At the same time, volar pads start appearing, first on the palm, and then on the apical ventral region of the fingers. These localized elevations precede the formation of papillary ridges, that will form on these pads. Between weeks 6.5 and 10.5, these pads grow rapidly, and separate in the palm. Then, from weeks 11 to 16, the pads regress (or rather, grow less than the hand and therefore disappear). During this time, the primary differentiation of ridges also takes place. For a link between the shapes of volar pads and the resulting general pattern of ridges, see Wertheim and Maceo (2002). The primary ridges appear first as cell proliferations localized in the basal layer of the epidermis at around the 10th week of gestation (according to Kücken (2004), the time of the initiation of ridge formation given in the literature varies from the 10th to the 13th week of pregnancy). These proliferations fuse together to form ledges. These ledges are the primary ridges, which are still immature and will develop downward into the dermis (Champod et al., 2004). Rather than speaking of 'fusing together' of ledges, Kücken (2004) speaks of both cell proliferation and folding in the basal layer, citing a number of authors. Also, he develops a mathematical model based on a buckling process, controlled by stresses in the basal layer that mimicks observed ridges well.

While the hand is growing, the number of primary ridges increases; new ridges form between the existing ones where gaps exist due to the expansion of the surface (Ashbaugh, 2006). New developing ridges may also form bifurcations if their development starts on the side of a developing ridge (Ashbaugh, 2002). Also, the formation of ridges does not start simultaneously on the whole finger surface: it starts at the apex of the volar pad, along the nail furrow, and in the distal interphalangeal flexion crease area (Champod et al., 2004). These three fronts advance until the dermal surface is covered. The primary ridges define the basic configura-

tion of the volar skin surface (Babler, 1991). At the 14th week, sweat gland ducts form at the bottom of the primary ridges and project into the dermis (Kücken, 2004). At 15 to 17 weeks gestational age, secondary ridges start to form (Babler, 1991). Simultaneously, primary ridge development terminates. It is then that ridges appear on the surface of the epidermis as fingerprints. Between the 17th and 24th week, secondary ridges continue to grow. In the 24th week, bridges or anastomoses start forming between primary and secondary ridges. Dermal papillae (or papillae pegs) are formed between these bridges (Hale, 1952), which are characteristic of the final dermal ridge (Babler, 1991).

The ridge pattern is definitely fixed in the dermis. New epidermal cells form in the basal layer of the epidermis. The new cells are formed, and then progress simultaneously with neighboring cells from the basal layer to the skin surface, where they are exfoliated (Wertheim and Maceo, 2002). Three types of attachments are described by Maceo (2005): the primary/secondary ridge attachment, the basement membrane zone and cell-to-cell attachments. General structural support for the surface ridges is ensured by the primary and secondary ridges at the bottom of the epidermis. The papillae pegs and epidermal anastomoses reinforce this system (Maceo, 2005). The basement membrane is generated by the basal cells of the epidermis and the dermis and attaches the basal cells of the epidermis to the dermis. More specifically, the basal cells of the epidermis have hemidesmosomes projecting fibers down toward the dermis, while the dermis projects fibers up towards the epidermis; these fibers projected by both the dermis and the epidermis make up a fibrous sheet, the basement membrane, that locks the two layers together. The third and final type of attachment is the cell-to-cell attachment between the cells of the epidermis. Two structures link these keratinocytes: Desmosomes and focal tight junctions. Desmosomes are on the cell surface and have fibers extending into the cells, while focal tight junctions are small zones where the plasma membranes appear fused together (Flaxman, 1974). Interestingly, the basal cells of primary ridges divide to create transient-amplifying cells, i.e. cells that can divide while they are in the supra-basal layer, while the basal cells of secondary ridges do not (i.e. cell division only occurs at the stratum basale). Since the primary ridges correspond to the ridges on the surface while the secondary ridges correspond to furrows, and that the ridges on the surface are submitted to more friction than the furrows, and the primary ridges therefore need to keep up a higher rate of creation of cells (Maceo, 2005). Since cells originate in the basal layer, between the dermis and the epidermis, and move jointly to the surface, only damage that alter this basal layer will result in permanent scars visible on the surface (Champod et al., 2004).

2.2.2 Studies on heredity and factors influencing ridge development

Simply put, studies have put forward that there clearly are genetic factors influencing ridge configuration; however, it has also been shown that fingerprints are

not determined by genetics, therefore allowing for variation due to the environment of the fetus. The first indication of a genetic component is that there are statistical differences in the distributions of general patterns and ridge widths between different ethnic groups (Chakraborty, 1991). A second information indicating the presence of genetic factors is that particular phenotypes in ridge patterns are linked to hereditary diseases. These are even used to diagnose some diseases, in particular syndromes caused by changes in the number of chromosomes (Schaumann and Opitz, 1991). A link between prenatal selection (spontaneous abortion) and dermatoglyphs has also been shown by Babler (1978). There are, however, environmental factors that cause syndromes including manifestations in the ridge skin, such as alcohol consumption by the mother, some medications, as well as viral infections during pregnancy. Interestingly, experiences on monkeys have also shown that the mother's psychological stress can provoke changes in papillary patterns (Schaumann and Opitz, 1991). Finally, family studies, generally based on general patterns or ridge counts, also show genetic links. Studies on twins' fingerprints have been published (Jain et al., 2001, 2002; Srihari et al., 2008), that allow the observation that the fingerprints of identical twins can be discriminated but are more similar than between random individuals or heterozygotic twins. This observation not only shows that there are genetic as well as environmental effects, but also that these two types of effects are still observed when using automated feature extraction and matching on the minutiae level.

A genetic influence on fingerprints has therefore been established; Jones (1991) even suggests to ask systematically for ten-prints of family members (brothers, sisters, parents) when a latent comparison leads to an exclusion while the print shows similarities with the latent. According to Babler (1991), the genetic component influences the development of ridges indirectly through pad topography, growth rates, and stress on the epidermis. A final important discovery concerning environmental factors is that the resemblance between the total ridge count of brothers and sisters in a family increases as family size increases. According to a hypothesis, this effect of the family size is due to the changes of the amniotic environment, which is most important between the first and the second pregnancy. This effect would therefore be strongest in small families (Schaumann and Opitz, 1991). Also, although environmental effects have been shown to exist, those known to exist (contrarily to the amniotic environment hypothesis) result in illness (viruses, alcohol, etc) and cannot, therefore, be the kind of environmental influence that would explain that (or show whether) all fingerprints are distinguishable. The twin studies, however, do show that there are environmental factors influencing the development of ridge skin in a normal context. In both of the twin studies cited above (Jain et al., 2001, 2002; Srihari et al., 2008) no false match was observed, but the studies were carried out on fully rolled impressions, not in a forensic setting. With respect to this setting, one single observation is interesting. In a proficiency test in 1995, a latent was included along with the inked print of the twin (whether it was a homozygotic twin is not

stated) of the actual donor of the latent. The rate of false identifications on this comparison was of 19% (Cole, 2006), which does put into question the possibility of systematically distinguishing one twin from another based on a latent print of small size. The 81% of respondents who did not erroneously identify this latent to this print do show, however, that even in this partial impression sufficient information was present to determine that the mark did not come from this finger.

2.3 The Identification process

Currently, the procedure used in fingerprint identification is known under the acronym ACE-V, which stands for Analysis, Comparison, Evaluation and Verification (Ashbaugh, 1991, 2000; McRoberts, 2002). While the analysis, comparison and verification steps will be treated here quite briefly, the evaluation is the heart of the present study; indeed, the goal of this thesis is to elaborate an evaluative tool that could, in time, replace or complement present-day decision making in this step. It may be worth noting that the other steps are far from being uncontroversial: the number of features noted on any given mark will vary from examiner to examiner (see 2.3.1 for details). In the comparison phase already some evaluative decisions are taken by the examiner: whether a discrepancy is a difference leading to exclusion is often decided in this phase. Finally, the setup of the verification is much discussed: must it be blind or not? Must only identifications be verified? Who verifies the identifications carried out by a fingerprint examiner? What happens when the verifier disagrees with the initial examiner? What are the consequences when the initial examiner or the verifier has made a mistake? While these questions are out of the scope of the present thesis, they are of paramount importance when ACE-V is implemented as a standard operating procedure.

It is in particular the analysis and the comparison phases that will have an impact on a system composed of the examiner carrying out these steps, and then inputting his or her results into an evaluative tool such as the one presented here. Indeed, the exact minutiae marked in the analysis phase will have a direct impact on the LRs generated by the evaluative tool. Also, most comparisons never reach a proper evaluation phase: the print is excluded as being from the same source during comparison or declared insufficient for comparison (sometimes identification) purposes in the end of the analysis phase. In most cases these exclusions will be true negatives, but in some instances severe distortion or effects due to the substrate on which the fingerprint has been left may lead to divergent features that then lead to exclusion, without an appropriate assessment of the origin of the difference. The evaluative tool proposed here will, most certainly, only be used in cases where no discrepancy is observed, and the examiners' question pertains to the value to attribute to the correspondences observed between mark and print. This of course increases the reliability of the system for cases where the result supports the prosecution hypothesis: these are the cases where the system profits the most from the synergies

between the examiner and the evaluative tool, in the sense that these conclusions will be reliable. The conclusions supporting the defense, however, will include all false negatives attributable to the examiner, as well as all of those attributable to the evaluative tool. We may therefore expect an increase in misleading evidence in favor of the defense when using the system, but also a decrease in misleading evidence in favor of the prosecution.

2.3.1 Analysis

In the course of the analysis phase, the mark (as well as the inked comparison print) is observed in order to know which papillary surface it originates from, which level of detail is present and what is the quality of the mark. Three levels of detail are generally mentioned (SWGFAST, 2002; Interpol European Expert Group on Fingerprint Identification, 2004), where level 1 is the general pattern, level 2 are the minutiae, or rather the specific ridge path, and level 3 are the finer details: ridge edges and pores. In the course of the analysis it is determined whether the general pattern, the delta, minutiae and pores and ridge edges are visible. Also, the presence of distortion, its direction and extent are determined. Ideally, all characteristics that will be used in the comparison phase are marked during this analysis. The quality of the overall impression, as well as a degree of confidence in each characteristic is established. Finally, the fingerprint examiner judges whether or not the mark shows features in sufficient quantity and quality to allow a meaningful comparison (i.e. whether this mark can lead to an identification or an exclusion).

It could be expected that, when two examiners analyze the same mark, that they annotate the same characteristics; this is not the case. Even their number varies (Langenburg, 2004; Evett and Williams, 1995). In the qualitative-quantitative approach to fingerprint evaluation (this quantitative-qualitative approach is explained below, in section 2.3.3). this is not seen as a problem: first of all, features need not be numbered or counted; secondly, the only postulate is that two examiners with the same training should arrive at the same conclusion (e.g. identification, exclusion or inconclusive) when comparing the same area of friction ridge skin (Ashbaugh, 1991), regardless of the features used to that effect. This comes down to the fact that it does not really matter whether the characteristics they observe are the same ones (or whether there is the same number).

2.3.2 Comparison

From a purely practical point of view, several methods are used that facilitate a systematic comparison between the mark and print. These methods have been published by Olsen and Lee (2001) and formalize eight fashions to compare a mark and a print. These are the Osborn grid method, the Seymour trace method, the photographic strip method, the polygon method, the overlay method, the Osterburg grid method (used for comparison as well as for subsequent evaluation), the microscopic

triangulation method, and finally the conventional method (Olsen and Lee, 2001). All except the conventional method involve either grids or superposition, while the conventional method relies on simple side-by-side comparison. As its name indicates, the conventional method is probably the one used most frequently. All other methods do not accord very well with elastic distortion between the two prints, using either some grid or some kind of overlay or a combination of the two.

A ground rule in the comparison of fingerprints is to always start on the mark, and look for the feature seen on the mark on the print subsequently. The converse, to look for features on the *mark* that have been observed on the *print* is not considered good practice, as it can lead to the observation of features on the mark that are not visible and are due to observer effect (Wertheim, 2000; Ashbaugh, 1991; Office of the Inspector General, 2006). Observer effects in different scientific endeavors are listed in Risinger et al. (2002). These examples show how insidious such effects are. Even the reading of dials is influenced by expectations (Risinger et al., 2002)! However, observer effects are 'most potent where ambiguity is greatest' (Risinger et al., 2002). In fingerprint comparison, typically, the latent print is analyzed, and then used to sift through a certain number of prints; the print that has been retained for further comparison already has some features in common with the latent print, such as the general pattern and a focal group. Then, more observations of similarities between the two prints are added. There is a moment when every feature on the latent is expected to be found on the inked print. Conversely, and notwithstanding the fact that features must first be observed on the latent in order to counter as much as possible observer effects, it should also be observed whether there are features on the rolled inked print that should be present on the latent. These features would be in the region where it is thought that the latent comes from, and there is no smudging that would make that feature invisible. The influence of observer effects in this stage can lead to the erroneous detection of correspondences, the erroneous non-detection of differences, as well as to the 'explaining away' of detected differences. Also, while the methodology (ACE-V) separates comparison and evaluation, the author believes that most of the evaluation is terminated once the comparison phase is concluded: indeed, the judgement of whether a feature is in correspondence, whether it is important (i.e. of high value), whether a difference leads to exclusion or not, is at least partly carried out during the comparison phase. It is therefore not only in the evaluation (where observer effects certainly play a role also) but already in the comparison phase that the influences of expectations on human perception have an impact. To deny the possibility of observer effects in fingerprint examiners (Leadbetter, 2007) does not seem helpful at this point in time, and the extensive research on such effects (although not, in general, directly applicable to fingerprint examination as such) does not suggest that observer effects (or context effects) are easy to control by the scientist herself. In the fingerprint context, observer effects have been shown to exist even in experienced examiners (Dror et al., 2006).

2.3.3 Evaluation

In the evaluation phase, one of several identification criteria may be used. Two sets of criteria are actually applied for the evaluation of fingerprint criteria: numerical standards and the so-called holistic or quantitative-qualitative approach. Constant in these two approaches are the conclusions that result routinely: Identification (print and mark come from the same source), exclusion (print and mark do not come from the same source) and finally, inconclusive (insufficient detail is present to either individualise or exclude). This set of possible conclusions has even been set as a requirement by the International Association of Identification (Anon., 1980); going against these accepted conclusions here results in the exclusion from this professional body. The Scientific Working Group on Friction Ridge Analysis, Study and Technology (SWGFAST), another North American group, also only admits these three conclusions (SWGFAST, 2002, 2003).

Another constant requirement for all approaches is the importance of the absence of any discrepancy. A single unexplained difference must, according to all approaches to evaluation discussed here, lead to exclusion.

Numerical Standards

Numerical standards, the need to observe a given number of correspondences between a mark and a print, have been used almost since the beginning of the identification of latent prints. The bases for these standards are quite blurry; they are probably based on several texts, suggesting different numbers for those standards, such as Locard's tripartite rule (Locard, 1931), a demonstration including 16 corresponding points in prints from different fingers by Bertillon (1912) (who tried to highlight the importance of the absence of differences rather than the number of corresponding minutiae), and Galton's probabilities (Galton, 1892). In 2002, the inventory of the different fingerprint standards used in Europe were published (Anon., 2002), and they range from 8 to 16. Two resolutions adopted by the fingerprint profession (McCann, 1973; Margot and German, 1995) go in the direction of abandoning numerical standards; the wording is almost identical. The 1973 resolution by the IAI (International Association for Identification) reads:

...no valid basis exists at this time for requiring that a pre-determined minimum number of friction ridge characteristics must be present in two impressions in order to establish positive identification. ...

The second resolution (Margot and German, 1995) replaces 'valid reason' by 'scientific reason', since valid reasons can be found in national legal texts. Numerical standards are still used in many countries, and even at the FBI, 12 points may be used as a quality assurance measure (Budowle et al., 2006).

Quantitative-Qualitative approach

Also called the 'holistic approach', since all details are taken into account, including also their quality. This is the approach that has replaced numerical standards in the countries where such a move has taken place. It has been described by Ashbaugh (1991):

A print found at a crime scene may have one, two or all three levels of detail, depending on its clarity. Often the various detail levels are present to varying degrees in different parts of the same print. Clarity, quality and quantity of unique detail dictates the friction ridge area size required for individualization (p 44)...Unclear prints display large accidental formations with little intrinsic shape. In these instances identifications are based more on quantity. (p 45)... Forensic identification investigators, having varying degrees of knowledge and experience, perceive the comparison differently. This also affects the size of friction ridge area required for individualization. Different levels of knowledge and experience coupled with available quality and quantity of ridge detail dictates that a preset number or size of ridge detail cannot be established as a basis for identification. Examiners of equal experience and training should arrive at an identical conclusion when comparing the same area of friction ridges.

In this approach, the examiner therefore evaluates correspondences and divergences, weighing quantity against quality. This evaluation is based on the experience and the knowledge of the examiner in question; conclusions of examiners should correspond *if* they have equal experience and training. This is, arguably, a reliable method, as long as the exactitude of the examiners' conclusions is assessed regularly. Also, and this joins a point made in the introduction, it is necessary for the experience to be acquired in the same setting (under the same conditions) as the ones under which it is applied. Also, the experience is only useful if it is acquired in an environment where the conclusions arrived at by the examiner are tested against some ground truth (Haber and Haber, 2008).

It does not make sense to consider untested opinions held by the examiner as experience, since he cannot be shown to be wrong (if such was the case) and therefore would not necessarily learn from that experience. Haber and Haber (2008) require quantitative measurement of training and experience; this may not be sufficient. Indeed, there may be differences in training and experience that cannot be measured in quantitative units (such as the individuals' learning curve), and to standardize training and experience in this sense will not lead to a valid assessment of the examiners' competence. It is true, however, that when the evaluation is a function of the examiners' training and experience as mentioned by Ashbaugh (1991), and two examiners who have the same level of training and experience should arrive at the same conclusion, then there should be some way of measuring these levels.

Also, the most straightforward way to measure examiners' competence (which is, in the end, the relevant question, rather than how much training and experience they have), would be to base such an evaluation on fingerprint examinations. To measure it in this way would lead to circular reasoning if it is assessed whether two examiners who have scored identically in the evaluation of competence also arrive at identical conclusions in a comparison for testing whether they arrive at the same conclusion. If they arrive at the same conclusion on the testing comparison, no knowledge is gained (they were chosen because they concluded identically on a batch of comparisons); on the contrary, if they score differently, that does nothing to help sustain that two examiners of equal competence conclude identically. It does not necessarily lead to refusal of this hypothesis: it can simply be argued that the test to evaluate equal competency was not fit for that purpose (which would, whatever the test, always be possible, since it was sufficient to include one more comparison, in particular the one used as a test, in the evaluation to observe the divergence between the examiners and conclude to different levels of competence). Now, an experiment meant to test observer effects (but whose results are quite revealing for examiner repeatability in spite of this different goal) may help here: if the same examiner, past a certain number of years of experience, examines the same print twice, he should also arrive at the same conclusion. This is not necessarily the case, as shown by Dror et al. (2006). Now, while it is agreed that the sample was small, that the context created in the study may not have mimicked casework contexts, and that the examiners were submitted to a strong context effect, this still casts much doubt on the claim that two examiners with the same training and experience should arrive at a same conclusion for a given comparison. These conclusions should, if this were the case, be independent of contextual bias, and it is the author's view that it would be difficult to better standardize the examiners' competence than by observing twice the same person.

Since therefore the opinions of examiners cannot be considered simply the result of their training and experience or their competence, all of which seem extremely difficult to standardise (if it is considered that opinions of examiners correspond if they had the same training and experience), this approach does not seem promising. A more transparent and easily explainable approach are statistical models that aid the examiners decision, and some of these models are explained below.

Existing statistical models of fingerprint features

Although not used presently in operational settings, it has been proffered to be the way forward (Saks and Koehler, 2005). The use of statistical models will yield conclusions that are less than absolute, and may therefore be conceived of as lessening the strength of fingerprint evidence, but they build on solid observations of data. The 'experience' that is included in these models in the form of repeated impressions of the same finger, as well as impressions of many different fingers, may not be

perfect. In particular, imperfections concerning the description of the features used (never all features that can be observed on a mark can be included), as well as the way in which repeated impressions of the same finger are acquired, will be present. Their advantage is transparency: we can describe exactly what these models are based on, the data, the assumptions, the modeling steps, and the features used: this is not the case with the examiners' experience. Also, they can be tested, and the error rates issued from such models can be defined, which is an advantage in the current North American judicial setting (*Daubert vs Merrell Dow Pharmaceuticals, Inc.*, 1993 and its progeny).

A selection of models is presented here in detail. Indeed, several models of so-called fingerprint *individuality* have been proposed, beginning with Galton (1892). This initial model was followed by other models by Balthazard (1911), Roxburgh (1933), Amy (1946, 1947), Kingston (1964), Osterburg et al. (1977), Stoney (1985); Stoney and Thornton (1986, 1987), Champod (1996), Meagher et al. (1999), Pankanti et al. (2002), Neumann et al. (2006, 2007), and Srihari and Srinivasan (2007), as well as a proposition to weight the minutiae found in a comparison depending on their type by Santamaria (1953), which is a notion also included in the report of the second European Expert Group on Fingerprint identification (Interpol European Expert Group on Fingerprint Identification, 2004). To be mentioned as well are tests carried out using an automated fingerprint comparison system, and computing likelihood ratios from the scores of this system (Ramos-Castro et al., 2005; Gonzalez-Rodriguez et al., 2005), which is very similar to the present study. There are fundamental differences with the present work: the number of minutiae used is not controlled, and the within-variability is modeled without giving much consideration to the data used for this purpose. In Ramos-Castro et al. (2005), the concept that scores as output by biometric systems can be used for the computation of LR is proven for fingerprints.

Reviews of most of these models are proposed by Champod (1996) and Stoney (2001), and the interested reader is referred to these reviews for all models predating 1996. The models described here will be the 50K study (due to the use of AFIS in this test), the model of Neumann *et al* and the models by Pankanti *et al.* and Srihari *et al.*.

The 50 x 50K study This study was conducted for the demonstration of fingerprint individuality in the context of a courtroom questioning of the use of fingerprint evidence in *United States of America vs Byron Mitchell* (1999), and has been discussed by Stoney (2001), Wayman (2000) and Kaye (2003). As the study's name indicates, 50'000 fingerprints were used, which makes it the study based on the most data available to date. Furthermore, all of these fingerprints were left loops (Stoney, 2001). Each of these prints was matched against all of these prints, yielding 2.5 billion comparisons, using the same algorithms as the FBI's AFIS. For each print the best match obtained was this same print: note here that the same print is

truly the exact same *impression* of a given finger. However, there were cases where another 'strong match' for this print was found, and these were subsequently found to be other impressions of the same finger. In a second step, partial prints including approximately 20% of the rolled inked print were generated, and again compared to the whole database. This comparison was a simulation of latent-to-print comparisons.

Once the scores had been obtained, the researchers fitted a normal distribution to the scores issued from comparisons of different fingerprints (Wayman, 2000). Based on this assumption of normality, and the scores obtained when comparing the same impression to itself, the probability associated with the z-score (the score obtained when comparing the print to itself, reduced by the mean of the scores obtained between different fingers and divided by the standard deviation of that distribution) was computed as $1/10^{97}$ (Wayman, 2000; Stoney, 2001). Then, this number has been multiplied by the world population ($5.9 \cdot 10^9$) and thus the approximate chance that two rolled fingerprints on Earth are identical is claimed to be $59/10^{88}$. In the case of the pseudo-latent print, an estimate for the 'rarity' of such a latent was carried out for each number of features observed in the pseudo-latents. Again, based on z-scores and normality assumptions, probabilities of between $1/10^{27}$ and $1/10^{97}$ are obtained (Stoney, 2001).

Two major points are criticized in this model: the data used and the modeling used. Indeed, the data included repeated prints from the same fingers: the scores issued from such comparisons have been excluded from the data before estimating the probabilities. This is exactly the kind of data needed, however: what are the scores obtained when comparing two different impressions from the same finger? In figure 2.1 the relationship between the scores used in this study and the data that should have been used is shown. Although the illustration shown in figure 2.1 is based on purely hypothetical distributions, the overall behavior is as shown. The 50K study therefore yields much lower probabilities of duplication than what is warranted in any application of fingerprints. It is indeed trivial to show that twice the same image of a fingerprint will be exceedingly rare.

The simplistic modeling using a normal distribution (without testing whether it actually fits the data) is the second point criticized by Wayman (2000). It is indeed doubtful that such scores would follow a normal distribution, since in another context, such score data has been modeled using a log-normal or gamma distribution (Wein and Baveja, 2005).

Finally, based on their probability that a non-mate print would match any fingerprint, they compute the probability that any fingerprint in the world would match the print, simply multiplying the world population by the probability value previously obtained. This is a basic error according to Stoney (2001), but here minor with respect to the other points mentioned above (although it will have a great influence on the final result, if maintained).

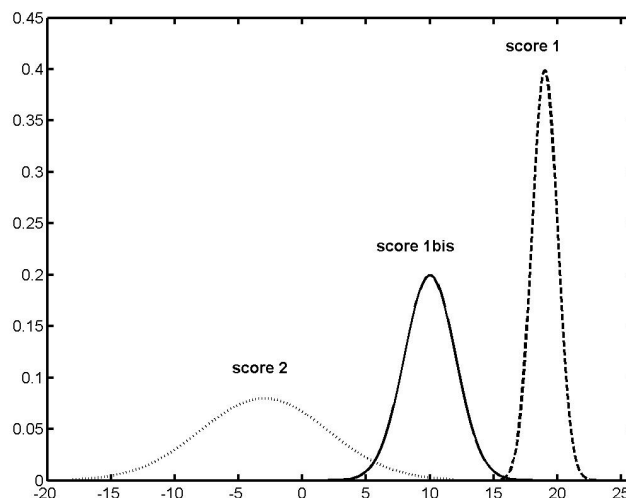


Figure 2.1: Illustration of 3 distributions of scores. Score 2: distribution of scores between different fingers; Score 1: the distribution used in the 50K study (comparisons between same impressions) and Score 1bis: distribution of scores in comparisons between different impressions of same finger

Neumann et al’s model This is the first model to actually use spatial relationships between minutiae, and taking into account the within-finger variability. It is also a truly evaluative model: the goal is not to show fingerprint individuality (as it was the case in the 50K study) nor to establish some probability of duplication, but to provide an evaluative tool for fingerprint comparisons. Since the author was one of the collaborators in the establishment of this model, some similarities with the present thesis may be apparent, and, of course, only limited critique concerning the overall approach can be expected here due to the fact that the authors views haven’t radically changed since the establishment of that model.

In Neumann et al. (2006), a database of 216 images from 4 fingers of two donors was used to model within-finger variability, and a background database of 818 fingerprints showing ulnar loops was used for the modeling of between-finger variability. In a first step, configurations of 3 minutiae were extracted using Delaunay triangulation (Bebis et al., 1999), a technique that has also be used to index large fingerprint databases for efficient searching (Liang et al., 2006). These configurations were described using the general pattern of the print, the region (centre, delta, right and left periphery), type and direction of the three minutiae, as well as the length of the side of the triangle separating the minutia from the next one. The likelihood ratio was then separated into the part concerned with discrete variables, and the part including continuous variables: $LR = LR_d \cdot LR_{c|d}$. Discrete variables were used for the comparison of triangles to the relevant part of the database. Frequencies of occurrence for this data were used in the denominator of the LR, and the numerator was set to 1 for the discrete variables. Continuous variables were

compared between mark and print using the Euclidean distance. The overall LR therefore became $LR = \frac{1}{f(GP) \cdot f(R|GP) \cdot f(T|GP,R)} \cdot \frac{p(d|x_d, y_d, S, I)}{p(d|x_d, y_d, \bar{S}, I)}$, where GP is the general pattern, R is the region, T is a cumulated indicator of the three minutiae types, d is the euclidean distance, x_d and y_d are the discrete variables of the latent and the suspect's print, respectively, S is the prosecution hypothesis (the two impressions come from the same finger), \bar{S} is the defense hypothesis (the two impressions come from different fingers) and finally, I is information relevant to the evaluation. $p(d|x_d, y_d, S, I)$ and $p(d|x_d, y_d, \bar{S}, I)$ were estimated, for right loop fingerprints, from feature vectors from a common source and from different sources, respectively, and continuous functions were fitted using kernel density estimation. Note that LR_d has not been fully tackled in the paper.

The results thus obtained were LRs, and were assessed on 2000 non-matching and 2000 matching configurations of 3 minutiae using Tippett plots. This shows whether the system works with reasonable rates of misleading evidence. This model has then been augmented to be able to include any number of minutiae (Neumann et al., 2007), using radial triangulation (rather than Delaunay triangulation, as was the case in Neumann et al. (2006)). The descriptor of a minutiae configuration is slightly changed: the direction of the minutiae is recorded with respect to the image, and in addition to the other features, the length of the side of the triangle linking the minutia to the centroid of the configuration is included, as well as the surface of the triangle including minutia k , $k+1$ and the centroid of the configuration. The region has been abandoned in this model. The euclidean distances are now computed on normalized variables in order to avoid confounding the effect of each variable in the distance measure with it's units of measurement. Normal mixtures are used for the modeling of within- and between-finger variability, where within-finger variability was not only based on data, but also on a model of distortion based on data. Four datasets of unrelated fingers were available: 321 Ulnar loops from right forefingers, 365 Ulnar loops from right middle finger, 73 arches from right forefingers, and 131 arches from left forefingers.

Testing showed that rates of misleading evidence decreases when the number of minutiae in a configuration increases. Also, LRs in favor of the prosecution increase in value as the number of minutiae increases.

As the authors state, two main drawbacks of the model are the modeling of distortion (based on a single ulnar loop finger), and the dearth of data for general patterns other than loops. Also, the metric used to compute a distance between two configurations has not been the centre of attention, and there may be a better metric than a simple euclidean distance. Another, and this can hardly be changed as easily as the first two, is that there is no possibility to evaluate minutiae configurations where the center of the configuration is not visible. In other words, all ridges in the convex hull defined by the minutiae in the configuration must be visible. All minutiae included in the surface analyzed must be noted, otherwise LRs will be much too large (due to the fact that the databases that the between-variability

distribution is based on are established by sampling neighboring minutiae). The fact that minutia type is taken as a valid information, thus ignoring connective ambiguities, is another small concern, but a remedy can easily be found (such as computing LRs with both types and adding them in a weighted fashion, given some data on how often a bifurcation is observed on a mark when the minutia observed on the corresponding print is a ridge ending).

Pankanti et al's model This model estimates the probability of false correspondence between minutiae on different fingerprint images, such as the probability that a fingerprint showing 36 minutiae points will share 12 of these points with another randomly chosen fingerprint with 36 minutiae (this particular probability is estimate at 6.1×10^{-8}) (Pankanti et al., 2002). The probability computed is : given an input fingerprint containing n minutiae, what is the probability that an arbitrary fingerprint containing m minutiae will have exactly q corresponding minutiae with the input? Here, you may notice that falsely detected minutiae are admitted (not all minutiae on the input need to find a matching minutia on the template print; indeed, non-matching minutiae are ignored). Also, the matches are symmetrical: if a minutiae is absent on the template or on the input, and present on the other impression, there is no difference in the probabilities. In forensic settings, we expect that most of the minutiae of the template are absent in the input print, and we expect that all minutiae from the input are present on the template. In this model, minutiae are described by their (x, y) coordinates, as well as the angle of the ridge on which it resides, θ . After alignment, a minutia in the input is considered as matching a minutia in the template if the distance between the two minutiae is smaller than some radius r_0 , and if the difference between the angles is smaller than some value θ_0 . The probability that two minutiae will correspond in position only is the area of tolerance (πr_0^2 , hereafter C) divided by the area of overlap found between input and template (A), and the probability of correspondence in angle only is angle of tolerance ($2\theta_0$) divided by 360. The probability that exactly ρ minutiae match between the n input and the m template minutiae is:

$$p(A, C, m, n, \rho) = \binom{n}{\rho} \left(\frac{mC}{A} \right) \left(\frac{(m-1)C}{A-C} \right) \cdots \left(\frac{(m-\rho+1)C}{A-(\rho-1)C} \right) \times \\ \times \left(\frac{A-mC}{A-\rho C} \right) \left(\frac{A-(m-1)C}{A-(\rho+1)C} \right) \cdots \left(\frac{A-(m-(n-\rho+1))C}{A-(n-1)C} \right) \quad (2.1)$$

This is the probability of observing ρ out of n minutiae that are matching concerning their location. Reformulating this equation yields a hyper-geometric distribution of ρ with parameters m , M , and n , where M is $\frac{A}{C}$. The probability that q among the ρ minutiae match in direction is given by $\binom{\rho}{q} (l)^q (1-l)^{\rho-q}$, where l is the probability of two position-matched minutiae having a similar direction. Here, position and direction of minutiae are considered independently; however, it is considered by

Pankanti et al. (2002) that this should not be the case. Also, in a next step, instead of considering the whole overlap area A , the authors that minutiae can only lie on ridges, which reduces this area to $M = \frac{a}{2r_0}$, where $2r_0$ is the length tolerance in minutia location. The parameters r_0 , θ_0 , l , ω , A , m , n , and q are estimated from data (450 mated pairs of fingerprints). The model was tested on a database from 167 individuals, where 4 repetitions of 4 fingers were acquired using a livescan device, for each individual, yielding 2672 fingerprints. A second dataset was also acquired using another livescan device.

This model does not answer the question of whether a latent can be attributed to a fingerprint uniquely, or allow the evaluation of the results of the comparison between a mark and a print. The results provided do give an estimation of the probability of matching exactly 12 out of 12 minutiae (on the input fingerprint) to a template (showing 12 minutiae) and also give an idea of the influence of falsely detected or erroneously undetected minutiae. While within-finger variability is considered by the tolerances r_0 and θ_0 (as well as the allowance for the presence of variable numbers of minutiae) these tolerances are overly simplistic in the sense that deformations between different fingerprint impressions should go in the same direction. If a minutia on the input fingerprint is displaced upwards with respect to the matching minutia on the template, neighboring minutiae will not, generally, be displaced downward, due to distortion phenomena. Also, this is a simple point matching model, where points are distributed randomly along ridges; there is no consideration of the fact that some minutiae are more rarely observed than others. There is no evaluation of where on the fingerprint minutiae can be found with higher probability, while it is known that there is a higher minutia density in the center and delta regions (Champod, 1996). Whether the minutiae matched are truly neighbors or not is not considered; indeed, the minutiae matched between two impressions may be anywhere on the fingerprint, with several nonmatching minutiae between them. For example, on one print two unmatched minutiae may be inside the convex hull of matched minutiae, while on the other there may be none. While in a setting where such discrepancies have already been verified by an examiner and not lead to exclusion this is acceptable (since in a smudged mark we do not expect to see all minutiae), this is not the case in an automated setting, where the reason for absence of intervening minutiae is unknown. Also, the asymmetrical relationship (one degraded and one perfect representation) between a mark and a print in a forensic setting is not at all captured by this model. This was not the goal of this model, although fingerprint examiners were used to annotate minutiae and matches on the datasets. When comparing theoretical and empirical matching performance (between the proposed model and an automated matcher), the empirical data is several orders of magnitude lower than the theoretical performance. The authors (Pankanti et al., 2002) attribute this to noise, errors in locating minutiae and the fragility of the matching algorithms. It is quite possible that the independence assumptions used in the model also contribute to this difference. The fact that

mismatches are ignored weakens this model further. It is not, here, considered that this model adds much to the understanding of fingerprints or, as the title of the paper says, their individuality. Finally, It does not answer the related question of whether a partial mark can be identified (or linked) reliably by examiners to a given inked fingerprint, be it unaided or with the support of a probabilistic model.

Some of these concerns are addressed by a later model by Dass et al. (2005) and later Zhu et al. (2006, 2007), assessing the probability of random correspondence (PRC) by using finite mixture models to represent minutiae locations and directions. The mixture model used is composed G mixture components, each component consisting of the multiplication of a normal (modeling minutia location) and a Von-Mises distribution (modeling minutia direction). This mixture is then constrained to the fingerprint area. The mixture is fitted to the input and template fingerprints individually and used for generating the random minutiae in those two impressions separately. The probability of obtaining exactly w matches out of m and n minutiae on the query (Q) and template (T) prints then is: $p * (w; Q, T) = \frac{e^{-\lambda(Q,T)} \lambda(Q,T)^w}{w!}$ for large m and n ; this is a Poisson distribution with parameter $\lambda(Q, T) = mnp(Q, T)$ and $p(Q, T) = P(|X^Q - X^T|_s \leq r_0 \text{ and } |D^Q - D^T|_\alpha \leq d_0)$ where X^Q and X^T are the (x, y) coordinates of minutiae chosen from the template and the query fingerprint (according to the mixture) and D^Q and D^T the directions of such minutiae. The Poisson distribution is a reasonably good approximation when $m, n \geq 40$. In a next step, the mixture models are fitted on 'master' prints, where minutiae from different impressions of the same finger are combined.

The great problem of this model is the requirement that m and n both be large; this renders it quite inapplicable to latent prints, although it can be argued that, in the fingerprint having left the mark, more than 40 minutiae are present, and that therefore the q minutiae found (and subsequently matched to the suspect's print) are a subset of the minutiae available on the whole print. Also, while this model is very interesting for a general idea of what can be obtained from points with a direction that are distributed according to this mixture, it does not model the minutiae present in the prints accurately (although better than a uniform distribution does): for example, there are minutiae in some instances whose direction is perpendicular to the ridge flow actually observed. The clustering of minutiae is captured, and this is extremely interesting. Minutiae locations are still considered as independent, and nonmatching minutiae are still not considered. Also, this model does not (and is not supposed to) capture the specific value of a given minutiae configuration, which, from the authors' point of view, would be far more interesting, even as a basis for PRC computation if such a computation was deemed necessary.

Srihari et al's model The most recent model considered has been established by Srihari and Srinivasan (2007) and Fang et al. (2007). It is based on the model developed by Zhu et al. (2006, 2007). Additional features are used with respect to this model (rather than only minutia location and direction): so-called ridge

types. Ridge types have first been described in a simple way, where only three such types were included, and then expanded to 16 such ridge types (Fang et al., 2007). Ridge types are defined by sampling points along the ridge at equal intervals in the neighborhood of a minutia. In the model with three ridge types (right turn, left turn, unknown), a ridge point is considered to be right or left according to the angle between the orientation of the connection between the minutia and the ridge point and the minutia orientation. These ridge types are then modeled using a uniform distribution and included in the model based on minutiae by Zhu et al. (2006), yielding the following model:

$$f(s, \theta, \mathcal{T} | \Theta_G) = \sum_{g=1}^G \tau_g f_g^X(s | \mu_g, \sigma_g) \cdot f_g^D(\theta | \nu_g, \kappa_g, \rho_g) \cdot f_g^T(\mathcal{T} | a, b) \quad (2.2)$$

where $f_g^X(s | \mu_g, \sigma_g)$ is the probability density function of a bivariate Normal distribution over the positions of minutiae, ($f_g^D(\theta | \nu_g, \kappa_g, \rho_g)$) is the probability density function over the orientations, ($f_g^T(\mathcal{T} | a, b)$) is the uniform distribution over the ridge types. s is the (x,y) position of the minutia, θ is the direction and \mathcal{T} is the ridge type, while Θ_G are the parameters of the distribution used. G is the number of mixture models, τ_g is the non-negative weight for that model, with $\sum_{j=1}^G \tau_j = 1$, and μ_g, σ_g are the parameters (mean, covariance matrix) of the bivariate normal distribution for class g of the mixture. The parameters of the von Mises distribution for component g of the mixture are ν_g, κ_g, ρ_g , and the parameters of the uniform distribution are a and b . This uniform distribution is to be replaced by the observed frequencies of the ridge types in a database. Each model g in this mixture represents a cluster of minutiae. The minutiae location (x, y) corresponds to the g th cluster and the orientation and ridge type therefore also correspond to that cluster; dependence between location, direction and ridge type is therefore modelled here.

The probability that two randomly chosen ridge types would match, given a probability of 1/3 for each of the types and given that a match is declared when either the two ridge types compared are the same or when one of them is unknown, is 7/9. This is judged as too high (Srihari and Srinivasan, 2007), and more ridge types are therefore added. Two anchor points along the ridge are chosen (the 6th and the 12th point sampled starting from the minutia considered, where the distance between the points sampled is equal to the distance between ridges). Sixteen ridge types are defined according to the properties of these two anchors, and their relationship to the minutia. Then, empirically observed frequencies for each of these sixteen ridge types are used to replace the uniform distribution. A match between the ridge types is declared when the difference between the template and input ridge types is no larger than one (the indices of the ridge type being ordered logically from 1 to 16). Not surprisingly, smaller PRC is obtained for this model (including a new measure, i.e. ridge types) than in Zhu et al. (2007).

The criticism of this model remains the same as those for the model by Pankanti et al. (2002), mainly that the particular problem of the mark cannot be included

in this model, and the problems when using a number of matching minutiae given a number of query and template minutiae. Modelling of within-finger variability is inexistent and replaced by thresholds for accepting or rejecting the match of a minutia between query and template. Also, again, it is a model used to estimate discriminative power rather than the value of a given fingerprint comparison, at least in the form used. The probabilities considered are the multiplication between the characteristics of the marks and the characteristics of the print (i.e. both mark and print are generated using the model). The declared goal is again the demonstration of fingerprint individuality; again, the numbers given for the probability of random correspondence do show that this is an improbable event. Given the premises of probability distributions such a probability cannot be zero in any event, and therefore the individuality of fingerprints (as postulated in the titles) cannot be shown in this way. Additionally, here, ridges must be clear and defined around the minutiae, and some of the 16 ridge types (although all of them have been found in the database used) do not correspond to observations on real fingerprints (i.e. types 4 and 13 in Srihari and Srinivasan (2007)).

Conclusion on statistical models Drawbacks are present in all models presented up to now. Many do not answer the question asked in the present study: evaluating, for a given mark, the quality of the correspondence with a given print and the rarity with which such a match is expected to happen. With the exception of the model by Neumann et al. (2007), a match is considered as a binary decision, based on tolerance values to allow for within-finger variation. In the last two models, the fact that nonmatching minutiae are simply ignored greatly increases the PRC; this is reasonable when treating automatically extracted minutiae, but does not at all approximate the selectivity of the fingerprint itself. In a forensic setting, the presence of a nonmatching minutia is the criterion allowing to exclude a donor, preventing false matches. Here, only a high number of matches is considered (a minimum of 12 matching minutiae out of 26, 36 or 46 minutiae present on query and template in (Fang et al., 2007)). It furthermore seems unreasonable to model the minutiae present in a fingerprint and to then compute PRC's based on these models of minutiae, rather than the minutiae themselves; in this sense, the PRC's reported based on empirical observations are much more reliable, although influenced by noise, falsely detected minutiae etc.

Most of the models presented above compute the expected probability of random correspondence; this corresponds to the discriminatory power used in other subjects (such as paint analysis in the domain of forensic science, see (Tippett et al., 1968)). This assessment allows the definition of the overall (or mean) performance of a system. It has been highlighted that this is not a relevant information in a given case (Stoney, 1984).

The interpretative canvas presented here will follow the theoretical bases presented in Neumann et al. (2006, 2007), and will not be based on generative models

for minutiae, nor on huge accumulations of pairwise comparisons as was the case in the 50K study (Meagher et al., 1999). Rather, the present study aims at establishing relevant aids in a forensic evaluative setting. If this model was to be tested on large numbers of marks, it could yield some information concerning the selectivity of latent-to-print matches, although this is not the goal. This is also another major advantage of the model used here over approaches computing PRC: a model established with the goal of estimating a "value" for a given comparison can be used to establish the discriminative power of the method used, while a model established with the goal of computing a PRC cannot necessarily be used to compute the value of a given comparison.

2.4 Automated Fingerprint Identification Systems

2.4.1 History

The automation of fingerprint identification started first with a patent (Maurer, 1960), filed in 1956 but published only in 1960. This was followed by a paper by Trauring (1963). In this paper, feature extraction is described, as well as a matching process. Trauring (1963) only proposes the use of his described algorithm for verification purposes, and not for 1:n searching.

By 1969, the FBI was convinced that automated 1:n searches were (going to be) feasible, and contracted an external company to automate the matching of minutiae. Simultaneously, research was starting in England and France, who both focused on the search of latent prints. This was at the time a major problem: indeed, while one-finger classifications existed, they were hardly used (Cole, 2004). Blind searches (without a suspect) of crime-scene marks were therefore impossible. The FBI's problem was the size of its 10-print database: at the time they held more than 16 million sets of criminal fingerprints (Woodward et al., 2003). After going through a semi-automatic punch-card system, the Royal Canadian Mounted Police implemented the first actual automatic fingerprint identification system (AFIS) in 1978 (Woodward et al., 2003).

It is, however, in the 1980s that automated identification systems really became operational. While generally smaller systems were implemented in American cities, counties, and states, as well as in European and Asian countries in the beginning of the 1980s, the FBI's IAFIS (integrated AFIS) was built in the 1990s. In 1995, IAFIS started communication with the Boston police department (Komarinski, 2005) and it became operational in 1999 (Woodward et al., 2003). IAFIS was important not only on a crime solving level, but it also made it necessary to set a certain number of standards. Since the smaller systems across the United States had been built by different societies, the data, at this point, was not compatible between these systems. The need for a national database generated the need for a data transmission standard. This ANSI/NIST standard for the Interchange of Fingerprint Images (as

well as the Image Quality Specification for scanners, livescans, etc) now exists and is used across the world, thus enabling not only national but also international data exchange.

The evolution of AFIS is not stopping: these systems have, of course, grown faster, more reliable and more accurate. Electronic submittal of fingerprint images to the FBI was possible by 1995 (Woodward et al., 2003). Another major change was the passing from 500 dpi to 1000 dpi in the image resolution, a change in the ANSI/NIST standard that occurred in 2000 (calling for the addition of variable density images) (Woodward et al., 2003). Presently, the probably largest database for criminal searches is held by the FBI in the United States, and included, in 2005, 46 million records (Komarinski, 2005).

2.4.2 How it works

First of all, a caveat on this section: AFIS systems are developed by private companies. These companies do not divulge the mechanism which makes their system work in detail. Some basic principles are known, but the exact feature extraction and matching algorithms remain confidential. AFIS are not only comparison systems; they are also repositories of data, comprised of several databases. Here, it is important to know only that the latent and tenprint impressions are separated in two different databases: the latent cognizant and the unknown latent databases. Of course, in an operational AFIS, more than only the fingerprint image is stored, most importantly alphanumeric data (as a minimum the name, date of birth, reason for arrest in the case of inked prints, and the case and latent identification numbers for latent prints).

There are two steps to the automated comparison of fingerprints, whether in a verification or in an identification setting: feature extraction and matching. The extracted features, generally minutiae as well as ridge flow direction are stored in minutiae databases; these are the databases actually used by the matcher (Komarinski, 2005).

Three different types of searches are generally possible in AFIS: Tenprint to tenprint, latent to tenprint and finally, latent to latent searches. Tenprint-to-tenprint comparison allows the determination of whether the person printed is already in the system (and to know which name was given on previous occasions when his fingerprints were entered. Latent-to-tenprint searches are those that are mainly considered here: an unknown mark is found on a crime scene or object, and is compared to a database of inked prints in order to find a suspect. Finally, latent-to-latent searches are used to know whether the person having left the mark under examination has also left marks in another context. This last option does not allow the direct identification of a suspect, but is useful to link cases.

Typically, the input is a gray scale image, with darker ridges on a lighter background. The resolution of this image may vary, but must be known. The region where the fingerprint is located is then detected, and segmentation (into background

and fingerprint) is performed. Although algorithms for direct feature extraction from gray-scale images exists (Maio and Maltoni, 1997), the image is then generally converted to a binary (black and white) image. This demands the use of filters, such as Gabor filters. The ridges are then generally thinned to a so-called skeleton, which allows easy detection of minutiae. These different image processing steps are described in detail by Maltoni et al. (2003). While automatic feature extraction as implemented in the leading AFIS works quite well on inked prints, this is not always the case on very degraded latent images. Due to the importance of having the correct minutiae for comparison purposes, minutiae are manually checked on marks as well as on the inked prints (Komarinski, 2005). AFIS are generally using mainly minutiae-based matching methods. Minutiae are described by their position and their direction, as a minimum. Additional features are added, depending on the system: overall pattern, core or delta location, image quality for the whole image, minutiae quality, nearest neighbors, ridges crossed between neighbors, the quadrant the minuta is in, and the length and curvature of the ridge a minutia is located on are the characteristics listed by Woodward et al. (2003). Once these features are extracted, they are confronted to the database using a matching algorithm (Woodward et al., 2003). For the matching of minutiae, the two fingerprint images are often aligned, although other methods exist (Maltoni et al., 2003). Then, decisions are taken for all minutiae on the mark concerning whether they match a minutia on the comparison print or not; the number of mates found during this matching process is maximised (Maltoni et al., 2003). A review of feature extraction and matching techniques up to 2004 is available (Yager and Amin, 2004).

Generally, fingerprint matching is not performed in a single step. First, additional data can be used to filter the database (such as gender etc). Then, the database to be searched can be further reduced by using the general pattern of the searched print. These strategies become less and less used as computers get faster, at least for databases that are not too large. Otherwise, successive matchers can be used: a first (fast) matching algorithm winnows the database, and is followed by a second algorithm. In AFIS, these algorithms yield match scores, that then lead to a sorted list of candidates. This list can be limited by the minimum score allowed to enter the list (Threshold-based), or the list may be of predefined length, including the prints with the highest scores (Rank-based). The main difference is that in the first type of selection, if no matching candidate is found, the output list will be empty, while when using rank-based list, the same number of candidates will be output. Of course, hybrid systems exist, where list length is predefined and a minimum threshold must be exceeded in order to include a candidate in the list.

2.4.3 Concluding remarks on AFIS

Automated identification systems have emerged amazingly quickly. Before the development of digital treatment of fingerprints, there was no way of detecting features or of comparing them. Storing of digital images was a problem: a 500 dpi greyscale

image of the 8 fingers that were scanned by the FBI in their first digitalisation campaign from 1977 to 1980 was just less than 5 MB in size, and disk space was expensive (500\$/MB) (Woodward et al., 2003); in a first step, therefore, only extracted characteristics were stored. Once digital acquisition, feature extraction and storage were possible, the problem of matching remained to be solved. All of these obstacles were removed in less than 20 years, all fingerprint cards of the agencies acquiring a system scanned, and the systems were operational, putting an end to manual searches of ten print cards, enabling blind searches of latent prints and finally, eliminating the need for the use of fingerprint classification systems. All of these technical solutions made it possible to have larger and larger repositories that remained usefully searchable.

The historical increase in the size of the database to which a latent print is compared will test this application of the biometric even more in the future, as mentioned in the introduction. Indeed, before the implementation of automated systems, latent prints from a crime scene were only compared to suspects in that case (or known local offenders committing this type of crime). Then, with the advent of automated systems, the latents were compared to known offenders. As mentioned above, in the beginning, these databases were local, and therefore concerned offenders from a given region. Presently, databases searched are national, and even international searches are possible (although the databases are generally separate for each nation, with the exception of Eurodac (Conseil de l'Union Européenne, 2000)). Generally, the databases used are still databases containing fingerprints of known offenders. Now, the latest developments are to create databases of the whole population of a given country, first of all for security purposes. In England, at least, the right to use this population-wide database for searching crime-scene latents is foreseen to remain possible (Office of Public Sector Information, 2006).

These developments are going to test the biometric, because the database against which the latents are compared becomes less and less one of the relevant population: from the 'most relevant' population (the suspects found by the police), to the local delinquents, to delinquents who were known farther away from the place of the crime, and finally, to a population who has, for the most part, never taken part in any delinquent act and will never do so. This means simply that the fingerprints' discriminatory power will be, in the future, tested far beyond the historical data that defenders of this biometric so readily use to demonstrate its individuality as well as the reliability of fingerprint identification. This testing may or may not lead to problems, although the case of Brandon Mayfield can be taken to show that very similar fingerprints will be retrieved when a mark is searched in sufficiently large databases. If such problems should appear more frequently as databases grow larger, this could lead to a change in the use that is made of the data obtained in a mark-to-print comparison.

Chapter 3

Methodology

3.1 Probabilistic approach

From the holistic approach described in the introduction, it becomes clearer that identifications are carried out subjectively, and based on experience. Furthermore, the conclusion of a comparison is, for most fingerprint expert groups, exclusively identification, exclusion or inconclusive. This does not seem coherent, since just before an identification conclusion can be reached, a particular mark cannot be deemed useless. In this thesis, one approach which may aid evaluation of fingerprint evidence is presented.

The first step for modelling probabilities associated with Level II features is to measure distances (in some sense) between minutiae configurations. Secondly, in any model for fingerprint feature evaluation, the fact that no two appositions of a given papillary surface are exactly alike needs to be considered. This approach is based on probabilities. Several statistical studies had been carried out previously, and some have been presented in 2.3.3 while the remainder is discussed in Stoney (2001). The main problems highlighted by Stoney (2001) with respect to the models he discusses are:

- no consideration of the configuration of minutiae as such;
- most are based on untested independence assumptions;
- none of them has been tested on a large database.

The model by Neumann et al. (2006, 2007) has solved, at least partially, all of these problems, but has created new ones, as discussed in chapter 2.3.3. Two of the models proposed (Champod, 1996; Neumann et al., 2006, 2007) employ a likelihood ratio approach (although in the first one the numerator is not addressed):

$$LR = \frac{p(E|H, I)}{p(E|\bar{H}, I)} \quad (3.1)$$

Where:

LR is the ratio of likelihood of the evidence if H is true, divided by the likelihood of the evidence if \bar{H} is true

- E is the evidence, the concordances and discordances observed on the mark and the print respectively,
- H is the hypothesis that the same finger is at the origin of the print as well as the mark and
- \bar{H} is it's inverse, that the mark originates from another finger than the print.
- I is any other information may impact on the within- and between finger distributions, such as for example the sex, the ethnic origin or the age of the author of the crime. In this thesis, no such information is ever formally considered, since it would have to be determined individually for each case.

In the approach presented here, an AFIS is used in order to extract the 'evidence'. The scores employed by the system are the proximity measure between two minutiae configuration. These scores are entire numbers ($S \in \mathbb{N}$)¹, and therefore data is ordinal. However, since they can take values between 0 and above 10000 they will be considered as continuous. The likelihood ratio that will be modeled is therefore

$$LR = \frac{f(s|H)}{f(s|\bar{H})} \quad (3.2)$$

Where s is now the score obtained for the comparison, and H , and \bar{H} have the same definition as given above (3.1). As will be shown in the rest of the document, in the present study, minutiae configurations will be considered, no independence assumptions will be made, and the model will be established on large databases, including also a small testing step. These different elements are shown visually in figure 3.1, where $f(S|H)$ is noted as 'Within' and $f(S|\bar{H})$ is noted as 'Between'. Indeed, $f(S|H)$ is the distribution of scores if the same finger is at the source of both the mark and the print; it is therefore a within-finger distribution. Similarly, $f(S|\bar{H})$ is the distribution of scores if different fingers are the sources of the mark and the print, respectively; it is therefore termed 'Between-finger variability'. More precisely, and in particular in the approach used here, since the AFIS score will be based on the best match between mark and print (such as found by the examiner for the within-finger variability and by the system for the between-finger variability) the distributions are not truly based on the entire finger, but on the closest configuration found on that finger. 'Numerator' and 'Denominator' in figure 3.1 refer to the two elements of the LR, obtained using the within- and between-finger distributions as well as the score of a given comparison.

¹In this thesis, upper case letters will denote random variables (such as S), while the same letter in lower case (s) will indicate a precise value taken by this random variable. The letter H for hypotheses has been excluded from this convention. Also, the letter p is used to denote probability distributions of discrete variables, while in general f is used for densities. Cumulative distribution functions, in both cases, are again indicated using capitals (P , F).

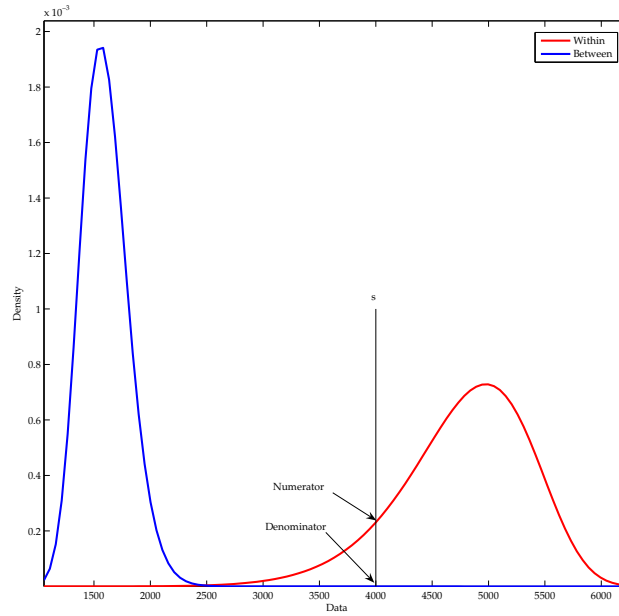


Figure 3.1: Illustration of the elements of the Likelihood Ratio

3.1.1 Considerations for within- and between-finger variability

As seen above, the numerator of the LR is $f(s|H)$; this is the value of the within-finger variability distribution function $f(S|H)$ for a precise score. Within-finger variability has been considered to be 1 in past works (Champod, 1996), but this position has been improved since. Then, one idea was to capture the variability of *marks* that could be obtained from the suspects' finger. This is the approach used implicitly by Neumann et al. (2006, 2007). This view has not been taken here; indeed, it is preferred to try to mimic the way the evidential score itself is obtained, i.e. by comparing a mark to a print. The within-finger variability has therefore been based on the scores obtained from comparisons between marks and prints from the suspects' finger in the present study. Also, it is considered that the properties of the marks (development technique, surface on which the mark was left) must be considered. Therefore, within finger variability as considered here is $f(S|x, y, H)$, where x and y are the properties of the mark and the print considered in the comparison. The properties of the mark define the minutiae used. The prints properties are included here since they allow the selection of the finger used to establish within-finger variability. Furthermore, these properties include the fact that the print is rolled and inked, and in the case of the mark the development technique. The position is taken that the data on which within-finger variability is based should mimic the comparison carried out between the mark and the print

in question; that therefore, the distribution must be based on comparisons between developed marks and inked prints, using the same number of each, in order to capture the variation that could be present between any mark from the suspect, and any print from that suspect. H , rather than being phrased as "the same finger is at the origin of the print as well as the mark" should be phrased, "the suspect's finger is at the origin of print and mark". In the first phrasing, it is understood that that 'same finger' is the suspect's, since the print is supposed to be of known origin. But that hypothesis intimates that there is a generally applicable within variability (e.g. that scores from a same source always behave in the same way, independent of the exact source they are from), which mustn't be adapted for the case at hand, exception made of the characteristics of the mark and the print. It is, however, truly the second that will be modeled here. For each finger, a within variability distribution is established, based on repeated impressions of the suspects' finger.

The between finger variability $f(S|\bar{H})$ will be written $f(S|x, y, \bar{H})$. The mark is compared to the database of fingerprints, which warrants the conditioning by x , the marks' characteristics. the conditioning by y can be left aside since $f(S|x, y, \bar{H}) = f(S|x, \bar{H}) \cdot f(y|\bar{H})$ and that, under \bar{H} , the probability of observing the suspects' configuration is 1.

For within-finger variability, that will mimic as closely as possible the comparison between the mark and the suspects' print, several prints will be used. The print (or rather its set of characteristics extracted) is therefore considered to be a random variable, where the constraint is that these repeated prints are acquired from the suspects finger that is under examination, and that they are acquired under the same conditions as the comparison print used for the evidence score.

3.2 The AFIS used

The system used in the present study is a Sagem DMA. Also, several extensions have been custom made for this study by SAGEM. The first one is for the automatic acquisition of tenprint cards. It is called `ei_batchscan.exe`, and takes all files stored in a given directory. The filenames must be of the form:

`id.page0.0x0xWidthxHeightx500.raw,`

and must therefore be in `.raw` format and at 500dpi. A second program allows the definition of marks and prints to be automatically compared (`raw_dump.py`), and the third allows the automated (and listwise) comparison of the selected marks and prints (`spec.exe`). It is through this automated extraction/comparison process that it possible to obtain all of the scores when a given mark is compared to all of the fingerprints in the system. An overview of the commands used to extract scores is given in Appendix B.

A further tool programmed by SAGEM allows the extraction of the general patterns attributed to the fingerprints in the database (PatternExtractor.py).

All outputs are organised in textfiles, and indexed by the prints' number (number of the ten-print card and the finger number).

The way in which this AFIS is organised includes 4 databases: the log database (saving actions on the database), a WIP database (work in progress), the AFIS database (including marks and tenprint cards) and an administration database. Several processes linked to these databases and the task of the AFIS (storing, comparing, retrieving fingerprints) exist.

3.3 The Hypotheses

Two main hypotheses have been tested here: the first one concerns within- and the second one between-finger variability. In both cases, ideally, a generally applicable probability density function can be found; otherwise, the result of the testing of the following hypotheses will be a guide on the acquisition of data for their estimation on a case-by-case basis.

3.3.1 Hypothesis 1: Within Variability can be modelled using a generally applicable probability density function

Hypothesis 1a: The density used for modelling the within finger variability becomes stable as a given number of observations is reached

Above a certain number of scores obtained, the within-variability density function and, as a consequence, the numerator of the likelihood ratio for a given comparison stabilises in the sense that addition of more data does not cause this distribution to change much. In order to be able to give likelihood ratios which are robust, this stability must be attained. This minimum number of comparisons for the estimation of within-finger variability must be known whether a generally applicable function is, at a later point, found or not. Indeed, if a generally applicable distribution can be determined, it is in the present study that this number of comparisons must be obtained for the conclusions to be reliable and valid. If no such stable distribution is found, this is a first step towards the description of the data that must be acquired on a case-by-case basis. This hypothesis is tested in chapter 4, section 4.2.

Hypothesis 1b: Marks used for the modelling of within variability can be substituted by livescan images or slaps from ten-print cards

If the within-finger distribution is shown to be influenced only by the difference between flat apposition of fingers and rolled impressions, then marks can be substituted by any kind of flat impression. This hypothesis is intimately linked with hypothesis 1d (that within finger variability depends on the number and positioning

of minutiae). If, indeed, it is only the positioning and number of minutiae, rather than the way of acquiring the fingerprint image, that are decisive, then livescans or inked prints could substitute marks for the estimation of the within-finger variability distribution. Rolled prints are not considered here as a substitute for marks, since the distortion that is present on rolled prints is very distinctive and does not generally correspond to distortions that are observed on marks. This replacement, and the reason for the present hypothesis, is interesting if the distribution has to be estimated separately for each case. The acquisition of fingerprint images is in all cases time-consuming; for the acquisition of repeated marks, however, the time required is superior to the time needed for slaps or livescans, for several reasons. First of all, on marks, it is far from certain that the particular minutia configuration found on the evidence is present. This means that, while the number of scores needed and therefore the number of marks where the configuration is present is determined under hypothesis 1a, the number of marks that actually have to be developed is likely to be superior. Second, the development and imaging steps for marks are time consuming and there is a need for equipment (working laboratory, chemicals, imaging techniques, etc.) that is far superior to that of livescans or inking. This hypothesis is tested in chapter 4, section 4.3.

Hypothesis 1c: Within variability for the evaluation of a given mark can be deduced from a generally applicable distribution

This hypothesis includes two subhypotheses, 1c.i and 1c.ii.

Hypothesis 1c.i: Within finger variability is independent of general pattern and finger number

Hypothesis 1c.ii: Within finger variability is independent of donor

Either of those hypotheses may be refuted. If the testing of 1c.i shows that within variability is dependent on either finger number or general pattern or both, generally applicable densities may still be found for each combination of general pattern and finger number, as long as hypothesis 1c.ii holds. Variables linked to the donor, such as age and sex, will be investigated, and if they influence the density modelling within variability, an investigation of the way in which those variables influence the properties (resistance to pression) of the finger cushion itself may be undertaken. Also, the feasibility of finding a generally applicable density depends on the results of hypothesis 1d, since if the densities depend on the particular minutia configuration, no such generally applicable distribution can be found. The results on this hypothesis (and the subhypotheses) are inferred from the results obtained in section 4.5 of chapter 4.

Hypothesis 1d: Within finger variability depends on the number and positioning of minutiae

From the fact that the score is a proximity measure and some preliminary observations, it has been seen that the score obtained in comparisons will lessen when the number of minutiae decreases. It is also thought that it is possible that it decreases if those minutiae are grouped in a way that is not particularly discriminating : ridge endings in the delta region for instance. The way in which scores are computed is unknown: however, the AFIS used is reliable (Wilson et al., 2003). This leads to the expectation that the scores obtained vary logically with the increase in the number of minutiae, and can indicate whether some configuration is very similar to the configuration it is compared to, as well as some weight of this similarity. Indeed, if we accept that some configurations are less discriminant than others, it would be logical that the more discriminant ones yield higher scores. This hypothesis is tested in chapter 4, sections 4.4 and 4.5.

Hypothesis 1e: Repetitions of inked prints show variability and should also be used for the description of within variability

Rolled prints are subject to easily discernible distortion effects (see figure 3.2). In figure 3.2 these are particularly visible in the upper part of the prints. Whether this

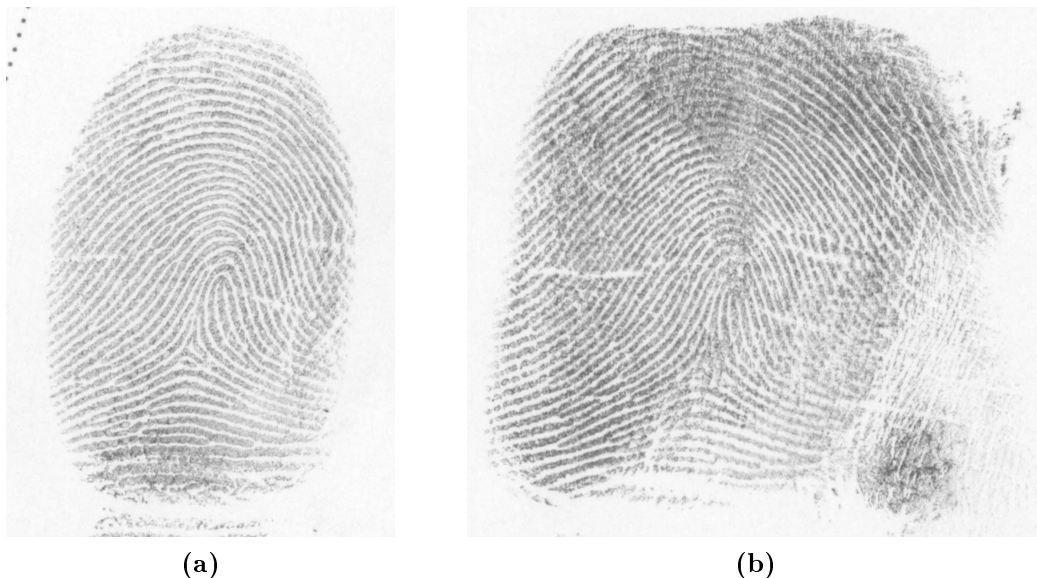


Figure 3.2: Slap (a) and rolled print (b) from a ten print card

distortion leads to variability, and how the variability due to prints compares to the one observed in marks is tested in hypothesis 1e.i. The remainder of hypothesis 1e concerns how to handle this variation due to inked prints.

Hypothesis 1e.i: Scores issued from the comparison of one mark to several rolled inked prints show variation

This hypothesis is tested in section 4.3 of chapter 4. Furthermore, the importance of this variation is compared between marks and prints. It is important to know not only whether the prints show variation, but also whether the variance in scores due to this variation is comparable, smaller or larger than the variance in scores due to the variability of marks. The remainder of hypothesis 1.e intimately depends on the results of this first hypothesis: if repeated inkings show much less variation than marks, it is not feasible to decrease the number of marks acquired by using more prints, nor to compare the number of marks to the same number of prints. These methods would both artificially decrease within-finger variability, since in this case, the suspect's inked print could be thought of as being simply a good (and therefore constant) representation of the finger surface.

Hypothesis 1e.ii.: the number of marks used can be decreased when the number of rolled inked prints is increased

It has been determined that variation was present in the rolled inked prints of a given finger. It is considered here that if such variation is present, there is no reason to consider the one inked suspect's print as a given, and that therefore several inked prints must be used. If this is considered to be true, there are two ways of using the information obtained from repeated rolled inked prints:

1. Use the same number of marks as determined in the testing of hypothesis 1a, and compare them to the same number of rolled inked prints, leading to n^2 comparisons.
2. Decrease the number of marks used, and obtain n comparisons overall.

The second option is the one tested here. Also, if the increase in the number of prints used sensibly reduces the variability present in the within-finger distribution, it does not seem reasonable to use quite as many inked prints as marks. This hypothesis is tested in chapter 4, section 4.3.2 on page 81.

Hypothesis 1.e.iii.: marks can be replaced by the same number of slaps or livescan images

This hypothesis is rather a reformulation of the general hypothesis 1b in view of the results of hypotheses 1e.i and 1e.ii: it is not self-evident that if these kinds of impressions could replace the total number of marks, that they can also replace the potentially reduced number of marks after the non-refusal of hypothesis 1b.i. This hypothesis is tested in the same section (4.3.2) as hypothesis 1e.ii.

3.3.2 Hypothesis 2: Between finger variability can be modelled by a generally applicable probability density function

Hypothesis 2a: The density used for modelling the between finger variability becomes stable as a given number of observations is reached

An evaluation of the evolution of the between-variability distribution as the database for between-variability increases is necessary, since it is thought that above a certain number of tenprint cards, this density will remain stable, and that this number is smaller than the database available. Again, and for the same reasons of robustness as in 1a, it is necessary to reach that stage. If this is not possible, at least the evolution of the between variability can be monitored. This hypothesis has been tested in chapter 5, section 5.3.

Hypothesis 2b: Between finger variability is independent of general pattern and finger number

The scores obtained when comparing a mark to the database containing only prints from other fingers than the one having left the mark may or may not be influenced by the fact of choosing only comparisons from fingers which show the same general pattern and / or which are from a finger with the same number. This hypothesis will be tested for different regions of the finger: it is for instance possible that it cannot be refuted for minutiae arrangements situated in the periphery, but that it can be refuted for minutiae arrangements from the delta area. Chapter 5, section 5.4 presents the testing of this hypothesis.

Hypothesis 2c: Between finger variability depends on the number and placement of minutiae

As in hypothesis 1d for within-finger variability, it seems reasonable to expect distributional differences between scores obtained for highly discriminant minutiae configurations with respect to configurations that are less discriminant. Here, however, scores are expected to decrease as the minutia number increases or for more discriminant configurations. These hypotheses are tested in section 5.5 of chapter 5.

Chapter 4

Within-Finger Variability

4.1 Introduction

The assessment of within-finger variability is an important part of this thesis. Fundamentally, this chapter will help to address the question whether the distribution of scores obtained when comparing marks to prints from the same source is generalizable or not. It will also clarify how within-variability samples should be acquired be it for such a generalizable distribution or on a case-to-case basis. It is grouped according to hypotheses, where the samples used for the testing of these hypotheses as well as the results are presented together. In the cases where one sample has been used for the testing of several hypotheses, it is described only the first time. Samples are presented first by the description of the images. Furthermore, the minutiae marked on these images are shown and described. Finally, the comparisons used are defined. The final sample is the data obtained when comparing the minutia sets chosen on the images to the comparison prints. Some of the following results have been the subject of a Master thesis (Egli, 2005), and these will be declared.

4.2 Evaluation of sample size

4.2.1 Material and Methods

Images

It has been tested how many observations are necessary in order to obtain a robust distribution. For this, livescan images have been used, and this sample size will determine the number of developed marks to be acquired. Sample size determination was done in the course of a master thesis (Egli, 2005).

704 images of the right thumb of one female donor have been acquired using a livescan device (Smiths Heimann Biometrics, ACCO 1394). These images have a resolution of 500ppi and are in bitmap (.bmp) format.

These 704 images are acquired under four different distortion and pressure conditions. 64 series of 11 images each have been acquired in two different sessions,

using 11 different directions of distortion. Ten of these directions of distortion are illustrated in figure 4.1. The 11th position was central without any intentionally introduced distortion.

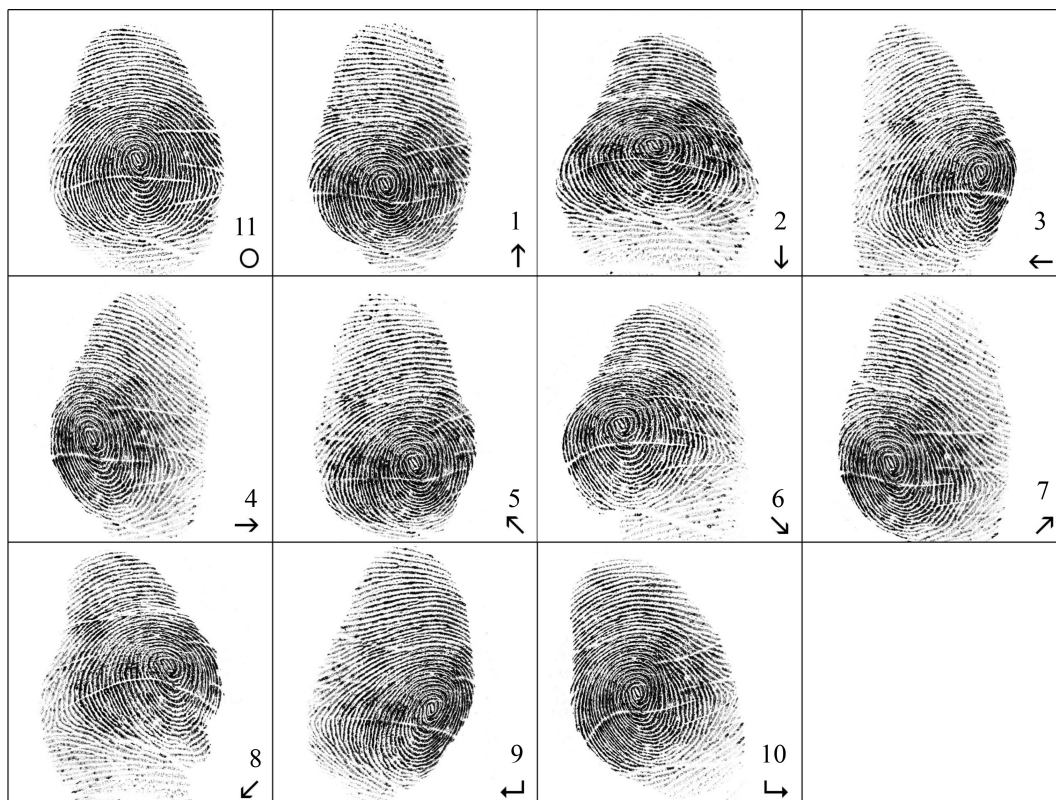


Figure 4.1: Schematic representation of the directions of distortion. Image courtesy of A. Anthonioz

The four pressure and distortion positions were normal and extreme distortion at 50g and 100g pressure. The four different sampling conditions are therefore:

- A : normal distortion at a pressure of 50g
- B : normal distortion at a pressure of 100g
- C : extreme distortion at a pressure of 50g
- D : extreme distortion at a pressure of 100g

Extreme distortion is obtained by moving the finger on the livescan device in the direction opposite the intended distortion direction. Afterwards, the finger is moved back rapidly in the intended direction. As those two movements together result in more constraints on the finger, they cause more distortion. For each condition, 8 series of 11 images were acquired on two separate days, resulting in 704 images. In order to be able to get scores, a comparison image was chosen, an inked print of the same finger. However, two images have been excluded, and results are therefore based on 702 scores.

Minutiae configuration

A minutiae configuration of 6 minutiae has been chosen and is illustrated in figure 4.2. Since the configuration of six minutiae had been chosen arbitrarily (but in a



Figure 4.2: Illustration of the fingerprint with the initial configuration of 6 minutiae

way that left the minutiae grouped), some of the minutiae were not visible on many livescan images. It can already be seen on figure 4.2 that these minutiae are very close to the edge of the part of the inked print that is actually reproduced; therefore another configuration of 6 minutiae has been chosen and is shown in figure 4.3. This particular configuration has been chosen for proximity to the center, as well as not being influenced by the delta area. The minutiae chosen are grouped, none has been left out inside the perimeter determined by the minutiae. Furthermore, the minutiae are alternating in orientation in the ridge flow. The minutia configuration has, in all cases, been automatically coded in a first step. In a second step, minutiae were manually corrected; all minutiae that are not part of the selected configuration have been erased in the impression inserted on the 'mark' side of the AFIS, and the presence, placement and orientation of the minutiae included in the configuration have been checked on that impression.

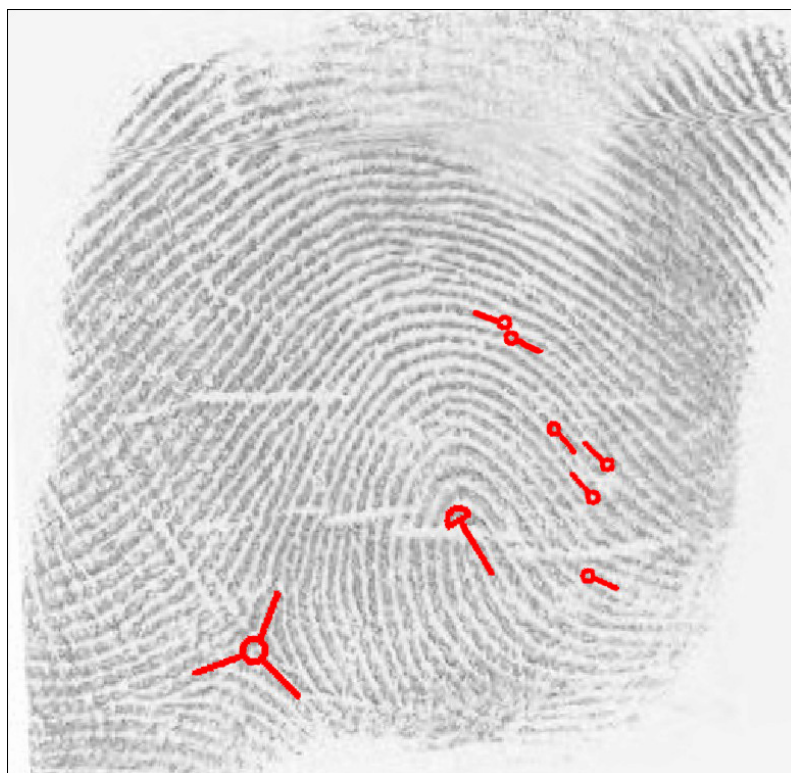


Figure 4.3: Illustration of the fingerprint with a new 6 minutiae configuration, called hereafter the first configuration

AFIS comparisons

The AFIS used for this study allows the extraction of the comparison scores between a list of marks and a list of prints. In the database, these two types of impressions are very much distinct and stored separately. The scores are a measure of proximity between two sets of minutiae, one from the mark and one from the print. The system is optimal for the case where the minutiae on the mark are a subset of those of the print; the set of minutiae compared is the one noted on the mark. The score is the proximity measure between that set of minutiae and the most similar subset on the print. One of the important criteria in the calculation of the score is the presence of a minutia which is on the mark and on the print. The absence of a minutia on the print which shows on the mark is penalized (decreases the score), since the print is considered as a complete reproduction of the finger surface, or at least a more complete reproduction than the mark. The penalty (again, in the sense of a decrease in the score) is less if a minutia which is on the print is not on the mark. The absence from the mark of minutiae present on the print is expected, since the mark is an less perfect reproduction of the skin surface.

In this study, the livescan images have first been introduced as prints and one corresponding rolled inked print is chosen among those already in the database and used as a mark. Minutiae configurations have then been selected (marked) on

the inked print. This allows to save a lot of time, since it avoids the repetitive annotation of the minutiae considered on all livescan images. These minutiae have, in this initial phase, not been checked on the livescans (inserted as 'prints' in the AFIS in this step). Scores are different if the subsample of minutiae is chosen on the mark and compared to a complete inked print or if all visible minutiae are marked on the mark and a subset selected on the print. In the second case, the score is naturally lower, for the reasons exposed above. It is considered at this point that this will have no influence on the sample size needed for stable estimation of the scores' distribution. The results thus obtained have been checked using 2 samples of livescan images that were annotated with the 6 minutiae used and compared to a single fingerprint (see figure 4.4). In these two verification samples, after the

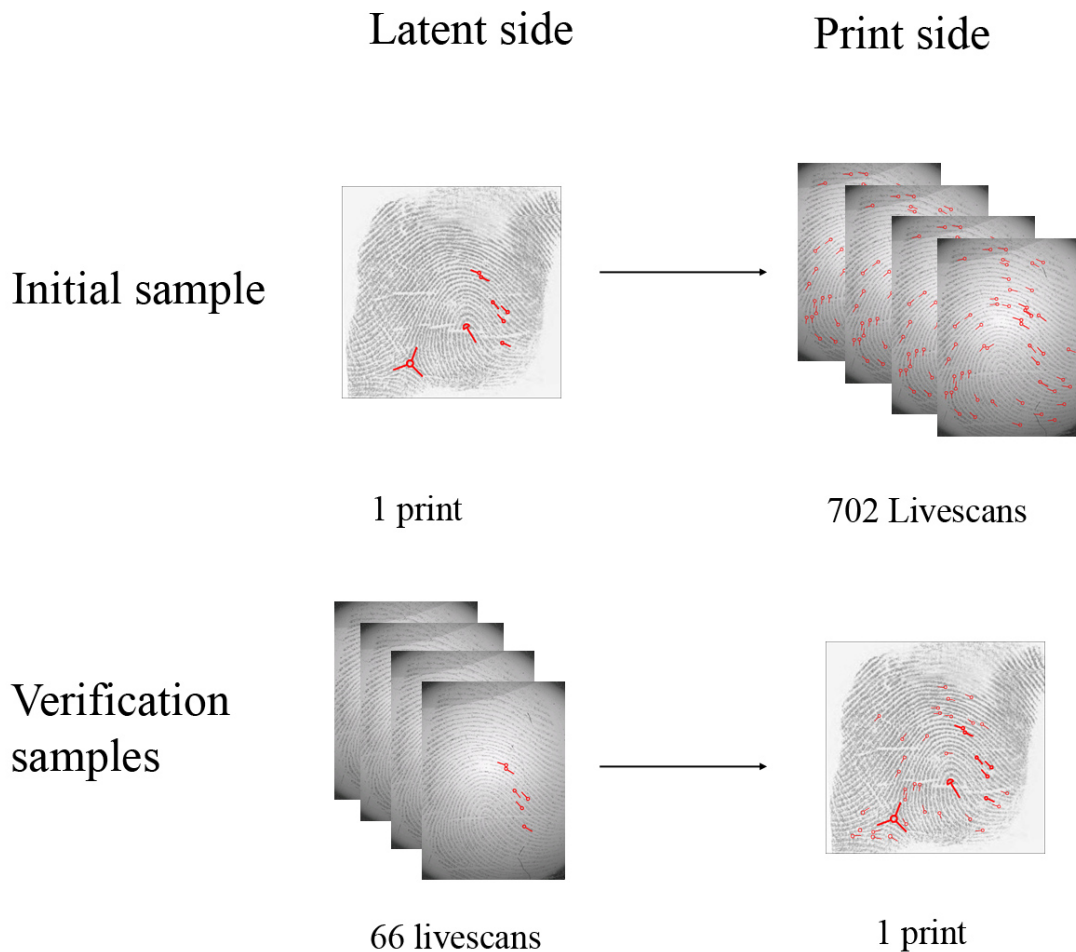


Figure 4.4: Schematic representation of comparisons used

automatic coding for the print as well as the livescans, the presence (as well as the position and orientation) of the minutiae on all impressions used has been verified, and corrections to the automated coding were carried out when necessary. While for

the livescans (inserted as marks into the AFIS in this phase) all minutiae not part of the selected configuration have been erased, on the inked print all minutiae found by the automated extraction are kept; the only two operations carried out on prints are the addition of minutiae missing among those from the selected configuration and the modification of minutiae that are part of this configuration if their placement or orientation does not correspond to what would normally be expected.

If a stable distribution is obtained for less than 702 scores, the hypothesis that the particular number of scores needed is sufficient will be tested by selecting the minutiae set investigated on two subsamples including that number of livescans rather than the print, and comparing the results on these two subsamples. It is considered that if those two random samples also show a good correspondence between each other, the population is considered to be well represented by them.

Quantile-Quantile plots

Quantile-Quantile (QQ-plots) or probability plots (Barnett, 1975; Hyndman and Fan, 1996) will be largely used for the visual evaluation of fits between distributions throughout this thesis. They show the quantiles of the sample against theoretical quantiles, or the quantile of one sample against the quantiles of another sample.

If $F(x)$ is the cumulative distribution function (which can either be empirical or a theoretical distribution) and $0 < p < 1$, the quantiles of a distribution are defined as $Q(p) = F^{-1}(p) = \inf\{x : F(x) \geq p\}$. p is based on the sample of observations. It is a vector of length n (the sample size), starting at $\frac{0.5}{n}$ and going in steps of $\frac{1}{n}$ up to $\frac{n-0.5}{n}$, where n is the number of observations in the sample. p may change in function of the programs used, since these are the plotting positions, and there is no unique rule concerning how these should be chosen. This plot is therefore a graphical representation of the samples' observations against either the theoretical quantiles of the chosen function or of the sample quantiles of two samples. Deviations from a straight line indicate a bad fit be of the observed to the theoretical distribution, or between the distributions of the two compared samples. When two samples are plotted against each other, the values plotted are the corresponding percentiles of the samples (in Matlab[®], the percentiles are again derived from p). In this case of comparison between two empirical samples rather than between a sample distribution and a theoretical distribution, the number of observations n used is the one in the smaller sample). The theoretical quantiles for the Weibull distribution are $\hat{Q}(p) = \log(\frac{1}{1-p})$.

4.2.2 Results

Results on the 704 livescans

Description of the data

The histogram for the 6 minutiae illustrated in figure 4.2 shows a very long tail with one bin between 1000 and 1050 containing a large proportion of observations (see figure 4.5). The marks resulting in these relatively low scores have been investigated,

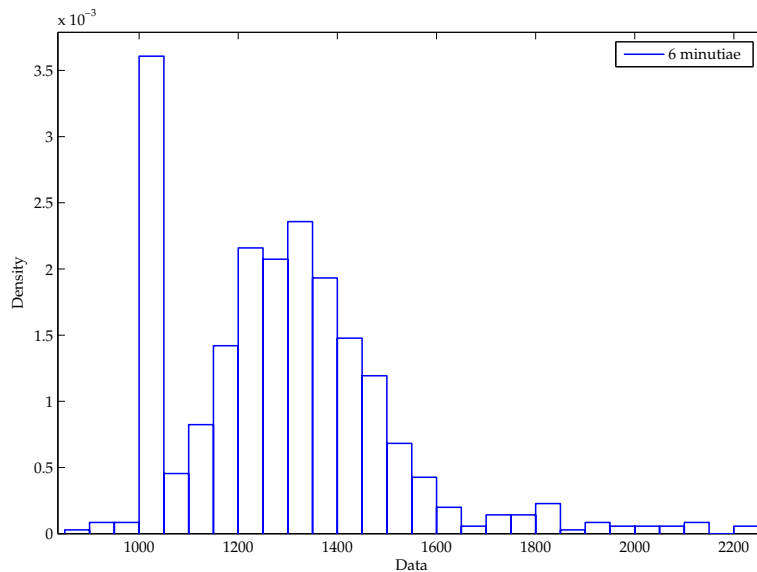


Figure 4.5: Histogram of scores for 6 minutiae

and it has been verified that one of the six minutiae is absent in many of these images. This absence of this particular minutia is most frequently observed in distortion positions 4 and 9. Several options were possible:

1. consider this variation as a part of within-finger variability. This option has not been retained because the goal of the study is to aid, in the end, an examiner who asserts a correspondence of a given number of minutiae. The within-variability considered here therefore needs to be the variability of a given minutiae arrangement when all points are visible.
2. eliminate all marks not showing one or more minutiae from the arrangement examined. This is a valid solution, even though it decreases sample size.
3. choose another minutiae arrangement, farther away from the edge of the print. This solution has been chosen, although the procedure offers no guarantee that all minutiae will be present on all 704 livescans.

A new minutiae configuration has therefore been selected, and is the one shown in figure 4.3. After verification of presence of minutiae, 2 images had to be excluded.

The sample used is therefore of 702 images showing the complete new 6 minutiae configuration. A histogram has again been created. However, since bin rules have

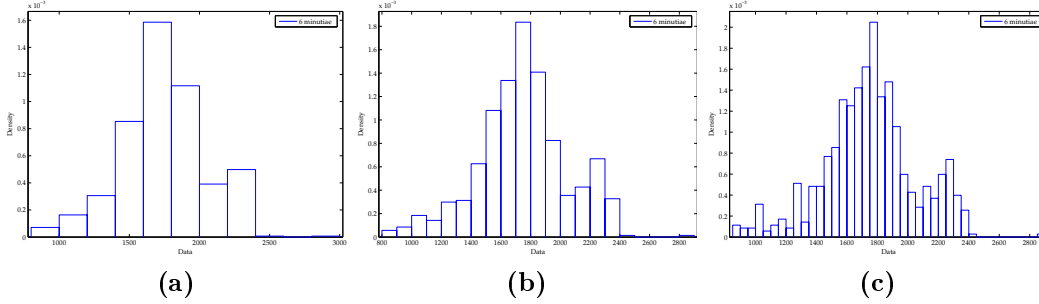


Figure 4.6: Histogram of scores for the second 6 minutiae group using the Sturges (a), Scott (b) and Freedman-Diaconis Rules (c) respectively

some influence on the aspect of this histogram, three different rules have been used for the establishment of the number of bins, respectively the Sturges (Sturges, 1926), Scott (Scott, 1979) and Freedman-Diaconis (Freedman and Diaconis, 1981) rules (see table 4.1 for these rules on bin width).

Table 4.1: Bin width in histograms according to three rules

Rule name	Bin width
Sturges	$h = \frac{R}{1+3.322\log_{10}(n)}$
Scott	$h = 3.46 \cdot s \cdot n^{-1/3}$
Freedman-Diaconis	$h = 2 \cdot IQR \cdot n^{-1/3}$

Here, R is the range of data, n the number of observations in the sample, s the standard deviation, and IQR the interquartile range ($q_{0.75} - q_{0.25}$). Also, the Sturges rule can be re-written as $h = \frac{R}{1+\log_2(n)}$. The resulting histograms are shown in figure 4.6. The number of bins computed according to these three rules are 11 (Sturges), 17 (Scott) and 27 (Freedman-Diaconis). The distribution is bimodal for this 6-minutiae arrangement. This bimodality is also visible on the plot of the empirical cumulative distribution function (figure 4.7), where the distribution first tapers off and starts to increase again between 2000 and 2200. Below this point, the distribution function is very regular. The source of this bimodality may lie in the sample acquisition methodology and does not have to be due to natural variation of repeated appositions of fingerprints.

The distribution of distortion directions in the second small mode of the distribution is shown in figure 4.8a), and shows that two positions are over-represented in these high scores. These positions are 3 and 8, both of which are the result of distortion movements towards the left (3 is from right to left, and 8 is from the

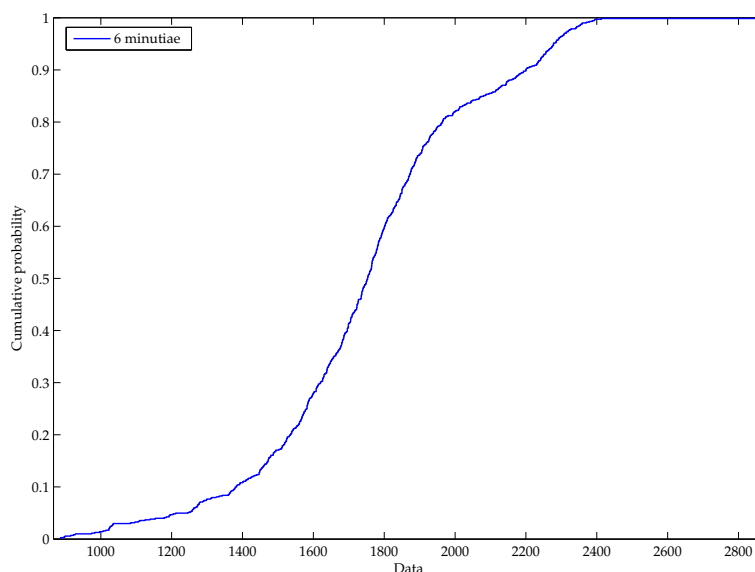


Figure 4.7: Empirical cumulative distribution function of all samples for 6 minutiae

upper right to the lower left corner). On the scatterplot in figure 4.8b), it can furthermore be seen that position 8 has higher scores and is more frequently observed in this second mode: it can therefore be assumed that this second mode is due to the choice of the 6 precise minutiae in the lower left quadrant of the fingerprint. Unfortunately, at this time, no information concerning the distribution of distortion directions in fingermarks is available. Such a distribution would allow the weighting of the results for each direction, which is at present uniform, according to it. It is quite probable that some directions are more frequent than others when objects are used normally, but the observation of this normal use is far from trivial. At this time, it is therefore not known whether, as a result of the distribution of marks, there should be such a second mode in the distribution, nor whether there should be several.

An Analysis of Variance (Anova) applied to the observed scores and the categorical variables distortion direction (X1), condition (X2) and day (X3) confirms the influence of the distortion direction on the scores obtained (see table 4.2). These p-values (noted as Prob > F in tables 4.2 and 4.3), even though they are based on the assumption of equal variance, normal distribution and independence of the disturbances, are very indicative of an effect of direction and day and absence of influence of condition. In particular, the independence assumption is not violated here, and the method is robust to modest violations of the first two assumptions.

When all interaction effects are taken into account (table 4.3), the result for those factors is still the same, and only the interaction effect between the two factors which have an effect (X1 and X3, corresponding to distortion direction and day of acquisition) is significant at 5%.

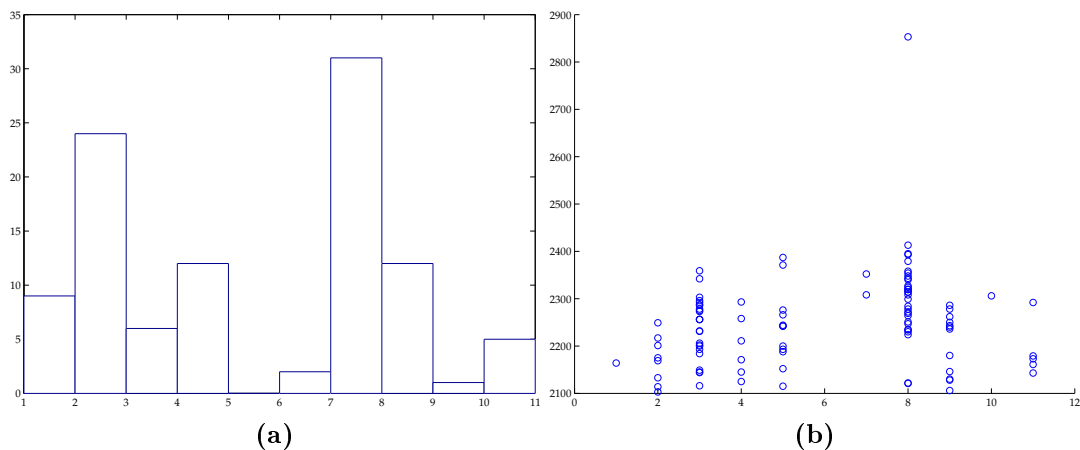


Figure 4.8: Investigation of distortion direction in higher mode (in terms of score)

Table 4.2: Analysis of Variance without interactions

Source	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
X1	11880113.3666	10	1188011.3367	7.6944	9.9238e-12
X2	188221.4801	3	62740.4934	0.40635	0.74848
X3	2784164.5622	1	2784164.5622	18.0323	2.4705e-05
Error	106226251.4954	688	154398.6214		
Total	121087275.6899	702			

Table 4.3: Analysis of Variance with interactions

Source	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
X1	11890893.247	10	1189089.3247	8.0203	3.2173e-12
X2	192478.7671	3	64159.589	0.43275	0.72962
X3	2773353.7027	1	2773353.7027	18.7061	1.7791e-05
X1*X2	5425686.4243	30	180856.2141	1.2199	0.19683
X1*X3	3136087.8723	10	313608.7872	2.1153	0.021575
X2*X3	374322.9272	3	124774.3091	0.84159	0.47139
X1*X2*X3	6094397.4112	30	203146.5804	1.3702	0.092214
Error	91179627.6786	615	148259.5572		
Total	121087275.6899	702			

The boxplot shown in figure 4.9a) shows the influence of the distortion directions 1 to 11 on scores. Both the mean and the variance vary according to the direction in which the distorted livescans have been acquired. This observation is verified by the Anova, where this variable has an influence. The lack of influence of the variable 'condition' is shown on the boxplot (figure 4.9b); all four boxplots, where each corresponds to a given pressure combined with extreme or normal distortion, are centred around the same score values, and the width of these boxplots is also similar. The boxplot of scores according to the variable 'day' (figure 4.9c)) does not show the differences that the Anova indicated in these overall results; either the effect detected in the Anova is due to violation of the assumptions of this method, or it cannot be seen in the overall results, because the distribution of observations changes for each distortion direction by day. This is indeed the result of the boxplot shown in figure 4.9d).

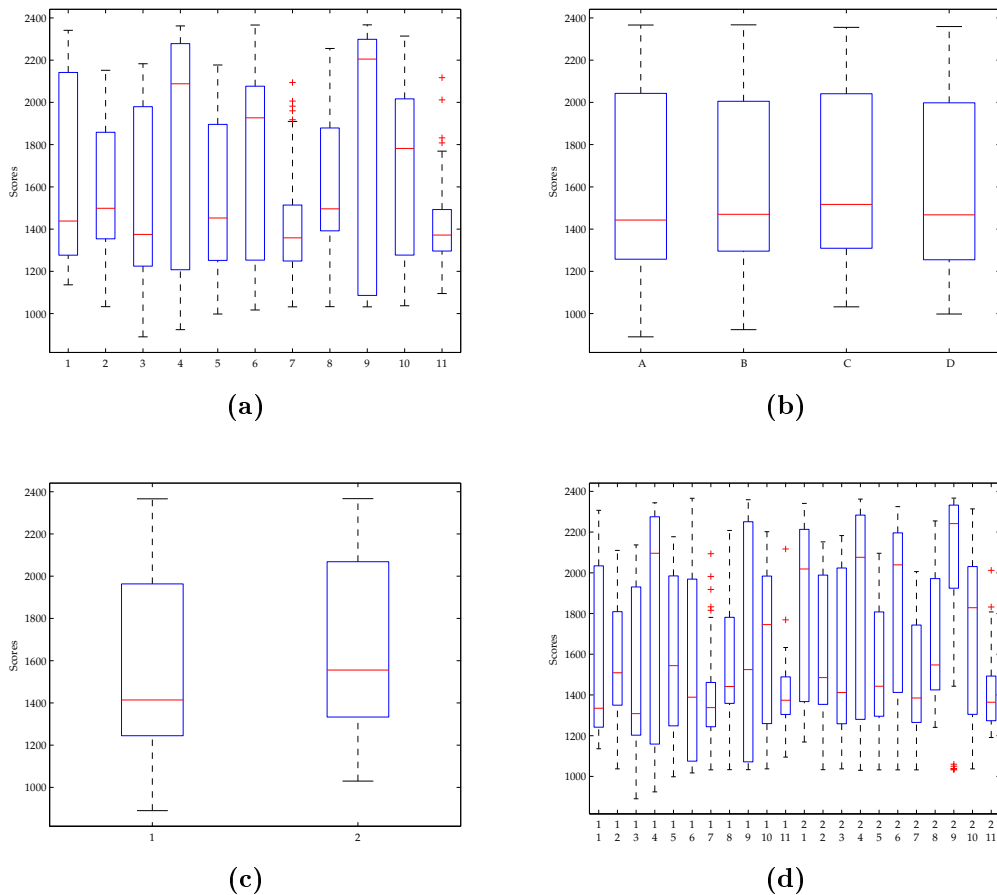


Figure 4.9: Boxplots of the results divided by the variables a) distortion direction b) condition c) day and d) the two conditions day (top x-axis indication) and position (bottom x-axis indication)

An influence of the acquisition conditions was, in opposition with these results, expected. More distortion is visually observed in the 'extreme' conditions B and D and pressure is subjectively expected to influence the way a finger moves across a surface. This absence of influence on the scores does not mean, however, that there is no effect on distortions as such. It only means that the *scores* are not influenced; this may be due to the way the AFIS computes these scores.

On the other hand, the variable 'Day' was not expected to influence the scores. The reasons for this variable having an effect may be the substances deposited from the skin to a surface, which are known to vary even on a given day. As a livescan has been used as an acquisition device, this variation was not expected to reproduce on the images and, a fortiori, the scores. Another reason may be a learning effect, since the protocol is quite complicated for the donor of the fingerprints. On the boxplots, the influence of variable 'Day' on the scores is not well visible, even though scores on day 2 seem to be slightly higher. Finally, the boxplot of day * condition, again fails to show clearly an influence of the day overall, however when comparing for a given position the boxplots of day one to the one from day 2, scores are mostly a little bit higher on day 2.

In view of these results, **stratified sampling will be used, where a fixed number of fingerprints will be chosen by day and by position**. No separate modelling for each distortion direction will be used, since results will need to be given for 'within-variability' rather than 'within-variability when the direction of distortion is given'. This decision, however, may need to be reviewed depending on results on developed marks, and be put into question for real cases, where the direction of distortion might be determined on the mark recovered and being evaluated.

Sample size

In order to estimate the sample size needed for a reliable estimation of within-finger variability, the initial sample (acquired as shown in the upper part of figure 4.4) has been randomly divided into 2, 4, 8 and 16 parts (including 351, 176, 88, and 44 samples). One of each of these subsamples has been visually compared to the distribution of the 702 scores, and to another of the samples. Some of the results are shown below in figure 4.10 in the form of Quantile-Quantile-plots. On these QQ-Plots it can be observed that down to 88 observations (1/8th of the total sample) the results of the subsample are a good representation of the results obtained on 702 scores. However, even though the plot (in figure 4.10 d) of the sample containing 44 observations does not show very bad fit, when comparing two of these samples, it seems clear that reproducibility of the distribution is not reached anymore with a sample of 44 observations. More than 44 observations are therefore needed, and 88 are sufficient. Since the observations from the Analysis of Variance have shown how the subsample to be drawn has to be stratified by day and position, two possibilities for sample size remain: 66 or 88 observations.

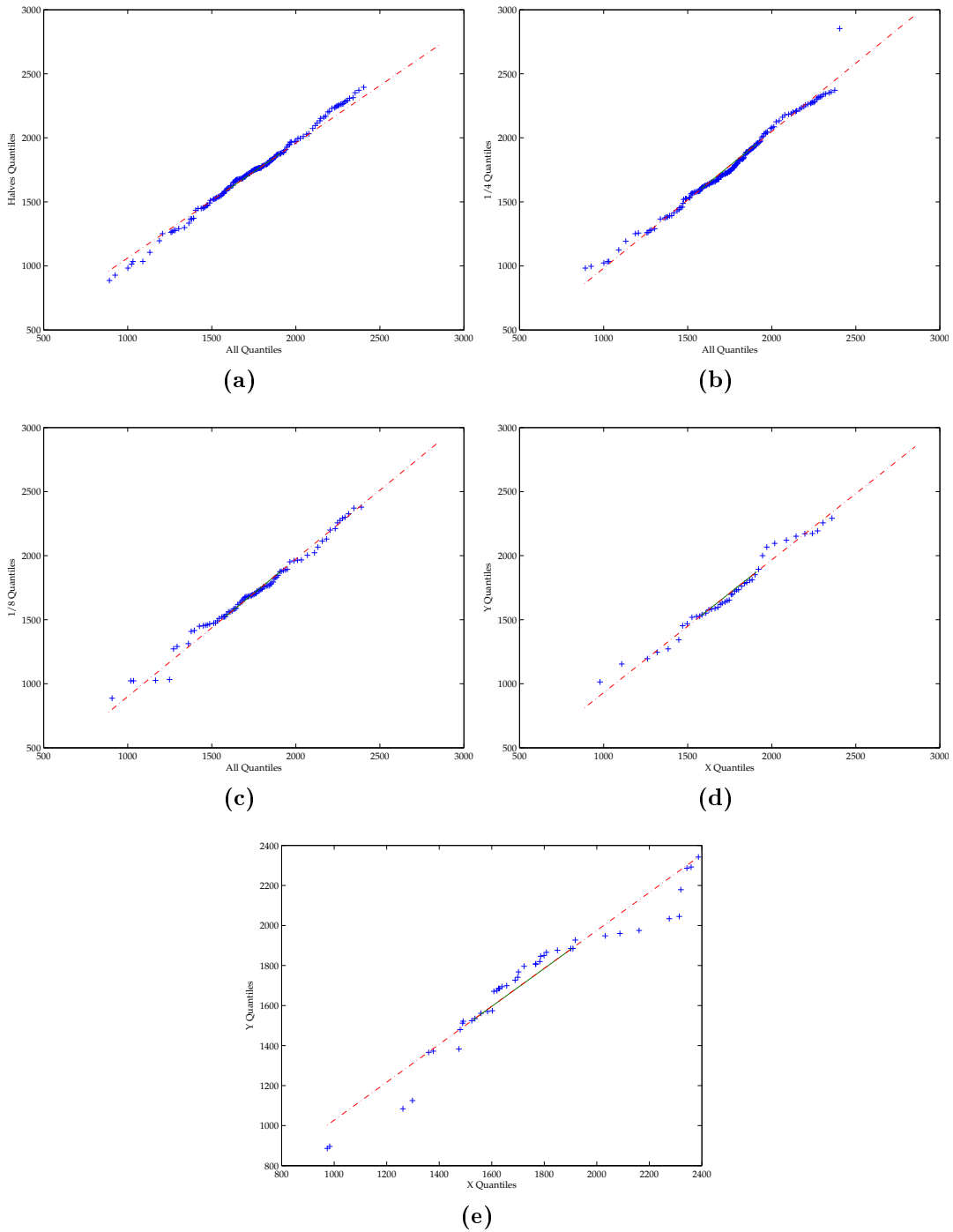


Figure 4.10: Quantile-Quantile plots for decreasing sample sizes: a) 1/2, b) 1/4, c) 1/8, d) 1/16, and e) two samples containing 44 observations

Two subsamples of the 702 results obtained have been drawn without replacement, containing each 66 observations. Two observations have been excluded, and the second sample has also been adjusted to this new sample size of 66 observations. A QQ-plot has been drawn using these two samples in order to see if such a sample may suffice to obtain a similar distribution twice. The result is shown below, in figure 4.11. The two samples are considered to show that they are from the same distribution, and **a sample size of 64 will therefore be used for the rest of this study**. Two verification subsamples of the livescan images, containing 66

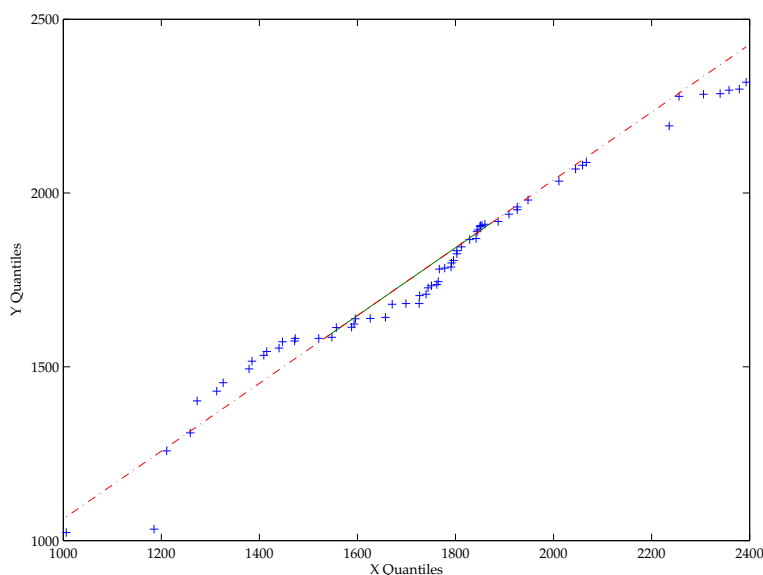


Figure 4.11: QQ-plot of two subsamples containing 66 observations

observations each, have therefore been drawn, where each contains 3 observations per position and day, and the 6-minutiae configuration has been annotated on these 132 livescans. The scores of these verification samples have then been extracted according to the lower part of figure 4.4. This is for the reason mentioned in 4.2.1, that scores change if the smaller number of minutiae is noted on the image considered as the mark or on the print. Where up to now results were based on comparisons where the smaller number of minutiae was on the print, from now on the subset of minutiae will be marked on the mark (which is substituted here by livescans). These two samples, called Sample 1 and Sample 2 hereafter, will be used for modelling, the first for the establishment of the model and the second for verification purposes.

Results on subsamples

The QQ-plot comparing these two samples (figure 4.12) does not contradict that this sample size is sufficient, even though a departure from the ideal diagonal is present.

In order to compare these results, obtained on livescan images, to results obtained

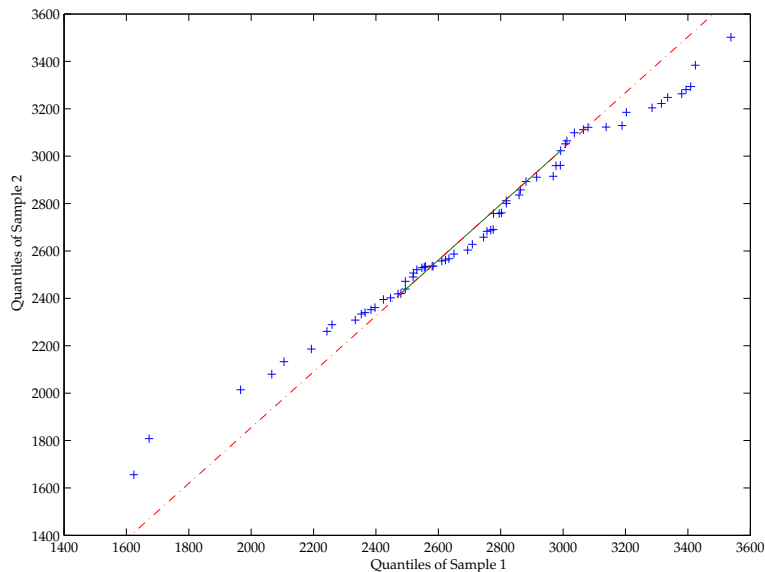


Figure 4.12: Comparison between samples 1 and 2

using marks, at least 66 marks are therefore needed. Generally, it will from now on be considered that a sample size of 66 different images for the mark is sufficient. This is not equivalent to considering that 66 different scores are sufficient. Up to now, the 66 scores used were based on the comparison between one configuration marked on a inked print to 66 configurations marked on different livescan images; this is the current minimal standard. In the following section, comparisons will be carried out to see whether the number of images used to obtain 66 scores can be decreased. This could be achieved by using more than one inked print and compare the configurations marked on these prints to a smaller number of 'mark' configurations.

4.3 Comparison between marks, livescan images and rolled inked prints

In this section, it will be investigated whether the images used for the modeling of within-finger variability must be from marks detected using frequently used techniques or whether less time-consuming methods can be employed for the acquisition of within-finger data. Also, it will be determined whether the variability observed in marks is different from that in livescan images. Indeed, it is thought that the way that the minutiae positions vary is more random in marks than in livescan images, that only show distortion. This is because distortion is a rather smooth process, at least locally. Therefore, minutiae in a configuration will have a tendency to spread out, for instance. Differences in minutiae placement due to detection methods are

thought to be less smooth: a bifurcation could, for instance, not be completely detected and therefore seen on the image as a ridge ending. This would introduce a position that differs with respect to the neighboring minutiae. These neighboring minutiae would not necessarily be subjected to the same effect; therefore, the distances between minutiae could vary more randomly.

4.3.1 Material and Methods

Data

Marks have been acquired using four different detection techniques: powdering and cyanoacrylate fuming for nonporous surfaces, and 1,8-diaza-9-fluorenone (DFO) as well as ninhydrin for porous surfaces. The solutions used were prepared according to Margot and Lennard (1994). The surfaces used were the inscriptible surface of CDs of different brands and white photocopy paper (Xerox[®] Business Paper, 80 $\frac{g}{m^2}$). No particular distortion was introduced on these marks. The number of marks showing all minutiae used is different for each detection method (see table 4.4), due to the complications presented by deposition and detection of marks. More marks than those mentioned here had been deposited, but some of these were not, after detection, of sufficient quality or did not show all of the selected minutiae.

Table 4.4: Number of marks showing the configuration of interest acquired for each method

Method	Number of marks
Cyanoacrylate	29
Powder	30
DFO	24
Ninhydrin	25

Furthermore, the two verification samples of livescan images used in section 4.2 has been used in order to compare results obtained on livescan images to those obtained on marks. Following initial results (see 4.3.2), a new sample of 64 livescan images in the central position has been annotated and used. Finally, 80 ten-print cards of the donor used have been established; while the rolled inked print is used on the print side, the slap impressions on the bottom of these ten-print cards have also been tested to see whether they can be used as substitutes for developed marks. Not all slaps and rolled impressions showed the chosen minutiae configuration properly. The comparisons used in the following sections are explained in table 4.5.

The finger used is again the right thumb of the same donor as the one used with the livescan. Also, the same 6-minutiae configuration as described in 4.2.1, and shown in figure 4.3, has been selected on the marks. Again, first, all minutiae were detected automatically. Then, all minutiae not part of the configuration were erased

4.3. Comparison between marks, livescan images and rolled inked prints

Table 4.5: Datasets used in this section (4.3)

Section	Marks	Prints	dataset name
Investigation of variance due to different rolled inked prints (p. 62)	24 DFO marks	24 rolled	
Modeling of the data (p. 64)	2 samples of 66 livescan images	1 rolled	
	4*22 marks	15 rolled	
Comparison between marks and livescan images step 1 (p. 72)	1 sample of 66 livescan images	1 rolled	
	4*22 marks	15 inked prints	
Comparison between marks and livescan images step 2	1 sample of 66 livescan images	66 rolled	
	29+30+24+25 marks	66 rolled	
Comparison between marks and livescan images step 3	64 livescan images in central position	66 rolled	
	29+30+24+25 marks	75 rolled	
Detection Method (p. 75)	29+30+24+25 marks	66 rolled	All
	29+30+24+25 marks	1 rolled	AllMa1P
	1 mark	66 rolled	1MaAllP
	all marks from a given method	1 rolled	1Me1P
	all marks from a given method	66 rolled	1MeAllP
	all marks from a given method	same number of rolled	1MeFewP
	64 central livescan images	66 rolled	LS
	78 slaps	75 rolled	TP

on the marks. Finally, the minutiae configurations have been checked and corrected on the marks as well as the inked prints before carrying out the AFIS comparisons between the marks and rolled inked prints from the same finger. Now, the rolled inked prints of this finger from a total of 75 Ten-Print cards, which all show all six minutiae selected, have been used instead of a single rolled inked print.

A background database of 10000 ten-print cards has also been used for some computations involving LR's carried out in this chapter. A reasonably good fit to this between-finger data obtained when confronting marks to this database has been obtained using a lognormal distribution; this model has therefore been used here. Since at this point the between-variability (and the denominator) will be constant for comparisons between methods for the modeling of within-finger variability, no further description of this data is given at this point; please refer to chapter 5 for details on the data and modeling steps that have been undertaken for between-variability in a further stage.

In order to verify whether the variation in the scores due to the use of different inked prints has been verified using two-way Anova (Analysis of Variance). These results have been checked visually using histograms of the variances obtained when comparing one mark to several prints, and when comparing one print to several marks.

It has been decided to introduce a modeling step before the comparison between the different distributions of the datasets used. Distributions have been investigated in order to verify whether they fit the data. Two families of distributions were considered: the two-parameter Weibull distribution, and the Extreme Value distribution. The two-parameter Weibull distribution has the density

$$f(X|\alpha, \beta) = \frac{\beta x^{\beta-1}}{\alpha^\beta} \exp(-(x/\alpha)^\beta) \quad (4.1)$$

or, by substituting α by $\lambda = \alpha^{-1/\beta}$

$$f(X|\lambda, \beta) = \lambda \beta x^{\beta-1} \exp(-\lambda x^\beta) \quad (4.2)$$

The extreme value probability density function is

$$f(X|\mu, \sigma) = \sigma^{-1} \exp\left(\frac{x-\mu}{\sigma}\right) \exp\left(-\exp\left(\frac{x-\mu}{\sigma}\right)\right) \quad (4.3)$$

Modeling has been carried out using first of all QQ-plots. Since these plots do not allow a formal decision concerning the goodness of the fit (i.e. the affirmation that a sample has come from a given distribution), further tests have been carried out. Distances have been calculated between observed samples and the distributions which had been pre-selected using QQ-plots. These distances, between distributions p_1 and p_2 are:

The Bhattacharyya distance (Liu et al., 2007; Bhattacharyya, 1943):

$$D_B(p_1 \parallel p_2) = \sum_{i=1}^n \sqrt{p_1(i)p_2(i)}$$

The variational distance (Steel and Székely, 2006):

$$D_v(p_1 \parallel p_2) = \sum_{i=1}^n |p_1(i) - p_2(i)|$$

The harmonic mean (Liu et al., 2007):

$$D_m(p_1 \parallel p_2) = \sum_{i=1}^n \frac{2p_1(i)p_2(i)}{p_1(i) + p_2(i)}$$

The Kullback-Leibler distance (Kullback and Leibler, 1951):

$$D_{KL}(p_1 \parallel p_2) = \int_{-\infty}^{\infty} p_1(x) \log \left(\frac{p_1(x)}{p_2(x)} dx \right)$$

here, the discrete case has been used:

$$D_{KL}(p_1 \parallel p_2) = \sum_{i=1}^n p_1(i) \log \left(\frac{p_1(i)}{p_2(i)} \right)$$

The Jeffreys distance (Jeffreys, 1946), which avoids the fact that $D_{KL}(p_1 \parallel p_2)$ is unequal to $D_{KL}(p_2 \parallel p_1)$

$$D_J(p_1 \parallel p_2) = \sum_{i=1}^n p_1(i) \log \left(\frac{p_1(i)}{p_2(i)} \right) + p_2(i) \log \left(\frac{p_2(i)}{p_1(i)} \right)$$

Modifications of two of these distances are used; both the Bhattacharyya and harmonic mean measures should be 1– the measure reported above; in view of the evaluation procedure used for these distance measures (see below), the inclusion of this factor would add nothing. They have been calculated on the basis of the histogram of the sample data, using the Freedman-Diaconis rule (see table 4.1 for the determination of the bin width). For each observation $x(i)$, the frequency of the bin in which this observation was encountered was taken to be $p_1(i)$, the observed distribution. For p_2 , the cumulative distribution function ($F(X)$) fitted to the sample was considered; if the lower edge of the bin in which $x(i)$ is observed is e_j and the upper edge is e_{j+1} , $p_2(i)$ is

$$p_2(i) = F(e_{j+1}) - F(e_j)$$

In order to evaluate the distances thus computed, 1000 random samples of size n have been drawn from the distribution $f(X \mid \Theta)$, which had been fitted to the sample, and the distances between these samples and the theoretical distribution have been computed in the same way as for the observed sample.

For the evaluation of whether marks could be substituted by inked prints or livescan images, likelihood ratios have been computed using different within-finger variability datasets. These LR's have then been compared using a simple correlation

measure (see 4.4); this allows to evaluate whether LRs obtained using a within variability based on impressions other than marks correlate (e.g. behave in a similar way) with the LRs obtained on the basis of within variability estimated using mark-to-print comparisons.

$$R(i, j) = \frac{C(i, j)}{\sqrt{C(i, i)C(j, j)}} \quad (4.4)$$

where C is the (here: 2 by 2) covariance matrix between the LRs obtained from one and the LRs obtained from another within-finger dataset.

Then, in a second step, Tippett plots (Evelt and Buckleton, 1996) have been used in order to assess the differences due to these different data in the within-variability on the quality of the LRs obtained on this minutia configuration. Tippett plots are a visual representation of distributions of likelihood ratios obtained under each of the two hypotheses, H and \bar{H} . On such a plot, a function of the cumulative distribution functions of the LRs obtained under each of the hypotheses are plotted. The plotted functions are, indeed, $1 - F(\log_{10}(LR))$. For an example of such a plot, please refer to figure 4.24 on page 80. Such plots help assessing the overall system performance; they show whether the LRs obtained under the two hypotheses differ. The larger the separation between the two curves plotted, the better is the systems capacity of obtaining small LRs for comparisons under \bar{H} and large ones under H . Furthermore, the proportion of LRs above 1 obtained for observations under \bar{H} and the proportion of LRs below 1 under H can easily be assessed from these plots. These two proportions are called 'rate of misleading evidence in favour of the prosecution' or RMEP in the first case and 'rate of misleading evidence in favour of the defense' or RMED in the second case.

4.3.2 Results

Investigation of variance due to different rolled inked prints

The result of an Anova carried out on mark to print comparisons where marks were developed using DFO clearly shows that variance in the inked prints exists, that it is significant, and even of the same order of magnitude as the variance observed in the marks. The results reported (see table 4.6) are based on a random sample drawn from the inked prints, in order to have an equal number of observations when one mark is compared to prints, or one print is compared to marks.

When the variance observed for each of the marks (compared to the 24 prints) is compared to the variance observed for each of the prints (compared to the 24 marks developed using DFO), similar results are obtained (see figure 4.13). These plots have been checked for the other development techniques as well. While the results are not always exactly comparable with the figure shown here (for marks developed using cyanoacrylate, the variance due to prints is tendentially larger than that due to marks, while for ninhydrin developed marks the tendency is inverted), overall, the variance due to marks and due to prints is at least of the same order

4.3. Comparison between marks, livescan images and rolled inked prints

Source	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
Marks	$6.46 * 10^6$	23	280909	28.63	0
Prints	$6.13 * 10^6$	23	266412	27.15	0
Error	$5.19 * 10^6$	529	9813		
Total	$1.78 * 10^7$	575			

Table 4.6: Analysis of Variance of inked prints and marks

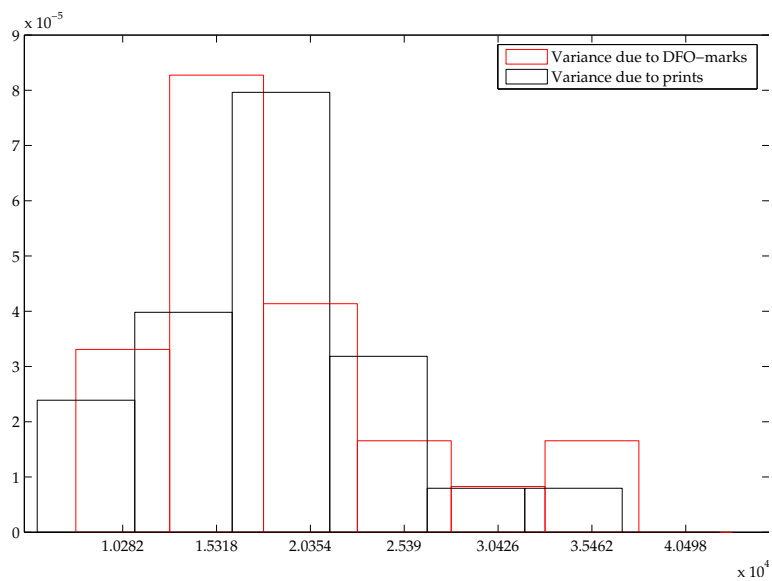


Figure 4.13: Histograms of variances within marks and within prints

of magnitude. And, **for all development methods, the results of the Anova show a significant effect due to the rolled inked prints. Therefore, several prints should be used.**

The variance in prints is most probably due to other sources than the variance observed in marks, although it is possible that in both cases it is due to the distortion introduced by the deposition. However, since there are most certainly distortion effects during the rolling of prints, these are here thought to be largely more important than the effects during the deposition of marks such as carried out here. Marks were deposited *without* introducing distortion on purpose. Due to the fact that therefore the variance observed is thought to be due to different phenomena, and that it is generally of the same order of magnitude between marks and between prints, as many prints as marks should be used for the acquisition of within-finger variability data.

Modeling of the data

The sample of livescan images

A Weibull distribution has been selected on the basis of the shape of the histogram of 66 observations of scores from livescan images. The histogram with the density superimposed, the Weibull probability plot and the empirical cumulative distribution functions (ecdf) for samples 1 and 2 of 66 livescan images each compared to an ecdf based on a random sample size 66, drawn from a Weibull distribution, are shown in Figure 4.14. Also included in this figure are the confidence interval of the ecdf based on the sample from the Weibull distribution. The distance measures have been calculated for these data, and the results are shown in figure 4.15. The random samples are based on a Weibull distribution with parameter estimations based on sample 1 (red line) which explains why sample 2 is systematically farther away of the mode of the histogram of distance measures.

All the distances observed on the samples of livescan images are highly likely according to the histograms of random samples distances (see figure 4.15). The Weibull distribution is therefore considered to be a good fit. Additionally, the fact that the distances obtained using sample 2 fall well within the distribution of distances indicates that these two samples come from a same population, which indicates that the conclusion on sample size from section 4.2.2 holds.

The sample of marks

Following the results obtained on livescan images, a Weibull distribution has again been fitted to the data obtained using developed marks. This distribution presents a reasonably good fit, although departures in the tail are visible (see figure 4.16a). An Extreme Value distribution has also been fitted, and the QQ-plot comparing the sample to this distribution can be seen in figure 4.16b), whereas the histogram with the fitted probability density function (pdf) is shown in figure 4.17a) for the

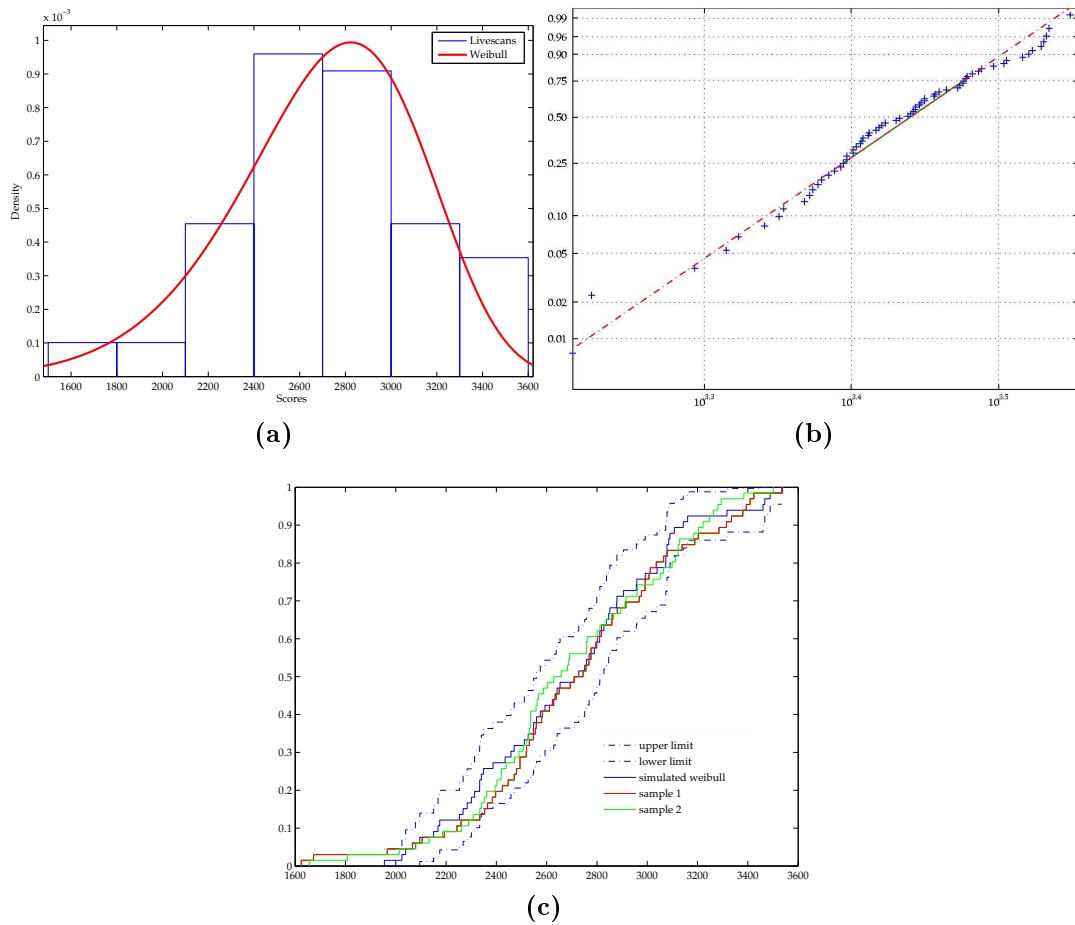


Figure 4.14: Fit of the Weibull distribution illustrated by a) the histogram of the sample and the Weibull density, b) a Weibull probability plot and c) the empirical cumulative distribution function (ecdf) of two samples of livescan images compared to a simulated Weibull ecdf with its upper and lower confidence bounds

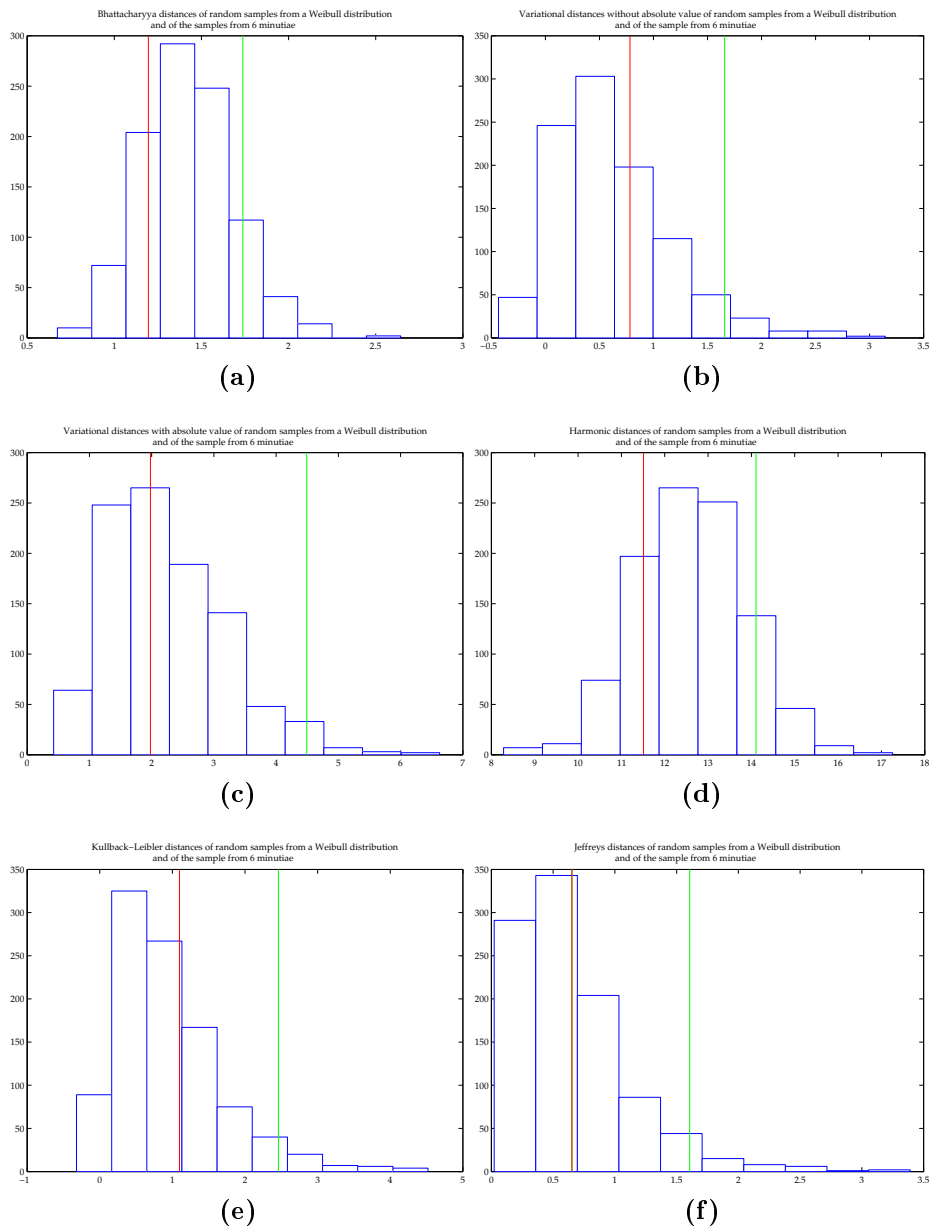


Figure 4.15: Distances to Weibull distribution for the first (red line) and the second (green line) sample of livescan images and random samples (histogram) where the distances are a) Bhattacharyya b) Variational distance without absolute value c) Variational d) Harmonic mean e) Kullback-Leibler and f) Jeffreys

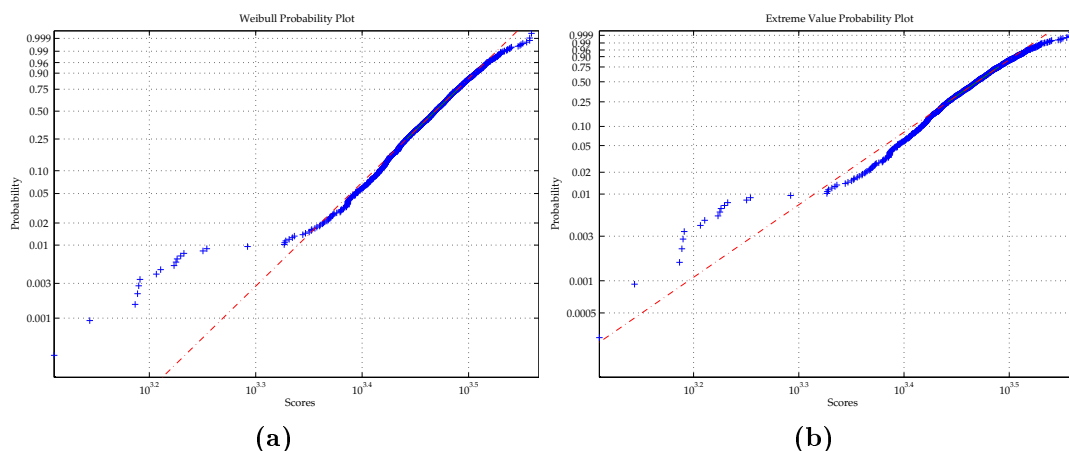


Figure 4.16: QQ-plot of the sample of marks and a) a Weibull distribution, b) an Extreme Value distribution

Weibull distribution, and in figure 4.17b) for the Extreme Value distribution.

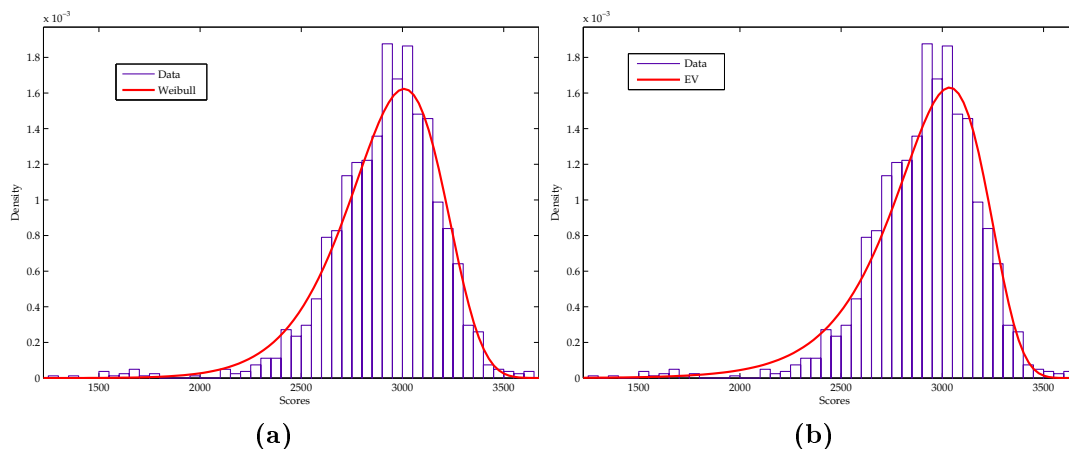


Figure 4.17: Histogram of scores from marks for 6 minutiae with a) the fitted Weibull pdf b) the fitted Extreme Value pdf

The QQ-plot against the Weibull is clearly more linear (see figure 4.16), however, the departure in the tail of the Extreme Value distribution is less important. Both distributions have been used for the computation of the distances, since both seem to fit the data quite well. In figure 4.18 the comparison between the samples distances to a Weibull distribution fitted using maximum likelihood estimation of the parameters and the histogram of distances obtained on 1000 random samples from the Weibull distribution with the parameters estimated from the sample are shown. These distances show no alarming difference between the theoretical and the observed distributions; two of them, however (the variational distance when no

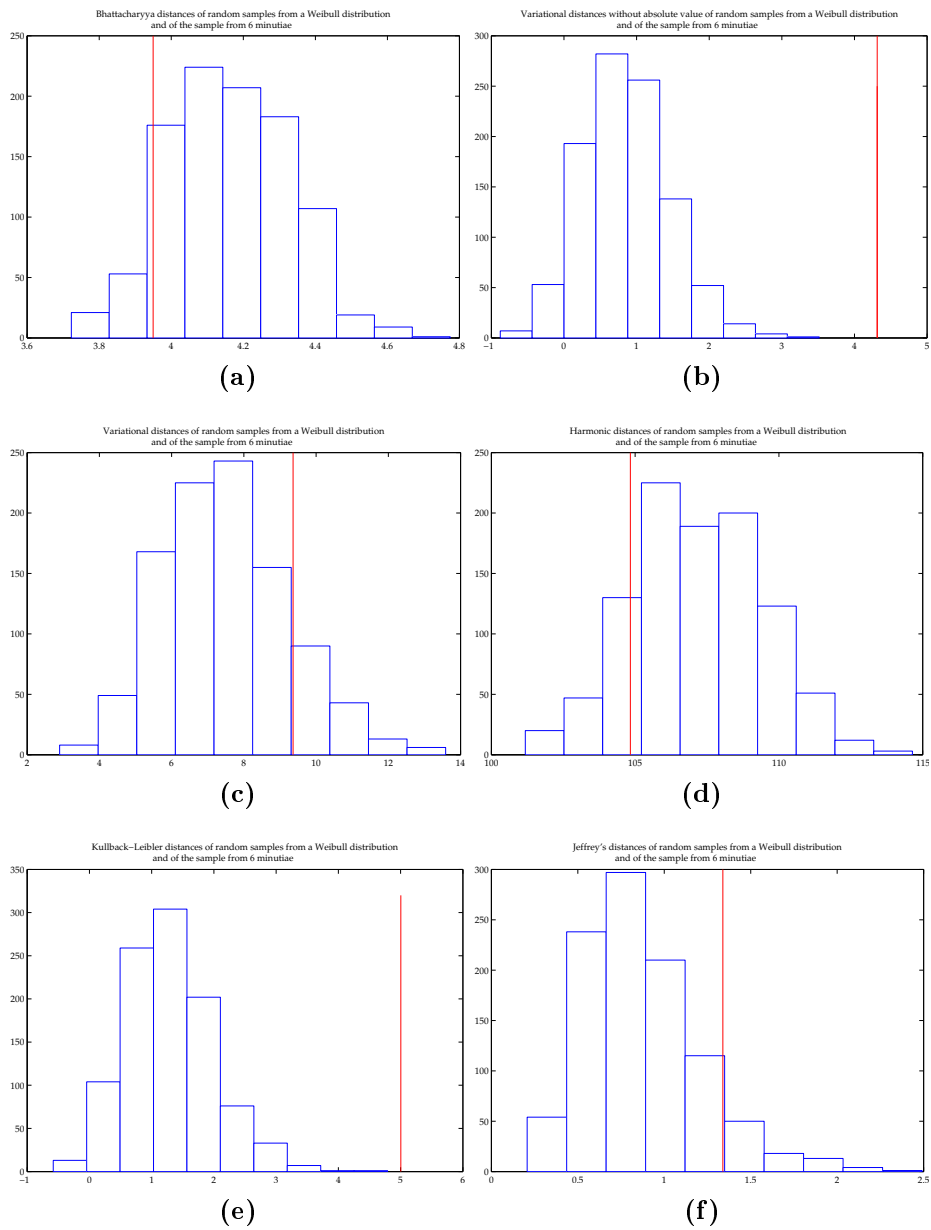


Figure 4.18: Distances to Weibull distribution for the sample (red line) and random samples (histogram) where the distances are a) Bhattacharyya b) Variational distance without absolute value c) Variational d) Harmonic mean e) Kullback-Leibler and f) Jeffrey's

absolute value is used (4.18b), as well as the Kullback-Leibler distance (4.18e) show that the distance obtained for the sample is very far from the histogram obtained from the random samples. Both distances showing this difference are asymmetrical ($D(p_1 \parallel p_2) \neq D(p_2 \parallel p_1)$), and in both cases, when the observed frequency is higher than the distribution which is fitted, the distance measure will increase. These high frequencies are found in particular in the center of the distribution (see figure 4.17a).

In fact, when not taking into account observations between 2900 and 3050, the Kullback-Leibler distance decreases from 5.033 to 0.69, which is quite impressive, even though these bins are in a high probability density region of the observed distribution.

It has been checked if the same decrease appears in the random Weibull samples. When observations between 2900 and 3050 are not considered in the random samples, the Kullback-Leibler distances do not decrease, quite on the contrary. This can be seen by comparing figure 4.19, where the data between 2900 and 3050 has not been considered, with the original distances, shown in figure 4.18e. This is due

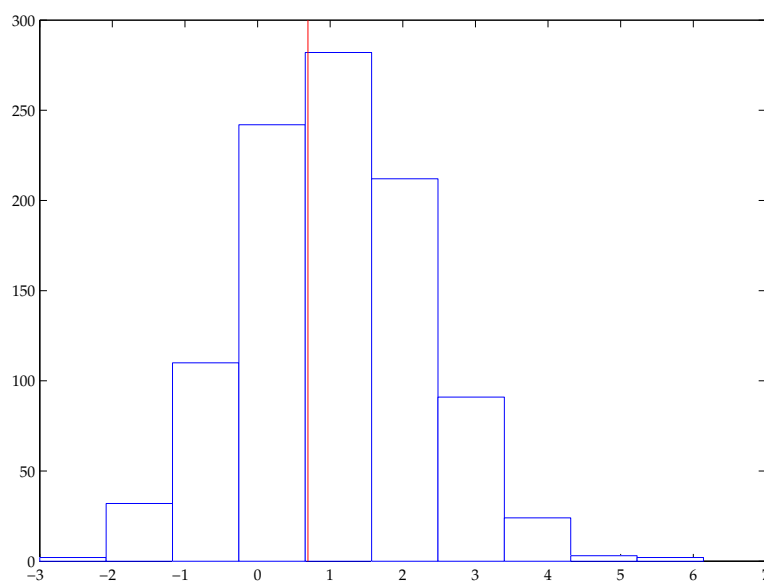


Figure 4.19: Histogram of Kullback-Leibler distances excluding part of the high probability density (HPD) region with the same distance observed on the sample superimposed

to the fact that these random distributions do not show more observations than the theoretical density predicts in this region.

When not taking into account the observations between 2900 and 3050, the samples variational distance without absolute value also decreases: the observed distance for the sample goes from 4.31 to 0.85.

When considering the QQ-plot of the Extreme Value distribution (see figure 4.16b), nonlinear deviations can be seen, which are not present on the QQ-plot

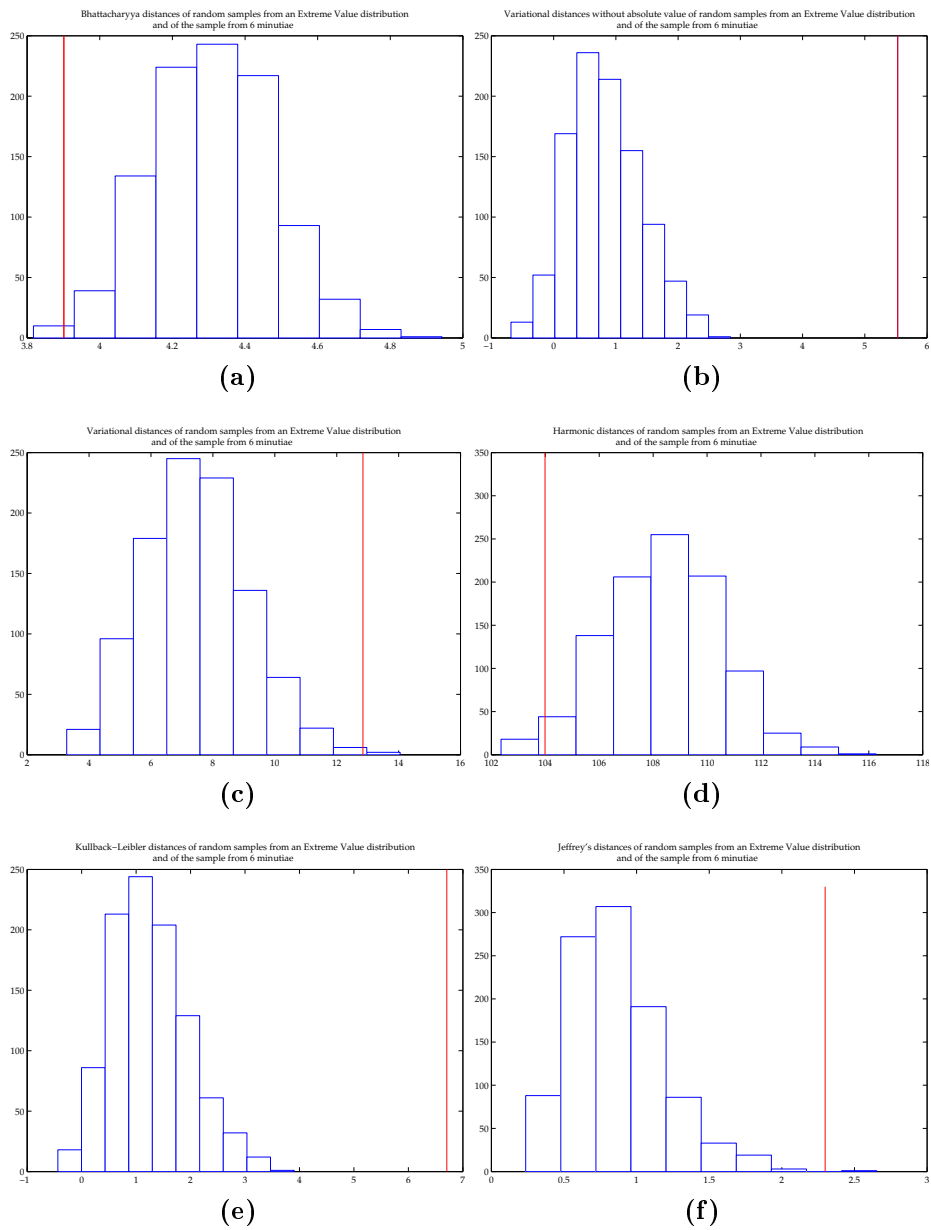


Figure 4.20: Distances to Extreme Value distribution for the sample (red line) and random samples (histogram) where the distances are a) Bhattacharyya b) Variational distance without absolute value c) Variational d) Harmonic mean e) Kullback-Leibler and f) Jeffreys

of the Weibull distribution (figure 4.16a). The fit of the Weibull distribution is therefore better.

This observation is reaffirmed by the results of the distance measures: The distance observed on the sample is systematically in a tail of the histograms of distances observed on the random samples drawn from an extreme value distribution (see figure 4.20). This was not the case for the distances to the Weibull distribution. The Weibull distribution therefore models the observed data better than the Extreme Value distribution considering the measures used, and will therefore be preferred.

In conclusion, **the Weibull distribution is accepted as a good model for the data** in view of these results, for several reasons:

1. Considering the two distributions retained (Weibull and Extreme Value), the Weibull is clearly preferable considering the goodness of the fit of the model to the data.
2. Overall, considering all distance measures, the sample corresponds well to what is observed on the random samples from a Weibull distribution.
3. The observations on the two distance measures which are not symmetrical are due to deviations in the high probability density (HPD) region of the distribution: therefore, these distances, which are summed over all of the observations in this region, have a great influence on the overall distance measure. The distance between the theoretical and observed distribution is not very large, but in the distance measure, it is multiplied by many observations falling in this region.

Comparison between marks and livescan images

A histogram of the scores obtained from marks acquired using the different development methods and livescan images is shown in figure 4.21. The data used for these histograms is based on the marks acquired using each development technique individually, compared to 15 fingerprints. The distribution obtained from livescan images is different from the one obtained based on marks. However, the major difference observed between the datasets is the width of the distribution: the livescan images' distribution is larger. This can be due to one of three reasons: either the distribution of scores from livescan images is different due to the acquisition method itself, or the difference may be due to the distortion introduced in the livescan images, which is absent in the marks, or, finally, it may be due to the size of the dataset, since for each detection method, the number of marks used here is of 22 for all development methods, but there are 330 comparisons overall, since 15 inked prints are used for the establishment of the densities, and there are 66 observations for the livescan images, where only 1 inked print has been used. When looking at the boxplots of these datasets, differences are less obvious (see figure 4.22), particularly when comparing all of the marks to the livescan images. The methods on nonporous surfaces have overall slightly higher scores than the methods on porous surfaces and the livescan images. The boxplot is, however, a symmetrical observation, whereas there is no doubt that the data is skewed. Formal testing (Kolmogorov-Smirnov test of equality of distribution at $\alpha = 0.05$) rejects the hypothesis that both the livescan images and the marks are random samples from a same distribution. When only the results for marks for the same inked print as the one used for obtaining the scores for the livescan images are used, the test also rejects the hypothesis of both samples coming from a same distribution. The same is true for each of the two samples of livescan images as well as both samples together.

The number of inked prints has been increased to 80, for the comparisons of both the livescan images and the marks. The number of marks used is also increased to the numbers reported in table 4.4. The first sample of livescan images is then tested against the mark-print comparisons for each print separately, using the Kolmogorov-Sminov test. The hypothesis of the two samples coming from a same distribution is rejected in 77 out of 79 cases.

Since this rejection is therefore not due to sample size, nor the inked print used for comparison, it may be due to acquisition modalities. A new sample of 64 livescan images is therefore used with the same 6 minutiae noted. These livescan images are all acquired in the central position (which is why the 66 livescan images are no longer available), as are the marks in this case. For a comparison of the histograms of the scores obtained for this new sample of livescan images and the marks with the probability density functions superimposed, please refer to figure 4.23. For this sample of livescan images, when the Kolmogorov-Smirnov test is carried out for each inked print separately, the hypothesis of both samples coming from the same distribution is rejected 14 times out of 79. One of these 14 is the inked print used

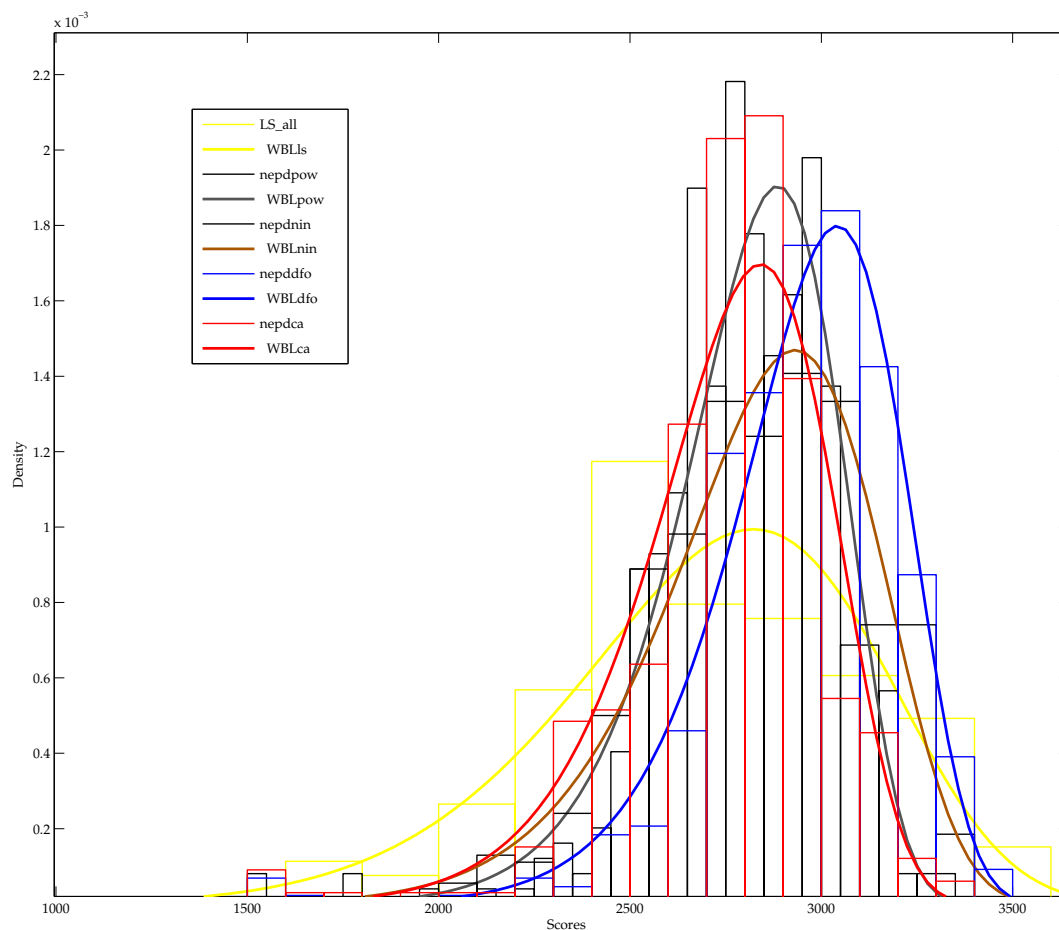


Figure 4.21: Overview of distributions of scores (x-axis): Histograms of livescan images (yellow), marks developed using powdering (black), ninhydrin (brown), DFO (blue) and cyanoacrylate (red), as well as the fitted Weibull distribution of these datasets (prefixed with WBL)

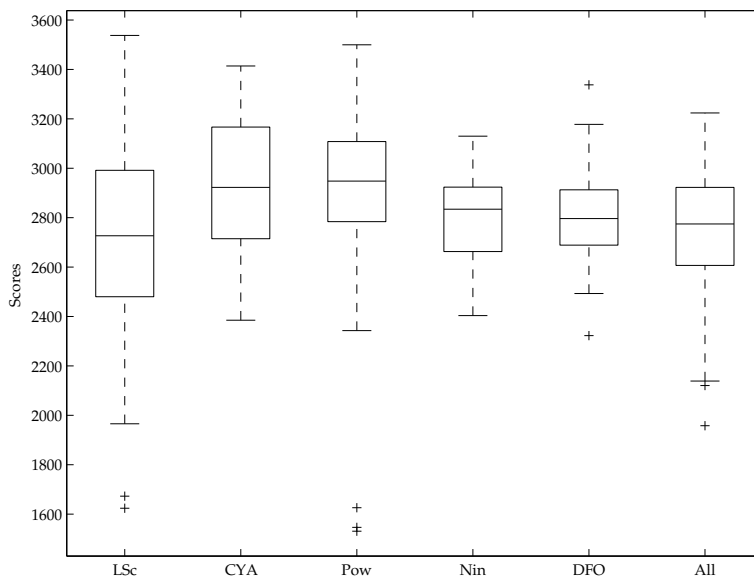


Figure 4.22: Boxplot of scores obtained from livescan images (LSc), marks developed using DFO (DFO), cyanoacrylate (CA), ninhydrin (NIN) or powder (Pow) and all marks (All)

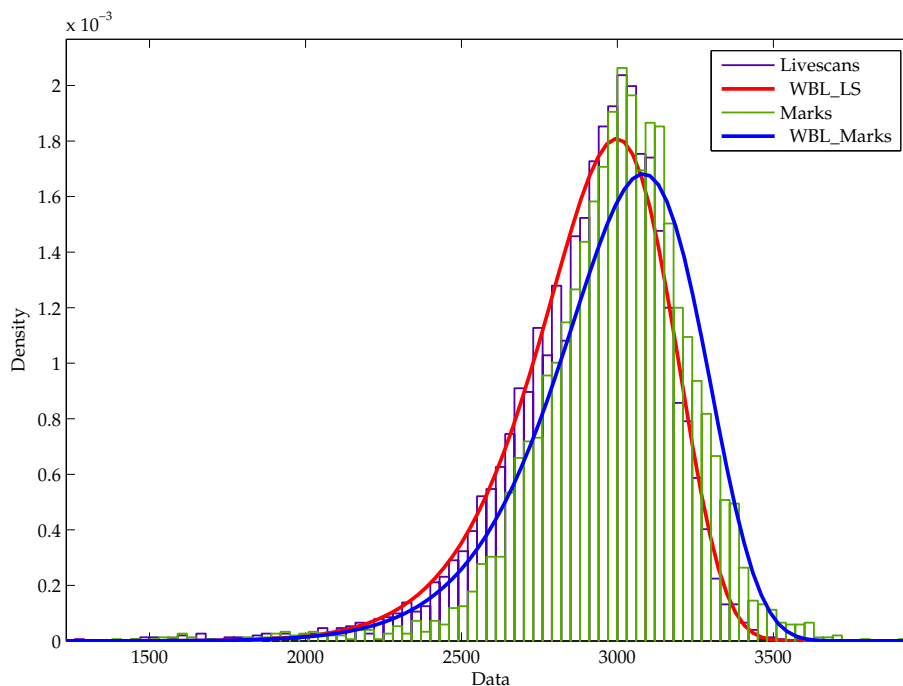


Figure 4.23: Histograms of scores obtained against 79 inked prints for marks and livescan images, with Weibull density superimposed

for the first sample of 66 livescan images. When all of the scores issued from marks are compared to all of the scores from the central position livescan images, the test rejects the hypothesis of a common distribution for both samples. This hypothesis is also rejected when the number of scores used is randomly subsampled to 5056 (the number of scores obtained for livescan images, whereas the total number of scores for marks is 8532). The same is true for 4% of independently drawn random samples of a size of 236 observations, issued from the Weibull distribution fitted to the marks, as well as for 5.4% of samples of 5000 observations, again issued from this Weibull distribution.

It is therefore overall feasible, without being optimal, to use livescan images instead of marks. This is true particularly for the case tested here, where all detection techniques were considered jointly. This is, however, not ideal, since the mark in question in a real case will have been detected using one or several detection techniques, and that figure 4.21 shows that there are differences in the distributions of scores depending on the development method.

The differences between the results as a function of the method used will therefore be investigated, where the four detection methods as well as inking will be considered using the impact on the likelihood ratio as the measure to be considered.

Detection Method

In order to investigate the effect of the different detection methods as well as the inking process on within-variability, the likelihood ratio has been used as a measure in order to compare the different ways of modelling within variability. The within variability considered is that of the suspects finger, and not the variability of the mark found on the crime scene; this renders necessary to use several inked prints if they show variability. Within variability is then modeled using different datasets (see also table 4.5):

- All marks (from all detection methods) and all inked prints, as has been done up to now, hereafter 'All'
- All marks (from all detection methods) compared to one print, hereafter AllMa1P
- One mark (different from the questioned) compared to all inked prints, hereafter '1MaAllP'
- All marks developed using the same method as the questioned mark and one inked print, hereafter 1Me1P
- All marks developed using the same method as the questioned mark and all prints, hereafter 1MeAllP
- All marks developed using the same method as the questioned mark and the same number of prints 1MeFewP

- The livescan images acquired in the central position and all inked prints, hereafter LS
- The slap impressions from the ten print cards and all (rolled) inked prints, hereafter TP

Within-variability has, following the results from section 4.3.2, been modelled by a Weibull distribution using these different datasets. For the between-variability, all of the scores obtained when confronting the questioned mark to the whole database (excluding prints from the same finger) has been used and has been modelled using a lognormal distribution as a first approximation. In order to compute Tippett plots, all mark-to-print comparisons acquired were used under H , while 2000 scores were randomly chosen under \bar{H} . The LRs obtained using these different datasets as basis for the modelling of within variability have also been compared using their correlations. These correlations were first computed using the LRs as obtained. Second, the correlation between the logarithm (base 10) of the LRs was used, in order to compare their correspondence in terms of order of magnitude. In order to compute correlations between LRs, 500 mark-to-print comparisons have been randomly chosen (with replacement) for each detection method (Cyanoacrylate, DFO, Ninhydrin and Powder), resulting in a total of 2000 LRs.

Table 4.7: Correlations between LRs obtained using different within-variability datasets

	All	AllMa1P	1MaAllP	1Me1P	LS	TP	1MeAllP	1MeFewP
All	1	0.86	0.65	0.76	0.94	0.91	0.92	0.84
AllMa1P		1	0.56	0.89	0.73	0.90	0.79	0.64
1MaAllP			1	0.59	0.67	0.55	0.70	0.71
1Me1P				1	0.67	0.78	0.81	0.72
LS					1	0.74	0.88	0.88
TP						1	0.83	0.66
1MeAllP							1	0.95
1MeFewP								1

The results in table 4.7 show that the LRs are not correlated strongly. Correlation values are overall high, particularly between the last two datasets, where one is in fact a subset of the other. Both the massive reduction in number of marks (to one) as well as the reduction in inked prints (to one as well) are deleterious. livescan images result in the second best model in the sense that it's correlation coefficient is second only to 'all', where all marks (108) and all inked prints (75) are considered. It can also be seen that a reduction in marks does not have a very large influence, as long as several marks are still used: 'All' is strongly correlated with all other observations,

except when marks or prints are reduced to a single impression (1MaAllP, 1Me1P). This effect is stronger when the reduction takes place in the number of marks. Since this extreme reduction in the number of prints or marks yields LRs which differ much from 1MeFewP, they will not be considered any longer. It can also be seen that **the modelling using livescan images yields better results than the modelling with inked prints**.

The computation has been carried out a second time, using therefore different samples in the likelihood ratio computations, and the results are shown in table 4.8. When comparing the numbers reported in these two tables (4.7 and 4.8), quite large variations in the correlations can be observed. These variations are, however, generally linked with the datasets that have already been determined as insufficient (reduction of the number of marks or prints to 1), and are therefore inconsequential.

Table 4.8: Correlations between LRs obtained from another sample of marks using different within-variability datasets

	All	AllMa1P	1MaAllP	1Me1P	LS	TP	1MeAllP	1MeFewP
All	1	0.85	0.67	0.66	0.94	0.90	0.92	0.83
AllMa1P		1	0.71	0.88	0.76	0.79	0.84	0.74
1MaAllP			1	0.78	0.57	0.67	0.74	0.66
1Me1P				1	0.59	0.62	0.79	0.75
LS					1	0.70	0.85	0.85
TP						1	0.83	0.65
1MeAllP							1	0.95
1MeFewP								1

When considering the correlations, the only method that could be used in order to obtain a dataset for the modelling of the within variability using less time investment than acquiring multiple marks is to use livescan images.

The correlations when the logarithm of LRs is considered, is higher, as expected. Only the correlation with 1MeFewP is reported in table 4.9. The results for the two samples of marks are shown side by side (1MeFewP_1 are the correlations from the log of the dataset used for table 4.7, and 1MeFewP_2 is based on the data reported in table 4.8). Again, **the best way to model the within-variability without a large time investment is to use livescan images. However, the within-variability can also be estimated by using the slaps from ten-print cards**, which corresponds to an even faster data acquisition, if it is considered that several rolled inked prints need to be acquired.

It has been observed that some of the LRs which do not correspond well between the different modelling options are above 1 for one option and below 1 using another option. In order to compare these different modelling options from that point of view, instead of considering only marks and prints known for coming from the

Table 4.9: Correlation of Log base 10

	1MeFewP_1	1MeFewP_2
All	0.9827	0.9802
AllMa1P	0.9539	0.9514
1MaAllP	0.6621	0.6623
1Me1P	0.9489	0.8443
LS	0.9802	0.9800
TP	0.9674	0.9605
1MeAllP	0.9945	0.9935
1MeFewP	1.0000	1.0000

same source, Tippett plots have been used. These are not Tippett plots in the classical sense, e.g. based on comparisons using a different source for each evidential comparison, since they are based only on marks from one finger with a single configuration. They can still aid the decision as to the data to be acquired for the modeling of the within-variability. They allow the assessment of the performance of the system used for the finger examined; they do not allow an assessment of the systems performance in general.

The modelling options retained for these Tippett plots are 1MeFewP, LS and TP. The result for marks developed using cyanoacrylate are shown in figure 4.24. The way these Tippett plots have been established is the following: All mark-to-print comparisons for cyanoacrylate marks compared to a print of the same finger were stored in a table (see for an example of a part of such data table 4.10). From this table, 2000 evidence scores were chosen randomly, with replacement. More precisely, a line and a column were chosen. The column corresponds to a given mark, while the line corresponds to a given rolled print.

In an analogous manner, the comparisons of the cyanoacrylate marks to fingerprints from other sources, stored in a similar table to that shown in table 4.10 were used to obtain 'evidence' scores under \bar{H} . Again, for a given Tippett plot, 2000 such scores were randomly chosen and used.

For the within-finger variability based on cyanoacrylate marks, a subset of the mark-to-print comparisons was selected; all 29 marks were chosen, and 29 out of the 75 ten-print cards were selected so that the number of marks and prints used was equal for the gold standard distribution. For cyanoacrylate, 841 scores were therefore available. A Weibull distribution was then fitted to this data, and the density value $f(s|H)$ was found using this distribution and the evidential score selected randomly; this value is the numerator of the LR for 1MeFewP. The evidence score was not excluded from the within-variability database when it was present. The fact that this score is left in the within-finger data does not have any impact; it is one score among many, and the fitting of a parametric distribution further reduces

Table 4.10: Example of within-finger data (cyanoacrylate marks)

Tenprint card number	Finger number	Mark1	Mark2	Mark3	Mark4	Mark5	
200402	1	2959	3050	2947	3102	2919	...
200404	1	3036	2969	2988	2996	2850	...
200403	1	2995	2901	2955	2918	2831	...
200405	1	2963	3051	2798	2967	3054	...
200620	1	3118	2989	2959	2959	2962	...
200621	1	3004	2887	2817	2858	2928	...
200622	1	2994	2889	2893	2938	2904	...
200623	1	3028	3070	3006	3109	3047	...
200624	1	2803	2916	2892	2988	2875	...
200626	1	3006	3098	3047	3001	2941	...
...

the impact of a single (not outlying) observation.

For the within-finger variability based on livescan images (LS), all livescan-to-print comparisons were used, and again, a Weibull distribution fitted. The numerator of the LR was then obtained using the score randomly selected from the (cyanoacrylate) mark-to-print comparisons and this within-finger variability; again, the value $f(s|H)$ was therefore obtained and constitutes the LR's numerator.

Similarly, for the within-finger variability based on ten-print card, all of the slap-to-rolled inked impressions comparisons were used, a Weibull distribution fitted and the score randomly chosen from the cyanoacrylate-to-print comparisons used to obtain the numerator.

Finally, the mark from which came the evidence score (the column) was compared to the whole database of other fingers (or rather, the column corresponding to the comparisons of this mark to all prints was selected in a table similar to that shown in table 4.10, but obtained from fingers other than the source). This yielded the data needed for the between-finger variability distribution. Here, a lognormal distribution was fitted, and the value of the density function at the evidence score value obtained. This is the denominator of the LR.

Between these three ways of obtaining the LR, the scores used as well as the between-finger variability are therefore identical; the only difference is the data used for fitting the Weibull distribution in order to obtain the within-finger variability distribution.

Two things are to be observed on the Tippett plots shown in figure 4.24. First, the separation between the curves concerning matching and nonmatching comparisons: the best separation is obtained using the slaps from ten print cards (TP); however, the model using marks from the same method as the evidence (1MeFewP) allows

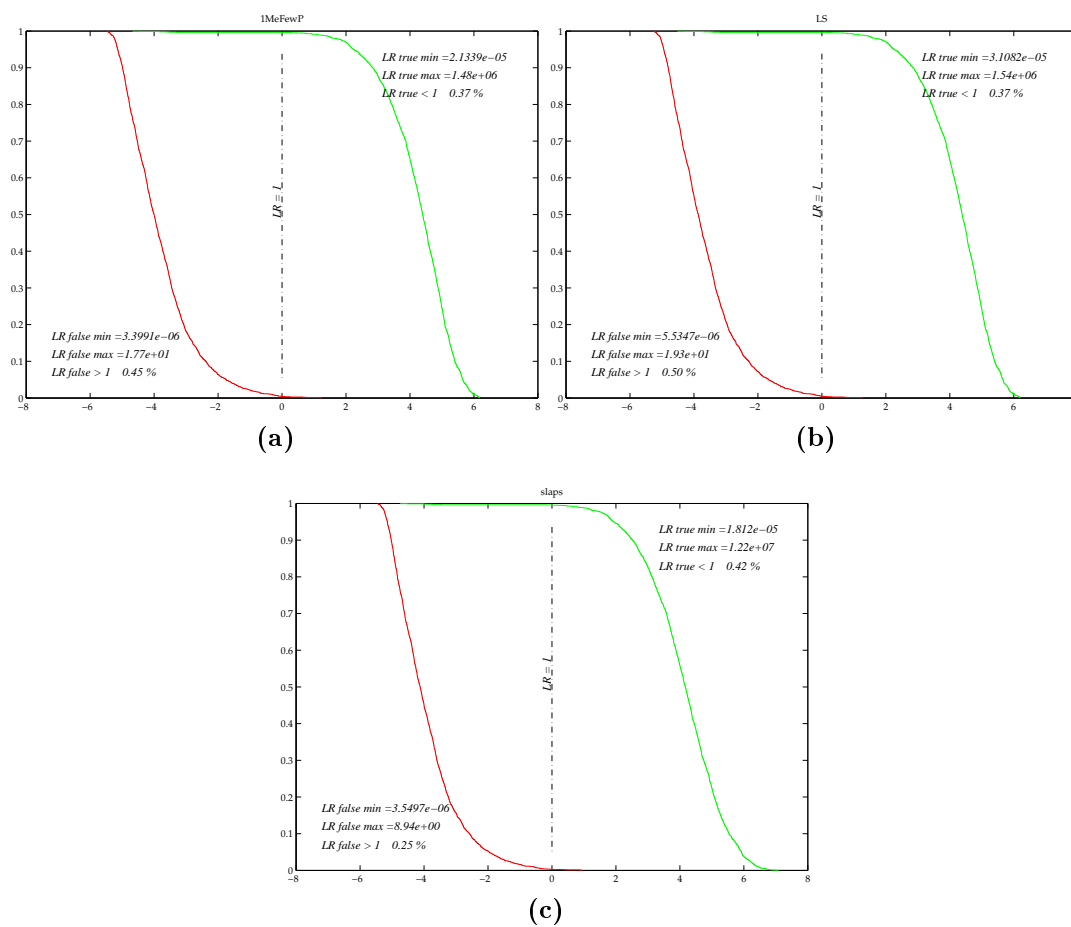


Figure 4.24: Tippet plots using different modelling options for within-variability for CA developed marks, a) 1MeFewP b) LS c) TP

a very good separation of the curve as well. Second, the methods using proxies for developed marks (LS as well as TP) show misleading evidence in favor of the prosecution in a lesser measure than the modelling using marks. The model using marks, however, shows less misleading evidence in favor of the defense, as well as overall the smallest percentage of misleading evidence. These are of course only approximations, since all of the Tippett plots are based on 2000 randomly selected scores under each hypothesis, and there are between 1584 and 1914 observations in the databases for each method under the hypothesis of common source: this means that 0.2% correspond to 4 observations among the LRs used for the Tippett under the hypothesis of common source, and may be due to a single observation of comparisons between marks and prints, since one observation may be chosen several times while another never. Oversampling has been used in order to obtain stable plots; it would, however, have been more judicial here to take each score as the evidence in turn, and establish the plot on the basis of these observations. The only influence this has is on the rates of misleading evidence, and even there this influence is expected to be small.

The rates of misleading evidence in favor of the prosecution (RMEP) and the defense (RMED) are reported in table 4.11 for the four different development methods used.

Table 4.11: Rates of misleading evidence for different modelling possibilities of within-variability for developed marks

	RMEP				RMED			
	CA	DFO	Nin	Pow	CA	DFO	Nin	Pow
1MeFewP	0.45%	0.20%	0.35%	0.85%	0.37%	0.06%	0.18%	0.43%
LS	0.50%	0.30%	0.40%	0.40%	0.37%	0.00%	0.18%	0.43%
TP	0.25%	0.20%	0.20%	0.30%	0.42%	0.00%	0.18%	0.54%

These rates correspond quite well between the different methods of obtaining the data for the estimation of the within-finger variability. Although the rates do not correspond exactly, they are not generally lower for the within-variability distribution based on developed marks (1MeFewP) than for those estimated using slaps or livescan images. Therefore, the three methods are judged equivalent with respect to rates of misleading evidence. Taken together with the results on the correlations in the order of magnitude of LRs, it is concluded that **livescan images or slaps can be used as the data on which within-variability is estimated.**

Reduction of the number of marks

Subsamples of observations have then been drawn on these three methods (1MeFewP, LS and TP) for modeling within-variability. In fact, the initial estimation of the number of observations necessary for the reliable estimation of the within-variability

was of 66. These 66 observations were, however, based on comparisons to a single print; since the comparison to multiple prints yields many more scores, the number of marks may be reduced. An equal number of marks (where livescan images and slap impressions from the ten-print cards are considered as marks here) and prints will be used; it is in fact not useful, in the light of the results above, to have a greater number of inked prints than marks. The number of marks and rolled inked prints chosen in a first step is 8, resulting in 64 scores overall.

The subset of methods for modelling within-variability is constituted of LS, TP and 1MeFewP. LS and TP are two methods of reducing time investment which still result in LR_s which correspond well to those obtained when using 1MeFewP.

The correlations of the logarithm base 10 of the LR_s thus computed between these subsets and the complete 1MeFeP dataset are shown in table 4.12.

Table 4.12: Comparison between complete and reduced datasets by the logarithm base 10 of the correlation between all LR_s for the mark-to-print comparisons available for within-variability

	1MeFewP (large)
LS	0.9911
TP	0.9917
1MeFewP (reduced)	0.99

Now, the largest correlation (after the reduced 1MeFewP dataset) is obtained when slaps are used for the substitution of marks, while very large correlations are also observed for the livescan images.

Again, Tippett plots are used in order to compare these different modelling options (figure 4.25); again, only the results obtained for cyanoacrylate marks are reproduced here. The Tippett plots for the other techniques show similar (or generally rather better) results to those shown in figure 4.25. The rates of misleading evidence in favor of the prosecution (RMEP) and in favor of the defense (RMED) are reported in table 4.13 for all development techniques used for the marks.

Table 4.13: Rates of misleading evidence for different modelling possibilities of within-variability for developed marks

	RMEP				RMED			
	CA	DFO	Nin	Pow	CA	DFO	Nin	Pow
1MeFewP	0.35%	0.20%	0.00%	0.65%	0.37%	0.06%	0.48%	0.43%
LS	0.95%	1.20%	1.30%	1.10%	0.37%	0.00%	0.12%	0.38%
TP	0.95%	1.20%	1.30%	1.10%	1.20%	0.06%	0.55%	1.89%

With respect to the full dataset, the comparison of 8 marks to 8 prints

4.3. Comparison between marks, livescan images and rolled inked prints

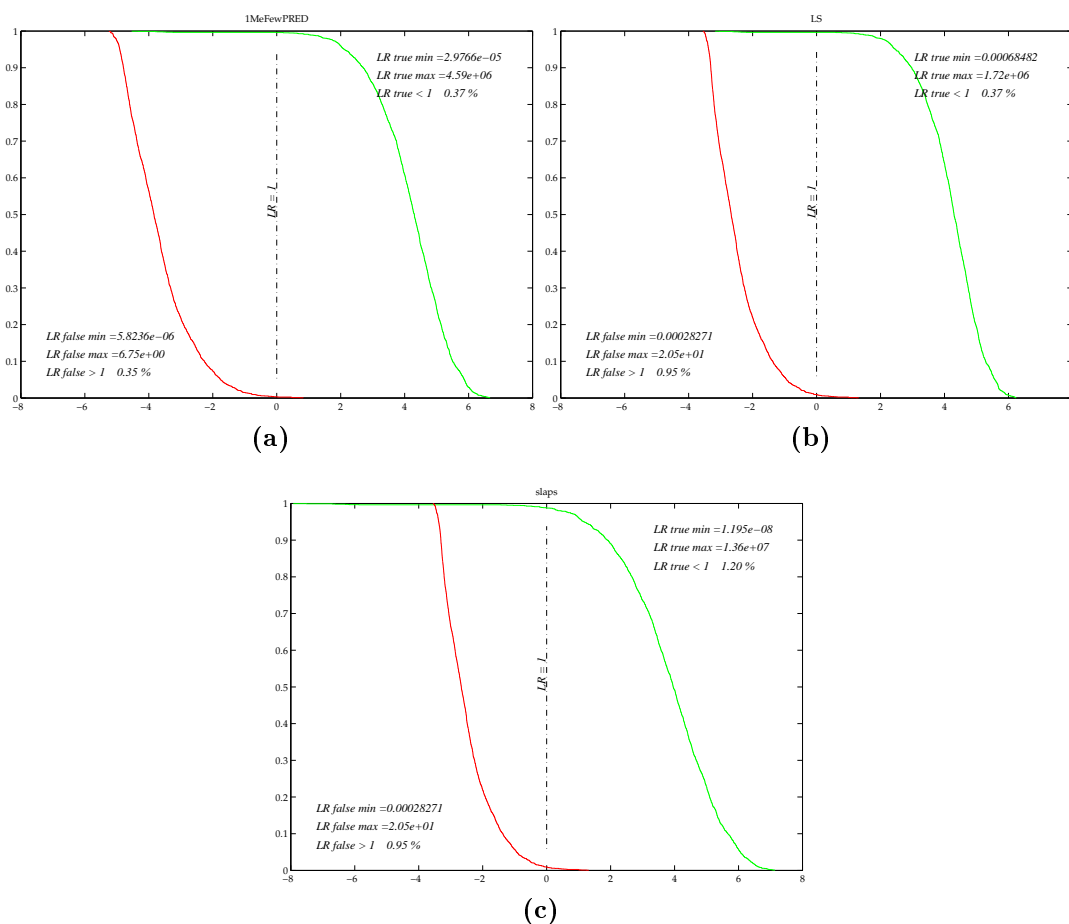


Figure 4.25: Tippett plots using different modelling options using reduced datasets for within variability for CA developed marks, a) 1MeFewP b) LS c) TP

yields LRs that are highly similar (in the sense of a correlation in the logarithm base 10 of LRs) to those obtained using the full dataset. Also, the modeling of within variability using the slaps from ten-print cards or livescan images instead of developed marks yield results that are equivalent to those obtained using developed marks, again in relation to the correlation obtained between these different results. The rates of misleading evidence, however, in particular in favour of the prosecution, increase. With respect to the time gained by acquiring these few impressions rather than a full dataset, the increase in RMEP is judged acceptable.

Kernel smoothing modelling

Here, another modelling method has been tested for within variability, kernel smoothing (ks) using a normal kernel. This is done in order to compare the parametric modelling used up to now to a nonparametric method, which fits the data closer and is based on fewer approximations. The disadvantage of nonparametric modelling, which is at the same time the reason why it was not chosen from the beginning, is that it is highly dependent on data, and may therefore result in large sample needs. This is why the results obtained on complete and reduced datasets are reported below. Also, this data-dependence implies that a change of database may introduce large variations in the numerator, and therefore in the LRs obtained. The rates of misleading evidence obtained using such kernel density estimation for the within-variability are reported, for each development method (of the evidential mark) separately. The data used for the estimation of the within-variability distribution using kernel density estimation are the 1MeFewP, LS and TP datasets; both the complete and reduced datasets are used here in order to verify the feasibility of data-reduction in this context. The data presented below is still based on a log-normal model for the between-finger variability density. The Tippett plots shown in this section are based on random sampling (with replacement) of 2000 evidence scores rather than the systematic selection used in the previous sections.

Table 4.14: RMED and RMEP obtained using ks-density for the within-variability for CA

CA	Complete		Reduced	
	RMEP	RMED	RMEP	RMED
1MetFewP	0.10%	0.25%	0.10%	0.85%
TP	0.45%	0.35%	0.00%	2.05%
LS	0.50%	0.40%	0.90%	0.30%

Between the parametric and the nonparametric approaches, very little difference is reported on the rates of error. In both cases, and in opposition to what was expected for the nonparametric approach, very little influence of the reduction of

Table 4.15: RMED and RMEP obtained using ks-density for the within-variability for DFO

DFO	Complete		Reduced	
	RMEP	RMED	RMEP	RMED
1MetFewP	0.05%	0.10%	0.20%	0.00%
TP	0.15%	0.00%	0.10%	0.25%
LS	0.75%	0.00%	0.05%	3.10%

Table 4.16: RMED and RMEP obtained using ks-density for the within-variability for Nin

Nin	Complete		Reduced	
	RMEP	RMED	RMEP	RMED
1MetFewP	0.25%	0.00%	0.35%	0.20%
TP	0.40%	0.30%	0.00%	2.50%
LS	0.35%	0.15%	0.00%	0.80%

Table 4.17: RMED and RMEP obtained using ks-density for the within-variability for POW

Pow	Complete		Reduced	
	RMEP	RMED	RMEP	RMED
1MetFewP	0.35%	0.55%	0.20%	0.85%
TP	0.20%	0.50%	0.10%	1.25%
LS	0.50%	0.20%	0.40%	0.30%

the size of the datasets is observed. This equivalence of results again validates the data reduction; if in this nonparametric setting there is no larger influence of dataset reduction, these 64 observations where only 8 are marks are truly sufficient for reliable estimation.

A difference is, however, observed, in the LRs for nonmatching comparisons. **The LRs obtained under the defense hypothesis \bar{H} using nonparametric modelling are much lower than using the parametric approach.** The Tippett plots obtained for CA are reproduced in figure 4.26, and can be compared to figure 4.25. This shows that the left tail of the Weibull distribution used for modeling

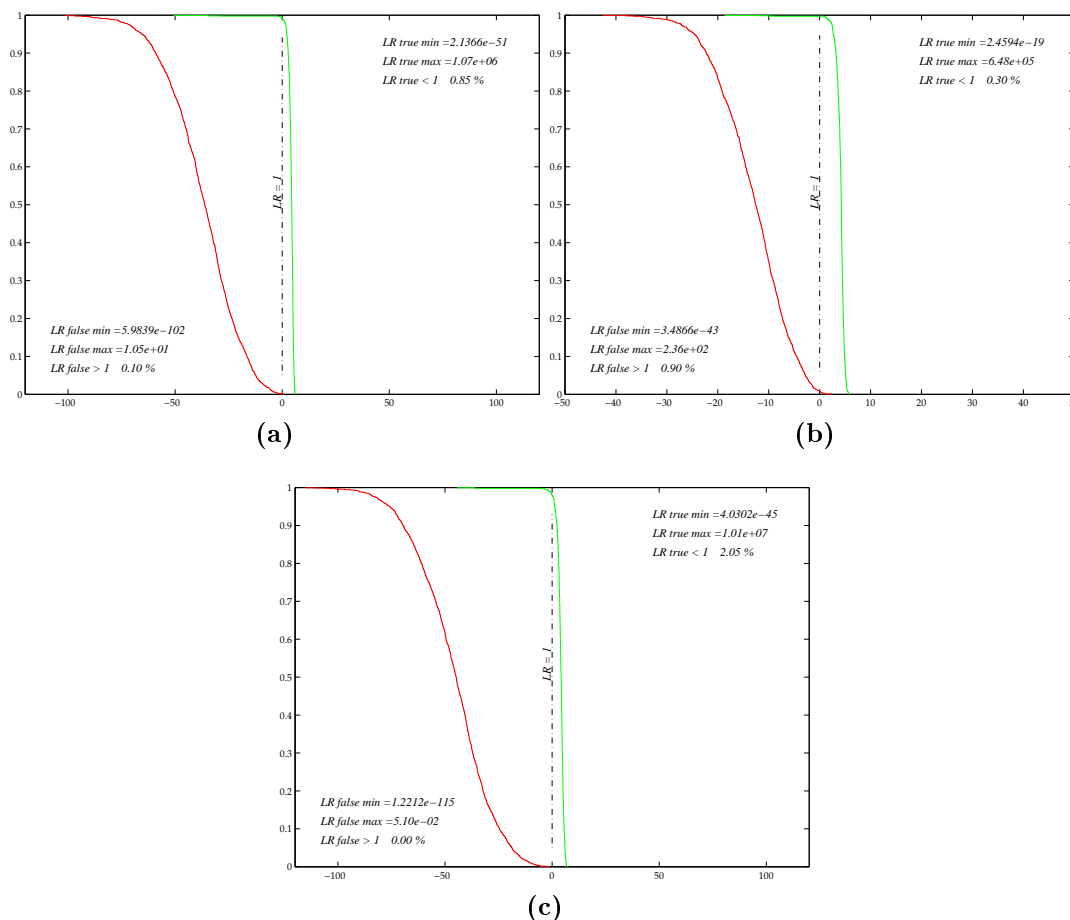


Figure 4.26: Tippett plots using different modelling options for within variability for CA developed marks, a) 1MeFewP b) LS c) TP

within-variability is heavier than the tail of the nonparametric density used.

The importance of the LRs obtained under \bar{H} using kernel density estimation is not warranted by the size of the dataset. It seems exaggerated to report LRs of 10^{-120} based on 10000 non-matching and 64 matching comparisons. The Weibull distribution continues to be the preferred modelling approach; the dataset size chosen, however (8 marks and 8 prints) remains sufficient for a change in modelling approach should this be necessary in the continuation of the

project. For the following sections, the full dataset continues to be used, since it is available.

4.4 Influence of the number of minutiae included in the configuration

4.4.1 Material and methods

The same developed marks as for the preceding sections have been used, likewise for the rolled inked prints. The minutiae configuration of 6 minutiae used above has been employed as a starting point, and neighboring minutiae have been added incrementally. The minutiae configurations of 6, 7, 8, 9 and 10 minutiae thus obtained are illustrated in figure 4.27. In this figure, the original configuration is annotated using a blue circle, while minutiae 7 to 10 are marked individually. After verification of the presence of the minutiae on the rolled inked prints, 5 ten-print cards have been excluded from further analysis, bringing the total of ten print cards used to 75.

The histograms of the scores have been compared visually. Then, the parameters of the fitted Weibull distributions for each number of minutiae are compared, and then used for direct estimation of these parameters based on very few observations from inked impressions of the suspects finger.

4.4.2 Results

After the extraction of scores from the AFIS through the comparison of the marks to the inked prints, histograms of the scores obtained have been plotted using the Freedman-Diaconis rule for bin width. These histograms, obtained when using 6, 7, 8, 9 and 10 minutiae, are shown in figure 4.28. In this figure, a Weibull distribution has been fitted to each dataset, and is superimposed on the histograms.

With each added minutia, the centre of the distribution is shifted towards higher scores, and the variance increases. Since with each new minutia, variation in location and direction is added, the increase in spread of the distribution does not come unexpectedly. Also, the overall increase in scores was to be expected, since more matching minutiae are present in this context, where impressions are known to come from the same finger. The parameters of the fitted Weibull distributions have been computed, and are shown in table 4.18.

It is concluded that **the variable 'number of minutiae' has a strong influence on results**; in particular the parameter α of the Weibull distributions fitted to these configurations where minutiae are added shows confidence intervals which do not overlap. Therefore, **within-finger distribution needs to be acquired**

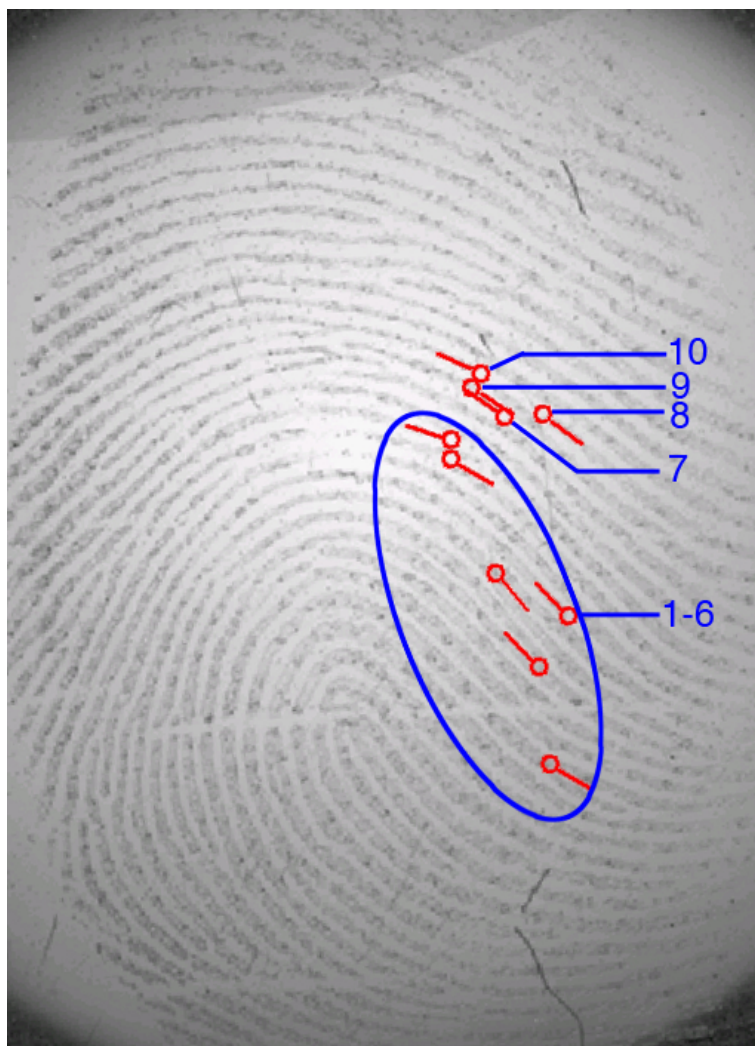


Figure 4.27: Illustration of the first minutiae configuration (1-6) increased from 6 to 10 minutiae

Table 4.18: Parameters (EST) and 95% confidence intervals (CI) obtained for Weibull distributions fitted to a configuration increasing from six to ten minutiae

	α			β		
	Est	CI		Est	CI	
6	3058	3053	3063	14.5	14.2	14.7
7	3579	3573	3585	13.6	13.4	13.8
8	4105	4097	4113	11.7	11.6	11.9
9	4878	4867	4889	9.9	9.8	10.1
10	5827	5814	5841	10.1	9.9	10.3

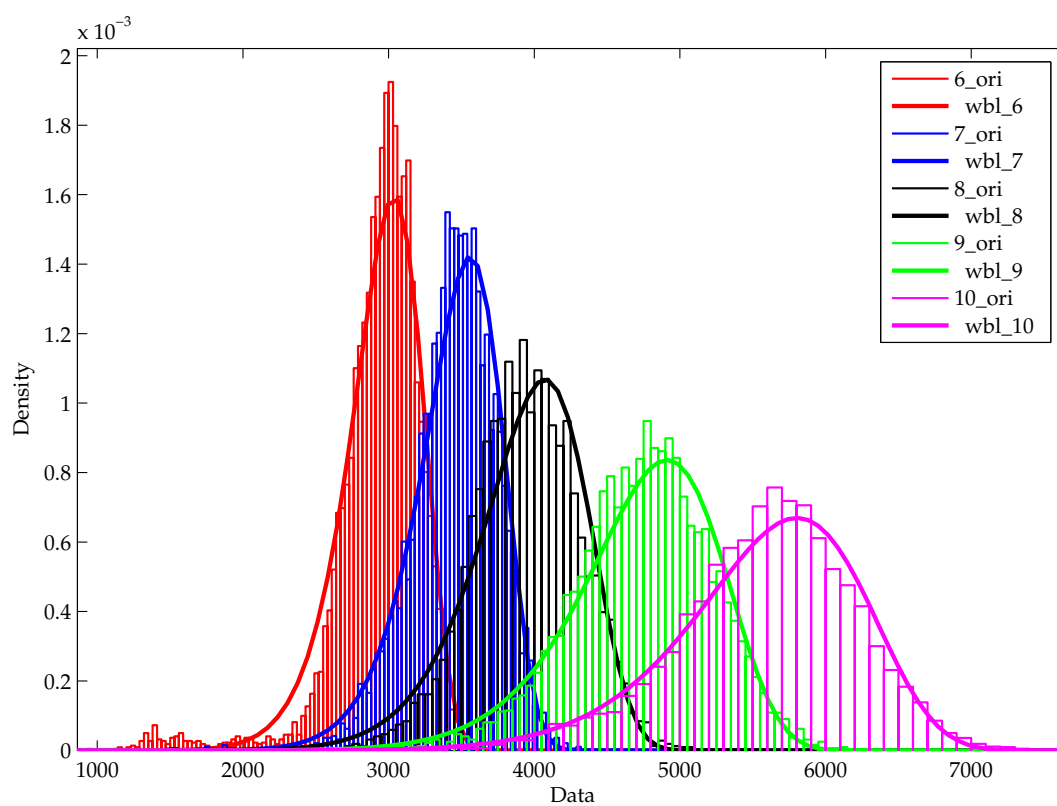


Figure 4.28: Illustration of the progression of the distribution of within-variability when adding minutiae. `ori` refers to the histograms of raw data from this minutiae configuration (with 6 to 10 minutiae), while `wbl_` refers to the fitted Weibull distribution

taking into account the number of minutiae included in the configuration. Furthermore, these results show that the behaviour of the within-finger distributions corresponds to what was expected: as the number of minutiae included in the configuration increases, the scores increase, and their variance increases as well.

One source of variation in the scores has therefore been clearly identified: it is the number of minutiae. Whether the precise configuration of minutiae also causes scores to vary is the subject of the next section (section 4.5).

4.5 Comparison between two minutiae configurations on the same finger

4.5.1 Introduction

Originally, the hypothesis underlying this chapter (hypothesis 1c: Within variability for the evaluation of a given mark can be deduced from a generally applicable distribution) included two subhypotheses. The first one is that within variability is independent of general pattern and finger number and the second one is that the within finger variability is independent of donor. However, it has been decided here to first choose a second, different configuration on the same finger, i.e. to ignore all variables included in the two subhypotheses detailed above, in order to see if, when all of these variables remain, distributions remain comparable. This will also allow to finalize the testing of hypothesis 1d (within-variability depends on the number and placement of minutiae); indeed, only the fact that the number of minutiae influences the scores has, up to now, been tested. Once two different minutiae configurations that are similar concerning their placement on the finger have been compared, the hypotheses concerning general pattern, finger number and donor can be further investigated.

4.5.2 Material and Methods

A new configuration of 6 minutiae has been chosen (referred to from now on as 'center' or 'second' configuration), on the same marks as used before and incrementally increased to 10. It is close to the center, as was the first configuration (from now on referred to as 'ori' in graphics), but on the other side of the core, towards the delta (see figure 4.29).

The number of marks showing this configuration is slightly smaller than for the first minutiae configuration: 99 marks have been used, and the number of marks for each development method used is shown in table 4.19. This new configuration is present on all rolled inked prints acquired: the number of rolled prints that can be used for the establishment of this new configuration is therefore 80.

All available inked prints have been taken into account as well as 99 marks. The distributions obtained for each number of minutiae are first compared visually, the

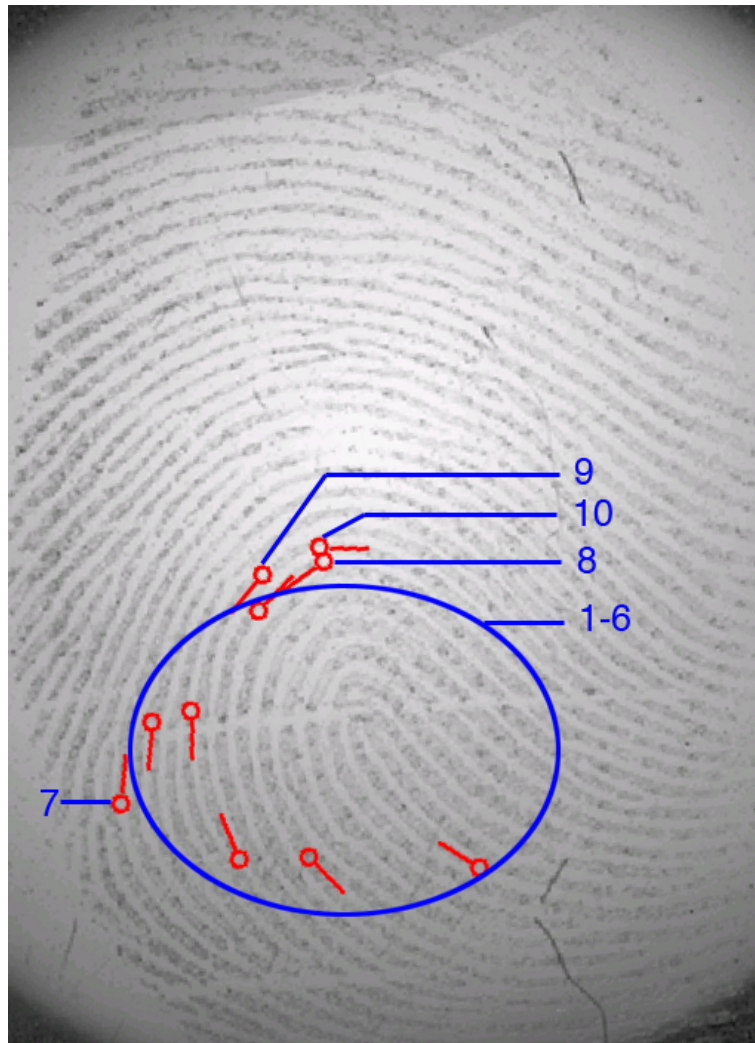


Figure 4.29: Illustration of the second minutiae configuration increasing from 6 to 10 minutiae

Table 4.19: Number of marks showing the second minutiae configuration for each method

Method	Number of marks
Cyanoacrylate	26
Powder	28
DFO	25
Ninhydrin	20

Weibull parameters are then presented, and finally, the Kolmogorov-Smirnov test is used for the formal investigation of whether the two samples come from a same distribution. A significance level of 5% has been chosen for these tests.

4.5.3 Results

Increasing the minutiae in the second configuration

A histogram showing simultaneously the scores obtained for 6,7,8, 9 and 10 minutiae has again been created and is shown in figure 4.30. The parameters of the fitted Weibull distributions as well as their confidence intervals are reported in table 4.20.

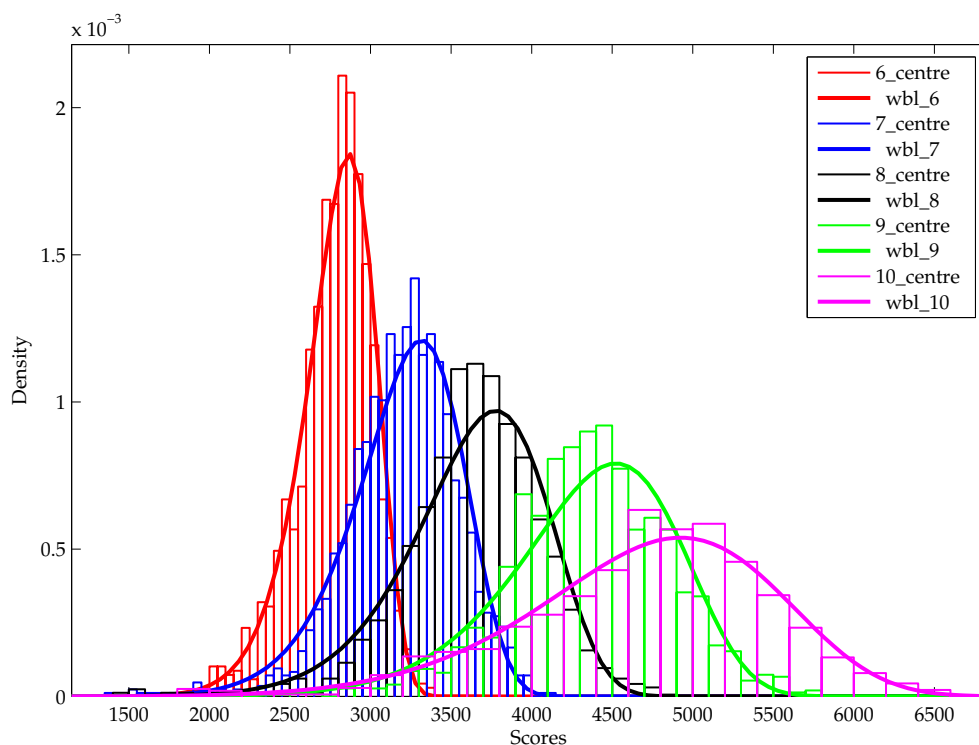


Figure 4.30: Illustration of the progression of the distribution of within-variability when adding minutiae to the second configuration

The same observations as for the first configuration still hold for this new configuration. As the number of minutiae increases, the scores increase as well as the variability observed in the scores distribution. The first parameter of the Weibull distribution increases with increasing minutia number, while the second parameter decreases. The distribution becomes more asymmetrical with increasing minutiae number; it is increasingly skewed to the right.

Table 4.20: Parameters (EST) and 95% confidence intervals (CI) obtained for a Weibull distribution for the second configuration of 6 to 10 minutiae

	α			β		
	Est	CI		Est	CI	
6	2894	2889	2899	13.4	13.1	13.6
7	3394	3388	3401	11.9	11.7	12.1
8	3898	3890	3906	11.3	11.1	11.5
9	4579	4569	4588	10.9	10.7	11.1
10	5371	5360	5383	10.6	10.4	10.7

Comparison of the two configurations for each number of minutiae separately

For the six-minutiae configurations, the histograms with the Weibull distributions superimposed are presented in figure 4.31. Although these two distributions show

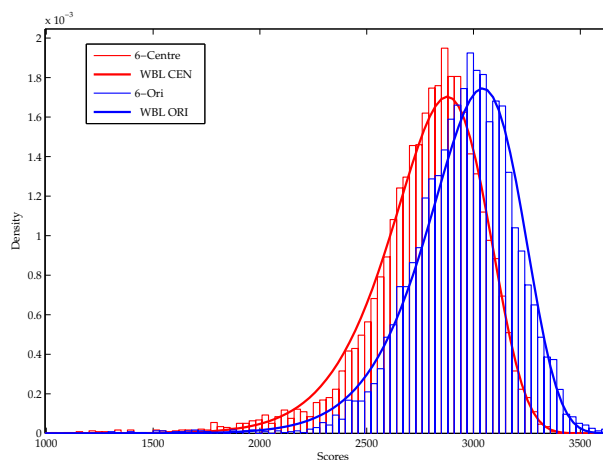


Figure 4.31: Comparison between the two 6-minutiae configurations (centre and ori)

similarity in scale, their location is clearly different. When examining the parameters estimated for the distributions, the 95% confidence intervals are disjoint for both parameters. They are [3053,3063] and [2889, 2899] for α for the original and the second minutiae configurations respectively, and [14.2,14.7] and [13.1,13.6] for β . The Kolmogorov-Smirnov furthermore rejects the hypothesis of the two samples coming from a same population ($p \ll 0.01$). The distributions of scores obtained from two configurations of 6 minutiae on the same finger and close to the centre are therefore different.

For 7 minutiae, the comparison between the histograms is shown in figure 4.32. Again, differences in location can be observed between these two distributions. The confidence intervals for the parameters of the estimated Weibull parameters for

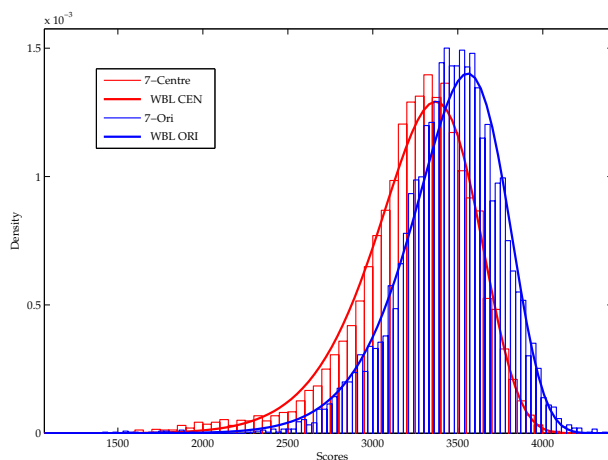


Figure 4.32: Comparison between the two 7-minutiae configurations (centre and ori)

these two configurations are [3573,3585] and [3388,3401] for α and [13.4,13.8] and [11.7,12.1] for β . These intervals are again disjoint, pointing towards two different underlying distributions. The Kolmogorov-Smirnov test rejects the hypothesis of a common underlying distribution for these two samples ($p \ll 0.01$).

Figure 4.33 shows the histograms and fitted Weibull distributions for 8 minutiae. Confidence intervals for the parameters are [4097,4113] and [3890,3969] for α and [11.6,11.9] and [11.1,11.5] for β . The hypothesis of the two samples being issued from a same distribution is again rejected ($p \ll 0.01$).

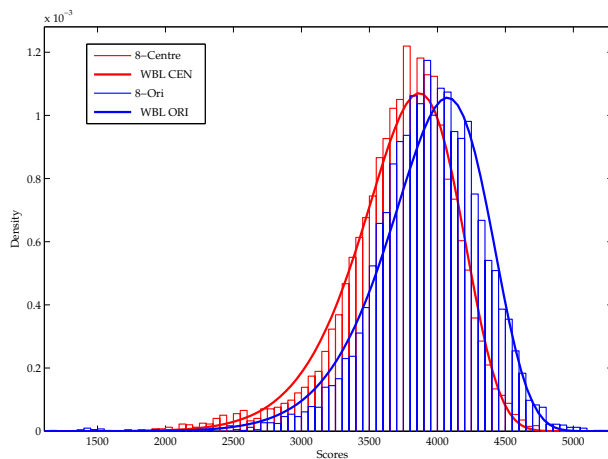


Figure 4.33: Comparison between the two 8-minutiae configurations (centre and ori)

For the configurations consisting of 9 minutiae, the same observations hold: the confidence intervals of the parameters for the second configuration are disjoint from those of the first one (α : [4867,4889] and [4569,4588] and β : [9.8,10.1] and [10.7,11.7]). The test rejects the hypothesis of equal distributions ($p \ll 0.01$). Also, on figure 4.34 the difference between the two distributions is visible.

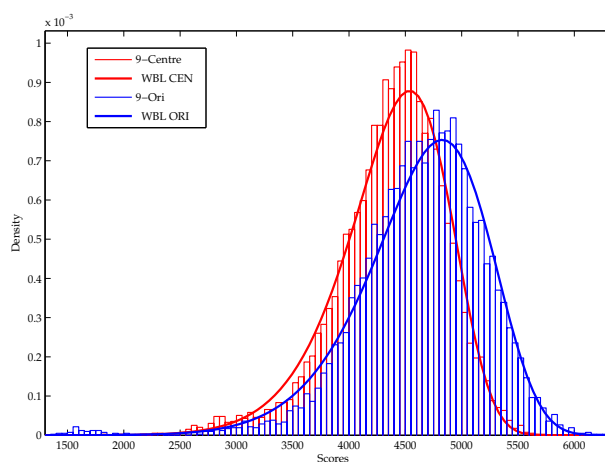


Figure 4.34: Comparison between the two 9-minutiae configurations (centre and ori)

Finally, for 10 minutiae, the visual comparison between the two distributions is shown in figure 4.35. The confidence intervals for α are $[5814,5841]$ and $[5360,5383]$

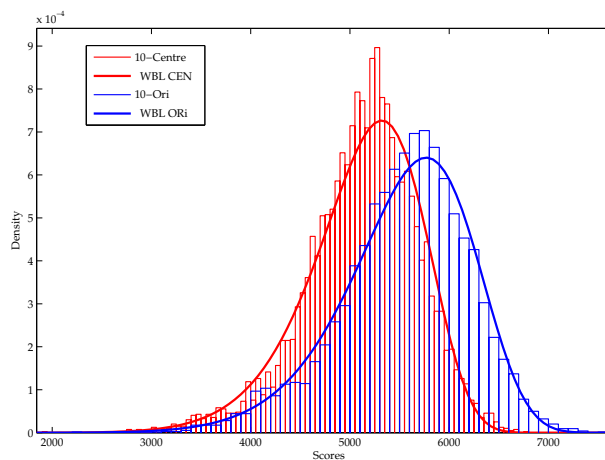


Figure 4.35: Comparison between the two 10-minutiae configurations (centre and ori)

and for β , $[9.9,10.3]$ and $[10.4,10.7]$. The hypothesis of equal distribution is also rejected.

The change in minutiae configuration therefore has an impact on the shape of the within-finger distribution. This influence will, however, be investigated further. The hypotheses to be considered for this investigation are as follows:

1. Is the difference observed in the scores for two configurations with the same number of minutiae due to the orientation of these minutiae?

and

2. Can the parameters of a distribution relative to a given minutia arrangement be related to the score obtained when the mark is compared to itself, the maximum obtainable score for a given configuration?

4.6 Influence of the orientation of the minutiae

4.6.1 Material and Methods

The first six minutiae show alternating directions (see figure 4.27), while the second minutiae configuration doesn't (see figure 4.29). A new configuration of six minutiae showing opposing directions as well has been chosen, again on the same finger, and is shown in figure 4.36 (this configuration will be referred to as 'third' or 'ter' in graphics). These minutiae have been noted on all marks which showed them (for a

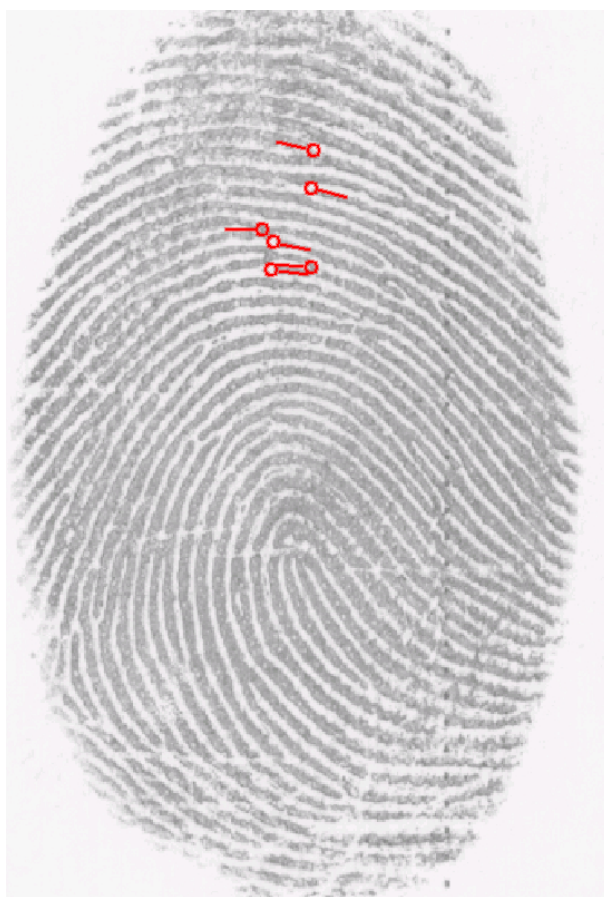


Figure 4.36: Third minutiae configuration showing alternating directions of minutiae

total of 112 marks, all methods together) and on 18 ten-print-cards. These ten-print cards are the same for both datasets. The results have been compared to data for the original 6 minutiae configuration, where 106 marks and 19 inked prints have been considered. This has been done in order to obtain comparable datasets, 2014

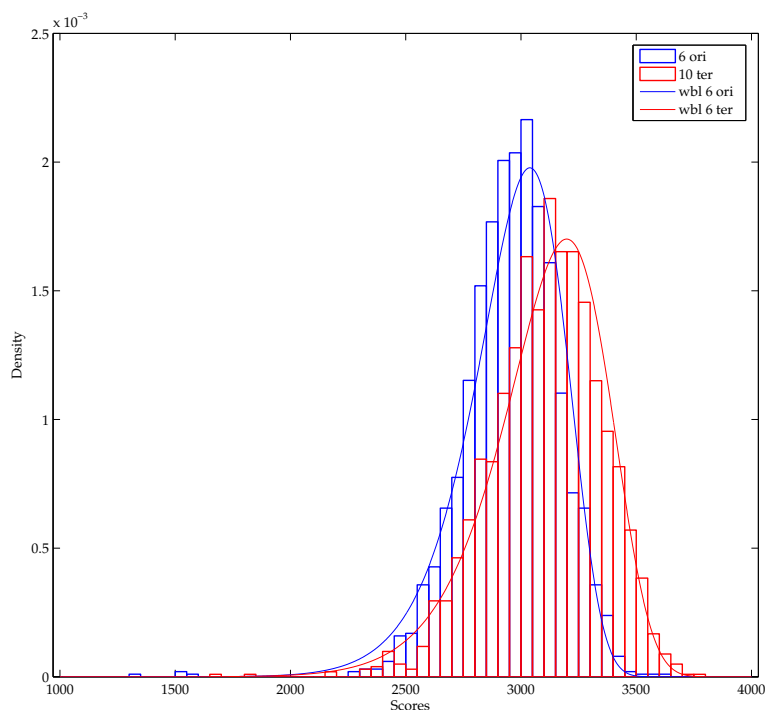


Figure 4.37: Comparison between the histograms and fitted Weibull distributions obtained for the original 6 minutiae (ori) and the third minutiae configuration (ter)

observations for the original dataset, and 2034 observations for the new one. The results obtained for this new configuration have been compared to the original six minutia configuration by visual comparison as well as a Kolmogorov-Smirnov test as before.

4.6.2 Results

The histograms are shown in figure 4.37. The Kolmogorov-Smirnov test rejects the hypothesis of both samples being issued from the Weibull distribution fitted on the other sample. The confidence intervals for α are [3042, 3059] for the first and [3203, 3223] for the third 6-minutiae configuration. For β , these confidence intervals are [15.8, 16.9] for the first and [14.3, 15.3] for the third configuration, respectively and are therefore again disjoint. Please note that the confidence intervals obtained here for the first configuration have changed with respect to the confidence intervals shown in table 4.18, due to the change in ten print cards. They are even disjoint for the second parameter, β . If the dataset used for the establishment of the parameters in table 4.18 had been used here, β would not be different between the two configurations; this other dataset, however, is not comparable to the one used for estimation here (due to the use of all rolled inked prints), and no particular conclusion can be drawn from this observation, except that not overly much importance should be attributed to rather small variations in this second parameter.

The hypothesis concerning the influence of the relative direction of minutiae can be rejected, since results obtained for two configurations on the same finger where minutiae directions alternate, lead to different score distributions. Other factors may influence the parameters of the distribution which can be used to model these data; however, another approach will first be tested: the link between the parameters of the Weibull distribution and the number of minutiae on one hand, and the link between the parameters and the maximum obtainable score for a given minutia configuration on the other hand.

4.7 Estimation of the parameters from the highest score possible for a given configuration

4.7.1 Material and Methods

Three inked slap impressions of the same finger have been chosen from the 80 ten print cards, and the three six-minutiae configurations have been annotated on these impressions. These same impressions have also been used as the comparison prints, and the (3*6) minutiae making up the configurations verified so as to be as similarly placed as possible. For each configuration of minutiae used up to now (6 to 10 minutiae for the original and the second configurations used, and 6 minutiae only for the third configuration used for the testing of the influence of minutiae orientation), 3 scores have therefore been obtained. These three scores are each based on the comparison of a (slap) impression to itself, where the exact same minutiae were annotated in exactly the same way as closely as possible.

Such comparisons, which are carried out in order to estimate the highest possible score for a given configuration, result in what will be termed 'self-scores' from now on.

4.7.2 Results

The original 6-minutiae configuration shown in figure 4.27 resulted, for the three impressions chosen, in the scores shown in table 4.21 under 'First'. The self-scores of the configuration of 6 minutiae shown in figure 4.29 are reported in that same table under 'Second', and the self-scores for the third configuration (shown in figure 4.36) are reported under 'Third'.

This is, overall, compatible with the distributions obtained for these minutiae configurations (see figure 4.38). In fact, the order of the self-scores (where the second configuration is lowest, the original configuration is in the middle and the third configuration has the highest scores) is the same as the order of the distributions shown: the second configuration has a distribution made up of overall lower scores than the original, whereas the third distribution has, overall, the highest scores.

Since this correspondence between self-scores and location of the distribution

Table 4.21: Scores obtained for the comparison to themselves of 3 flat impressions with the original 6 minutia configuration

Print	Configuration		
	First	Second	Third
1	3630	3353	3703
2	3591	3364	3636
3	3650	3577	3785
Mean	3623.67	3431.33	3708

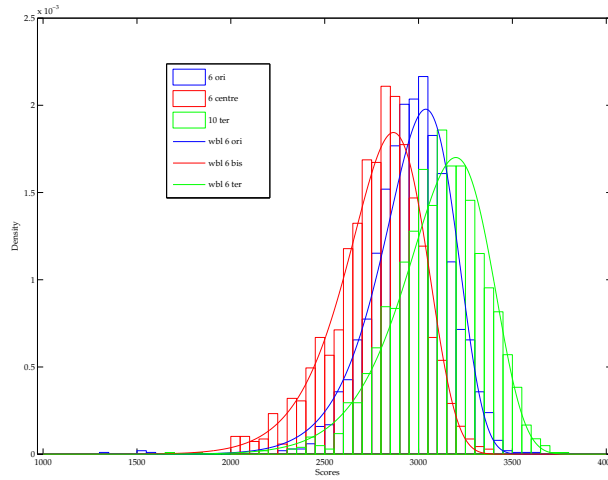


Figure 4.38: Comparison between the histograms and fitted Weibull distributions obtained for the first (ori), second (centre) and third (ter) minutiae configuration

exists, it is possible to try and see whether the first parameter of the Weibull distributions can be estimated using these self-scores.

A regression has been carried out, using the parameters α as predictors for the self-scores, for all of the minutiae configurations (first 6 to 10, second 6 to 10 and third of 6 minutiae). Although this does not answer the question which is asked in this context, which is the value of the parameter given the self-scores, the regression done in this way gives better results, since three observations have been made for the self-scores, and one only for the corresponding parameter. The inverse of the equation is then used in order to predict the parameter α from the self-scores. The equation allowing to predict the parameter α from the self-scores is the following:

$$\alpha = (s + 903.78)/1.4565 \quad (4.5)$$

where s is the self-score obtained for this configuration. The confidence intervals of the parameters used were extremely small, since their estimation is based on very many observations (around 8000, except for the third configuration). In order to obtain a more reasonable image of the interval in which this parameter can be found, subsamples of 66 observations have been drawn in the original datasets. 100 such subsamples have been used for each dataset. Confidence intervals for the parameter α have then been computed on these 100 samples, and the maximum and the minimum limits of these confidence intervals used. On figure 4.39, these intervals (which do not represent confidence intervals, nor will they contain the parameter estimate in 95% of samples generated) are represented by black lines in the mean of the self-scores. This figure represents the linear regression and its confidence intervals, as well as the parameters. Precise parameter estimates will, in the following, be based on the mean of the three self-scores which have been obtained for each minutia configuration. The use of a single self-score may be possible; this will, however, be tested when the generalisation to other fingers, donors, and other configurations of this model will be tested. The mean is used in order to slightly increase robustness. Logically, here, since the experiment is set up in a way allowing to obtain the highest possible score, the maximum should be used. This maximum score is very variable when the same impressions are annotated as marks and prints as closely as possible; it does not seem feasible, therefore, to use this maximum.

For the second parameter of the Weibull, β , the number of minutiae in the configuration is used as a predictor. The relation between this parameter and the number of minutiae n included in the configuration is shown in figure 4.40. No linearity can be detected in this relationship; also, the relationship between β and n is different for the first and the second configuration. It has been noticed previously that small changes in this parameter may occur when subsamples of datasets are used, and that (limited) differences in this parameter do not yield distributions that are too different. Since the relationship between this parameter and the number of minutiae does not need to be extrapolated, the mean of the estimated parameters from the data will be used and applied to new datasets. These parameters are reported in

4.7. Estimation of the parameters from the highest score possible for a given configuration

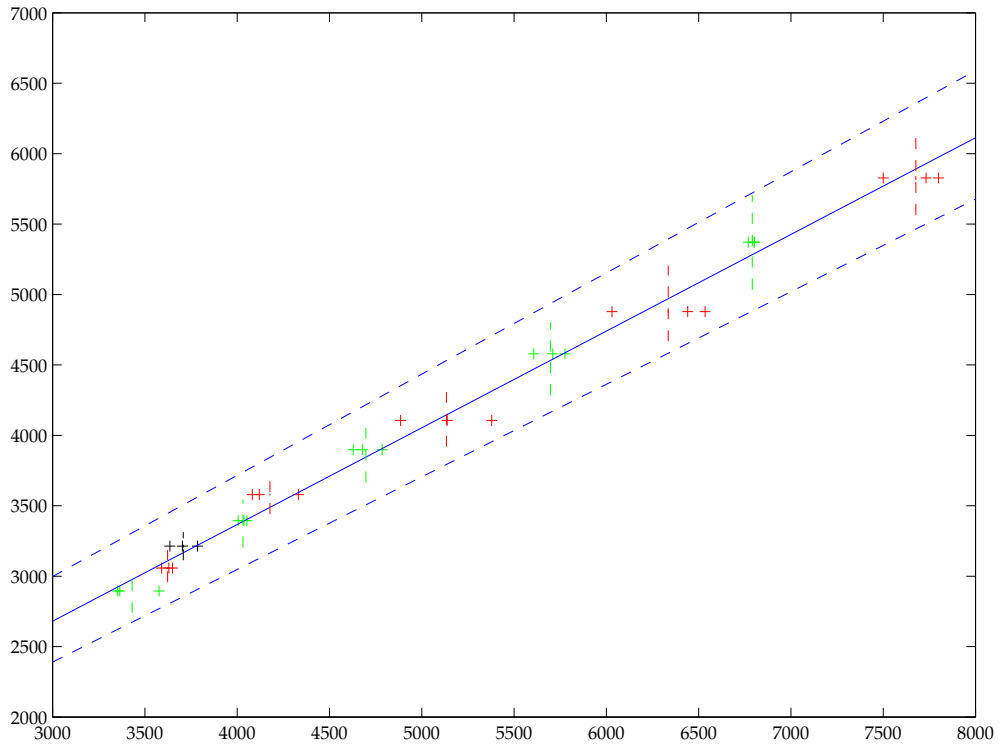


Figure 4.39: Regression of the parameter α on the self-scores of minutiae configurations

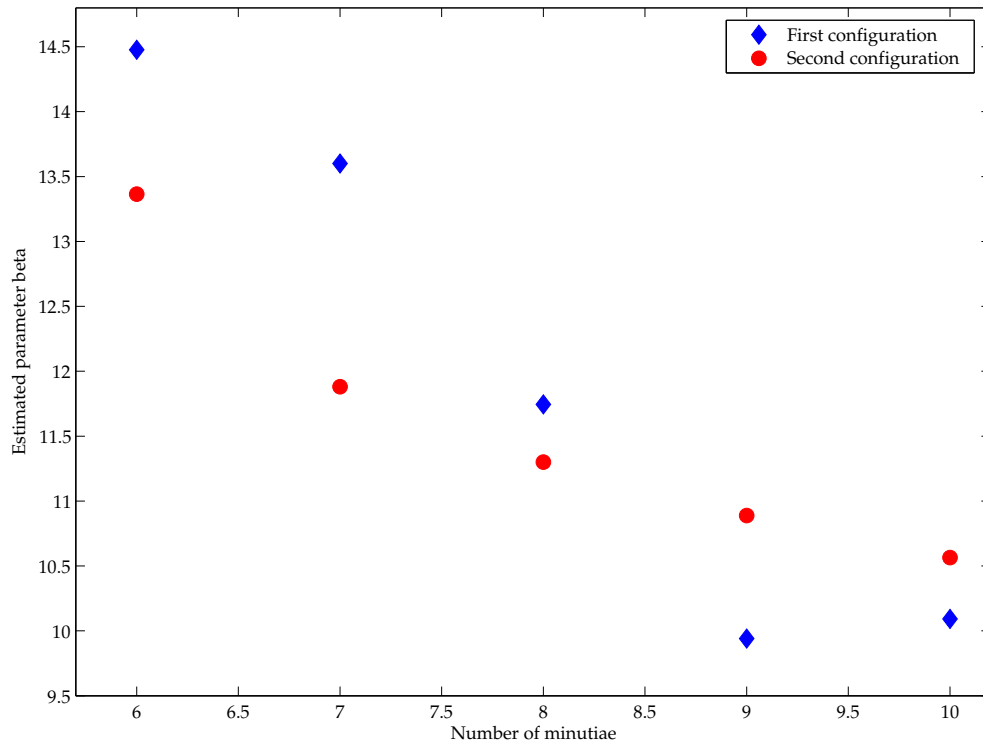


Figure 4.40: Regression of the parameter β on the number of minutiae in the configuration

Table 4.22: Estimators for the parameter β of the Weibull distribution

Nb of minutiae	parameter β
6	13.9
7	12.7
8	11.5
9	10.4
10	10.3

table 4.22. Of course, the distributions created using these estimated parameters do not correspond exactly to the distributions established from many impressions of the suspects finger. However, the approximation may be sufficient to obtain LRs which correspond closely to the ones observed when using the distribution obtained on the basis of multiple impressions. The comparison between the value of the numerators and of the LRs obtained based on the data on the one hand and those obtained when estimating the parameters using the equation 4.5 and the mean of the estimators for β obtained is the object of the next paragraphs. Correlations between the numerator and the LR obtained for a given mark will be investigated first, and then the Tippett plots obtained using the estimated parameters will be presented and analysed. As previously, the denominator used here is the same for either method of computation of the numerator (and based on a lognormal distribution fitted to the scores obtained by confronting the mark used as 'evidence' to the background database).

Comparison between numerators and LRs obtained by estimating the parameters based on data or by approximation using self-scores

On the first 6 minutiae configuration (and the configurations resulting when minutiae are added to it), the data concerning the numerator is different when comparing the two ways of obtaining the numerator for the distribution.

The explanation for the shape observed in figure 4.41 can be found in the two distributions used for within-finger variability, shown in figure 4.42. Below score values of approximately 3000, the value of the distribution obtained when using the within-variability data is higher than the one obtained using the self-scores; above scores of 3000, this relationship is inverted. The same value of the pdfs occurs twice, once on the left hand side of the mode, and once on the right hand side. For these two values of the data-based distribution, in one case the corresponding value of the self-score based distribution will be lower than the one observed (for scores below 3000) and once higher (above 3000).

The correlation coefficient for the numerator when 6 minutiae are used is reported, with all other correlation coefficients for the original minutiae configura-

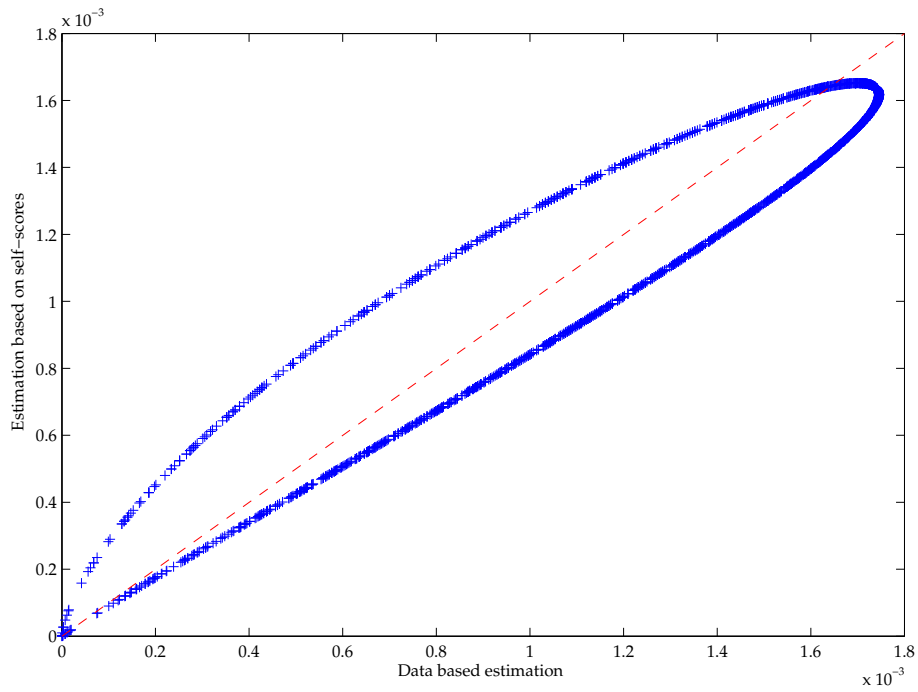


Figure 4.41: Numerators obtained when estimating the parameters of the Weibull based on the data on the abscissa and when estimating the parameters based on the model on the ordinate for the first 6-minutiae configuration

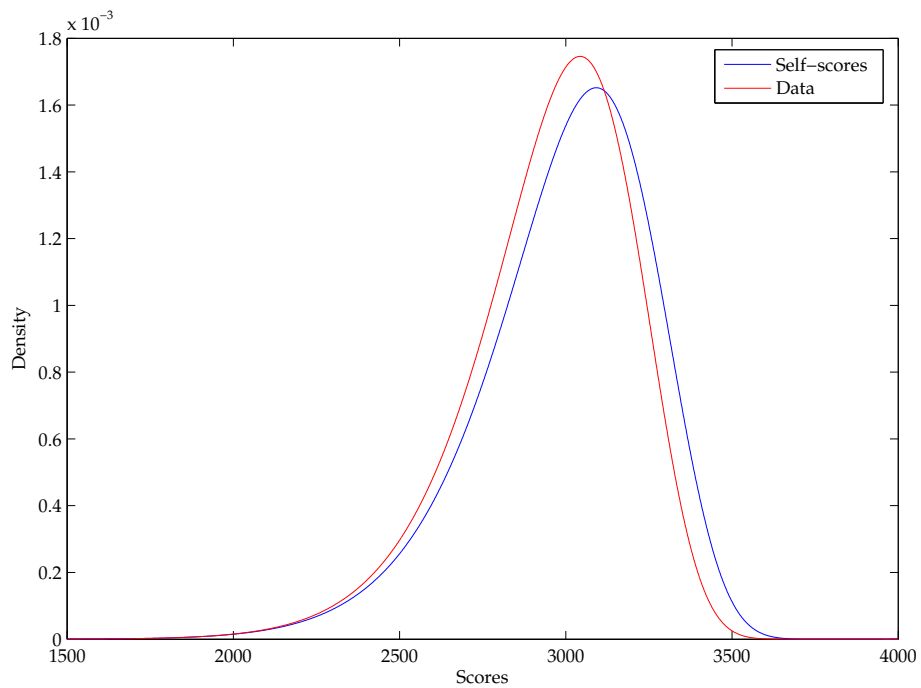


Figure 4.42: Illustration of within-finger distributions for 6 minutiae estimated based on data or self-scores

tions, in table 4.23. The correlation coefficients have also been calculated between LRs obtained when using the observed parameters and when using the parameters estimated, and are reported in the same table 4.23. In both cases, only results for comparisons between impressions known to come from the same finger are reported. The correlations obtained for the logarithm base 10 of the numerator for comparisons under \bar{H} are all above 0.99.

Table 4.23: Correlation coefficients obtained between numerators and LRs for the original 6 to 10 minutiae using Weibull parameters estimated on the basis of within-finger variability data and self-scores

	Numerator	Log ₁₀ Numerator	LR	Log ₁₀ LR
6	0.94	0.96	0.97	0.99
7	0.88	0.92	0.98	0.99
8	0.99	0.99	0.98	0.99
9	0.96	0.98	0.99	0.99
10	0.99	0.99	0.99	0.99

These correlations are extremely high, and tend to confirm the possibility of using estimated parameters instead of acquiring multiple appositions of the suspects finger. The same observations can be made on the second configuration. The correlations between numerators and LRs are reported for comparisons under H in table 4.24. Under \bar{H} , again, only correlations of the the logarithm base ten of numerators have been computed; these were again all above 0.99.

Table 4.24: Correlation coefficients obtained between numerators and LRs for the second 6 to 10 minutiae using Weibull parameters estimated on the basis of within-finger variability data and self-scores

	Numerator	Log ₁₀ Numerator	LR	Log ₁₀ LR
6	0.90	0.93	0.94	0.98
7	0.99	0.99	0.97	0.99
8	0.98	0.99	0.97	0.99
9	0.99	0.99	0.99	0.99
10	0.97	0.98	0.99	0.99

Again, the correlations obtained for the second set of configurations are very high, and therefore tend to show the validity of such a modeling approach. The advantage of this approach is that no high number of prints or marks must be acquired in order to model within variability for a given person. The correlations reported are based on all of the data. In some of the datasets, very high observations are present (outliers, which are very far away from the dataset). However, the exclusion

of these data has been investigated in order to examine their influence on the correlation coefficient, and, even though the correlation decreases when excluding those highest observations, it does not lower much when the \log_{10} of the results are considered (from 1 to 0.99, for the second 10 minutia configuration, where the 9 highest observations had been excluded). This is also why the logarithms of numerators have been preferred for the comparisons under \bar{H} . It is indeed in these comparisons, where numerators need to be computed in the extreme tails of distributions, that the largest differences were expected. However, it can now be confirmed that the order of magnitude between numerators (and consequently LR_s) computed on the basis of the approximation or estimations from data correspond, at least in order of magnitude. The Tippett plots for the original configuration, between 6 and 10 minutiae, are included below, juxtaposed with the Tippett plots where the parameter estimates are based on the data.

These results show that, based on 3 slap impressions from one finger, within finger variability can be estimated in an efficient and not very time-consuming way. While this approach has, up to now, been established and tested on data from a single finger, the results are promising. Tests have been carried out and are presented in the appendix and a further chapter (appendix A and chapter 6) on another donor. It is possible that using self-scores in this way, within-variability can be estimated without time-consuming data-acquisition. If the approximation using self-scores holds for another donor, within-variability is indeed a generalizable distribution, but only when taking into account the selectivity of the configuration used. This selectivity is here substituted by the maximum score obtainable for that configuration, which itself is approximated by using the AFIS to compare twice the same impression (and, for stability of the measure, by taking the mean of 3 scores obtained in this fashion).

The application of parameter estimation from self-scores to two fingers of another donor (D2) is presented in Appendix A. Overall, the detailed evaluation of the effect of the use of the approximation on the numerator, and therefore on the LR_s obtained, has shown that this approximation, although far from ideal, has very high probabilities of yielding very similar values as the estimation based on the data for both the donor on whose finger the model is established, as well as for another donor; generalizability is therefore possible. The results on donor 2 (presented in Appendix A do show some problems, but generally, large divergences between the approximated numerator values and those obtained from the data have a rather low probability of occurring. Improvements to this approximation could certainly lower the probability of obtaining numerator values that differ by more than an order of magnitude from what should be obtained, as seen from the data. The advantages of direct modeling of these parameters will be discussed in detail in the general discussion in chapter 7. Also, more work on the use of these approximated values is presented at the end of the chapter on between variability, where the effect of the approximations used on likelihood ratios is tested.

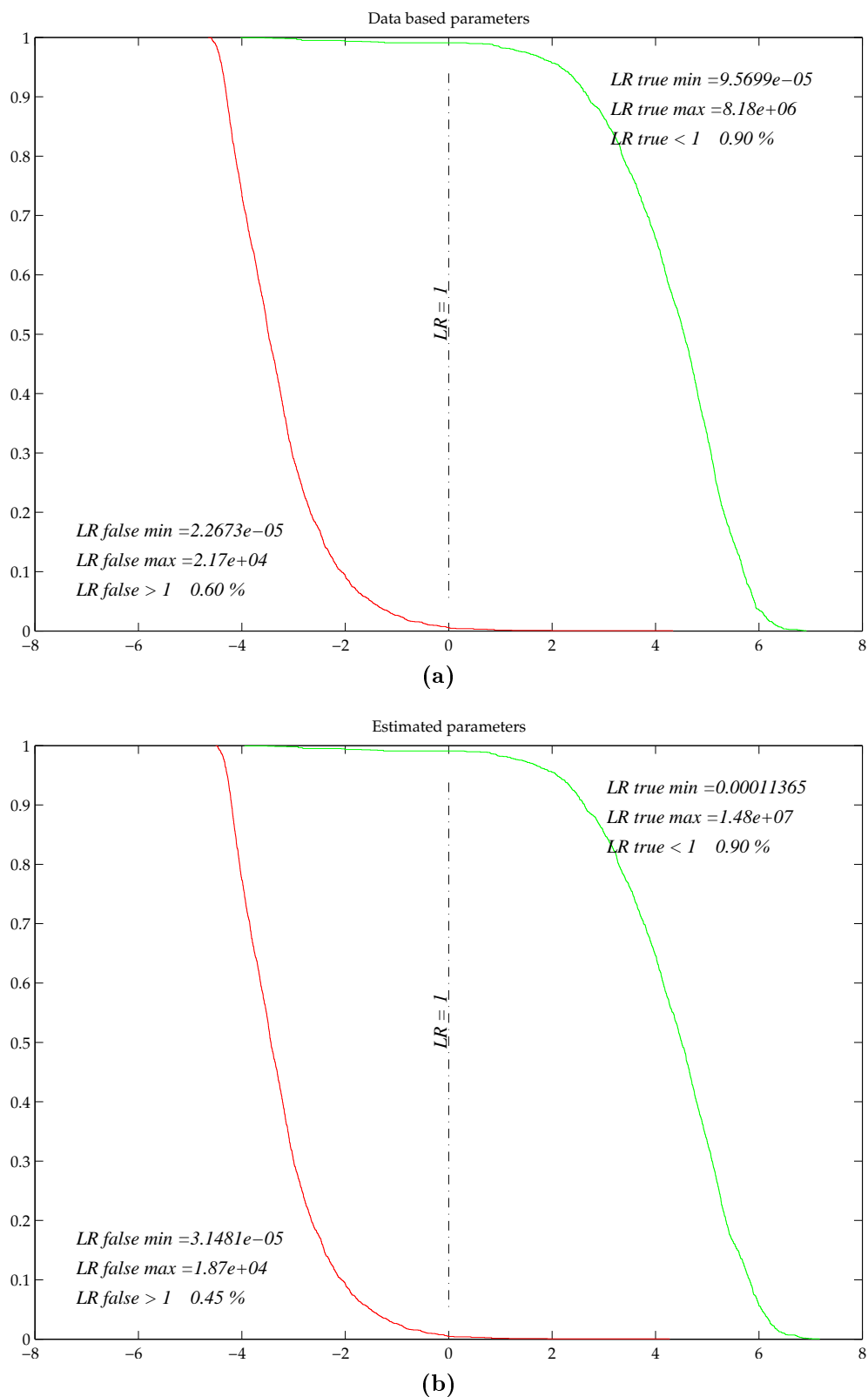


Figure 4.43: Tippett plots for the original 6 minutiae configuration using estimation of parameters for the within variability (a) based on the data and (b) based on self-scores and number of minutiae

4.7. Estimation of the parameters from the highest score possible for a given configuration

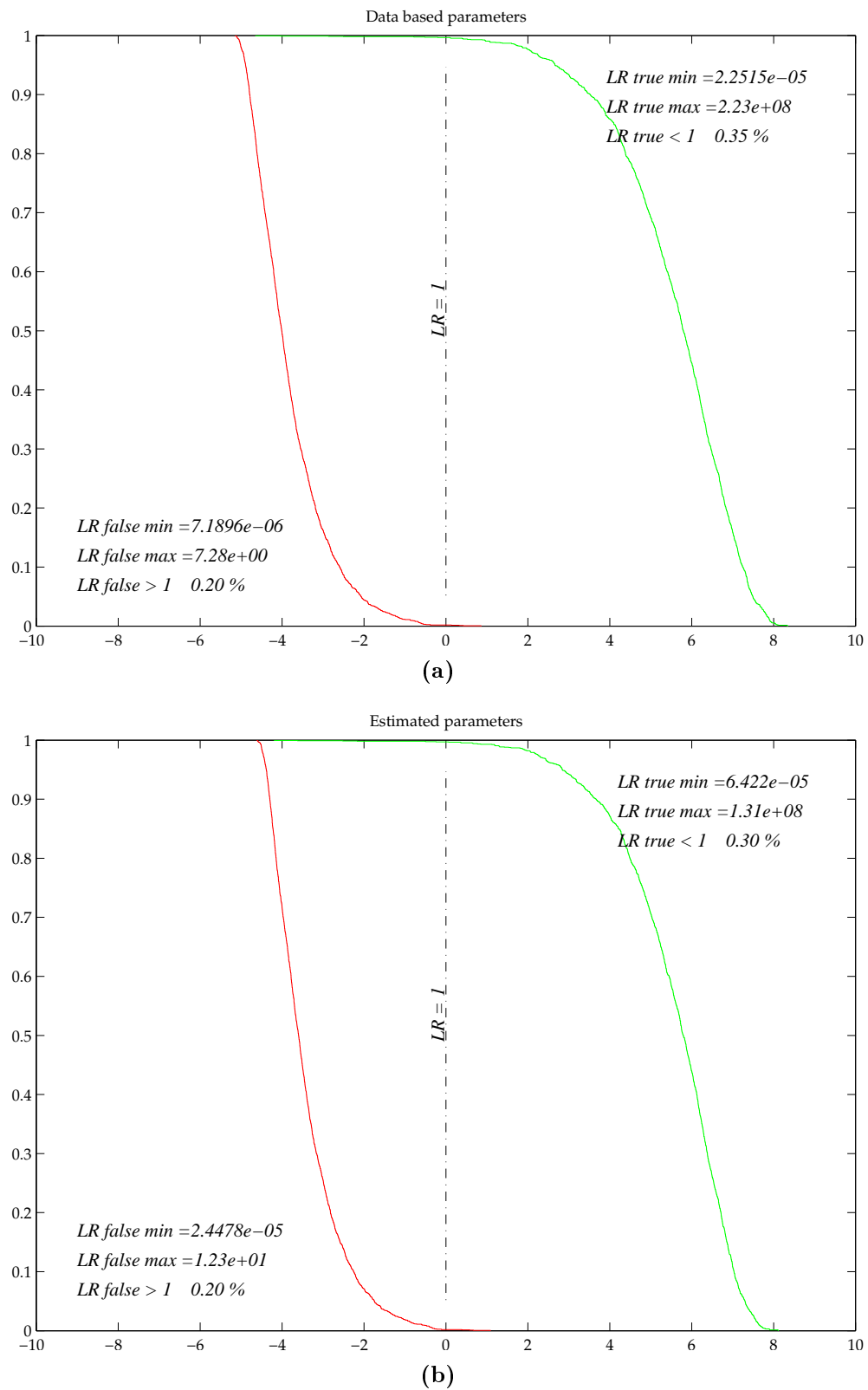


Figure 4.44: Tippet plots for the original 7 minutiae configuration using estimation of parameters for the within variability (a) based on the data and (b) based on self-scores and number of minutiae

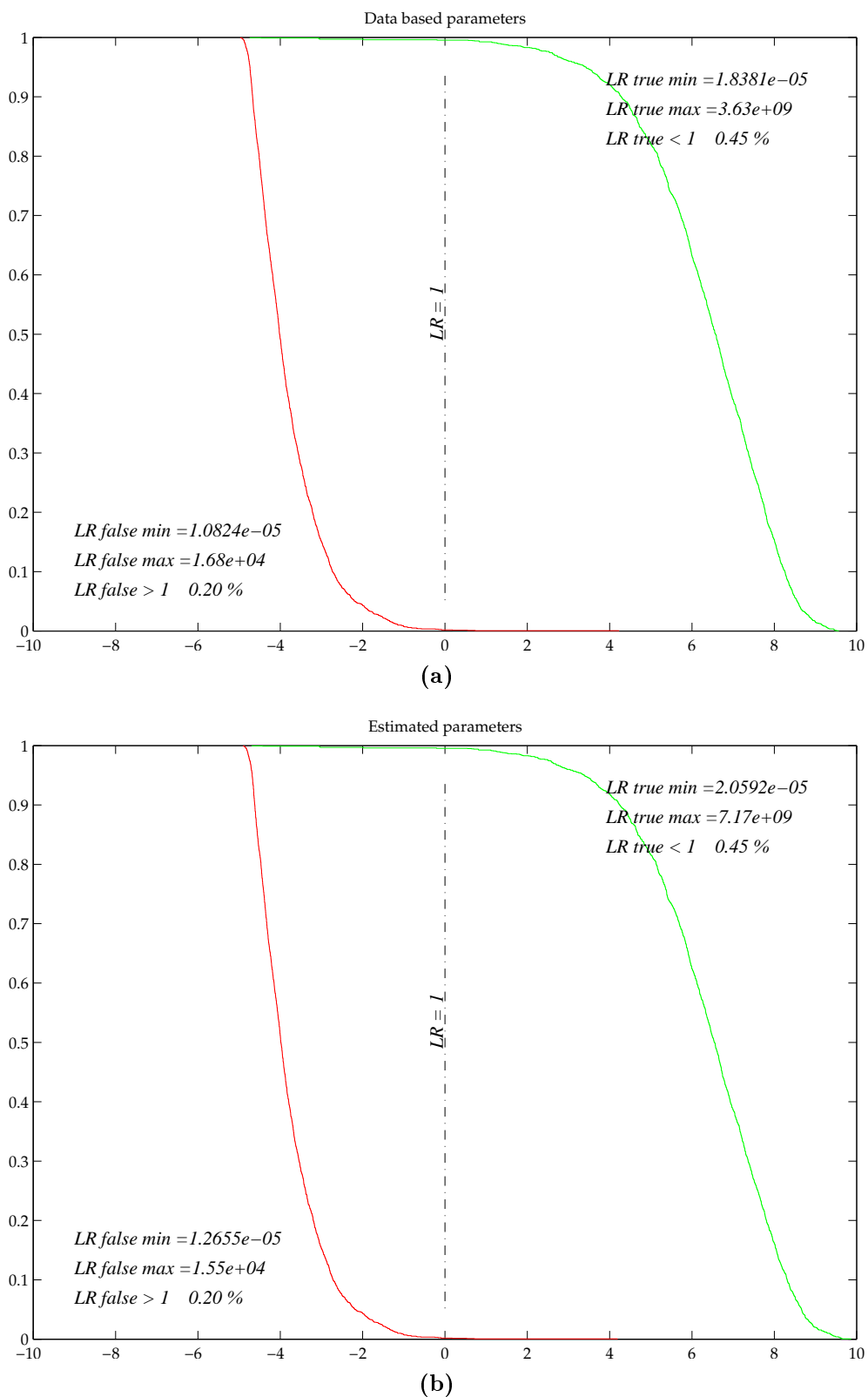


Figure 4.45: Tippett plots for the original 8 minutiae configuration using estimation of parameters for the within variability (a) based on the data and (b) based on self-scores and number of minutiae

4.7. Estimation of the parameters from the highest score possible for a given configuration

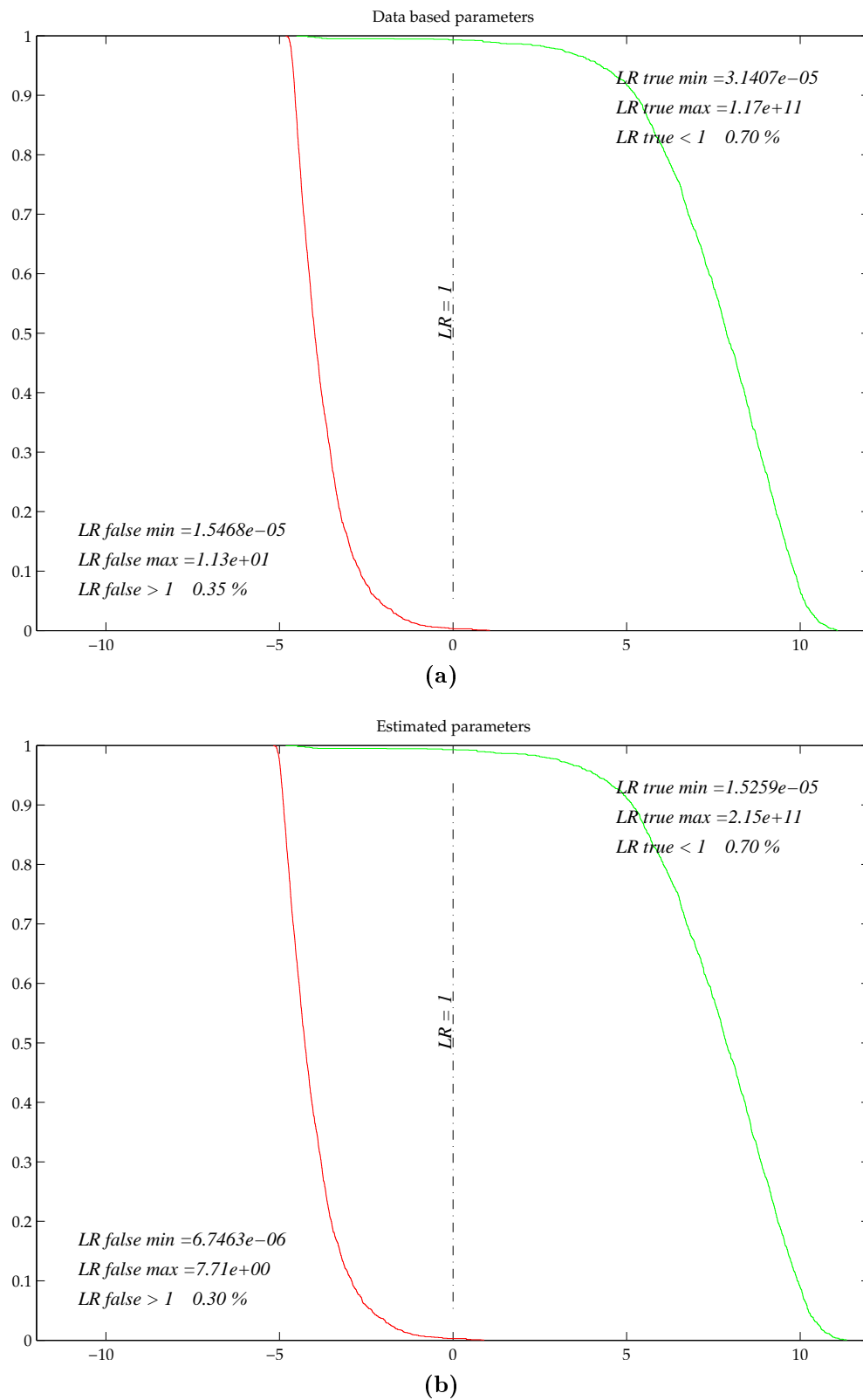


Figure 4.46: Tippet plots for the original 9 minutiae configuration using estimation of parameters for the within variability (a) based on the data and (b) based on self-scores and number of minutiae

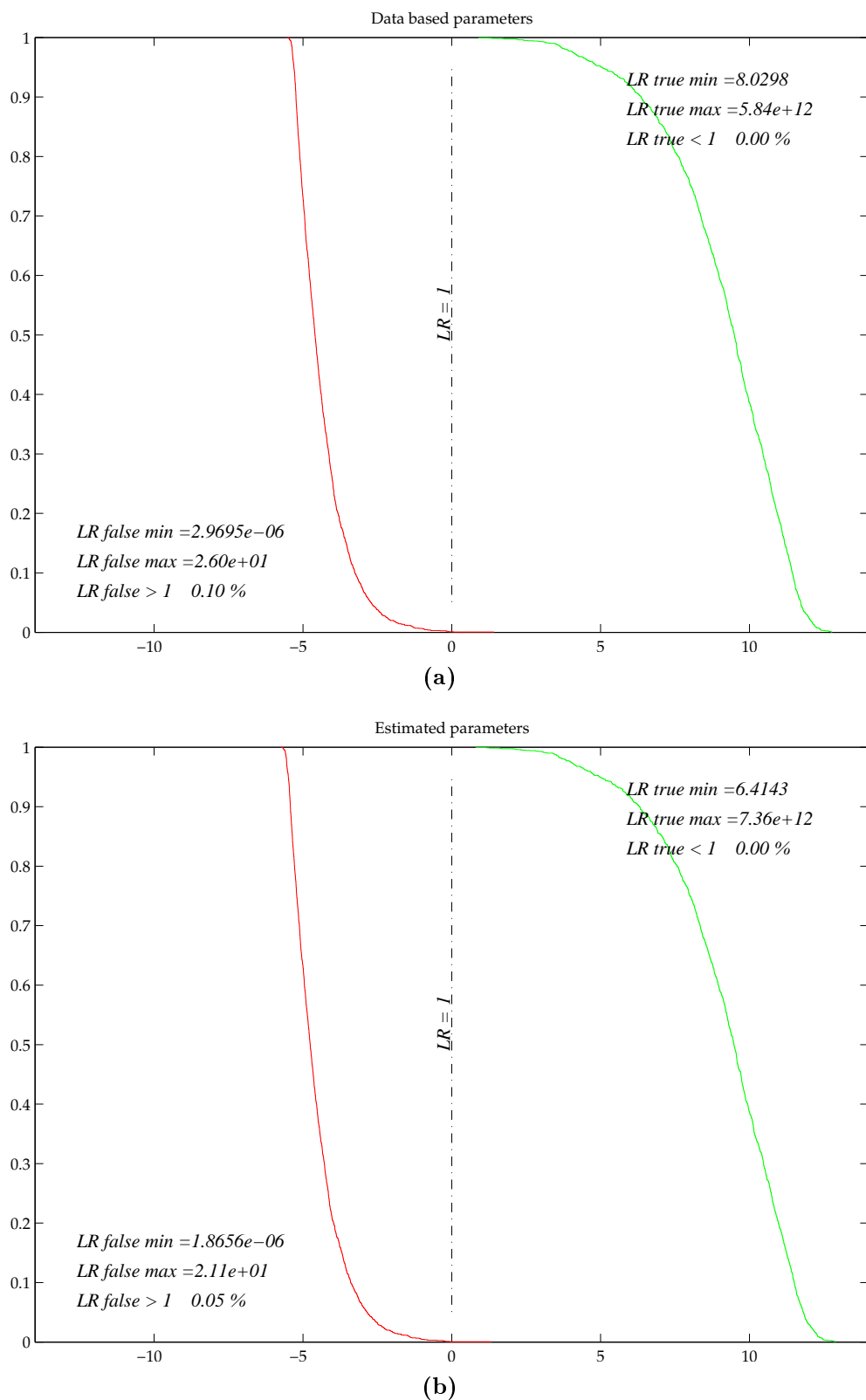


Figure 4.47: Tippet plots for the original 10 minutiae configuration using estimation of parameters for the within variability (a) based on the data and (b) based on self-scores and number of minutiae

The between-finger modeling used here, in order to obtain distribution values, does not truly allow a very precise estimation. Only the distribution of one mark has been used; in a casework scenario, this mark would be known, here, it is not. Therefore, these probabilities of obtaining scores above or below a certain value, while allowing to form a general idea of the probability of exceeding a limit, is not precise.

Chapter 5

Between-Finger Variability

5.1 Introduction

In order to be able to model the between-finger variability, the same questions need to be answered as those asked for the within-finger variability. First of all, a sufficient sample size needs to be determined, if this is possible with the dataset available. Then, the main questions to be answered are whether the distribution of scores obtained changes when only given general patterns or finger numbers are used. Of course, again, it needs to be investigated whether the between-finger distribution is dependent on the number and placement of minutiae: this time, this investigation is possibly less relevant from an operational point of view. It may, however, yield insights into the generalization possibilities of the distribution. It may be interesting operationally not having to extract all of the comparison scores of a mark to be evaluated when it is inserted into the database, then to fit a density function to these scores, in order to obtain the value of $f(s|\bar{H})$, but rather to have a generally applicable density (or family of functions) that can be employed directly. Not to fit a function to the data and only use observed frequencies is not a viable option. This is due to the fact that scores in the regions where LRs will generally be computed, in particular when H is actually true, are extremely scarce. The reason why LRs lend support to one or the other hypothesis is that observations are very improbable under one of the two hypotheses. The only way of not fitting a function and computing LRs is to use the proportion of observations at a given score, and to use some chosen constant for any score that hasn't been observed in the database, such as $1/n$, where n is the number of fingerprints in the database. This would result in the same probability for a score which is just above the highest score observed and a score that is, for example, 1000 above the highest observed score. This is not an approach which is considered rational here, since the probability decreases with increasing scores (above the mode of the distribution). This would therefore lead to unreasonably low LRs in support of H . Furthermore, while the extraction of all scores when comparing a given mark to the whole database is possible with the AFIS used here, this is due to a custom-made function (see B) allowing this automated extraction of all scores when a mark is compared to the whole database.

This is already an extension of 'normal' AFIS systems.

For these reasons, it is considered essential to fit a probability density function to the between-finger variability, and to try to reduce the data that needs to be acquired for the estimation of this function.

The ten print cards used in this thesis as a reference database are those that have been excluded from the Swiss central database when the central repository was purged (in function of the age of the donor). Within the central database, there are several sections: not only suspects' (and convicts') fingerprints but also immigrants' fingerprints; it is not known whether the ten-print cards used come from both databases, or are suspects' prints only. Not much is known about these fingerprints; they were excluded before the year 2003, when they were received at the University of Lausanne; when exactly they were inserted, excluded and whether the donors present are more frequently of particular ethnic groups than the general population is unknown, but likely due to the evolution of the Swiss population over the second half of the 20th century. A large majority of donors is male, however, since tenprints of females are designated using a color code; otherwise, the tenprint cards are totally anonymous.

For this reason, the frequencies of general patterns (as classified automatically by the system) are compared to frequencies previously published in the literature (see chapter 5.2 below).

5.2 Description of the general patterns present in the database

5.2.1 Material and methods

Here, the general patterns attributed automatically by the system have been used. Four general patterns are used by the system: Right and left loop, whorl and arch; an 'unknown' category is also used. The system automatically extracts ridge flow, and determines the placement of the centre and the delta(s); general pattern is then attributed, most probably based on this information. Again, the way in which general patterns are determined by the system is based on proprietary algorithms. The system over-classifies general patterns. This means that several general patterns are attributed to some fingers, so as not to exclude a part of the database from a search based on an erroneous information. Indeed, it is far from trivial to attribute general patterns to fingerprints in an automated way. Therefore, rather than to risk excluding a potential candidate print wrongly based on general pattern information, all general patterns that the system considers to be possible given the characteristics of a print, are saved. Frequencies of general patterns when not excluding over-classified prints are presented in table 5.1; here, every time a finger has been classified as a given general pattern it has been considered as being of this pattern, regardless of whether there was over-classification of that pattern. This means that

a finger that has been classed as right loop and whorl will be counted as both right loop and whorl and will be included twice in the frequencies presented. Since the divisor remains the total number of fingerprints, the total of the percentages shown for each finger is superior to 100%. In table 5.2, the proportions for each general

Table 5.1: Distribution of general patterns in the database counting the over-classed for each general pattern included in classifications

Finger Number	RT	RF	RM	RR	RL	LT	LF	LM	LR	LL
Right Loop	48.6	34.3	74.8	49.5	83.2	0.4	23.2	4.6	1.4	0.9
Whorl	56.1	44.6	28.0	61.7	35.6	42.7	39.4	25.5	48.9	27.7
Arch	3.9	20.4	12.7	5.4	5.6	5.4	21.4	16.3	7.2	7.7
Left Loop	0.5	26.1	3.6	1.7	0.8	61.3	43.3	75.9	64.3	87.4
Unknown	1.7	5.6	1.8	2.2	2.9	2.1	5.3	2.2	2.1	3.5

pattern obtained when excluding the over-classed prints are presented.

Table 5.2: Distribution of general patterns in the database not counting overclassified dividing by uniquely attributed general patterns

Finger Number	RT	RF	RM	RR	RL	LT	LF	LM	LR	LL
Right Loop	43.6	26.7	70.6	38.4	77.2	0.1	10.5	0.5	0.3	0.1
Whorl	52.8	45.2	23.3	57.3	18.1	37.8	40.3	21.7	41.3	11.1
Arch	1.6	7.9	3.0	1.1	0.6	3.1	6.3	3.7	1.3	0.8
Left Loop	0.1	12.7	0.9	0.5	0.2	56.7	10.5	71.4	54.5	83.3
Unknown	1.8	7.5	2.2	2.7	3.9	2.3	7.3	2.7	2.7	4.8

Finally, in table 5.3, in presence of over-classification, the print in question has been counted to be within the first class in the list of possible classes determined by the automatic algorithm. Here, therefore, each print is attributed to exactly one of the possible classes.

As a comparison, numbers drawn from the data published on <http://home.att.net/~dermatoglyphics/mfre/>, coming from the FBI's database and compiled in 1993, are reproduced in table 5.4. This data is based on approximately 18 million individuals.

Also for comparison purposes, the numbers published by Cummins and Midlo (1943) are presented in table 5.5. These numbers are based on 5000 individuals (50000 fingerprints) and help to assess the variance expected between different databases. When comparing these frequencies, it is apparent that there are differences. In particular, the automatic classification results in more unknown general patterns. In the NCIC data consulted (table 5.4), these unclassified patterns are

Table 5.3: Distribution of general patterns in the database counting only the first classification

Finger Number	RT	RF	RM	RR	RL	LT	LF	LM	LR	LL
Right Loop	45.6	29.0	70.9	45.4	79.0	0.2	17.6	2.7	0.8	0.4
Whorl	50.2	36.2	20.5	49.7	16.5	36.4	32.1	18.8	35.9	11.6
Arch	2.3	9.3	4.8	1.7	1.1	3.5	8.0	5.6	1.9	1.6
Left Loop	0.2	19.9	2.0	1.1	0.5	57.8	37.0	70.8	59.3	82.8
Unknown	1.7	5.6	1.8	2.2	2.9	2.1	5.3	2.2	2.1	3.5

Table 5.4: Distribution of general patterns in the 1993 FBI database

Finger Number	RT	RF	RM	RR	RL	LT	LF	LM	LR	LL
Right Loop	50.8	34.5	72.5	49.7	82.3	0.5	16.9	1.6	0.4	0.1
Whorl	45.8	32.5	17.9	46.8	15.9	34.3	29.6	17.2	34.5	11.3
Arch	2.9	13.9	7.5	2.1	1.3	5.2	13.8	9.8	2.9	1.9
Left Loop	0.4	18.6	1.7	1.2	0.3	59.8	39.2	71.0	61.9	86.5
Unknown	0.1	0.4	0.4	0.2	0.2	0.1	0.4	0.4	0.3	0.2

Table 5.5: Distribution of general patterns according to Cummins and Midlo (1943)

Finger Number	RT	RF	RM	RR	RL	LT	LF	LM	LR	LL
Right loop	56	32	75	56	85	0.2	23	2.5	0.5	0.02
Whorl	44	39	22	43	14	34	37	23	30	10
Arch	2.5	11	6	1.8	0.5	4.5	10	8.0	2.8	1.2
Left loop	0.2	26	2.5	1.5	0.2	66	38	73	69	90
Unknown*	15	41	29	21	22	12	32	26	25	26

*Absolute numbers; unknown fingers not taken into account in the total.

missing or amputated fingers as well as completely scarred patterns (NCIC Codes XX and SR). In the automatically classified data used here (tables 5.1, 5.2 and 5.3), instances where the program considers all patterns possible are included in the 'unknown' class. Similar proportions of patterns are obtained when comparing either the over-classified for each pattern, or when taking into account only the first pattern in case of over-classification, to the FBI data. The FBI data used here is based on males only, while the data in the system contains all ten print cards received from the Swiss central database. Very few females are present, however, therefore this cannot explain the difference observed.

The three tables established from the data used in the present thesis (tables 5.1, 5.2 and 5.3) show some divergences; in particular, when over-classified fingerprints are not taken into account, fewer loops are obtained than when either all classes are counted or when only the first pattern is counted. When all classifications are counted, more whorls are present than when either over-classifications are excluded or only the first classification is taken into account.

Generally, the percentages obtained here are not completely divergent from the previously published data. Some large differences are, however, present. In right thumbs, here, more whorls than loops are detected, while both in the FBI database and the database published by Cummins and Midlo (1943), more right loops than whorls are present, for example. Trends are preserved (i.e. most radial loops are found on forefingers with respect to the other finger numbers), and differences are similar in size as those observed between the two previously published data sources. The first classifications are retained for further use, since they seem to be the least dissimilar from this previously published data. This may indicate that the classifications attributed to each fingerprint are ordered in the sense that the most probable general pattern is in the first place when using the automatic classification algorithm.

The differences between the general patterns in the presently used data and the previously published works do not invalidate the use of our data, since the relative frequencies of general patterns are comparable. This database will therefore be considered as a random sample of fingerprints from a population of suspects, and be used as such.

5.3 Evaluation of sample size

5.3.1 Material and Methods

Images

The data used are the images of the right thumb of donor 1 that have already been employed for the description of the within variability. These images are of fingermarks developed using DFO, Ninhydrin, dusting and Cyanoacrylate. As a database, a maximum of 685'245 inked fingerprints are used. These fingerprints

come from a little more than 68'524 ten print cards. The exact number of ten-print cards is of 68543; this is not exactly the number of fingerprints divided by 10, because some of the ten print cards do not show all ten fingers due to amputation or momentary lesions. Such events result in scores of 0 and have been excluded from the analyses. It is considered that they do not need to be considered in the between finger distribution.

Configurations

The same configurations as for the within variability of Donor 1 have been used. These configurations are:

- The first configuration, increasing from 6 to 10 minutiae, shown in figure 4.27.
- A second configuration, increasing from 6 to 10 minutiae, shown in figure 4.29.

The scores finally used are those issued from these 10 different configurations, divided by development method, compared to the database of fingerprints.

Methods

Subsamples of the whole database have, as in section 4.2 where the sample size for within variability was determined, been used. QQ-plots have been established in order to investigate which minimum sample size allows the estimation of the distribution of scores in a robust manner. It is, of course, possible that the overall sample size, of 685245, is insufficient, and that stability is therefore not attained. This investigation will be carried out on the basis of one mark compared to the database.

In a second step, the Kolmogorov-Smirnov test for the comparison of the distribution of two samples has been used in order to assess whether two samples of a given size result in acceptance of the hypothesis of equal distribution. Also, the evolution of the test statistic, $t = \max(|F_1(x) - F_2(x)|)$, as a function of sample size has been studied.

5.3.2 Results

First, successively smaller samples have been compared using QQ-plots. The plot comparing two samples of 5353 observations is shown in figure 5.1. The correspondence between these two samples is very near perfect, leading to the conclusion that this sample size is sufficient. It was then decided, since only few of the possible QQ-plots for this sample size can be analysed, to take a more automated approach.

Divisors were chosen between 2 and 2048 (in steps of 2, resulting in sample sizes of between 342622 and 335 scores). Then, two random samples of the overall size divided by the divisor were drawn, and these samples were compared using a Kolmogorov-Smirnov two sample test. The test statistic has then been plotted

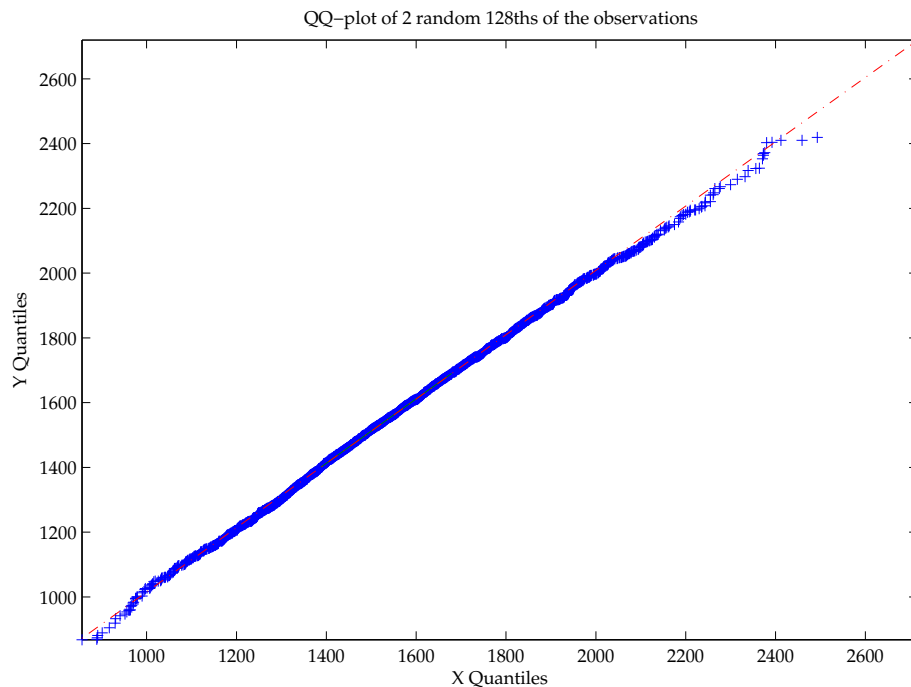
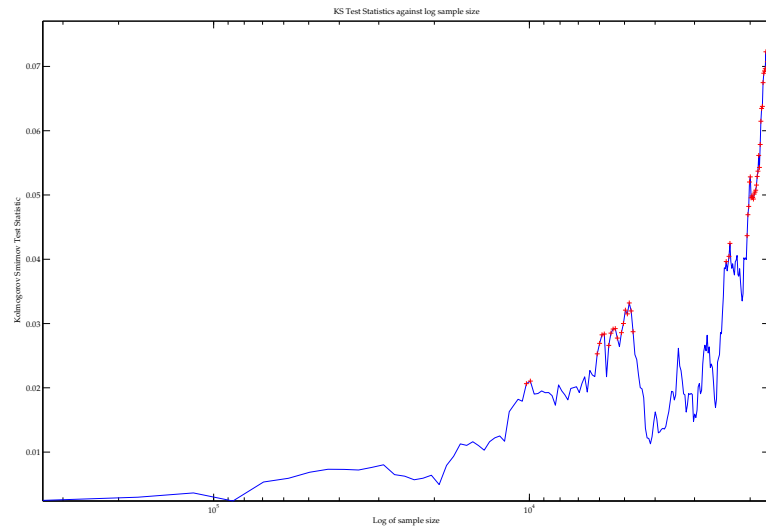
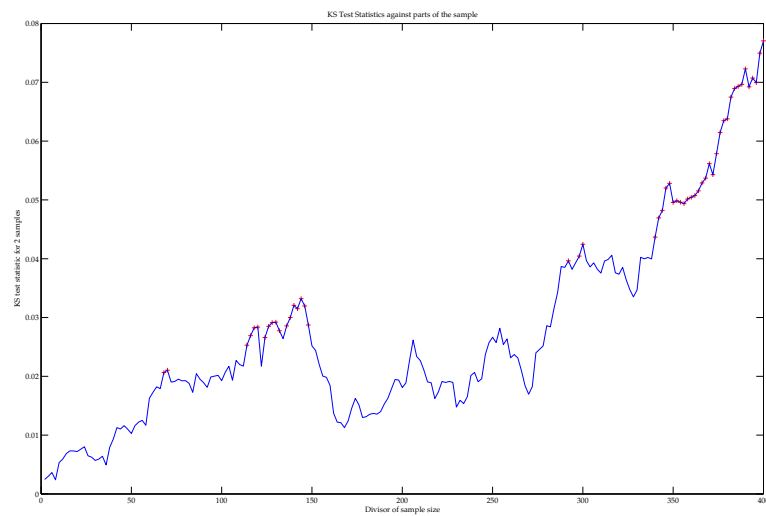


Figure 5.1: Comparison between two samples of 5353 observations of the between variability

against the divisor as well as the sample size; these plots are shown in figure 5.2. In the QQ-plot shown in figure 5.1 demonstrates that linearity is present; sample sizes of 5353 observations are therefore sufficiently large to obtain samples following the same distribution. In figure 5.2 a), it is shown that for sample sizes of more than 10000, none of the tests carried out refuses the hypothesis of similarity. Even with less than 10000 scores, only in reasonably few cases is this hypothesis rejected. When looking at figure 5.2 b), it is seen that a divisor of 68 or less (for a sample size of 10077) results in no refusal of the hypothesis of same distribution, and that a monotonous increase in the test statistic is observed from a divisor of 330 upwards (sample sizes of 2076 or less). Overall, samples of more than approximately 5000 observations yield reasonably stable distributions, but at least 10000 observations should be used if they are available. This result has been tested on other datasets. The first configuration has been used, and the marks visualized using different development methods and including up to 10 minutiae have been compared to the database. Then, the same approach as above has been used for each of these datasets, and there are 5 of the tests carried out refuting the hypothesis for a configuration of 9 minutiae, and 1 test refuting the hypothesis for configurations of 10 minutiae for sample sizes of more than 10000. The tests have been repeated for the second configuration as well. For configurations of 8 minutiae, 4 tests are failed and for configurations of 10 minutiae the test is failed once above a sample size of 10000. This does not show that this sample size is insufficient; even similar samples are expected to fail the test in 5% of tests carried out; here, the proportion of tests



(a)



(b)

Figure 5.2: Kolmogorov-Smirnov Test Statistics as a function of a) the log 10 of the size and b) the divisor of the sample used. In red, the comparisons where similarity of samples was refuted by the test.

that are failed remains below 5%.

These results also show that the presently available sample is largely sufficient for reliable estimation. Furthermore, meaningful comparisons between the different finger numbers can be carried out, since for each of these datasets (fingers 1 to 10), over 68500 scores are available.

Therefore, **the hypothesis 2a: The density used for modelling the between finger variability becomes stable as a given number of observations is reached is verified, and the minimum number necessary is of 10000 fingerprints.**

5.4 Dependence of between finger variability on finger number and general pattern

5.4.1 Introduction

The goal of the present section is to describe the influence of finger number and general pattern on the between-finger distribution of scores. A major difference with respect to previously published data is that here, the general patterns are classified automatically; furthermore, there is so-called overclassification present. This means that a given fingerprint may be associated with several general patterns, which is not the case when using manual classification. Finally, only 4 classifications are possible: right and left loop, whorl and arch (as well as unknown).

In the following section, a distribution is fitted to the between-finger data in order to be able to compare results on different general patterns more easily. Finally, it is considered that the development technique used for the visualization of the mark confronted to the background database may have an influence; therefore results are obtained separately for marks developed using different techniques.

5.4.2 Material and Methods

The images and configurations used as marks are the same as described above (section 5.3.1). As a database, the full set of ten print cards has been used for the examination of the influence of finger number and general pattern.

For both parts of the present section, concerned with finger number and general pattern, it is considered that as soon as a distributional difference is discovered, the hypothesis of dependence of the distribution on the variable examined is shown. If such a dependence exists, even in only some cases, then the variable will need to be taken into account systematically.

The marks from donor 1 all come from her right thumb: observations of right thumbs will therefore be compared to the other finger numbers. No comparisons between the distributions obtained when such a mark from the right thumb is compared to right middle and right ring fingers, for example, has been carried out.

Similarly, these marks come from a right loop; comparisons have therefore been carried out between the results obtained when a database containing right loops only is used, and the results obtained when only whorls are used. Arches and radial loops have not been used, due to the small number of observations obtained.

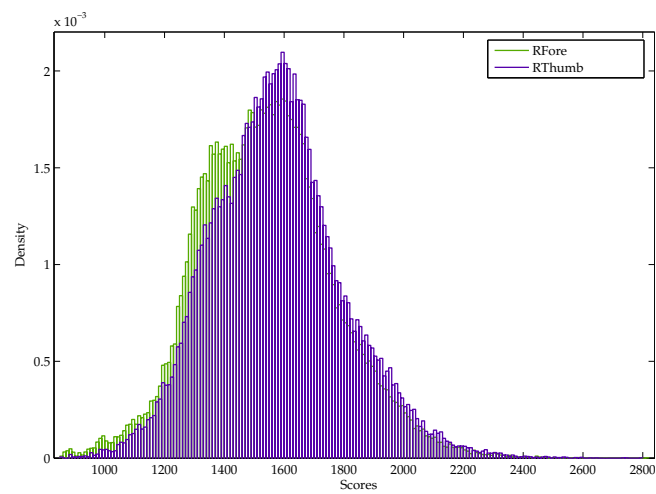
5.4.3 Results

The influence of finger number on the between-finger distribution

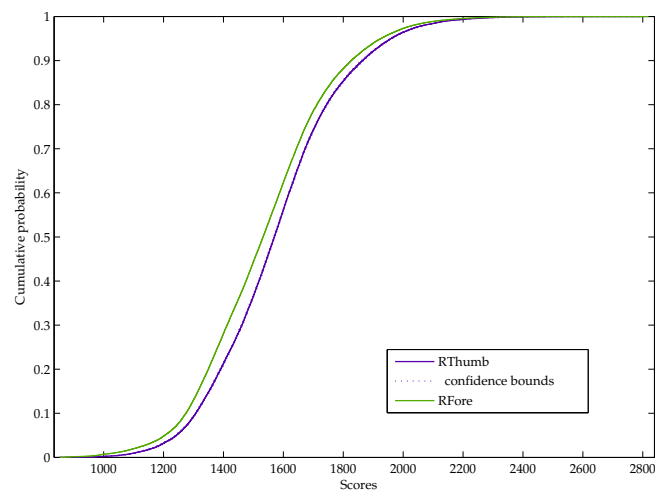
When the right thumb is compared to the right forefinger, the Kolmogorov-Smirnov test clearly rejects the hypothesis of the two samples coming from the same distribution ($p < 10^{-100}$). Visually, the histograms differ (see figure 5.3 a). In particular on the left of the mode, the histogram issued from forefingers has a shoulder that is absent in the thumbs' distribution. The empirical cumulative distribution function (ecdf, see figure 5.3 b) of the right forefinger is outside of the confidence intervals of the thumbs' ecdf. Only the QQ-plot (see figure 5.3 c) shows distributional similarity between the two sets of observations. For the comparison between the right thumb and the right middle finger, the results are less clear. Although the Kolmogorov-Smirnov test still rejects the hypothesis of equal distribution, the p -value is now higher ($p = 1.6 \cdot 10^{-5}$), and the plots are less dissimilar (see figure 5.4). When consulting these graphs, there is no alarming evidence of distributional differences between the two fingers. For the right ring finger and the right little finger, the results are similar to those obtained for the right middle finger. Although the Kolmogorov-Smirnov test rejects the hypothesis of distributional similarity ($p = 7 \cdot 10^{-10}$ and $p = 2 \cdot 10^{-8}$), the different plots (histograms, ecdf and QQ-plot, not shown) do not indicate great differences between the distributions of the thumbs and those two fingers.

The comparison between the right thumb and the left thumb, the left forefinger, the left middle finger, the left ring finger and the left little finger result in similar observations as those for the right forefinger: a very clearly negative result from the Kolmogorov-Smirnov test ($p = 2 \cdot 10^{-77}$, $p = 9 \cdot 10^{-45}$, $p < 10^{-100}$, $p < 3 \cdot 10^{-100}$ and $p < 10^{-100}$, respectively), with, again, a clear difference to the left of the mode, where the histogram of these fingers show a second, smaller mode, and ecdfs that are quite separated.

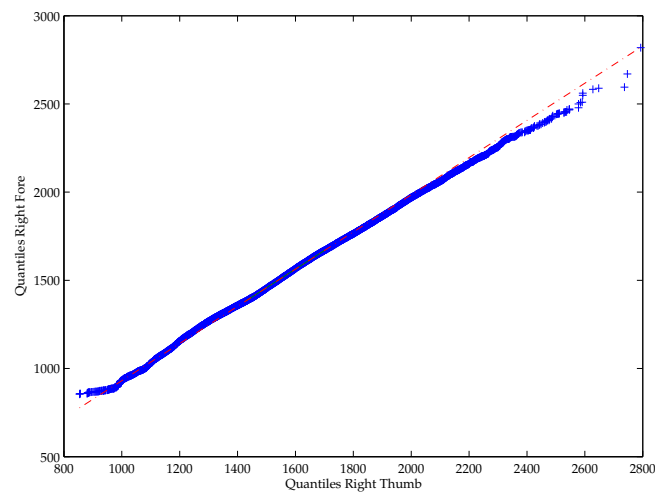
When the results obtained from the comparison of several marks (all those developed using cyanoacrylate for 6 minutiae configurations) to the database are compared between different finger numbers, these results can be verified by observing the overall behavior of the p -value of the Kolmogorov-Smirnov test. Some of the comparisons between the right thumb and the right middle finger pass this test (i.e. the hypothesis of both being samples issued from the same distribution is not rejected), and the p -values obtained in these comparisons are overall higher than those observed when comparing the right thumb to the right forefinger. When comparing the right thumb to the right ring finger, the p -values are slightly lower than



(a)

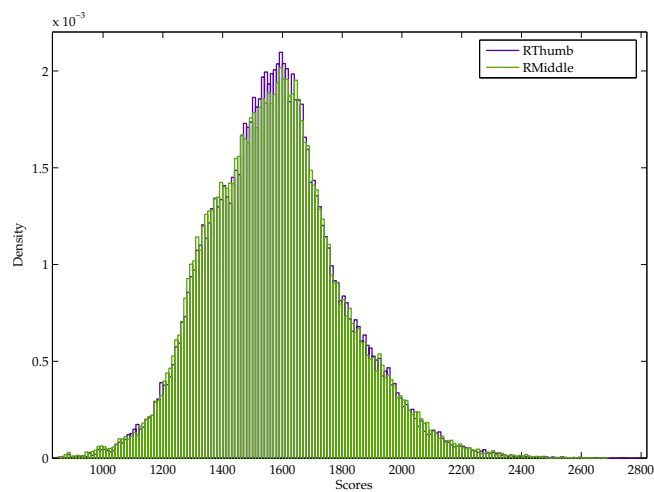


(b)

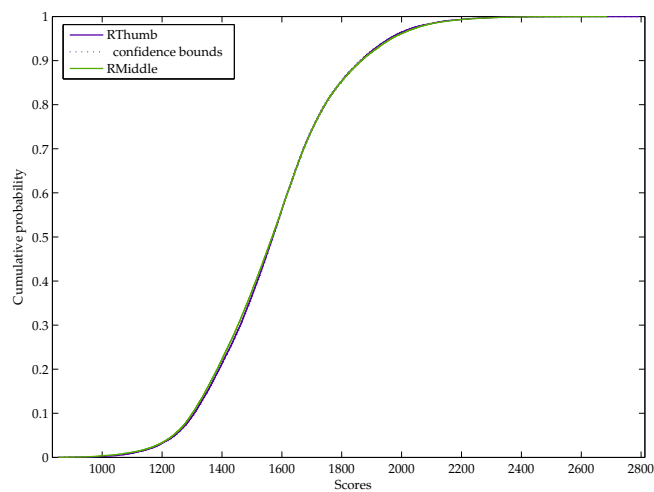


(c)

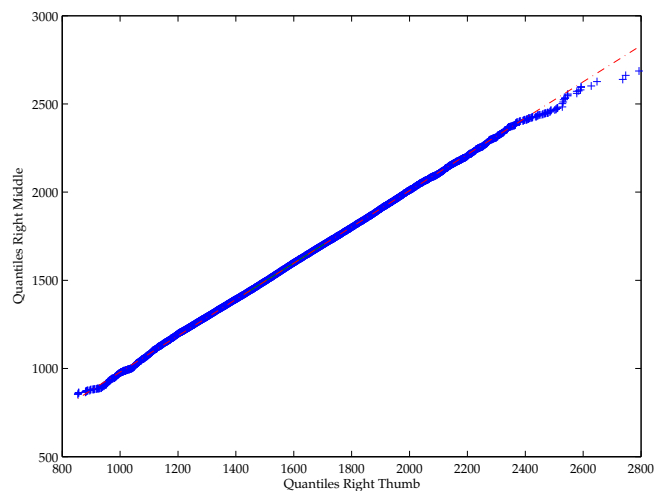
Figure 5.3: Comparison between the distributions obtained when comparing one mark against right thumbs and right forefingers a) histograms b) cumulative distribution functions and c) QQ-plot



(a)



(b)



(c)

Figure 5.4: Comparison between the distributions obtained when comparing one mark against right thumbs and right middle fingers a) histograms b) cumulative distribution functions and c) QQ-plot

for the middle finger, while being higher than for the right forefinger. Overall they are sufficiently high to accept the similarity of the distributions in view of what has been seen in figure 5.4, despite the rejection of this hypothesis by the formal test. The comparison between the right thumb and the right little finger again results in similarity of distributions in some cases, but in one case (for one mark) a clear divergence between the distributions is observed: this would tend to show that the similarity of distributions between different fingers also depends on the mark itself. Here, in particular, all marks used show the same configuration of minutiae, and therefore, the differences between marks are at a minimum. For the left thumb and the left forefinger, most p -values are quite high (i.e. close to acceptance to the hypothesis of identical distributions), with some exceptions. Again, this shows the distributional dependence of the between variability on the mark itself, and not only the minutia configuration. In the case of the left middle and ring fingers, the result from above is simply confirmed: the distributions of this finger and the right thumb are different. The difference between distributions is greatest between the right thumb and the left little finger.

Overall, from these results, it can be concluded that **when a mark is found where the source finger can be determined** (such as in anatomical sequences and the placement of several fingerprints on an object), **the between variability distribution needs to be based on the comparison of the mark to a reference database from the same finger**, although some fingers yield between-finger distributions that are more similar than others. Here, it has been observed that when a mark from a right thumb is compared to right thumbs on one hand and to right middle fingers on the other hand, similar distributions are obtained; this does not change the conclusion that a database from the same finger as the finger at the origin of the mark must be used.

On the other hand, when the finger number of the finger that left the mark is unknown, a stratified approach could be used (e.g. a mixture of distributions weighted by the relative frequency of occurrence of each finger in marks could be employed); in the following, a different view will be taken. The simplest way of extracting a between-finger variability is to compare the mark to the whole database. This is the best way of acquiring the general between-finger variability. Rather than to be based on published data that is not necessarily based on the proper database, the actual database of the considered population is used in this approach. There are therefore two arguments for simply comparing the mark to the database rather than to use a weighted mixture of distributions: the first one is that the proper population is included in this approach, while the second argument is simplicity.

Fitting of a distribution

Before investigating the impact of general patterns on the between-finger distribution, it has been decided at this point to try to find a distribution to fit to the data of between variability. The reason for fitting a distribution is that comparisons

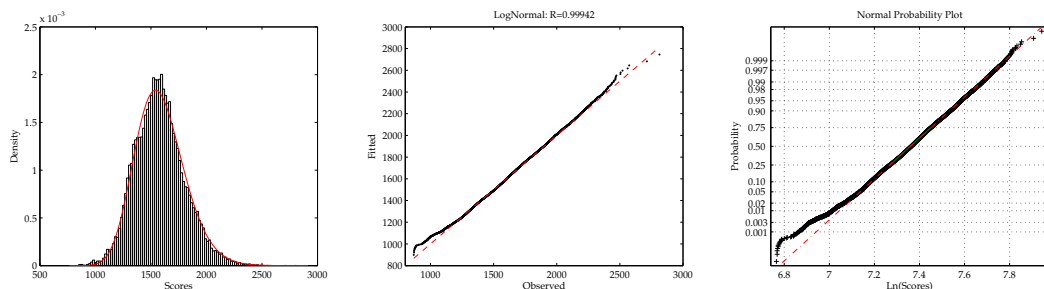


Figure 5.5: Comparison between the observed and the theoretical lognormal distribution. From left to right: Histogram and density, QQ-Plot, and a normal probability plot for the natural logarithm of between-finger scores obtained using a mark showing the original 6-minutiae developed using cyanoacrylate

between distributions will be easier. Secondly, from a more operational point of view, again, nonparametric estimation has been discarded (due to data-dependence issues). The simplest approach would have been to use the frequencies of scores observed in the data; this is not deemed useful here, since densities will need to be estimated in the far right tail of between-finger data, where no datapoint has been observed. Finally, the data quite closely follows a parametric distribution: the lognormal distribution (that is also mentioned in the literature, see Wein and Baveja (2005)). The probability density function of the lognormal distribution is

$$f(x|\mu, \sigma) = \frac{1}{x\sigma\sqrt{2\pi}} e^{-\frac{(\ln x - \mu)^2}{2\sigma^2}} \tag{5.1}$$

where μ and σ are the parameters, that are in themselves the mean and standard deviation of the natural logarithm of the variable. If X follows a lognormal distribution, $\ln(X)$ follows a normal distribution.

The lognormal distribution, while fitting the between data of some of the marks (6 minutiae, first configuration, developed using cyanoacrylate) closely, sometimes does not fit a part of this data. Some occurrences have been discovered where a shoulder is present on the left of the mode. For an example, see 5.5 a), where both observations can be made: a close fit of the lognormal distribution to the right of the mode, as well as a slight discrepancy between the data and the fitted model to the left of the mode, where a small shoulder is present in the observed data. Formal distributional tests have been applied to the natural logarithm of the data and the normal distribution. These different tests (Shapiro-Wilks, Lilliefors and Jarque-Bera tests) all refute clearly the hypothesis of normality of distributions of $\ln(X)$, for all 33 tested between variabilities. When considering diagnostic plots, however (see figure 5.5), deviances are relatively small and of little consequence. As this figure shows, the fit between the data and this distribution is quite good; a few problems are visible (which are present on other marks as well), and are enumerated below:

1. The mode of the observed distribution is higher than the mode of the theoret-

ical distribution. This difference may lead to the rejection of the hypothesis that this data follows a lognormal distribution. Here, this difference is not large enough to completely ignore this model for the data; indeed, at worst, the difference in density observed is of a fraction of an order of magnitude.

2. On the QQ- and the normal probability plots, a deviation in the left tail is visible. It concerns less than 1% of the data, and should not have an influence on casework LR that is of any consequence, since it concerns very small scores. Generally, casework LR are expected to be in the right tail of the between-finger distribution.
3. Small deviations are also present in the right tail, as evidenced again in the QQ- and probability plots. These deviations are small enough to be reasonable if the data is actually issued from a lognormal distribution.

The lognormal distribution also has many advantages, in particular as compared to another approach that was considered, the mixture of normal distributions: first of all, the lognormal distribution only models positive values, and the scores used here are strictly positive (after the elimination of zeros due to fingers that are absent or too scarred for analysis). The use of a distribution that is defined in the positive domain avoids truncating a distribution that includes zeros, or even negative numbers. Secondly, the lognormal distribution is skewed to the left, i.e. the tail where normally evidential scores will need to be evaluated is heavier than the left tail, which is bounded. This not only corresponds well to the data as evidenced by the quantile plots, but also has the advantage of letting this tail taper out slowly, not yielding extremely small denominators of the LR too quickly. The goodness of fit has also been tested on marks showing the first six-minutiae configuration but developed using the other methods (DFO, ninhydrin and powder). Examples of the fits obtained are shown in figure 5.6. **The lognormal distribution is, finally, accepted as a good model for the data.**

For each development method, the parameters of the lognormal have been estimated for all marks (still for the original configuration of 6 minutiae). In figure 5.7, the estimated parameter μ is plotted for all marks developed using cyanoacrylate with its confidence interval, once for the database of right thumbs showing right loops only, and once when the mark in question is compared to the whole database (all fingers, all general patterns). We can see that first of all, the first parameter (μ) estimated for the different marks varies over and above what is included in the confidence intervals obtained for these marks. This shows an effect due to the mark itself: even when the minutia configuration (and therefore the finger number, general pattern, placement on the finger and number of minutiae) and development method remain constant, different distributions are obtained for different impressions. The value of this parameter does not vary much, however; taking into account that the estimation is based on 31224 observations for right loops on right thumbs, the confidence intervals are extremely small. On the other hand, it is observed that

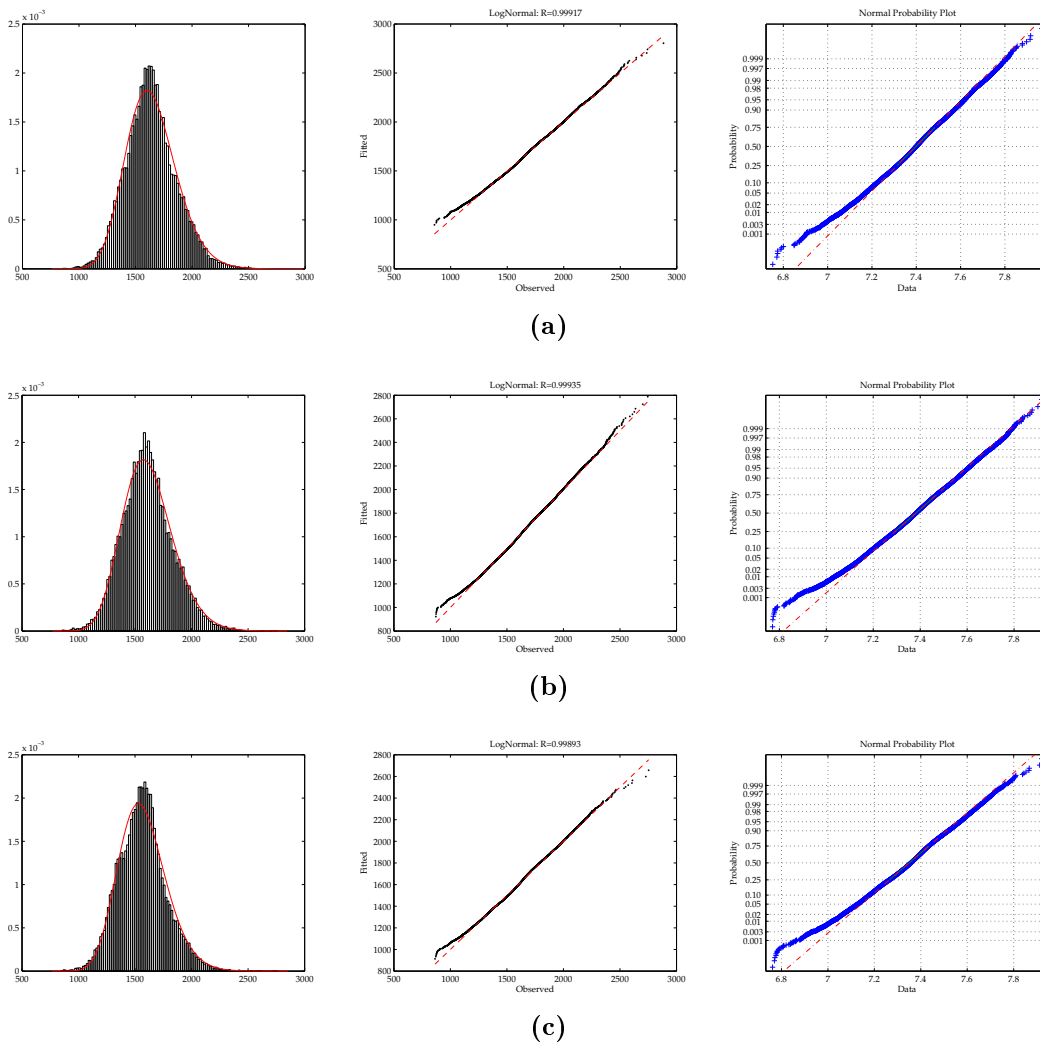


Figure 5.6: Comparison between the observed and the theoretical lognormal distribution for marks developed using a) DFO b) Ninhydrin and c) Powder. From left to right: Histogram and density, QQ-Plot, and a normal probability plot for the natural logarithm of the scores

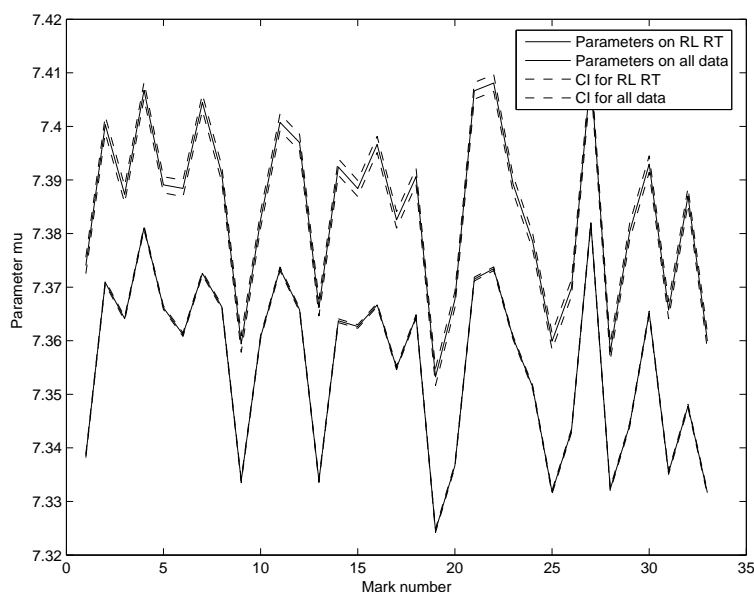


Figure 5.7: Comparison between the parameters μ obtained when confronting all marks developed with cyanoacrylate (using the original 6 minutiae configuration) with right loops on right thumbs and with the whole database

the estimation of μ on the basis of the whole database results in lower values for this parameter; this may be due either to the fact that all finger numbers are used or to the fact that all general patterns are included in this second dataset. The same observations have been made for the second parameter, σ (see figure 5.8). Again, the variation of this parameter exceeds the size of the confidence intervals for this parameter for each mark, meaning that in some of the possible pairwise comparisons of parameters obtained for different marks, the confidence intervals do not overlap. Furthermore, differences are observed between parameters when the database from right loops on the right thumbs only is used, or when the whole database is used. Two observations are made here: first of all, parameters estimated on the whole database are different from those estimated on the basis of right loops on right thumbs only. Secondly, this difference in parameters due to the database is smaller than the differences observed in parameters estimated on the basis of different marks from the same finger. As a consequence of these two observations, the impact of these differences between the parameters has been assessed by comparing two probability density functions visually. The largest difference in parameters has been chosen for this. One of the distributions chosen is the one where the largest first parameter is obtained here, and the second distribution is the one where the lowest such 1st parameter was obtained. The largest and smallest such parameters were chosen among those obtained for the comparisons between the cyanoacrylate marks and the database from right loops on right thumbs. Figure 5.9 illustrates the difference observed between these pdfs. The distributional differences shown in figure 5.9 will not have a significant impact. Indeed, when the maximum and

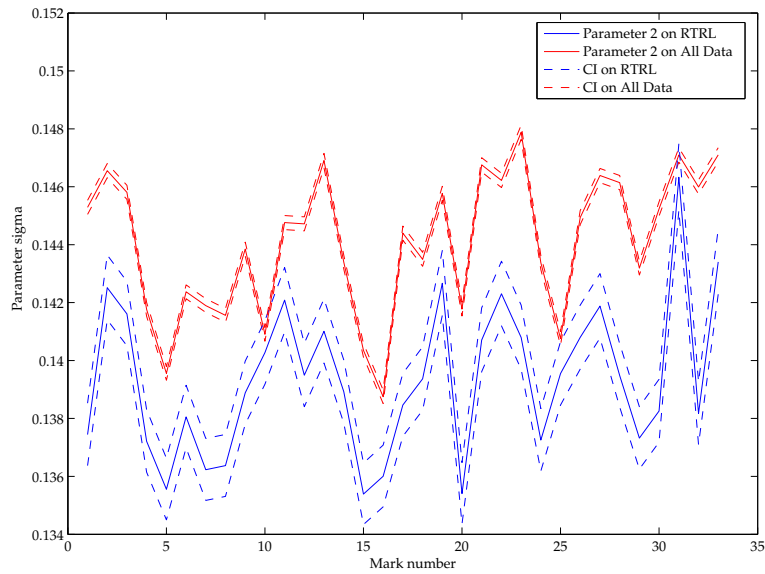


Figure 5.8: Comparison between the parameters σ obtained when confronting all marks developed with cyanoacrylate (using the original 6 minutiae configuration) with right loops on right thumbs and with the whole database

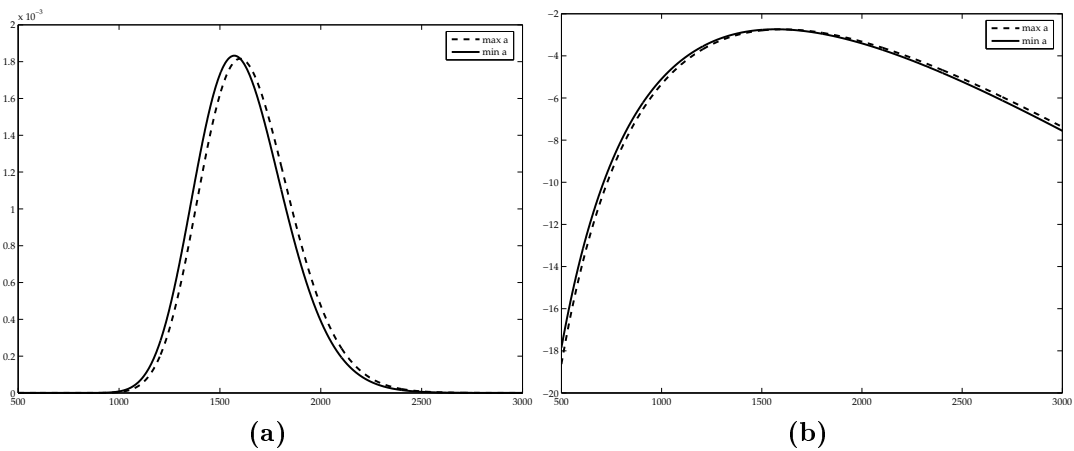


Figure 5.9: Comparison between the maximal and minimal parameter μ of the lognormal distribution obtained for the marks showing the original distribution of 6 minutiae; a) linear and b) \log_{10} scale.

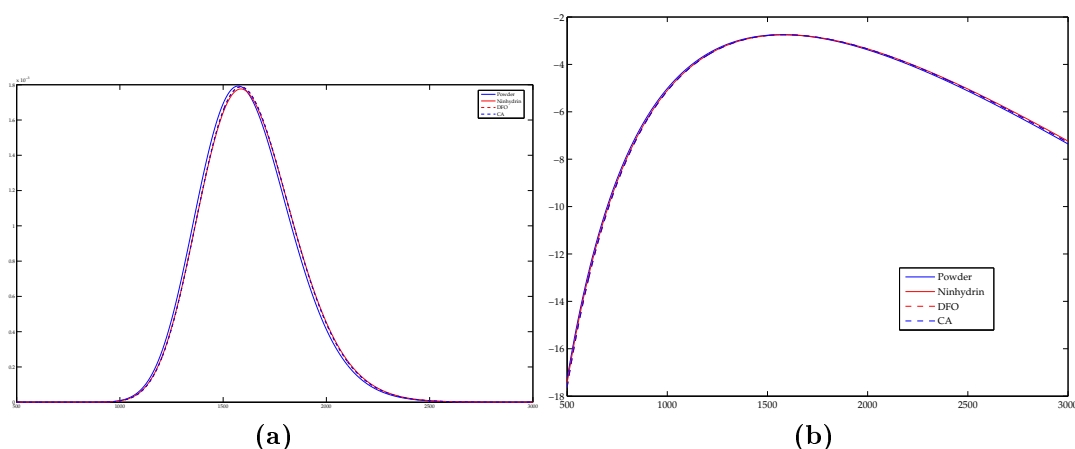


Figure 5.10: Comparison between the distributions obtained using the mean of each parameter separately for the four development methods used.

minimum parameters obtained on different marks are compared, the distributions are quite similar and in particular do not differ much concerning the denominators of the LR that will be obtained from them. While in the mode of the distribution, on linear scale, the differences are the largest, the plot on a log scale shows that their importance concerning their influence on the LR is small; it will be considered that the stability here is sufficient to be able to use a general between variability for all different marks showing a given configuration, and developed using cyanoacrylate, in spite of the fact that the parameters obtained for between-finger variability distributions from such marks have confidence intervals that do not overlap. Similar observations have been made for the other development methods, with slight differences: for powder developed marks, distributions correspond better than those shown here, while for DFO and ninhydrin, these differences between marks from the same finger are slightly larger than those shown for cyanoacrylate. These differences between distributions obtained when confronting different marks from the same finger with the same minutiae configuration to a given database remain, however, sufficiently small to accept that **a general distribution can be used for the marks developed using a given method**. To conclude this section, the four development methods have been compared; the mean of both the first and the second parameter for each method have been computed and used as the parameters for this comparison. In figure 5.10, the comparison between the four probability density functions is shown, again in linear as well as log scale. It is here that we see that the differences observed are most probably not due to true distributional differences but rather to random noise. Indeed, the fact that the four probability density functions obtained for the four methods using the mean of the parameters for each method correspond so perfectly indicates that there is one generally applicable probability density function, at least for a given configuration. One way of modeling between-finger variability for a given evidence mark directly follows from

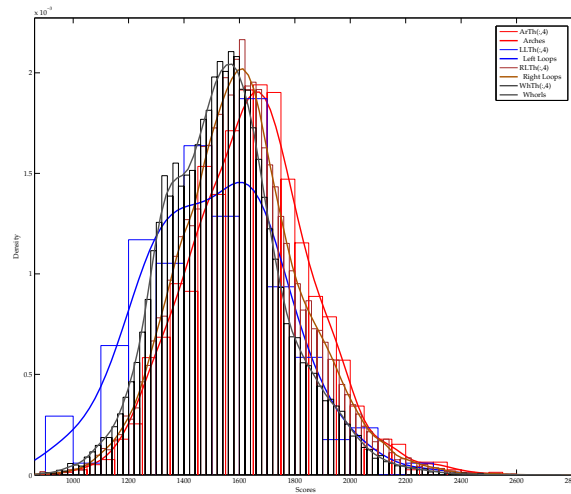
this: it is possible that a given pair of parameters applies for any between-finger variability. This hypothesis is tested directly in the chapter on the testing of LR's, where the mean of the parameters obtained here is used for the estimation of the between-finger variability and thus the denominator for comparisons involving a mark with a different minutia configuration.

The influence of general pattern

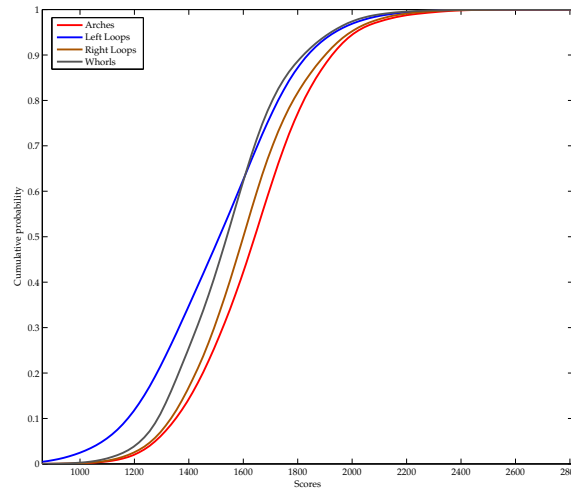
The automatic assignment of general patterns yields a sample of 67402 thumb impressions, excluding unknown patterns. All first classifications have been taken into account, and the fingerprints thus used are distributed according to general pattern in the following way: 1582 Arches, 171 Left Loops, 31374 Right Loops and 34519 Whorls. For the right thumb, only comparisons between right loops (the general pattern of the finger that actually left the marks used here) and whorls will be carried out, due to the lack of data for left loops and arches. As a visual example of the differences between all four distributions, however, see figure 5.11. This figure (as well as the remainder of comparisons) is based on the first configuration of 6 minutiae, annotated on a mark developed using cyanoacrylate. Superimposed on the data are nonparametric distribution functions based on kernel density estimation for comparison purposes.

It can be seen in figure 5.11 that differences exist not only between the two general patterns where few observations are present (left loops and arches), but also between the results obtained for right loops and whorls, where according to section 5.3, sufficient data is present. Indeed, the distribution obtained for whorls has its mode slightly to the left of the distribution for right loops. Furthermore, the distribution for whorls shows a shoulder for scores of between 1300 and 1400, where there is none for right loops.

A lognormal distribution has been fitted to this data, and again, the parameters obtained for each mark developed using cyanoacrylate have been compared (see figure 5.12a and b). The differences between these parameters are systematic: both parameters are smaller when the background database used is composed of whorls than when it is composed of loops. Figure 5.13 shows the effect of the maximal difference in parameters on the between finger variability density function; large effects are present in the right tails of these two densities. These differences obtained show that to use a distribution based on other general patterns than the one of the mark yields differences in denominators almost everywhere, and is prejudicial in these cases. Where great differences occur, these differences go in the sense of a lower probability of having obtained a score if the impressions are from different fingers when a whorl- instead of a loop database is used. Here, the database containing only right loops on right thumbs have been compared to whorls on right thumbs rather than the overall database; however, since **a difference due to general pattern has been detected** in this procedure, the results also preclude the use of a general database when the general pattern is known. As for finger numbers, **the database**



(a)



(b)

Figure 5.11: Comparison between the distributions obtained when comparing one mark from an ulnar loop on a thumb to arches, left loops, right loops and whorls separately a) histogram and nonparametric density function b) nonparametric cumulative distribution functions

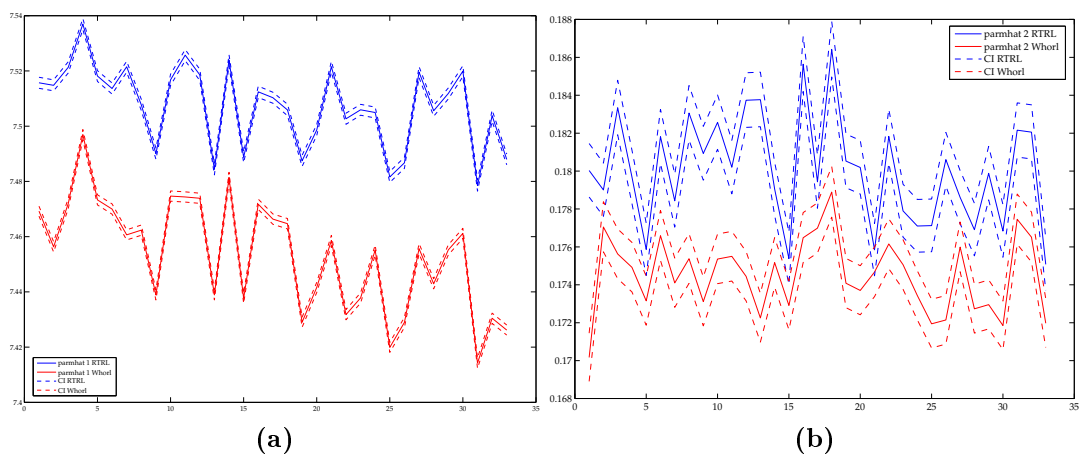


Figure 5.12: Comparison between the parameters obtained when comparing marks developed using cyanoacrylate from an ulnar loop on a thumb to right loops (blue) and whorls (red) separately a) μ b) σ

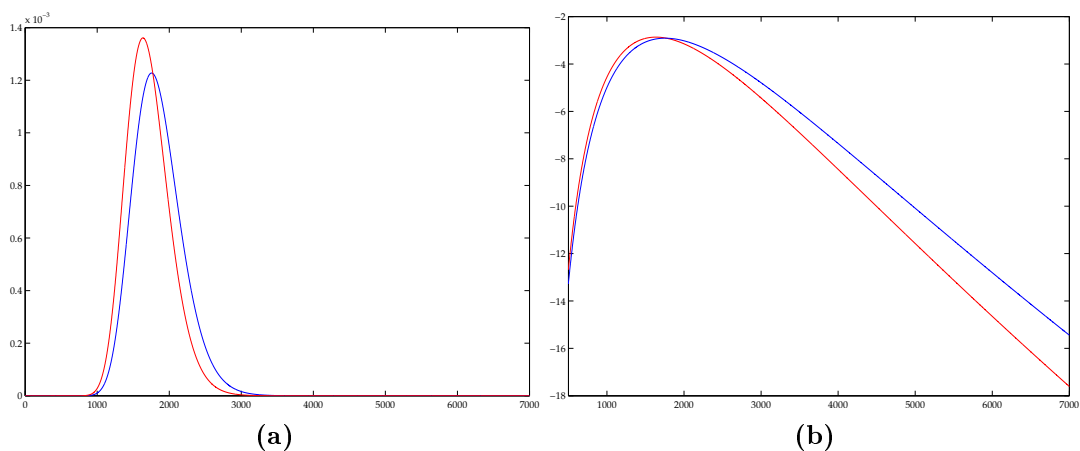


Figure 5.13: Comparison between the probability density functions obtained when using between finger databases of whorls (red) or right loops (blue) respectively a) linear scale b) \log_{10} scale

chosen based on the mark must therefore be used. If the general pattern is unknown, it is proposed here to still use the lognormal distribution (although in these cases there is often a shoulder present) and to try and approximate the parameters of the distribution of the 'same general pattern'. Indeed, here, the possibility of using a distribution for the between-finger variability that has the correct shape and parameters for a 'same finger and general pattern' distribution, while this finger and general pattern are unknown, may exist. Let us assume that we have a mark that does not allow the determination of finger number and general pattern. In the present work, it has been shown, up to now, that when comparing a mark to prints from the same finger number and the same general pattern, we obtain a lognormal distribution, while when the mark is compared to any finger number and any general pattern there is a shoulder to the left of the mode. Let us further assume that we have a way of estimating the parameters of the lognormal distribution that would be obtained when using only a database of fingerprints that come from the same (unknown) finger number and the same, but unknown, general pattern as the mark. The view is taken here that this distribution should be used, rather than an estimation on the whole database. Estimation on the whole database would correspond approximately to a stratified approach where distributions would be fitted to each finger number and each general pattern, and a combined denominator were computed where each finger number would have the same probability of $\frac{1}{10}$, and each general pattern would have the probability corresponding to its frequency in the database. When using the whole database for the estimation of the between-finger distribution, this stratification would be unnecessary and it has the advantage of taking automatically into account the fact that general pattern is not independent of finger number. The disadvantage is that the probability that the mark comes from a given finger should not be $\frac{1}{10}$, but the frequency with which marks are left by each finger.

The view taken here is that the best approach, if feasible, is to use the 'same finger, same general pattern' distribution. The reason is that it is thought here that the suspects' finger retained, even initially, has a much larger than average chance of coming from the same finger number and general pattern as the mark. This is due to the fact that strategies exist to 'estimate' finger number and general pattern on the basis of the mark, even if they are not visible. Some formations are more frequent on certain finger number / general pattern combinations and will be searched on fingers fulfilling these criteria first. This strategy does not amount to a determination that would allow its use for a stratified estimation of between-finger distribution.

The results of the sections above show that the between-finger variability is dependent on finger number. Therefore, and even if distributional similarities exist between some finger numbers, a database of the same finger as the one that the marks originates from should be used, if the finger that left the mark is known.

Also, it has been shown that between-finger variability depends on general pattern. Again, this makes it necessary to use a database for between-finger variability that is conditioned by the general pattern of the mark, if this general pattern is known.

For both characteristics, if they are not visible (or cannot be deduced) from the mark, the full database must be used. This is simpler than to fit distributions to subsets of the database and to then create a stratified model based on published data on the frequencies of general patterns, for example.

Finally, the differences observed between the between-finger distributions obtained from different marks (showing the same minutiae configuration) have been briefly analyzed. While the confidence intervals for the parameters of these between-finger distributions do not overlap, the impact of these differences in the parameters on the denominator is extremely small. The lack of overlap in these confidence intervals is therefore interpreted as being due to the size of the dataset (which is very large, therefore yielding a very small variance and confidence intervals) rather than to a difference between these parameters that will impact on the denominator of the LR.

5.5 Dependence of between finger variability on the number and placement of minutiae

5.5.1 Introduction

It has been seen that within finger variability distributions greatly depend on both number and placement of minutiae, and that this dependence is not easily attributable to minutiae directions or to their proximity to the centre or the delta.

This does not mean, however, that between-finger variability also depends on number and placement of minutiae. Indeed, this question is intimately linked to the way that scores are computed by the AFIS used.

In the following, the influence of the number of minutiae will be investigated in a first step, while their placement will be verified in a second step.

5.5.2 Material and methods

The same marks of donor 1 as used previously have again been employed. The minutiae configurations used are the first and second configurations, going from 1 to 10 minutiae. These configurations have been compared to the whole database, as well as right loops on right thumbs, resulting in 685245 or 31224 scores, respectively. These distributions of scores continue to be modelled using a lognormal distribution, in the light of the results obtained in section 5.4.3. Comparisons between distributions are carried out in similar ways as before; rather than using statistical testing, the divergence between distributions is evaluated considering its potential

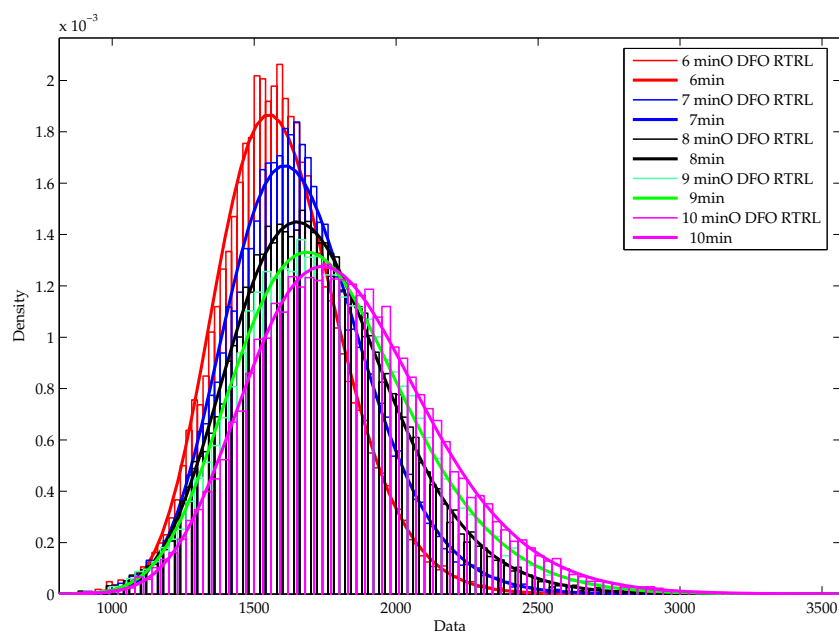


Figure 5.14: Between-finger distributions obtained for the first configuration on the first mark developed using DFO when increasing the number of minutiae and using a background database of right loops on right thumbs

impact on final LR values. Although manifest differences in the distributions with a low impact on LRs continue to be taken into account, the main criteria are, again, divergences in the tails rather than around the mode of distributions, which is where large differences may be observed in general.

5.5.3 Results for increasing number of minutiae

When analyzing a single mark, where minutiae are progressively added from 6 to 10, a similar evolution as for within-finger variability is observed: the centre of the distribution is (somewhat surprisingly) displaced towards higher scores, and the distribution flattens out. An example employing the first mark developed using DFO is shown in figure 5.14. When comparing the selected mark to the whole database, the same effect is visible, although the overall increase is lessened in this context (see figure 5.15); the distributions obtained for 7, 8 and 9 minutiae have their modes almost superposed, and their variance only changes only slightly.

The number of minutiae included in the configuration has, in the light of the results presented above, an influence on between finger variability.

Also, this observation can be generalized: the parameters for all DFO marks used here increase as the number of minutiae increases. This increase is not at the same level for each mark (see figure 5.16 a) for μ and b) for σ).

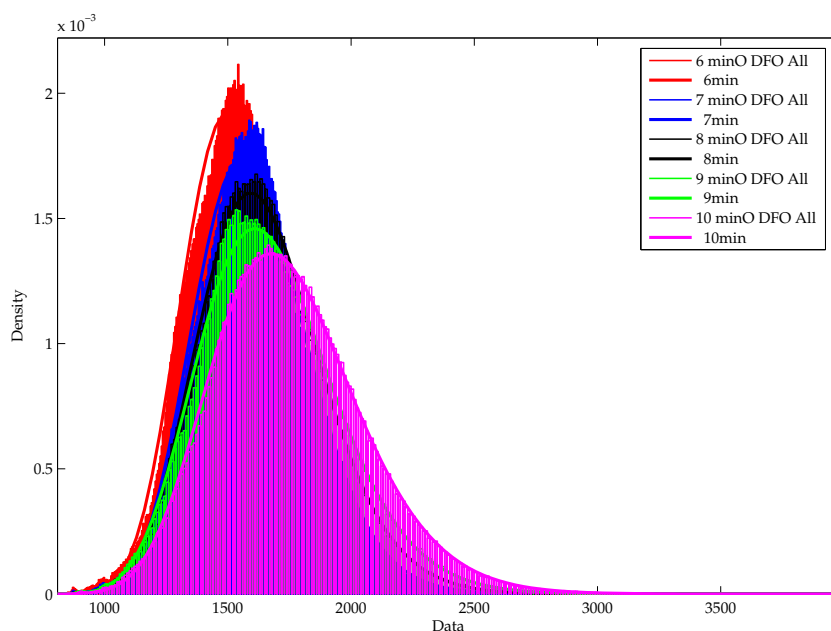


Figure 5.15: Between-finger distributions obtained for the first minutiae configuration on the first mark developed using DFO when increasing the number of minutiae and using a background database of all available fingerprints (all finger numbers and general patterns).

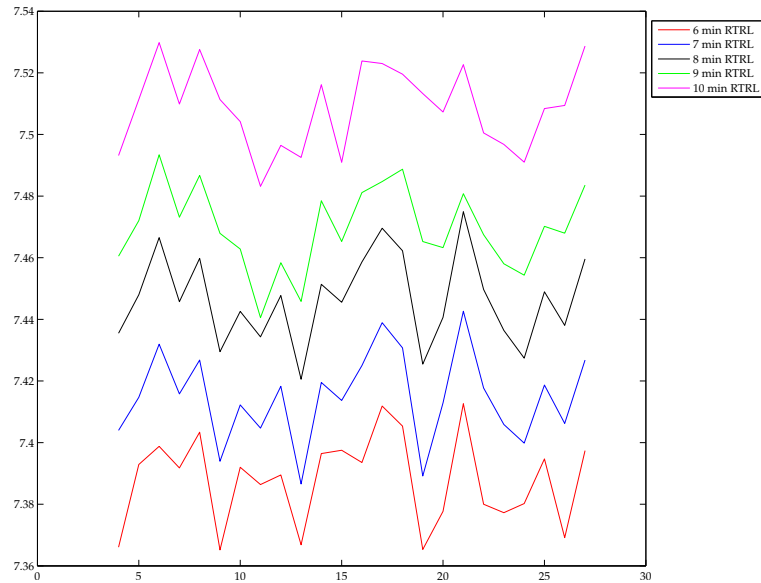
5.5.4 Results for differing minutiae configurations

The same finger of the same donor is again used, but between-finger distributions issued from the comparison of the second configuration annotated to the database are now compared to those from the first minutiae configuration. Marks developed using DFO are again used in this part of the thesis. Figure 5.17 shows the progression of the distributions when the number of minutiae is increased in this configuration. In this configuration, the distributions obtained when using 9 or 10 minutiae are almost identical; the reason for this observation is unknown, but this highlights a clear difference between the first configuration, where quite a regular increase in the expected score values was observed, and this second configuration.

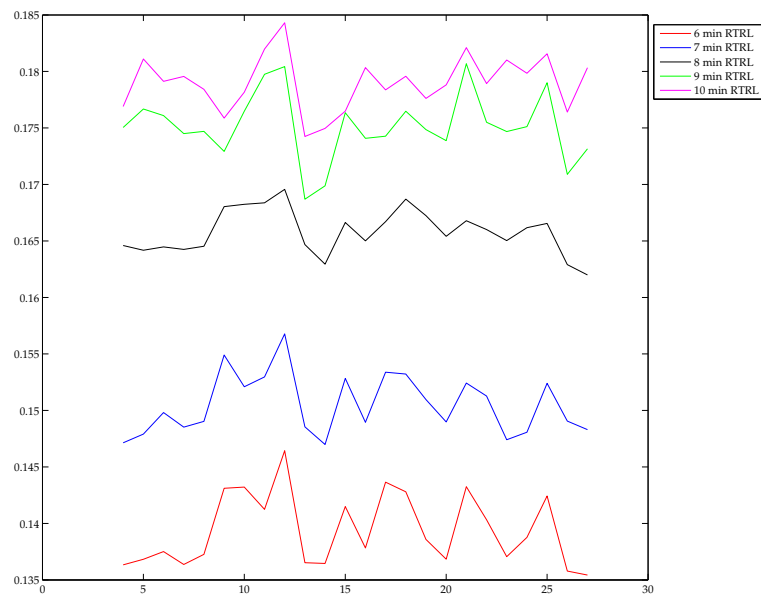
Figures 5.18 a) to e) show the comparisons between the probability density functions obtained for the first mark developed using DFO with the two different minutiae configurations, separately for each number of minutiae. The background database used is that of right loops on right thumbs.

These five figures show that **there are no large differences between the distributions obtained for the two configurations on the same finger**: although the modes are slightly different, the shape of the distributions corresponds, as does the scale, although not precisely.

It seems, from these results, quite feasible to fix parameters by number of minutiae (e.g. use the mean of the parameters obtained for a given configuration for the computation of the between variability and therefore the denominator for other



(a)



(b)

Figure 5.16: μ (a) and σ (b) obtained for the first configuration on marks developed using DFO, when increasing the number of minutiae and using a background database of right loops on right thumbs.

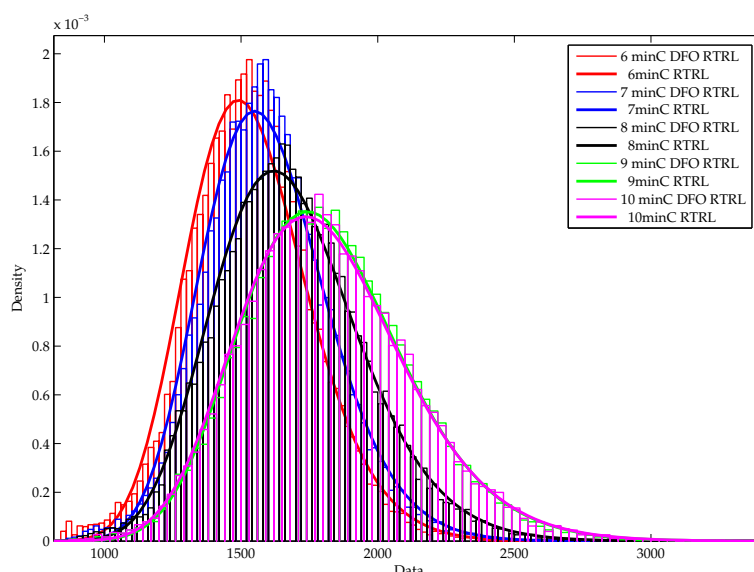


Figure 5.17: Between-finger distributions obtained for the second minutiae configuration on the first mark developed using DFO when increasing the number of minutiae and using a background database of right loops on right thumbs

configurations), at least for this finger; again, this result needs testing on the data from donor 2 (see chapter 6).

The situation is quite different when the whole database is used as the background database; when finger number and general pattern are considered unknown in this way, between-finger distributions vary widely between different minutiae configurations (see figure 5.19).

5.5.5 Approximation of parameters

As for within-finger variability, a way of approximating the parameters of the between-finger variability needed to be found; indeed, the extraction of the scores when confronting a fingerprint to a database is, although feasible, time consuming and may not be applicable operationally. Here, the parameters of between-finger variability are approximated using the 10 largest scores obtained when all general patterns and all finger numbers are taken into account. More precisely, the mean and variance of these 10 highest scores have been used to try to approximate the parameters of the between-finger distribution. This has been done for each number of minutiae separately.

The 10 largest scores have been chosen because they are readily available in AFIS; generally they are shown in the list of the best matches when a search is carried out. It would therefore be feasible to extract these scores easily. The reason why the 10 largest 'non-mate' scores are chosen from a database where no selection as to finger number and general pattern is carried out is that these approximations need to be applicable when the general pattern and finger number are not known from

5.5. Dependence of between finger variability on the number and placement of minutiae

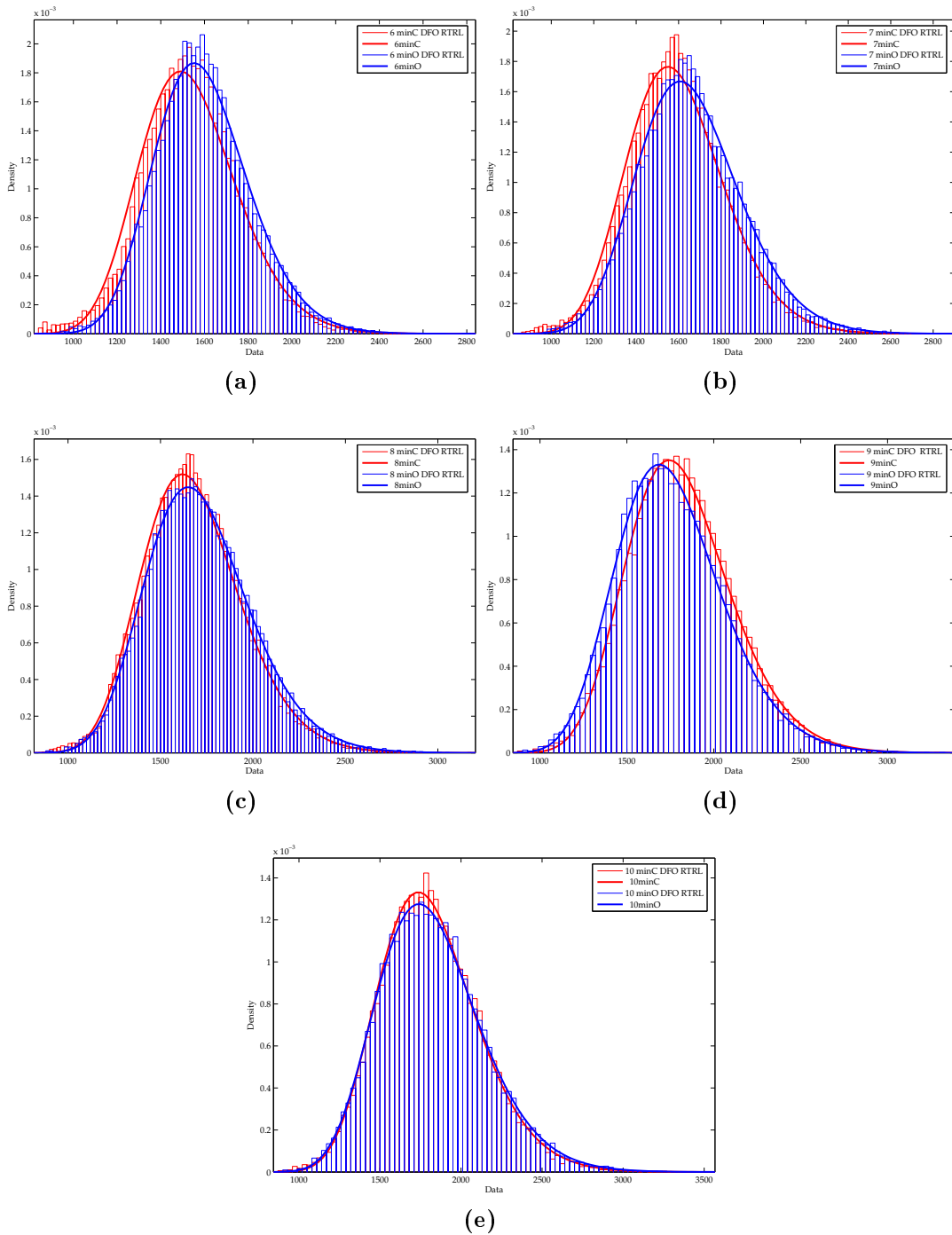


Figure 5.18: Illustration of the between-finger probability density functions obtained for the first and the second minutiae configuration on the right thumb of donor 1 using a) 6 b) 7 c) 8 d) 9 and e) 10 minutiae and a background database of right loops on right thumbs

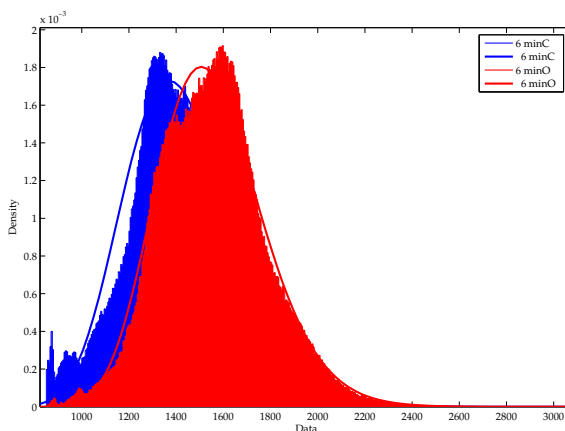


Figure 5.19: Illustration of the between-finger probability density functions obtained for the first and the second minutiae configuration on the right thumb of donor 1 when comparing the mark with 6 minutiae to the database including all finger numbers and general patterns

the mark; in such cases, there is no way of restraining the database to a subset, and the whole database needs to be used.

The first parameter, μ , of the lognormal distribution has been deduced from the mean of the 10 highest scores thus obtained, while the second parameter, σ , is deduced from a combination of the mean and the variance of these ten highest observations. In table 5.6, the different equations used for each number of minutiae and the two parameters are shown. The testing of these different approximations

Table 5.6: Equations for parameters of the lognormal distribution used for modelling between-finger variability

Parameter	μ	σ
6 minutiae	$0.6246 \cdot \log(\bar{s}_{10}) + 2.422$	$0.01199 \cdot (\log(\bar{s}_{10})/\log(Var(s_{10})) + 0.1282$
7 minutiae	$0.8113 \cdot \log(\bar{s}_{10}) + 0.9021$	$0.009652 \cdot (\log(\bar{s}_{10})/\log(Var(s_{10})) + 0.1415$
8 minutiae	$0.819 \cdot \log(\bar{s}_{10}) + 0.8089$	$-0.01174 \cdot (\log(\bar{s}_{10})/\log(Var(s_{10})) + 0.1772$
9 minutiae	$0.2981 \cdot \log(\bar{s}_{10}) + 5.034$	$-0.007286 \cdot (\log(\bar{s}_{10})/\log(Var(s_{10})) + 0.1827$
10 minutiae	$0.3947 \cdot \log(\bar{s}_{10}) + 4.248$	$-0.002005 \cdot (\log(\bar{s}_{10})/\log(Var(s_{10})) + 0.1817$

for the within- as well as the between-finger probability density functions are the object of a separate chapter (chapter 6).

5.5.6 Conclusions on between-finger variability

While considerations of variables influencing between-finger distributions may seem less interesting than those influencing within-finger variability, some important analyses of the behaviour of this distribution have been carried out in this chapter. If no such description had figured here, by default, it would have been possible operationally to confront the mark of a case to an available database, extract all the scores by conditioning on known factors of the mark (general pattern, finger number) and use some nonparametric estimation technique for obtaining the between-finger variability and the denominator of the LR.

First of all, a minimum number of comparisons necessary for obtaining a stable distribution has been estimated. While it was suspected that the distributions would depend on finger number and general pattern, this has been shown here. The same is true for the dependence on the number of minutiae and the behaviour of the distribution when the number of minutiae is increased. Finally, the differences obtained when different minutiae configurations (or even different marks with the same minutia configuration) are used have been observed. Also, it has been possible to use a parametric distribution for the fitting of these scores, which is considered as an advantage here for the same reasons as those discussed for the within-finger variability. The main reason is the possibility of obtaining robust estimates of the density in regions of low probability, where often no observations will have been made.

Finally, two possible ways of approximating the parameters of the between-finger distribution are proposed (and will be tested in the next chapter); the first one is to use fixed parameters for each finger number (computed as the mean of the parameters obtained from the marks developed using DFO of the original minutiae configuration) and the second one is to use an approximation based on the largest 10 scores obtained when confronting the fingerprint to the database. The 10 largest scores were chosen since they are readily available from the results of the AFIS.

Chapter 6

Testing of the different approximations using Likelihood ratios

6.1 Introduction

In the preceding chapters and sections, different propositions for approximating the distributions at the basis of the likelihood ratio have been made.

It has been proposed to estimate the parameters of the distribution of within-finger variability directly from three impressions compared to themselves. The mean of the 3 scores thus obtained, that are a description of the maximal score for a given configuration, has been used for the approximation of these parameters. These approximations have already been tested in the relevant section; the interest of the present section is to test the joint effect of the approximations used in both the numerator and the denominator.

For the between-finger variability, several propositions remain untested: the correlation between LRs obtained on full and reduced databases, where the reduced database contains only 10'000 impressions, an approximation using fixed parameters computed on the basis of the first minutiae configuration observed on DFO-developped marks of donor 1 (based on minutiae number only and using fixed parameters for all different configurations) and the approximation where the parameters of the between finger variability distribution are estimated based on the 10 highest scores obtained in the database, or rather their mean and variance.

All of these propositions are tested on first on the first configuration of donor 1, and then on one finger of another donor (donor 2). Impressions from this donor have been developed using powdering only. Also, they have not been used for the establishment of the approximations of the parameters.

6.2 Material and methods

28 marks of the left thumb of donor 2 are used along with the marks previously used from donor 1 with the first minutiae configuration. A configuration of 6 minutiae has been chosen on the marks from donor 2. Then, minutiae have been added progressively, and configurations of 7, 8, 9 and 10 minutiae have been obtained. This configuration is shown in figure 6.1



Figure 6.1: Minutiae configuration chosen on the left thumb of donor 2 showing the increments from 6 to 10 minutiae

These marks have been confronted to 12 inked prints of the same finger showing these minutiae, in order to obtain within-finger scores. Only 336 LRs can therefore be computed for this donor under H .

Then, the marks have been confronted to a database of 686260 rolled inked prints. This yields a distribution of scores, acquired as if neither finger number nor general pattern was taken into account. From these scores, those corresponding to left thumbs, and where the automatic classification algorithm includes Whorls in the possible classifications, have been extracted for donor 2. This smaller (34506

impressions) dataset represents between variability when considering finger number and general pattern as known. The same strategy has been used for donor 2, where right loops on right thumbs were retained (yielding 31224 scores).

Likelihood ratios obtained will first be described using Tippett plots. The evidential scores are chosen in the within- and the between-finger databases, respectively. The Tippett plots are constructed using 2000 LR_s under \bar{H} and either all LR_s obtained for the available scores for LR_s computed under H (when less than 2000 such scores are available) or 2000 LR_s (when more than 2000 scores are available). Less than 2000 scores are available for donor 2. When 2000 scores are randomly selected, a stratified selection of scores has been used. The same number of scores was randomly chosen for each mark separately (the code for this construction of Tippett plots is given in appendix C). The number of scores selected from the results for each mark is 2000 divided by the total number of marks used; when the result is not an integer, the next larger integer is used. Therefore, a number close to but larger than 2000 is obtained. The evidential scores selected under \bar{H} are always selected in the complete database of non-mate scores, even when reduced databases are used for the evaluation of scores (e.g. a database of 10000 scores or a database conditioned by finger number or general pattern). Once the evidential score is chosen, either the relevant databases for the computation of $f(s|H)$ and $f(s|\bar{H})$ are chosen (e.g. for the within-finger variability, all comparisons involving the configuration and for the between finger variability the comparisons where the 'evidence' mark is used and compared against all impressions of the background database, or a subset of this dataset depending on what is being tested), or the appropriate approximations are used and the parameters thus obtained are directly employed for the computation of the numerator and denominator values.

In a further step, the relationship between the different likelihood ratios will be examined: indeed, it is insufficient to obtain similar distributions of likelihood ratios as shown by Tippett plots. Rather, each LR obtained using the approximations has to be close to the LR obtained on the data. Then, numerators and denominators are also compared separately in some instances in order to complete the investigation of the influence of the approximations. Linear plots are used for this comparison; the same LR_s as those used for the establishment of the Tippett plots are employed for these graphs, e.g. exactly the same LR_s are employed twice: once for the Tippett plots and once for the establishment of these linear graphs. They are therefore based on the same data and sampling processes as described for the Tippett plots. Comparisons are carried out between estimation based on the data, for both the numerator and the denominator and LR_s obtained when both the numerator and the denominator are based on approximations using much less data. Also, a reduction in the data in the denominator estimation (to 10000 observations) is tested against the results obtained when all available data is used. Overall, 5 different ways of computing LR_s are compared:

1. data-based estimation for the within-variability, with a between-variability

estimated on the whole database (all scores obtained when confronting the evidential mark to the database of fingerprints from other sources, without conditioning by finger number and general pattern)

2. approximated within-variability and a between-variability based on a reduced dataset including all finger numbers and general patterns, but where only 10000 observations are sampled randomly
3. data-based estimation for the within-variability, and a between-variability based only on scores obtained from fingerprints showing the same general pattern/finger number combination as that of the finger that the mark originated from
4. approximated within-variability and a between-variability based on fixed parameters, that are the means of the parameters obtained for the first configuration from donor 1 on marks developed using DFO confronted to a database of right loops on right thumbs and finally
5. approximated within- and between-variabilities using the equations and the self-scores and 10 highest observations, respectively.

As all through the present thesis, a divergence of one order of magnitude in the likelihood ratio is judged acceptable.

6.3 Results on likelihood ratios

A first series of Tippett plots presents the results obtained when using a background database containing only right loops on right thumbs for the marks from donor 1 (see figure 6.2) and a background database of only whorls on left thumbs for the marks from donor 2 (see figure 6.3). For these Tippett plots, both the within- and the between-finger variabilities are estimated on data and no approximation is used. For the between-finger variability only the finger number and general pattern of the finger considered are included (right loops on right thumbs for donor 1 and whorls on left thumbs for donor 2).

These Tippett plots show relatively high rates of misleading evidence, in particular in favour of the prosecution, for 6 and 7 minutiae for donor 2 (see table 6.1; these rates are of 5.2% and 3.2%, respectively). Considering, however, that these rates are for rather small configurations of minutiae, these rates are acceptable.

The value of these misleading LRs is, in some cases, quite high, in particularly in favour of the defense. For example, as shown in table 6.1, the minimum value of the logarithm base 10 under the prosecution hypothesis is of -4.4 for the first minutiae configuration of Donor 1. As it should be, the separation between the two curves for impressions known to come from the same and different finger increases with increasing numbers of minutiae. Although the rates of misleading evidence

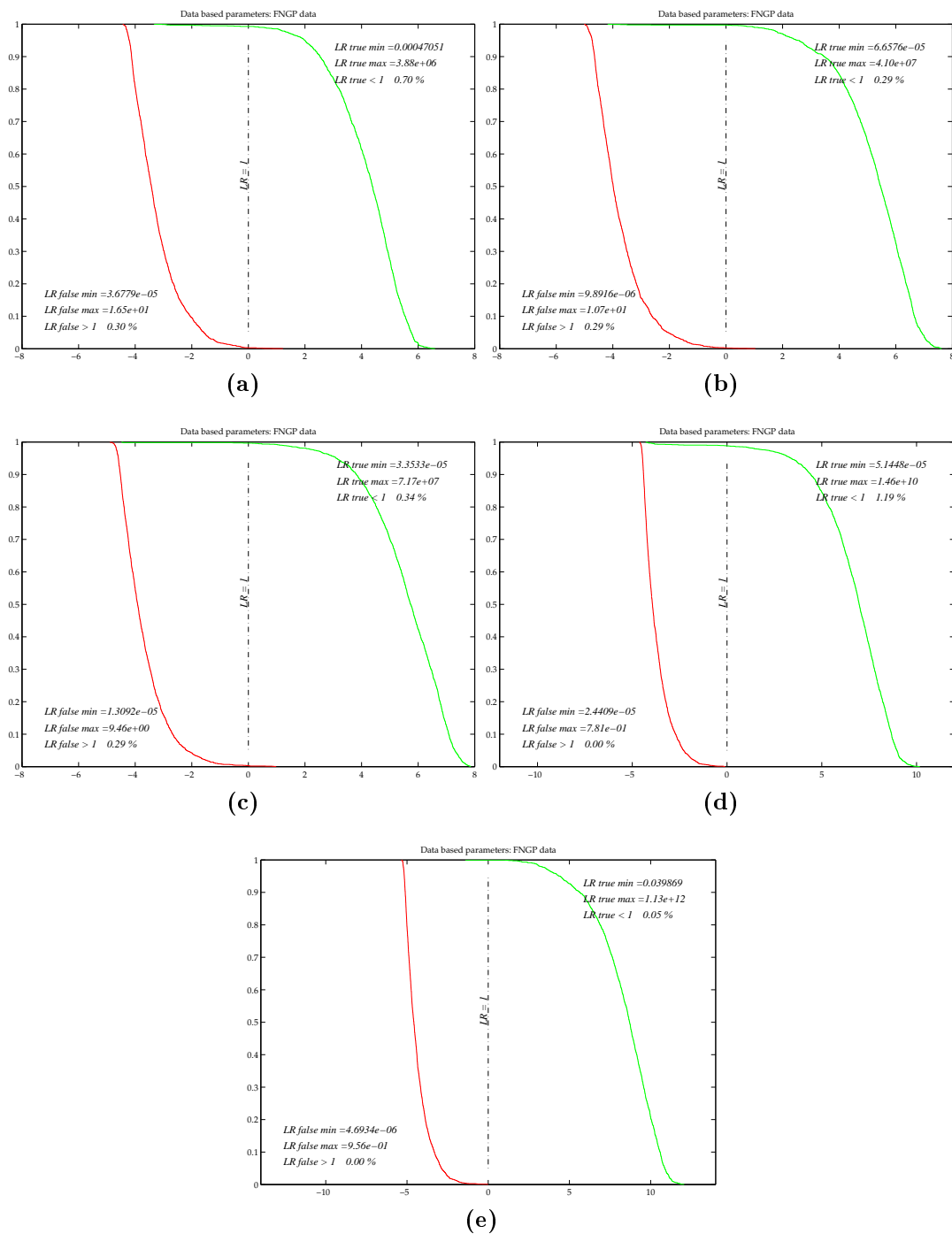


Figure 6.2: Tippett plots for the data-based likelihood ratio estimation for the first configuration on the right thumb of donor 1 confronted to a between-finger database of right loops on right thumbs for a) 6 b) 7 c) 8 d) 9 and e) 10 minutiae

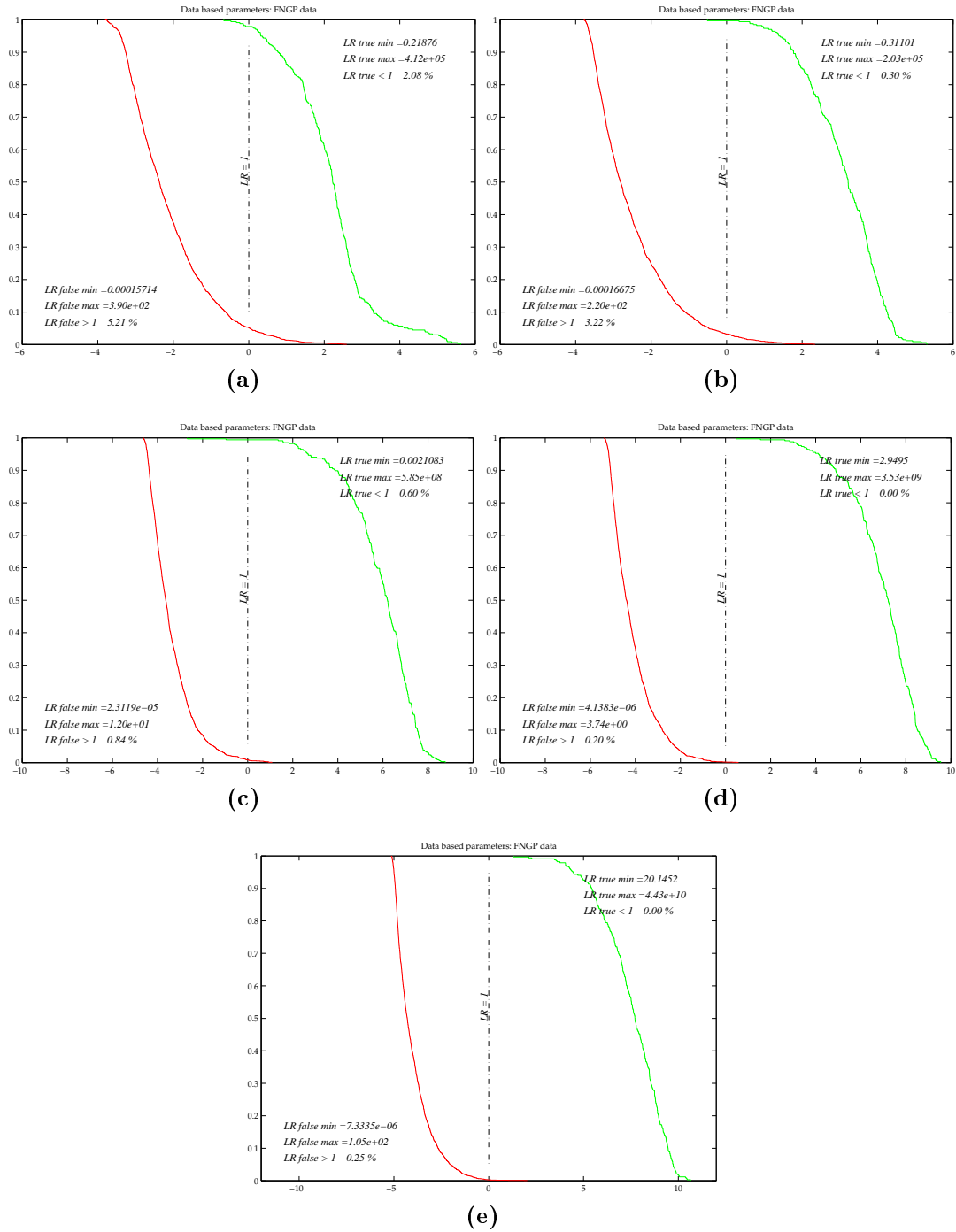


Figure 6.3: Tippet plots for the data-based likelihood ratio estimation for the configuration on the left thumb of donor 2 confronted to a between-finger database of whorls on left thumbs for a) 6 b) 7 c) 8 d) 9 and e) 10 minutiae

Table 6.1: Rates of misleading evidence as well as the minimum and maximum LRs obtained under both hypotheses for the first minutiae configuration on the right thumb of donor 1 (D1) and the left thumb of donor 2 (D2) when data-based estimation is used and the between-finger database employed is conditioned by the finger number and general pattern of the mark

Nb min	6 minutiae		7 minutiae		8 minutiae		9 minutiae		10 minutiae	
	D1	D2	D1	D2	D1	D2	D1	D2	D1	D2
RMED (%)	0.7	2.1	0.3	0.3	0.3	0.6	1.2	0.0	0.1	0.0
RMEP (%)	0.3	5.2	0.3	3.2	0.3	0.8	0.0	0.2	0.0	0.3
$\log_{10}(\min H)$	-3.3	-0.7	-4.1	-0.5	-4.4	-2.6	-4.3	0.5	-1.4	1.3
$\log_{10}(\max H)$	6.6	5.6	7.6	5.3	7.9	8.8	10.1	9.5	12.0	10.6
$\log_{10}(\min \bar{H})$	-4.4	-3.8	-5.0	-3.8	-4.9	-4.6	-4.6	-5.4	-5.3	-5.1
$\log_{10}(\max \bar{H})$	1.2	2.6	1.0	2.3	1.0	1.1	-0.1	0.6	-0.02	2.0

are rather high for low numbers of minutiae, therefore, the overall characteristics of the system are good. There is an exception to the overall improvement of the performance of the system; from 9 to 10 minutiae, the rates of misleading evidence do not decrease for donor 2 and the rate of misleading evidence in favour of the defense even increases from 8 to 9 minutiae for the first configuration of donor 1. In the case of donor 2, this may be due to the little data available: only 28 different marks of a single donor are available for these Tippett plots and have been used. In the case of donor 1, it is possible that there are some marks where the 9th minutia was annotated incorrectly; this is the most reasonable explanation for the increase, in particular since only the rate of misleading evidence in favour of the defense is concerned.

The Tippett plots when using the whole database instead of only confronting these marks to right loops on right thumbs for donor 1 and whorls on left thumbs for donor 2 are shown in figures 6.4 for donor 1 and 6.5 for donor 2. The results obtained on the whole database are very similar to those obtained on the database of the relevant finger number/general pattern combination; the usefulness of differentiating between these two series of results is therefore put into question.

When comparing the two series of likelihood ratios (obtained using a between-finger database of whorls on left thumbs only or composed of all impressions available) for donor 2, differences above one order of magnitude only appear for configurations of 8 or more minutiae, and only for LRs computed under H . For LRs under \bar{H} , no differences of more than an order of magnitude are observed between LRs where the denominator is computed from distributions in databases including only whorls on left thumbs or all fingers. For those LRs where such differences are observed (under H , for configurations of 8 or more minutiae), LRs are *larger* when the database used only includes whorls on left thumbs. For donor 1, differences of more than an order of magnitude are observed already for configurations of 8 minutiae,

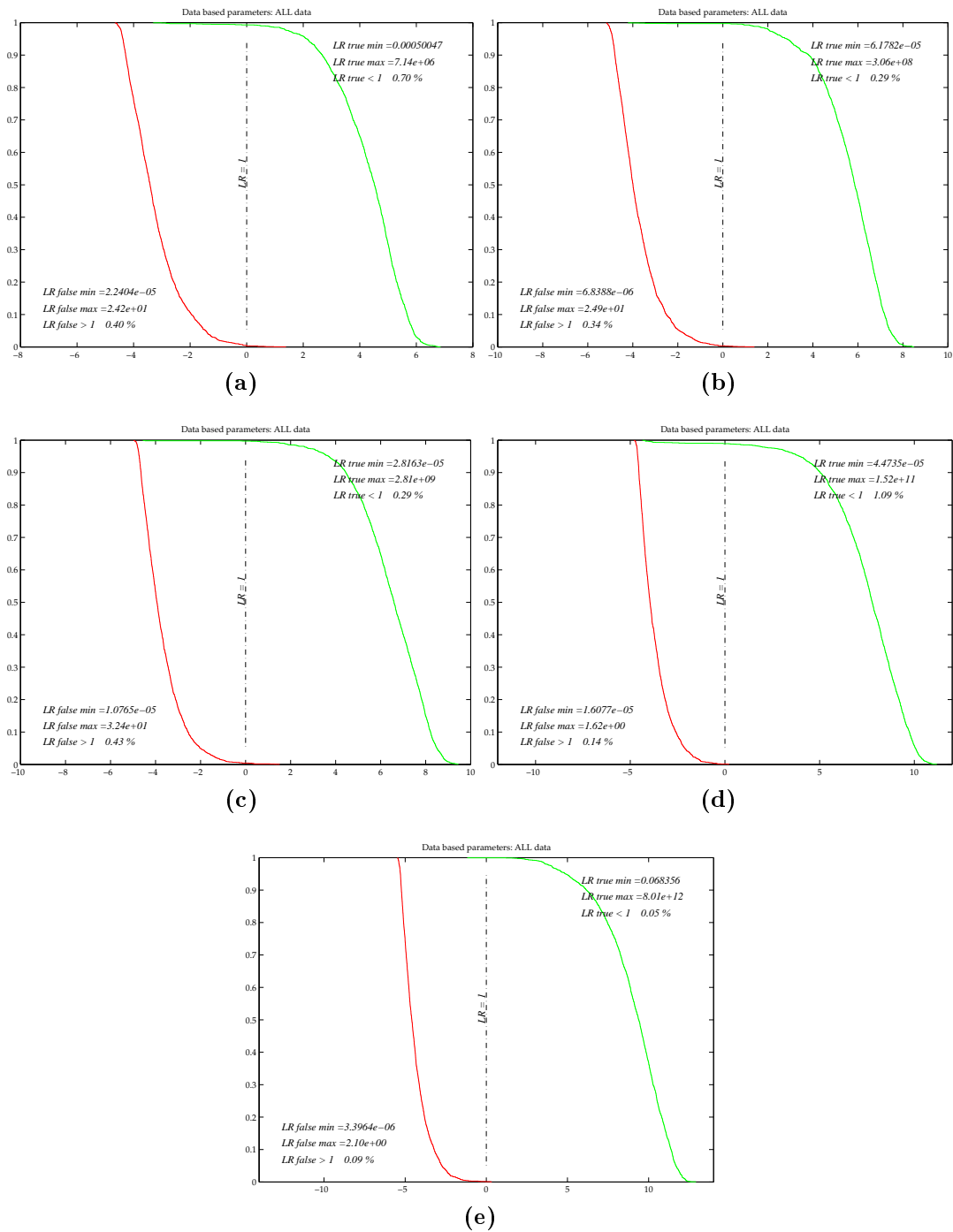


Figure 6.4: Tippett plots for the first minutiae configuration on the right thumb of donor 1 confronted to the whole background database for a) 6 b) 7 c) 8 d) 9 and e) 10 minutiae

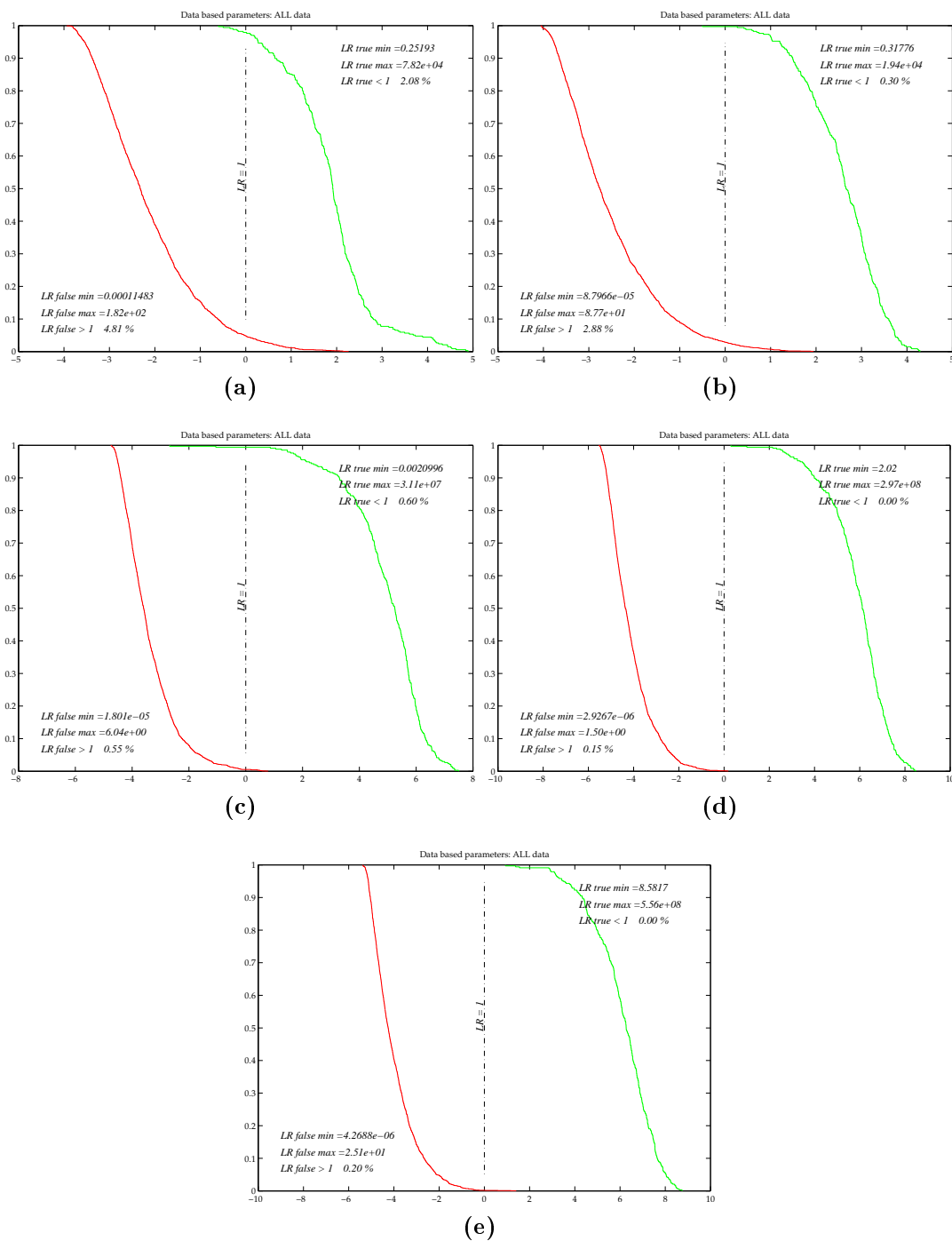


Figure 6.5: Tippett plots for the left thumb of donor 2 confronted to the whole background database for a) 6 b) 7 c) 8 d) 9 and e) 10 minutiae

under H ; here, LRs are larger when the database used is constituted of all finger numbers and general patterns. In figure 6.6, the reason for this difference between donors 1 and 2 is shown. This figure represents the between-finger distributions for donors 1 and 2 based on all data (red) and based on the relevant general pattern / finger number combination (green) for the mark showing 10 minutiae having obtained the highest score under H , as well as the within-finger variability (blue) and the maximum score obtained (under H) for this configuration. The reason why LRs are actually higher when left thumbs showing whorls are used for donor 2 is that the tail is less heavy in this case. For donor 1, the difference between the two between-variability distributions is smaller, and the two distributions have more similar shapes than for donor 2; however, the between-finger distribution obtained using the whole database has a lower mean than that obtained when conditioning by general pattern and finger number. For donor 2, it must be noted that in the extreme right tail of the between-finger variability this difference between tails becomes sufficiently important to cause large divergences between LRs obtained using these different databases for the denominator.

When using the reduced database (10000 randomly chosen prints from the general database) while still computing the numerator using a data-based approach, a perfectly linear relationship, with no difference larger than one order of magnitude, is observed between LRs based on this reduced dataset and the complete one. This database size is therefore truly sufficient. Only one example of the linear relationship between LRs obtained in this way and LRs obtained using the whole between-finger database (and still computing the numerator using a data-based approach) is shown, in figure 6.7. This figure is based on configurations of 10 minutiae on the left thumb of donor 2. Such figures have been established for minutiae configurations including 6 to 10 minutiae of donor 2, and the assumption that the database of 10000 observations allows the computation of LRs that are very close to those computed using the whole database holds. Therefore, the minimal database size estimated in chapter 5 holds when LRs are used.

Two approximation procedures are used for the between-finger variability: one based on fixed parameters (that are based on the mean of parameters obtained for the first minutiae configuration of donor 1 on the available marks developed using DFO, compared to a database of right loops on right thumbs) and one based on the ten maximal scores observed in the between finger database. In table 6.2 the rates of misleading evidence using these 2 approaches as well as the results for data-based estimation, where the between-finger variability is conditioned by finger number and general pattern, are shown for the first configuration of donor 1 (the configuration that the approximations are mainly based on). In table 6.3, the rates of misleading evidence obtained for these approaches are shown for donor 2. In these tables, first the results when a data-based approach is used with the database conditioned by general pattern and finger number is shown, then the approximation using the 10 maximal scores of the between-finger database and finally, the fixed

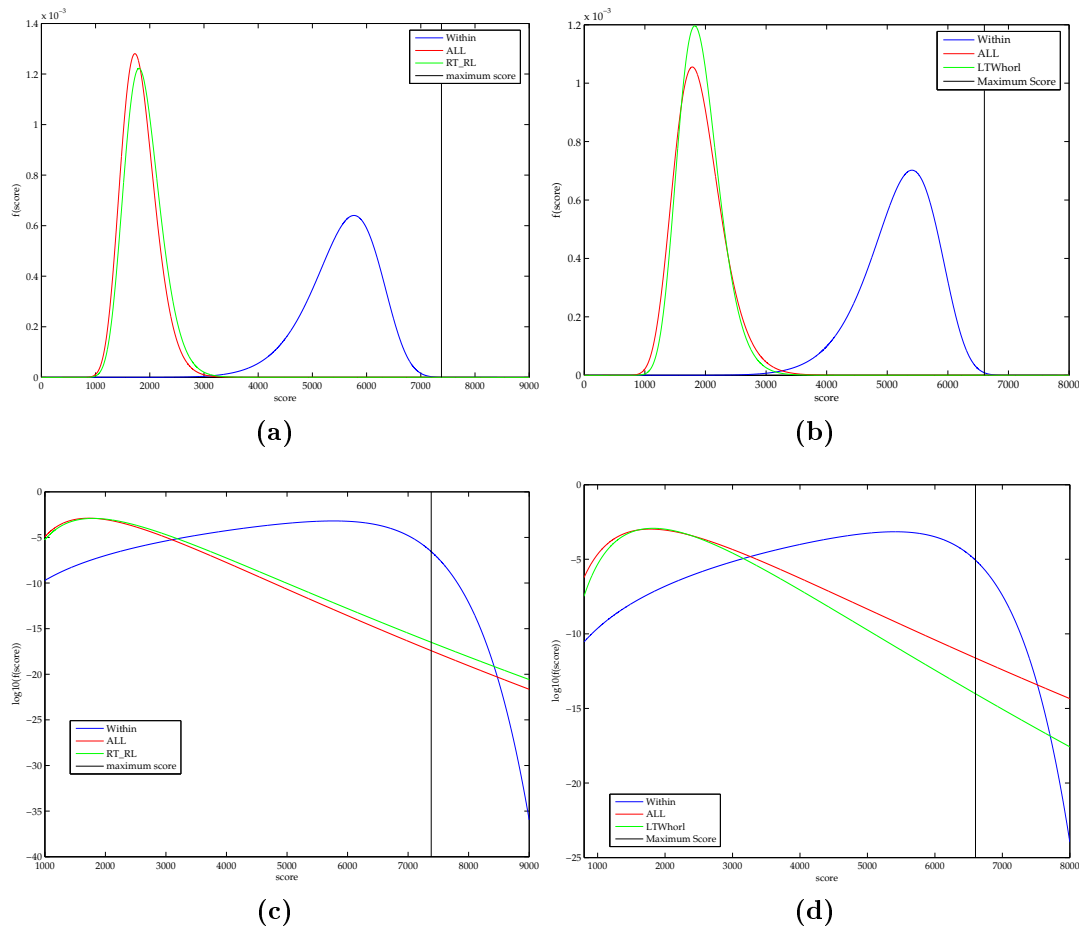


Figure 6.6: Illustration within and between finger variability for the mark having obtained the largest score in a) linear scale, donor 1 b) linear scale, donor 2 c) Log₁₀ scale, donor 1 (x-axis shortened for readability) and d) Log₁₀ scale, donor 2 (x-axis shortened for readability)

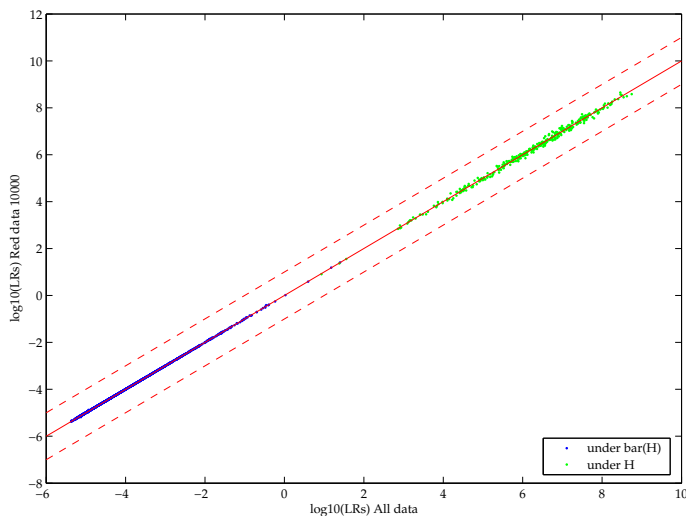


Figure 6.7: Comparison between LRs obtained for the configuration of 10 minutiae on the left thumb of donor 2, using data-based estimation for the numerator and the denominator, where in the denominator the whole dataset is used in one case and a dataset reduced to 10000 observations in the other case

parameters. These last two options also have approximated numerator values, while the data-based LRs are obtained using data-based estimation for both within- and between-finger variability.

Table 6.2: Rates of misleading evidence for 3 modelling approaches for the first minutiae configuration on the right thumb of donor 1

Nb Min	Data-based, FN & GP		Approximated		Fixed	
	RMED	RMEP	RMED	RMEP	RMED	RMEP
6 minutiae	0.70%	0.30%	0.74%	0.30%	2.78%	0.05%
7 minutiae	0.29%	0.29%	0.29%	0.39%	0.72%	0.10%
8 minutiae	0.34%	0.29%	0.34%	0.19%	0.63%	0.14%
9 minutiae	1.19%	0.00%	1.29%	0.00%	1.38%	0.00%
10 minutiae	0.05%	0.00%	0.05%	0.00%	0.05%	0.00%

The approximations hold well for donor 1 (see table 6.2); mostly, only small increases in rates of misleading evidence are observed with respect to the data-based approach. Only the fixed parameter yields more than a small increase for the rate of misleading evidence in favour of the defense, for 6 minutiae. For donor 2 (see table 6.3), these rates of misleading evidence indicate clearly that the approach using fixed parameters cannot be employed operationally; in particular, the rates of misleading evidence in favour of the prosecution for 6 and 7 minutiae are alarming and much larger than those expected from the data-based approach.

The parameters approximated using 3 self-scores for the within-finger variability

and the ten highest scores in the between-finger database for the between-finger variability hold quite well for both donors; when the rates differ from the data-based approach, they are even likely to be lower. Overall, although from these rates it is clear that the correspondence between the data-based LRs and their approximations is less ideal for donor 2 than for donor 1, the approximations do seem promising.

Table 6.3: Rates of misleading evidence for 3 modelling approaches for the minutiae configuration on the left thumb of donor 2

Nb Min	Data-based, FN & GP		Approximated		Fixed	
	RMED	RMEP	RMED	RMEP	RMED	RMEP
6 minutiae	2.08%	5.21%	2.98%	4.17%	0.00%	12.25%
7 minutiae	0.30%	3.22%	0.60%	1.78%	0.00%	7.24%
8 minutiae	0.60%	0.84%	0.60%	0.40%	0.60%	0.60%
9 minutiae	0.00%	0.20%	0.00%	0.20%	0.00%	0.25%
10 minutiae	0.00%	0.25%	0.00%	0.20%	0.00%	0.20%

While therefore the use of fixed parameters must be precluded, the other two options (data-based parameter estimation or approximation of parameters using 3 and 10 data-points for within- and between-finger distributions, respectively) cannot be easily differentiated using this indicator. Approximations have slightly higher rates of misleading evidence in favor of the defense (RMED) for small numbers of minutiae, while they also have slightly lower rates of misleading evidence in favor of the prosecution (RMEP) for low numbers of minutiae (6 and 7) for donor 2.

Whether the likelihood ratios obtained are equivalent is another question; the overall performance of the system using approximations is, however, at least equivalent concerning these rates. The minimum LR obtained using the approximations rather than the data-based approach is generally lower under H , while the maximum LR obtained is generally higher. Misleading evidence obtained using the approximations is therefore generally 'more misleading' than that obtained using data-based estimation. In figures 6.8 through 6.12, the comparison between the logarithm base 10 of LRs obtained using data-based estimation for the numerator as well as the denominator (where the denominator is based on all data) and the logarithm base 10 of LRs that are obtained using approximations for the numerator as well as the denominator, are shown for a) LRs obtained under H and b) LRs obtained under \bar{H} for the first configuration from donor 1. While deviations from the data-based LRs are visible for the approximated LRs, in particular for very large LRs obtained under H for 8 or more minutiae, the approximations perform well on this minutiae configuration. Furthermore, the discrepancies observed result in slightly too low LRs in this context, but remain very highly supportive of the hypothesis that both mark and print originate on the same finger. In figures 6.13

through 6.17, the comparison between the logarithm base 10 of LRs obtained with a data-based numerator and a denominator estimated using data-based estimation on a database conditioned by finger number and general pattern (right loops on right thumbs) and LRs that are obtained using approximations for both the numerator and the denominator are shown. Again, in part a) of these figures, LRs obtained under H and in part b) LRs obtained under \bar{H} are shown. Here, the discrepancies observed between the data-based estimation and the approximation remain within one order of magnitude throughout the data tested. The approximation therefore models well data-based LRs, whatever the background database used, but is particularly close to LRs where the background database is selected to come from the same finger number/general pattern combination as the evidential mark. Since these approximations are based on the finger on which they are tested here, this result is not unexpected for this minutia configuration in particular, that has been heavily employed to deduce the parameters for both the within- and the between-variability distributions. The 'hard' test is the one carried out on donor 2, that is the subject of the remainder of the present chapter.

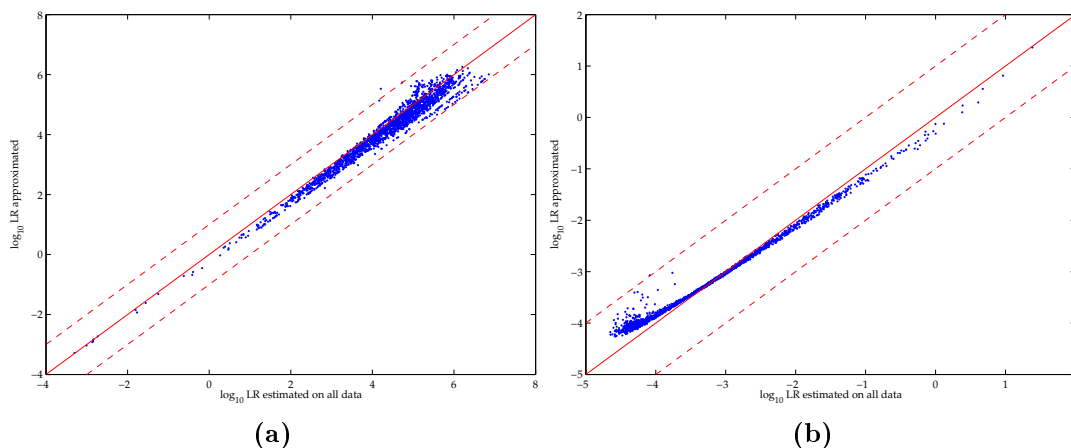


Figure 6.8: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on the whole database for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 6 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

In figure 6.18, the comparison between the logarithm base 10 of LRs obtained using data-based estimation and approximation are shown for a) LRs obtained under H and b) LRs obtained under \bar{H} . Clearly, the approximation, although overall resulting in almost the same rates of misleading evidence as the data-based estimation does not result in similar LRs, in particular, very low LRs (in favour of the defense) are much larger using the approximation, even up to the point where these values turn in favor of the prosecution. When analyzing LR values as a function of the score obtained, it is the data-based LRs that have the expected behaviour; under \bar{H} , the LRs become lower as the scores do, down to scores of around 1200, where

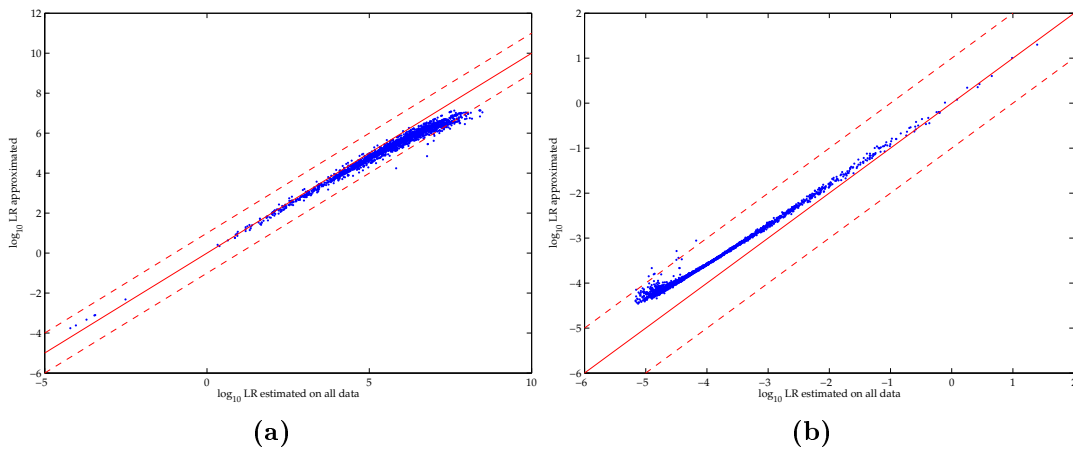


Figure 6.9: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on the whole database for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 7 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

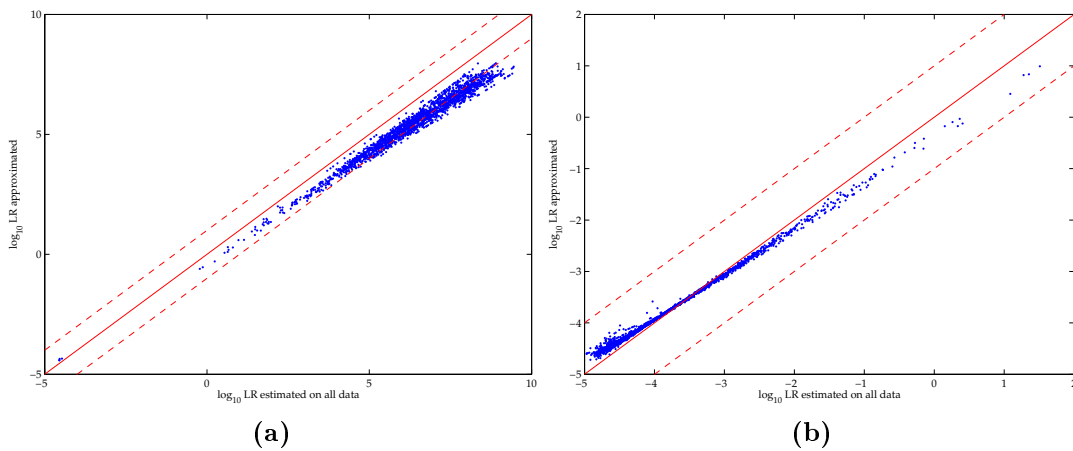


Figure 6.10: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on the whole database for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 8 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

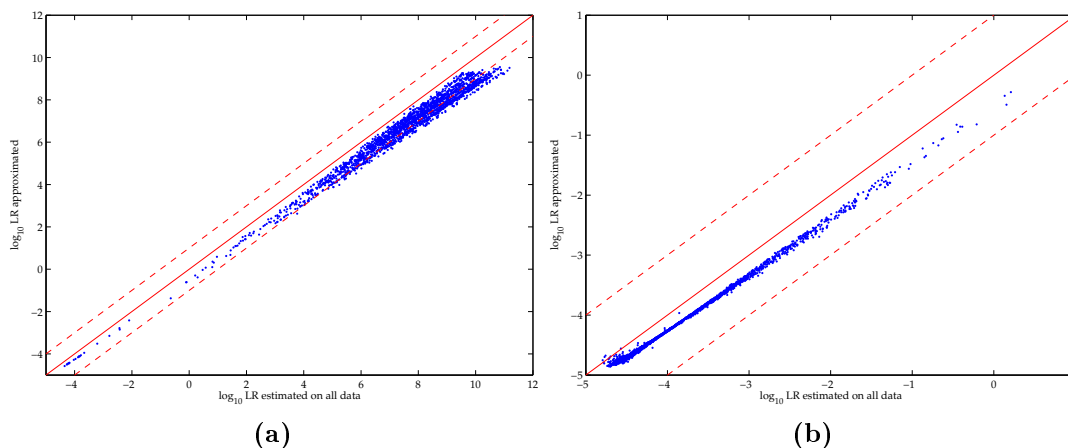


Figure 6.11: Comparison of the logarithm base 10 of LR obtained using data-based estimation (based on the whole database for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 9 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

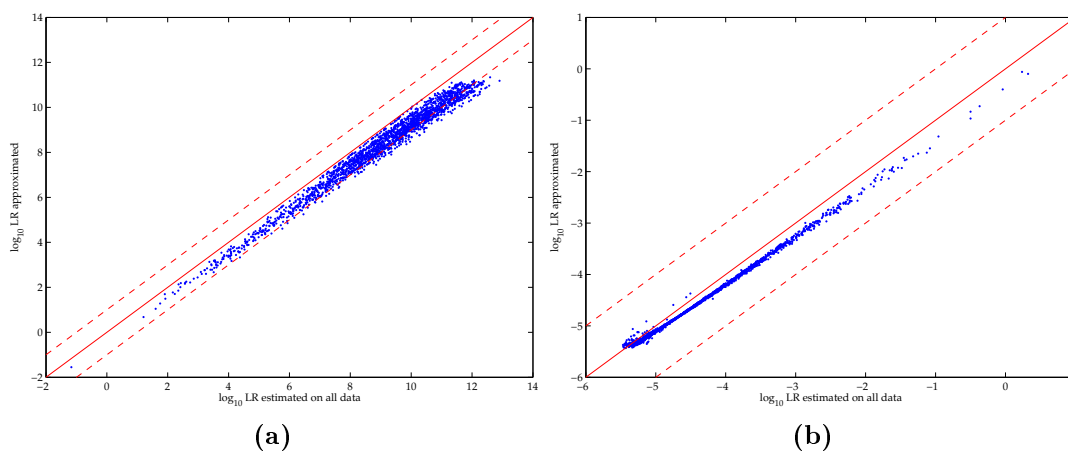


Figure 6.12: Comparison of the logarithm base 10 of LR obtained using data-based estimation (based on the whole database for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 10 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

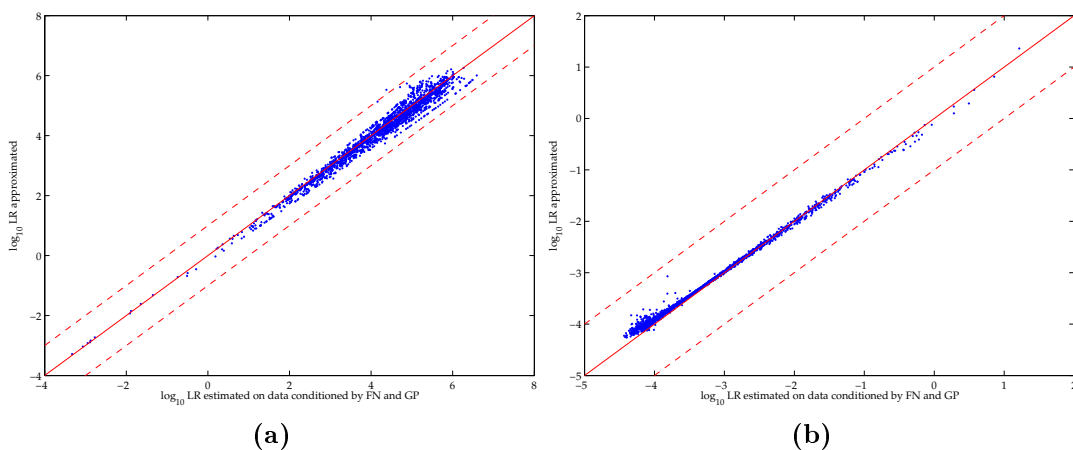


Figure 6.13: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on a database of right loops on right thumbs for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 6 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

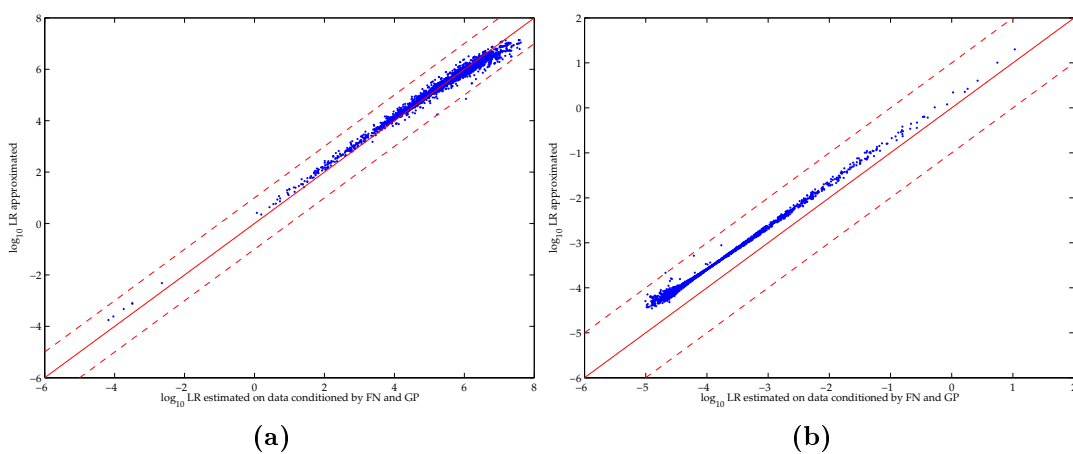


Figure 6.14: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on a database of right loops on right thumbs for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 7 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

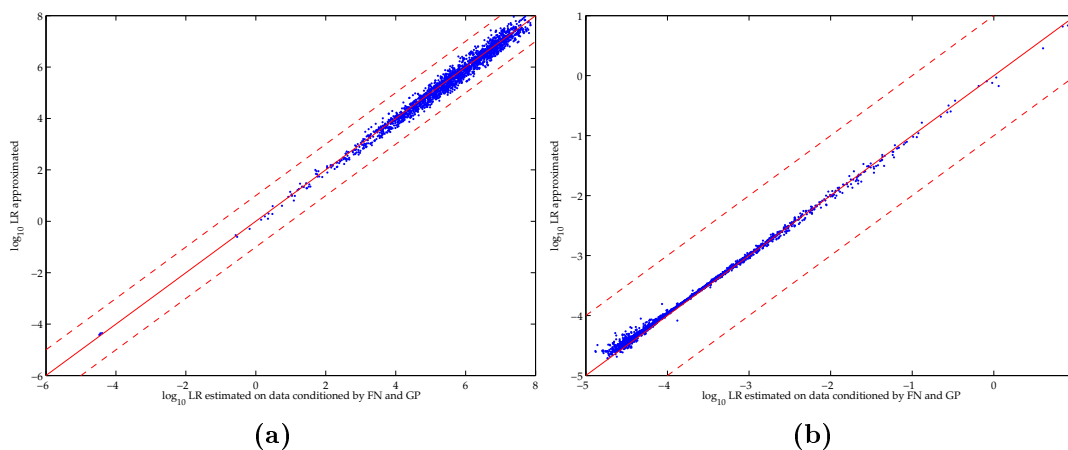


Figure 6.15: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on a database of right loops on right thumbs for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 8 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

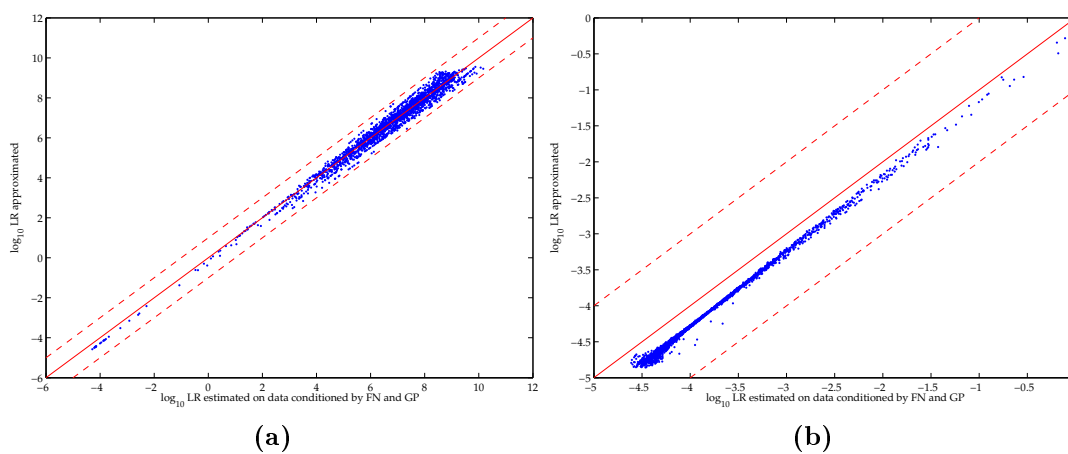


Figure 6.16: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on a database of right loops on right thumbs for the denominator) and using approximations in both the numerator and the denominator for the first configuration of 9 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

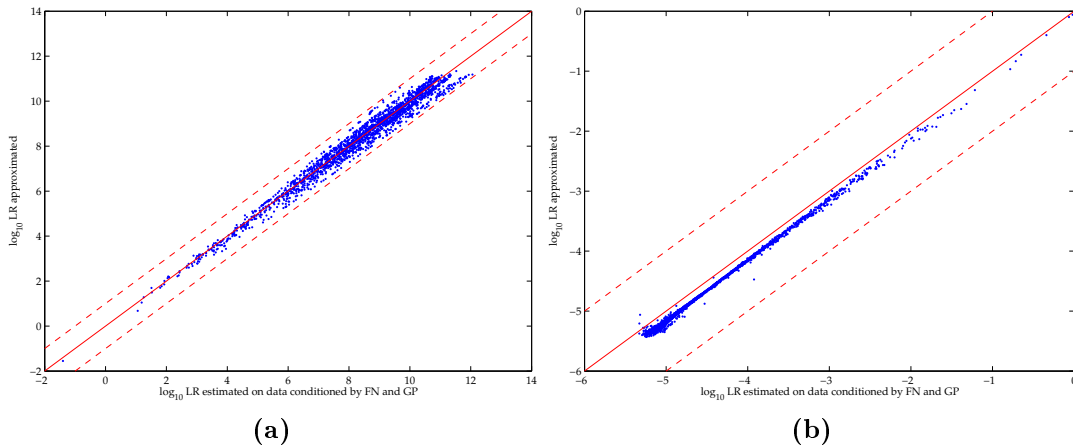


Figure 6.17: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (based on a database of right loops on right thumbs) and using approximations in both the numerator and the denominator for the first configuration of 10 minutiae on the right thumb of donor 1 under a) H and b) \bar{H}

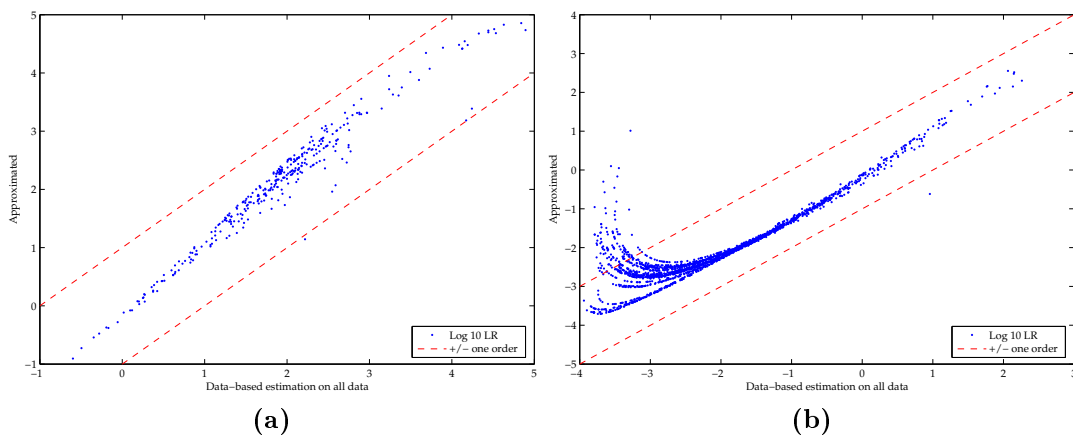


Figure 6.18: Comparison of the logarithm base 10 of LRs obtained using data-based estimation and using approximations in both the numerator and the denominator for the configuration of 6 minutiae on the left thumb of donor 2 under a) H and b) \bar{H}

the tendency starts to invert. For scores obtained using the approximation, this inversion starts much earlier (see figure 6.19 a) for this relationship for data-based LRs and b) for approximated LRs). Also, this relationship between the score and the approximated LRs can lead to a solution; if the differences in LRs are due to higher LRs being obtained for scores that are in the left tail of the between distribution, this can be remedied by observing the relationship of the evidential score to the within- and between finger distributions.

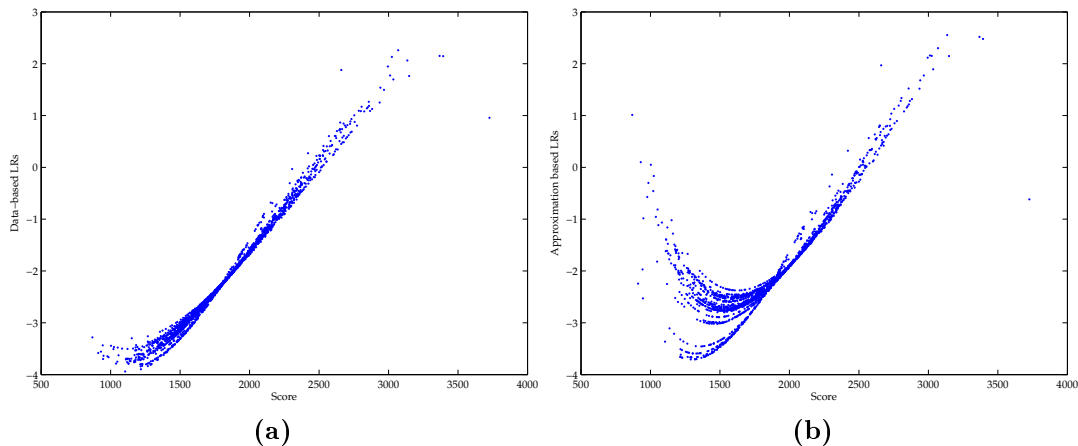


Figure 6.19: Relationship between score and LR under \bar{H} for LRs based on a) data-based estimation using all data for the between variability and b) approximated distributions

In figure 6.20, the minimal score obtained under \bar{H} , which is at the same time the score leading to the greatest difference between the logarithms base 10 between LRs based on data and LRs based on approximations is plotted at the same time as the within- and between-finger distributions. In this same figure (6.20), it can be seen that large differences in LRs computed using the approximation versus the data are observed mainly to the left of the mode of the between-finger distribution; since the mode at least of the approximated distribution is known when LRs are computed operationally using the information collected, such LRs could be, if used, at least tempered by the uncertainty associated with them. Furthermore, it is not necessarily expected that many LRs would be computed in this region, again in an operational setting. These are extremely low scores that are used here for the testing of the system; comparisons where LRs need to be obtained would generally at least be similar in aspect and therefore should, most probably, not lead to scores that are below the mean of the between-finger distribution.

The difference observed between data-based and approximated LRs is due to the denominator under \bar{H} ; the data-based denominators are systematically lower than those obtained from the approximations, while the approximation for the numerator is quite acceptable (see figure 6.21), although slightly skewed with respect to the data-based numerators.

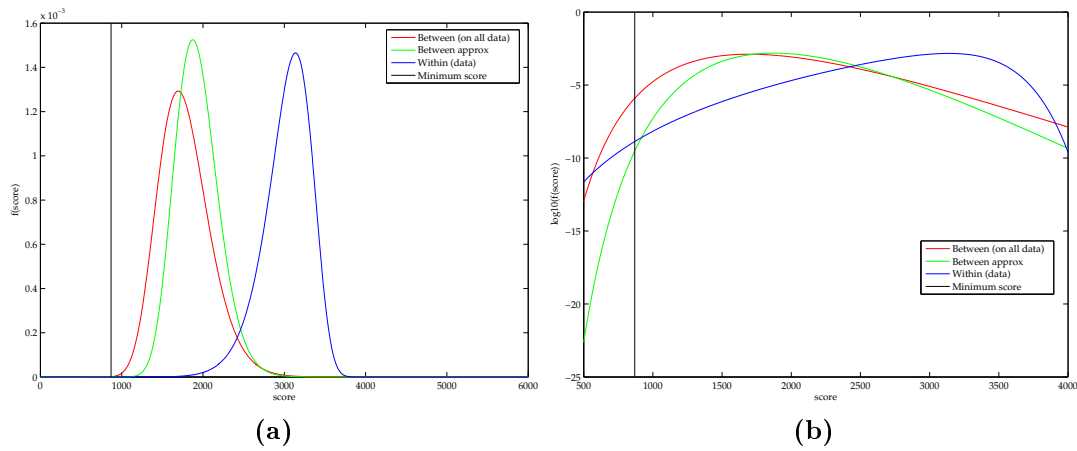


Figure 6.20: Relationship between the minimum score obtained under \bar{H} and the within- and between-finger distributions for LRs in a) linear and b) \log_{10} scale

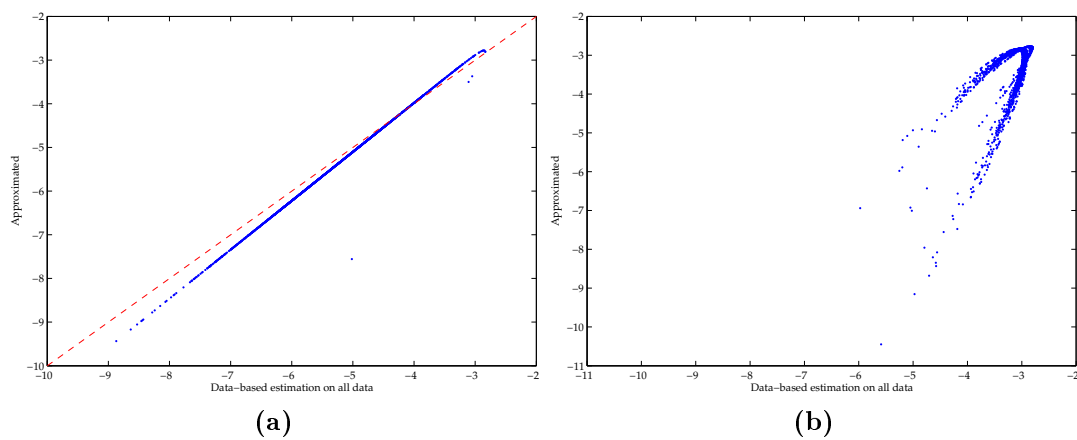


Figure 6.21: Relationship between the logarithm base 10 of data-based (using all available fingerprints for the estimation of between-finger variability) and approximated a) numerators and b) denominators, obtained under \bar{H} .

Under H , the differences observed in LR_s are mostly due to the *numerators* (see figure 6.22). In this figure, it is shown that while the approximated denominators are quite acceptable, for comparisons of impressions from the same finger, this time the approximated numerators are out of the accepted range. However, as shown in figure 6.18, the LR_s obtained under H are mostly within an order of magnitude of the desired value.

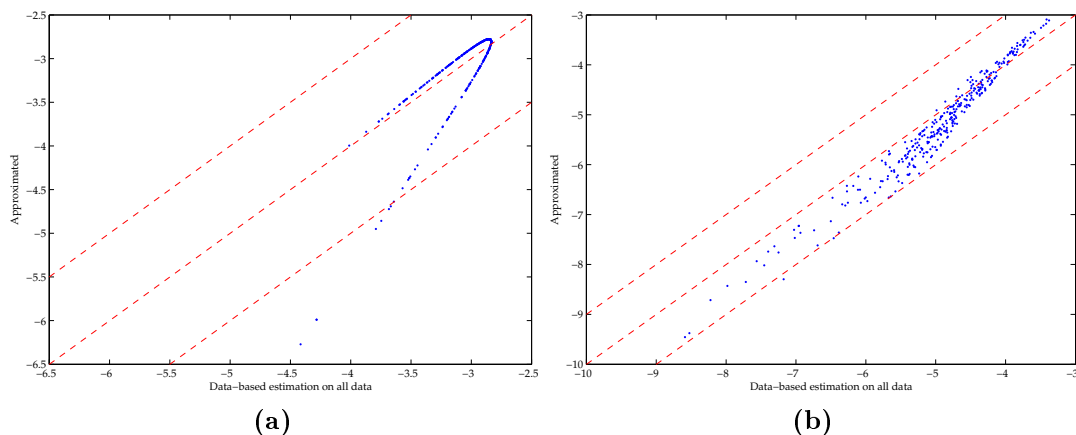


Figure 6.22: Relationship between the logarithm base 10 of data-based and approximated a) numerators and b) denominators (obtained from a between-finger variability estimated using all available fingerprints), obtained under H .

For 7 minutiae, while the results are not shown here, they are very similar to those obtained for 6 minutiae: overall, LR_s are acceptable under H but not under \bar{H} . Differences are due to the numerator under H , while they are due to the denominator under \bar{H} . Overall, these divergences are more pronounced for 7 than for 6 minutiae.

For 8 minutiae, approximated LR_s both under H and \bar{H} are within the tolerance limit of the LR_s obtained using data-based estimation (see figure 6.23 a) and b)).

Here, generally, both numerators and denominators under H as well as \bar{H} correspond well (see figure 6.24 for comparisons under H and 6.25 for comparisons under \bar{H}).

The most problematic deviation between the approximated and the data-based estimations is present for denominators obtained under \bar{H} (see figure 6.25 a); it is most probably due to these observations that there are some of the LR_s under \bar{H} (see figure 6.23 b) that are not close enough to the data-based estimation. Overall, however, these results from the approximations are almost acceptable.

For 9 minutiae, results indicate divergences of more than one order of magnitude (see figure 6.26). Of numerators (under H and \bar{H}) and denominators under each hypothesis, only the approximated denominators under H show deviations of more than one order of magnitude; the approximated denominators are too low. However, even if they exceed the fixed limit, they remain reasonably close to it. Also, again,

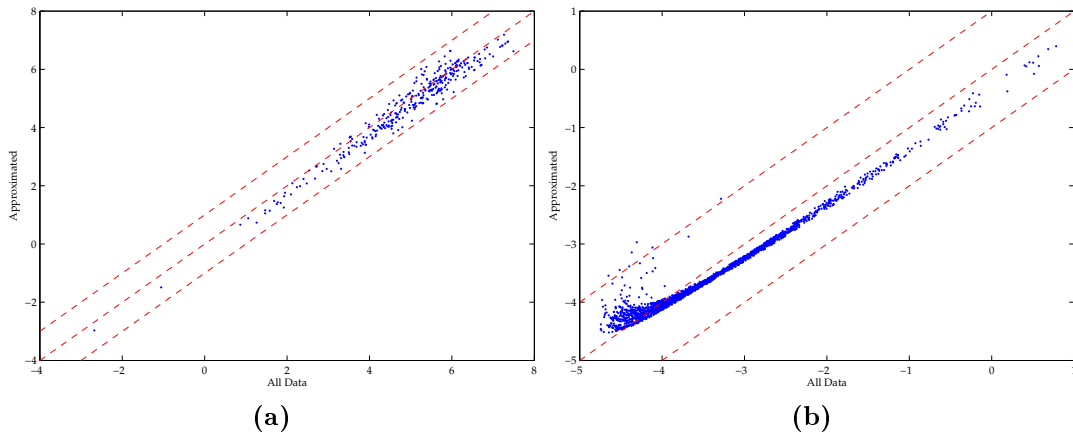


Figure 6.23: Comparison of the logarithm base 10 of LR obtained using data-based estimation (using all available fingerprints for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 8 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

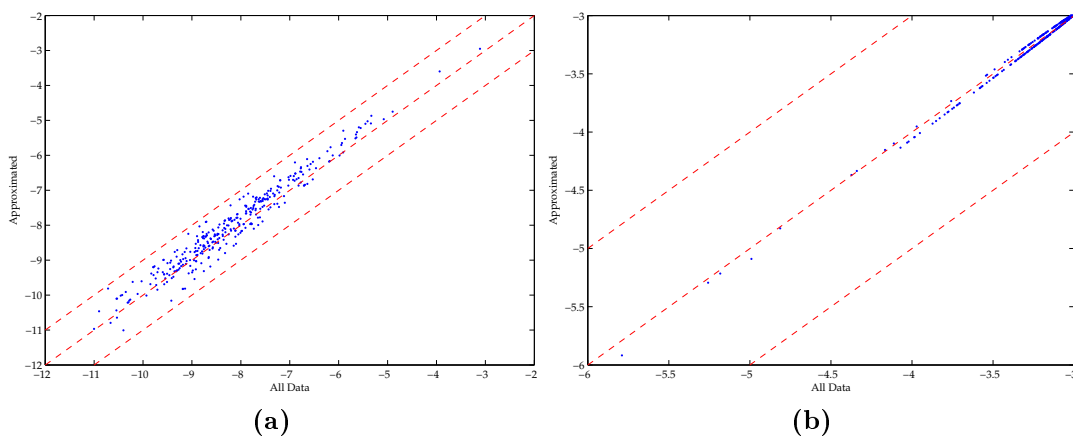


Figure 6.24: Comparison of the logarithm base 10 of a) denominators and b) numerators obtained using data-based estimation (using all available fingerprints for the estimation of between-finger variability) and using approximations for the configuration of 8 minutiae on left thumb of donor 2 under H

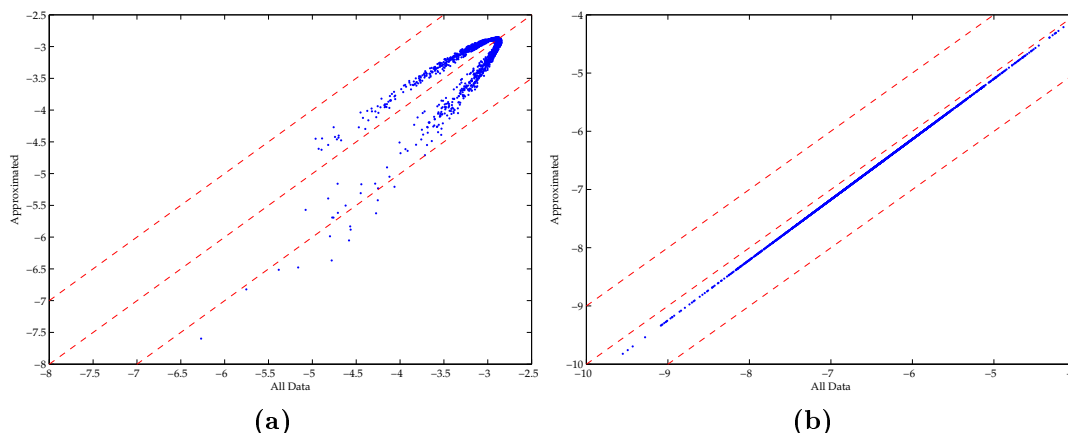


Figure 6.25: Comparison of the logarithm base 10 of a) denominators and b) numerators obtained using data-based estimation (using all available fingerprints for the estimation of between-finger variability and using approximations in both the numerator and the denominator for the configuration of 8 minutiae on left thumb of donor 2 under \bar{H}

the large deviations are mostly observed for extreme values; the impact of the difference observed between the approximated and the data-based LR is minimal in the sense that the LR obtained using either method lend much more support to H than to \bar{H} . Indeed, the deviations observed here occur only for LR that are very large using either method to compute them.

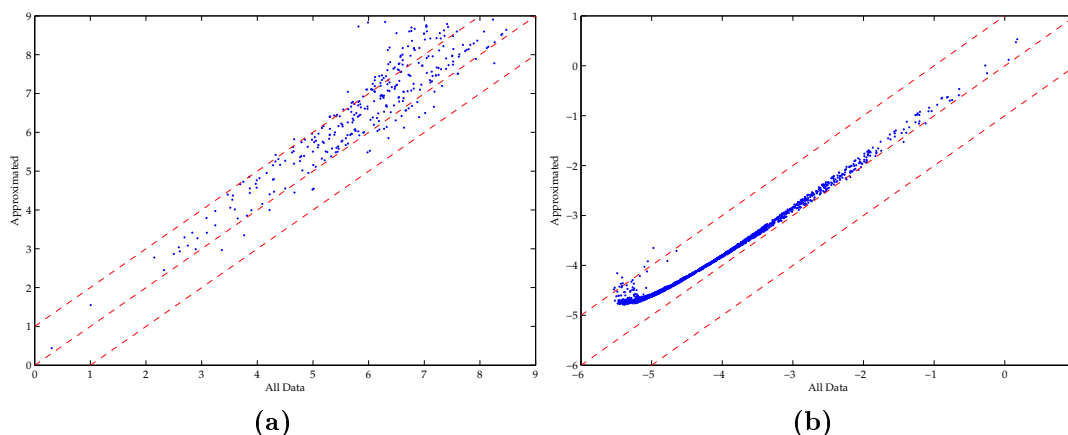


Figure 6.26: Comparison of the logarithm base 10 of LR obtained using data-based estimation (using all available fingerprints for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 9 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

Finally, for 10 minutiae, the comparison between data-based and approximated LR is shown in figure 6.27.

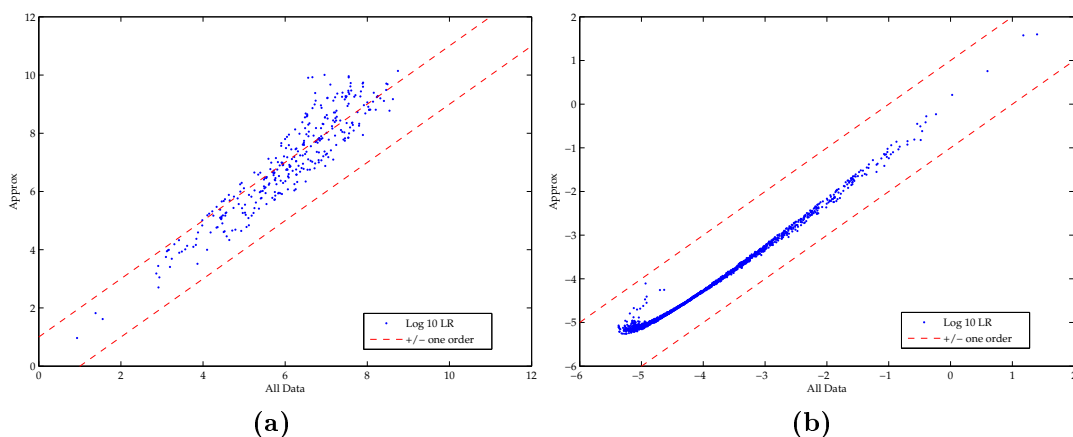


Figure 6.27: Comparison of the logarithm base 10 of LR_s obtained using data-based estimation (using all available fingerprints for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 10 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

Now, while LR_s obtained under \bar{H} using the approximation are comparable to the LR_s obtained using data-based estimation, this is not the case for LR_s obtained under H . Here, the approximated LR_s are systematically higher than those obtained using data-based estimation; as for 9 minutiae, this effect is particularly pronounced for very large LR_s (above 10^6). Indeed, denominators obtained using the approximation are too low under H , while the numerators obtained are, under both hypotheses, well within the fixed limits. Also, the denominators obtained under \bar{H} give no reason for alarm. It is therefore the right tail of the approximated between-finger variability that is not sufficiently heavy and causes the deviances in the LR_s obtained under H . Again, the impact of these deviations (although they are unfavourable for a suspect who is at the source of the finger leading to a score in this region when compared to the mark) is likely to be small. Indeed, scores leading to LR_s where these deviations are observed have only been obtained here for comparisons between impressions from the same finger, while using a very large background database.

When changing the between-finger database used for the estimation of between-finger variability to a database of whorls on left thumbs only (rather than using all available fingerprints) for the establishment of the graphs comparing the approximated to the data-based LR_s, the results shown in figures 6.28 to 6.32 are obtained.

While the correspondence between the logarithm base 10 of LR_s obtained using approximations in the numerator and denominator or obtained using data-driven estimation for both factors is still imperfect when the database used for the estimation of between-finger variability is restrained to the same finger number/general

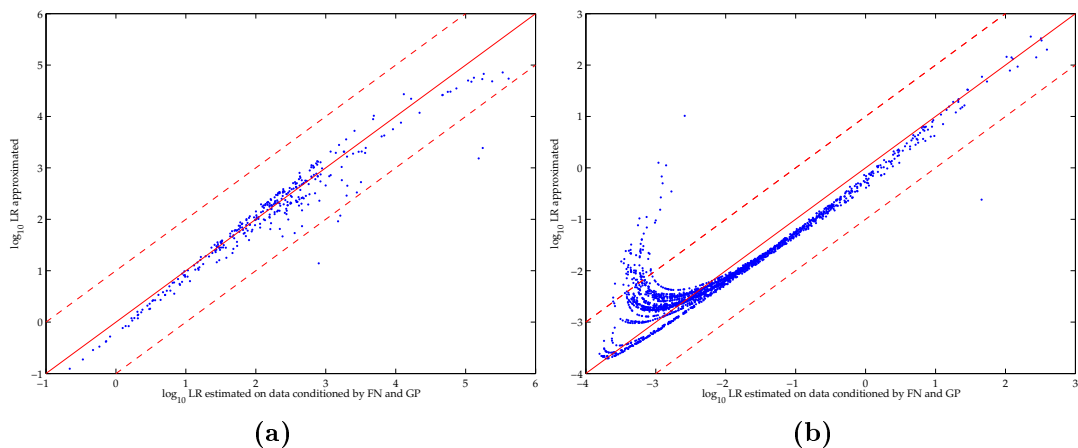


Figure 6.28: Comparison of the logarithm base 10 of LR obtained using data-based estimation (using only whorls on left thumbs for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 6 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

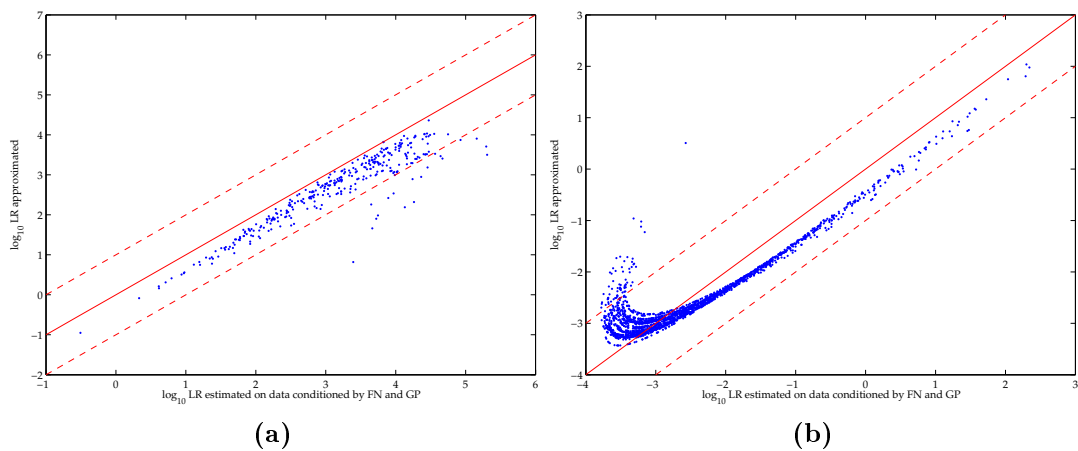


Figure 6.29: Comparison of the logarithm base 10 of LR obtained using data-based estimation (using only whorls on left thumbs for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 7 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

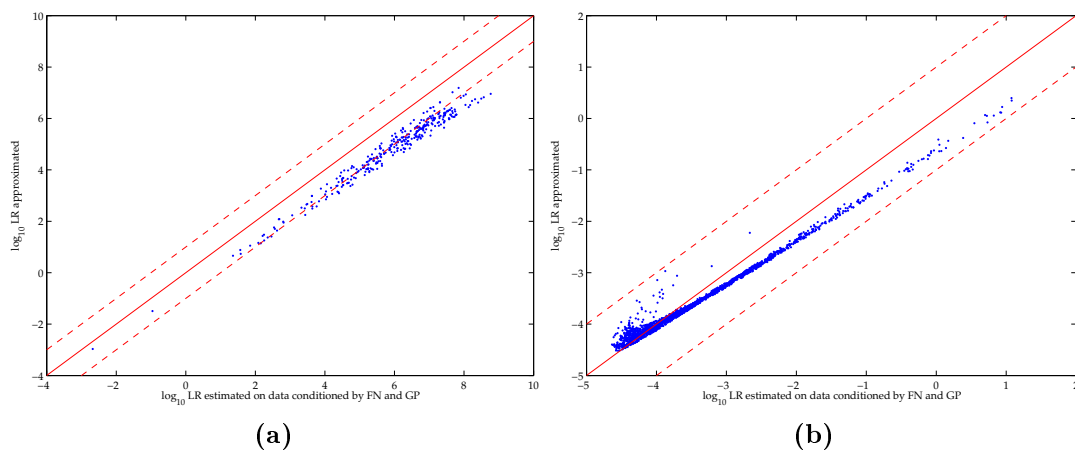


Figure 6.30: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (using only whorls on left thumbs for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 8 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

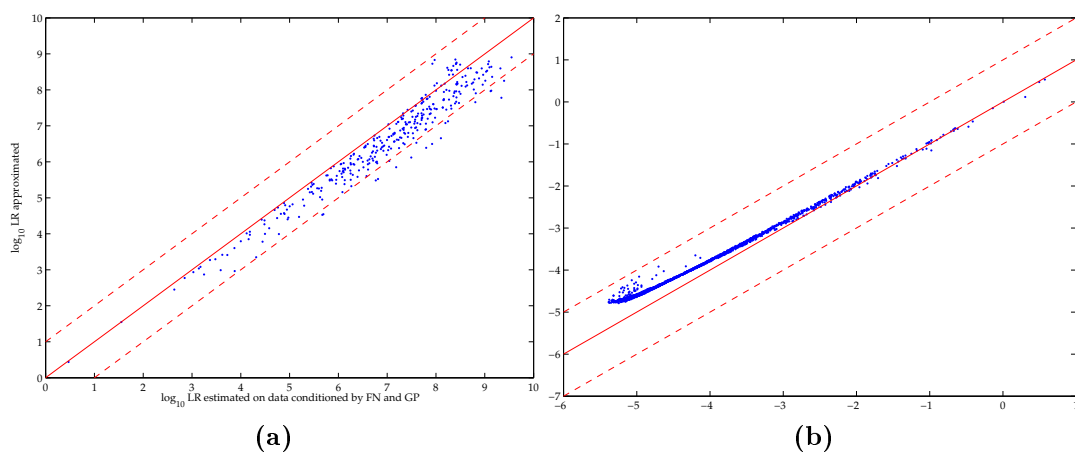


Figure 6.31: Comparison of the logarithm base 10 of LRs obtained using data-based estimation (using only whorls on left thumbs for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 9 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

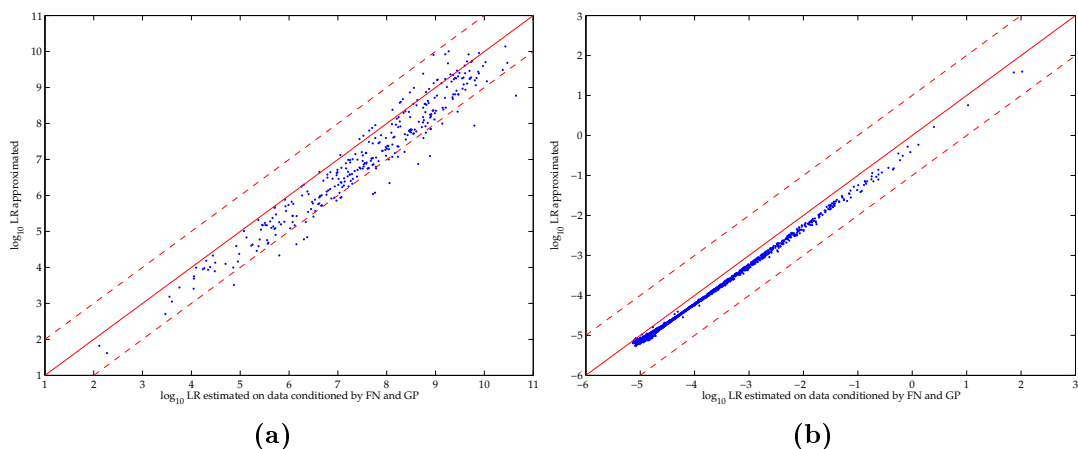


Figure 6.32: Comparison of the logarithm base 10 of LR obtained using data-based estimation (using only whorls on left thumbs for the estimation of between-finger variability) and using approximations in both the numerator and the denominator for the configuration of 10 minutiae on the left thumb of donor 2 under a) H b) \bar{H}

pattern combination as that of the mark, it is much better than that observed when between-finger variability estimation was based on the whole between-finger dataset. While results remain comparable to those previous tests for 6, 7 and 8 minutiae, the deviations observed in large LR obtained under H for configurations of 9 and 10 minutiae are reduced. Also, these deviations now go in the sense of obtaining lower LR when using the approximations rather than the data for the estimation of within- and between-finger variability.

6.4 Discussion of the results on the testing of LR

What has been shown here is that the approximations proposed have imperfections; it has, however, also been shown that these deviances between approximated and observed distributions are likely to have at most a moderate effect in operational use; large (more than one order of magnitude) deviations are observed mainly for extremely low scores for 6,7 and 8 minutiae, rather than for scores that are expected to be obtained for comparisons that indeed are to be evaluated by the present system. These are the only cases where the approximation lead to misleading results, i.e. LR that were closer to 1 or even above for comparisons between impressions from different fingers. However, in these cases, it is sufficient to be able to position the evidential score in relation to the between- and the within-finger variabilities in order to identify that it falls into the region where deviations were observed.

The deviations observed for larger numbers of minutiae (9 and 10) are more likely to be observed in operational settings; their impact, however, is much smaller than that of those observed for smaller minutiae configurations. Indeed, here, instead of

very large LRs in favour of H , now, LRs that are even larger are obtained. This is not unproblematic; however, upper and lower limits could be associated to these LRs, which would be likely to solve this problem.

Furthermore, comparisons with data-based LRs where a between-finger database consisting only of fingerprints with the same combination of general pattern and finger number resulted in even better correspondence between these data-based and the approximated results. Therefore, while the degradation in correspondence for donor 2 with respect to donor 1 is not negligible, it still yields acceptable or even good results and is therefore a viable approach to operational implementation of the computation of LRs based on scores as output by an AFIS.

This, although not very large, degradation of the correspondence between approximated and data-based LRs for donor 2 with respect to that of donor 1 does not allow the direct application of approximations to casework. It is not possible to know whether, in the case of another donor or a different finger number (such as index fingers) the approximation would hold as well as it has for donor 2. Since there is a certain instability in the fit of the approximation to the data-based estimation, which is evidenced by the difference between donors 1 and 2 observed here, the approximation cannot be considered generalizable at this point. Further validation of this approach is relatively easy to carry out, even during application of the model to casework using data-based estimation. During such data-based estimation, all the necessary data for the approximation is acquired; the only additional information needed for the approximation if data-based estimation is carried out are the self-scores (but the images to acquire self-scores are needed for the data-based estimation of within-finger variability; only the insertion of 3 slap impressions as 'prints' into the system and their annotation to match as closely as possible that used when they are inserted as 'marks' into the system are lacking).

The results obtained here do show that data-based LR estimation is robust and yields overall low rates of misleading evidence and rather large LRs in favour of the hypothesis known to be true. Furthermore, both the rates of misleading evidence and the values of the LRs go in the right direction as minutiae are added to the configurations; a decrease of the rates of misleading evidence is generally observed, while LRs lend more support to the true hypothesis as minutiae are added.

The approximations used are promising: divergences between the data-based and approximated LRs are generally small and the conditions in which they may be large are quite well defined. In the present work, no precise threshold in terms of score or density values can be given, because the large divergences generally depend not only on the probability density of one of the two distributions, but on the relationship between the two. An example shown in this chapter (see figure 6.20) may be taken to aid the determination of a region where approximation and data-based estimation do not correspond. However, in casework, such very low scores are not expected to be observed. It is thought that in general

such LR based evaluation would only be carried out when an examiner has carried out the comparison and has not been able to exclude. Therefore, the configurations of mark and print would already be more similar than those used here under \bar{H} , that are simply randomly sampled among all of the comparisons between the marks from a known source and the fingerprints known to come from different sources.

Chapter 7

Discussion

7.1 General approach

The point of view that the evaluation of forensic evidence in general and fingerprint evidence in particular can and should be carried out using statistical tools is taken in this thesis. This point of view cannot be considered as new: it is the one defended, for example, in Stoney (1985), Champod (1996) as well as Taroni and Margot (2000), Champod and Evett (2001) and Saks and Koehler (2005). Also, previous research has been carried out on statistical models in fingerprints. Only few used the likelihood ratio as the indicator of the probabilistic weight of the evidence: the model by Neumann et al. (2006, 2007) and the one by Champod (1996). The model by Neumann et al. (2006, 2007) is, however, the only one that estimates a numerator for the likelihood ratio. The probabilistic approach remains quite controversial, however, and even prohibited by professional bodies (SWGFAST, 2003; Anon., 1980). These professional bodies indeed require that conclusions be absolute. The view is taken here that while absolute conclusions may have had some reason for being in the absence of statistical models that were reasonably well tested and established on large datasets, now that such models become truly available, these reasons certainly no longer exist. The reason why these absolute conclusions had some grounds in that context is that it is, quite opposite to what should rationally be expected, easier to defend absolute conclusions than probabilistic ones. While absolute conclusions are accepted in court, subject to the experts' demonstration of their capacity to reach such conclusions, the presentation of probabilistic data is much harder, perhaps without reason. Such a presentation is subject to the verification of each step, the assumptions, data, modeling and final result. This also means that all that leads to the conclusion (i.e. the observations in the case, the assumptions and models, the method and data on which this process is based as well as the results of previous tests of the performance of this process) is (or can be) made transparent.

The likelihood ratios generated by the models used for within- and between-variability in the present thesis are not considered as being useful to the fact finder in the form of precise numbers. Although the result as such will be some high

precision number, it is not considered here that to take into account the precision is useful. Take, as an example, an LR of $3.45672 \cdot 10^8$. Indeed, if the LRs computed are undoubtedly quite robust concerning their exponent, it is very doubtful that with a change of data, in particular in the within-finger variability, the exact same number would be obtained. Also, while the number is very useful for the combination of different items of evidence, it is not necessarily a great aid to comprehension. The concept of likelihood ratios is not easy to explain, nor to understand. It is even worse when very large numbers result from computations, that must be viewed in a completely probabilistic setting in order to be understood properly; otherwise, these numbers would inhibit rather than aid a fair assessment of evidence.

Furthermore, the models for within- and between-finger variability that allow to compute LRs must be viewed as the best possible representation of what they should be. They are firstly based on data, and this data is acquired in a given way; this acquisition process, as well as the data itself, may lead to variations in the within-finger variability. Then, some way of obtaining $f(s|H)$ and $f(s|\bar{H})$ is devised in any model to compute LRs; here, choices are involved. The choice made here was to use a Weibull and a Lognormal distribution, fit them to the relevant data as defined previously, and obtain the numerator and denominator values from these distributions. These choices can and should be questioned, not only in the present model, but in all models. While it is hoped that LRs computed using different models will be coherent, this needn't necessarily be the case; at least numerical identity cannot be expected. Correspondence in the order of magnitude of LRs should, however, be possible. Otherwise, the only way to interpret the values of the different models would be to scrutinize the premises of the different models, and make a reasoned choice between them.

It is because in general the exact values of LRs are not viewed as being particularly useful in the communication of results (nor in the final decision made by the judge), that errors of up to an order of magnitude (or up to a change in the value of the exponent) have been allowed in all approximations made.

The results shown in the present thesis have been obtained by using a given system: a Sagem DMA. The scores and distributions obtained are most certainly not the same as those that would be obtained using any other AFIS. However, the present work not only yields these system-specific results, but more interestingly proposes a way of acquiring data for the establishment and testing of an interpretative approach based on AFIS scores. The goal being to be able to obtain likelihood ratios from these scores, practical approaches to the estimation of within- and between-variability are proposed. While some of the options selected here may not lead to general agreement (e.g. the use of parametric models for the within- and between-finger distributions), alternatives are mentioned and the reasons for not choosing them are made clear; if a similar model was to be established on the basis of a different system, different choices could be made.

One of the more salient choices made in the present thesis are the numbers of

minutiae that have been investigated; only configurations of between 6 and 10 minutiae have been used. While it is clear that not all numbers of minutiae can be investigated, the precise limits defined here can be challenged. The lower limit was chosen for practicability; indeed, very small configurations may be used, but in practice the use of very small configurations would lead to a large amount of additional work, mostly spent searching for very small configurations, that also have the disadvantage of being difficult to place on a fingerprint. The precise number of 6 minutiae was chosen here because such configurations of minutiae can reasonably be expected to be found on a comparison print without a necessarily huge time investment. This is not true, for example, for configurations of 3 minutiae, where the time needed to compare such a configuration to a comparison print is rather large. This is a subjective determination, and this number could be decreased, at least to 5 minutiae (this number is the limit set at this time in the AFIS used for the minimum number of minutiae needed to carry out a comparison using the system; even this limit can be as low as 3 minutiae).

The upper limit used here, of 10 minutiae, was chosen because it was expected that very large LRs could already be obtained for this number; otherwise, the system would not have been considered as an evaluative tool performing well on a very selective biometric which the fingerprint is. Here, indeed, very large LRs are obtained for 10 minutiae, showing that AFIS scores can usefully be employed for evidential assessment using LRs. It would be interesting to adapt the model to larger numbers of minutiae. If cases with larger numbers of minutiae did occur before such an adaptation has been carried out, a subset of minutiae could be used. A supplementary verification step would need to be included in such a case. Indeed, if any of the minutiae not considered in the LR computation initially was to lower the score obtained when added, that would be an alarm signal indicating possibly lack of correspondence between the mark and the print; such a minutiae would necessarily need to be included in the minutiae set used for the computation of the evidential score.

7.2 Within- finger variability

A minimal sample size necessary for the robust estimation of within-finger variability has been determined empirically. This minimum size is of 66 samples. This number may be subject to changes due to the data acquisition process. Here, a bimodality of the distribution of the results on 702 livescans had been observed (which may have been due to the precise minutiae chosen and therefore not necessarily present for any minutiae configuration), and it is on this sample that the sample size was based in a first step. This sample size may not be applicable to all other samples of fingerprints. In fact, the distribution of the scores is highly influenced by the distortion directions used in the acquisition of within-finger variability data; this dependence of the distribution on the data acquisition process may also impact on

the sample size need when data is acquired in a very different fashion than what has been done here.

In the present thesis, livescans that were not particularly distorted have finally been used, thus obtaining a similar distribution to the one issued from developed marks. The sample size chosen on the basis of distorted livescans has been verified on this new, undistorted data, and was sufficient to ensure reproducibility between two samples of this size.

The examination of the second mode in this distribution from distorted livescan images showed the dependence of the scores on distortion direction, and this has been confirmed by an Analysis of Variance. The data acquisition and modeling of distortion is therefore an extremely complicated undertaking: the probability of observing distortion in any direction is an unknown factor which influences directly the distribution of scores obtained in within-variability. This has not been taken into account in the present thesis: as soon as developed marks were employed, no distortion was introduced on purpose.

The investigation of this 'real' distortion, which includes the probability of observing a given distortion as well as its effects on the distance observed between two appositions of a given minutiae group, has already been a preoccupation in the past; now it is clear that the data acquisition is not trivial in planification. Here, a uniform distribution has been used for the probability of observing a given distortion direction in the acquisition of livescans; this way of acquiring data could, in time, be replaced by using the probabilities of observing directions of distortion in marks.

Further investigation of the effect of distortion on the distributions of scores would therefore be interesting, in particular for cases where the presence of distortion can be determined on the examined mark. However, in the present model, distorted marks can already be evaluated; they will, according to what has been seen on distorted livescan images in section 4.3.2, show a larger variance in scores. A model based on such distorted marks would therefore yield higher LRs under H , for scores that are not in the high probability density region (and lower LRs for scores that are in this region). Under \bar{H} , generally, LRs obtained using a model based on distorted marks rather than the one proposed here would be expected to be rather less favorable to the defense (since due to the higher variance in distorted marks the tail of the within-finger distribution would be heavier).

Apart from marks, the view is taken in the present work that inked prints should also be considered for the modeling of within-finger variability. It was thought beforehand that the inked print could be considered as a constant. This (rolled) inked print is acquired with the intention of having a faithful and reproducible representation of the fingerprint surface. The analyses carried out here have shown that there is variation in these rolled inked prints, leading to distributions that are similar to those obtained when comparing several marks and a single print.

Knowing that this variation is present, it has been considered that the within-

finger variability should take into account as many prints as marks. This is due to the way in which within-finger variability is considered here. It is not considered to be a representation of the distortions that can be obtained from the suspects' finger, but rather a representation of the possible comparisons between marks and prints from this finger. It is not considered either that the variability obtained should be as large as possible; rather, it should be realistic. The within-finger variability should, in the authors' view, mimic the mark to print comparison that yielded the evidential score. Then, the probability of obtaining this evidential score is found in a distribution of mark to print comparisons from a given finger, where the inked prints are acquired in the same way as the inked print that was used for obtaining the evidential score, and the marks in the same way as the mark used for the evidential score. This also means that the within finger variability computed here could not necessarily be applied in cases where the evidential comparison has been carried out using a slap rather than a rolled print. However, the number of data to be acquired, the distribution that can be fitted, and the fact that acquisition methods must correspond have been determined here, and can easily be adapted to almost any case scenario. Again, if distortion had been introduced into the marks acquired, it is possible that more variation would have been present in the scores obtained when using several marks and one print than when using several prints and one mark. Therefore, the use of as many prints as marks would reduce the variability of scores with respect to the use of a single print. Due to the fact that the within finger variability should mimic the way that the evidential score is obtained, a same number of prints as marks should, in this circumstance, still be obtained.

In the present data-acquisition process, minutiae have been marked semi-automatically; first, automatic detection was used and then, minutiae cleared, added or modified as needed. However, and perhaps in opposition to general practice, the minutiae used here were visible precisely, concerning their position, type and direction on the fingerprint. If one of the minutiae selected was not precisely visible on a given mark, this mark was not used any longer (even if the minutia could have been placed approximatively); in this sense, only very clear minutiae were included in the model. So while the present model does permit to give useful information to a court for fingerprints that show perhaps less minutiae than would be currently used for identification, these minutiae must be clearly defined on the mark (and the print), which relativizes the increase in the number of cases that can be usefully treated. It is considered in the present work that, for use in the model, it is sufficient if only such clearly defined minutiae are used; an increase in the number of cases where fingerprints can be usefully employed is still expected if the model was to be used operationally.

The estimation of within-finger variability has then been simplified using direct estimation of parameters based on 3 so-called self-scores. These are the scores obtained when inserting the same minutiae configuration twice: once as a mark and once as a print, in order to obtain the largest possible score for this minutiae

configuration. This approximation could save a lot of time; also, the likelihood ratios obtained when using it are generally close (i.e. less than an order of magnitude greater or smaller) to those obtained when estimating the parameters based on the data. Unfortunately, the tests using this approximation have shown that large deviations (of more than one order of magnitude) in numerators are obtained when using this approximation for scores that are in the far right tail of the within-finger distribution. While it is highly unlikely to obtain a score in this region, even when comparing two impressions from the same finger, these deviations remain problematic.

Deviations from data-based LRs have been observed in particular in the tails of the within-finger distribution; generally, excellent results are obtained in particular in the central part of the within-finger distribution. Also, only very few occurrences where estimation based on approximations lead to LRs that were in favour of the hypothesis that was not the one under which they had been obtained were observed. Generally, the impact of the deviations was minimal in the sense that, even in the presence of a deviation of more than what is admitted here (one order of magnitude), the overall impact of the LR should not have changed by much; if an LR of 10^8 had been obtained on the data, the approximations lead in some instances to LRs of 10^6 or, conversely, 10^{10} ; in all of these cases, this is evidence that is very highly supportive of the prosecution hypothesis, and it is doubtful that such differences would lead to large differences concerning their impact on the decision maker's conclusion.

The use of a parametric distribution also opens new possibilities; when considering that the data used here can be criticized (as is the case of any dataset) with respect to the representation of distortion, it could be considered that the within variability based on the data could be used as an indicator for the determination of a 'better' distribution to be used. Here, parameters were approximated so as to correspond as closely as possible to the data from the marks used. Since the marks used, however, were not acquired using distortion, the approximated parameters could be adjusted such as to include the possibility of distortion. Since it has been observed that livescans in the central position (without distortion) yield a within-finger distribution that is very close to that observed on marks, the effects of distortion observed on the livescans could be integrated into the parameter estimation. In the end, such a way of doing things would tend towards an intelligent choice of parameters rather than towards even more extensive data-acquisition procedures that would always remain imperfect. For the reasons mentioned above (the frequency with which marks that are distorted in any given direction is unknown), data-based estimation is not any closer to 'reality' than such an intelligent choice of parameters, that would take into account, of course, distortion as well as possibly the placement of the minutia group in relation to a distortion direction, and some indication of the quality of the marked minutiae.

Such an approach, where parameters are selected without being directly based on

data, would, of course, render necessary a large validation step, using, for example, likelihood ratio assessment techniques. The advantage of such an approach is that likelihood ratio values could be optimized such that they would be large, and in particular larger than 1, when H is known to be true, and small, in particular smaller than 1, when \bar{H} is known to be true. The disadvantage is of course the progressive abstraction of such a distribution: first, it is based very closely on data. In a second step (the approximation of parameters) it is less dependent on case specific data, and when such parameters are chosen as a function of general theoretical knowledge, as well as some case specific data, such distributions are more dependent on the knowledge than on larger amounts of data. While this removal of data-dependence could be viewed as problematic, it is quite possible that such distributions would yield more reliable results than data-based approaches, due to the difficulty of proper data acquisition, in particular in the forensic fields.

In general, a major advantage of using a model of within-finger variability is that it directly responds to one of the difficulties in fingerprint identification mentioned in the introduction. The difficulty of distinguishing dissimilarities from discrepancies, particularly when the comparison print has been chosen in a large database, is greatly reduced by such a model. The within-finger variability is a representation of the scores that are expected if the two impressions come from a same finger; whenever the comparison between a mark and a print has a very low probability of occurring under this hypothesis (and in particular when this comparison has a higher probability of occurring if the two impressions come from different fingers), the probability of being in the presence of a discrepancy rather than a dissimilarity is increased. In this sense, the within-finger variability model (as well as more generally the probabilistic approach proposed here) aids the examiner in this assessment of the characteristics compared.

7.3 Between-finger variability

The modeling of between-finger variability is in many ways much more straightforward. There are less considerations concerning the data to be made; the mark is confronted to the database of prints, yielding a distribution of scores.

The minimum number of prints to be included in such a database is quite low (10000); on the other hand, this is a large number of univariate data for modeling. This minimum number is much less subject to changes in the data acquisition process than is the number of data in within finger variability.

In this thesis, a database has been used where double entries are included; several ten-print cards from the same person are, in some cases, present. Due to the time investment necessary and the supposedly very small impact on the distribution of scores, these double entries have not been tracked and eliminated. Furthermore, in real cases with real databases, there are generally double entries for some individuals.

Effects due to finger number and general pattern have been observed, as well as effects due to the marks used; different distributions were obtained for different marks from the same finger with the same minutiae configuration. These effects were significant. However, the very large sample size used results in very small confidence intervals for parameters. This in turn leads to rejection of similarity of distributions although these distributions may be sufficiently close for our purpose: to estimate LR_s within one order of magnitude of the LR based on the proper data. This is why, in some instances, the result of a formal test has been reconsidered in favour of an analysis of the likely impact of the differences between distributions.

On second thought, the database to be used is less evident to determine than noted in the introduction: should only the marks' characteristics (finger number, general pattern) be used, if known? Or should the suspect's fingers' characteristics also be considered to determine the database to be used? Should, generally, the whole database be used? These characteristics of the suspects' finger indicate that the observed minutiae configuration has more chances to appear on a given finger number and general pattern; in this sense, the second option is likely to be more favourable to the suspect. The between variability distribution used would therefore be $f(S|x, y_G, \bar{H})$, where y_G represents the general characteristics (finger number and general pattern) of the suspects' finger; both the suspect's and the marks' characteristics are taken into account. If the suspects' characteristics are not used for database determination, the between variability is $f(S|x, \bar{H})$. Of course, if the suspects' fingers general characteristics are taken into account for the computation, the probability of observing these characteristics should also be integrated, yielding a denominator of $f(s|x, y_G, \bar{H})p(GP|FN)p(FN)$, where $p(GP|FN)$ is the probability of observing this general pattern (*GP*) on the finger number (*FN*) in question and $p(FN)$ is the probability of observing a crime scene mark from the finger number in question, which may be quite low (for little fingers on the left hand, for example).

In the present thesis, the conditioning by the suspect's finger number and general pattern is not thought to be correct; however, the approximations used open a new possibility for the computation of between-finger variability. What has been proposed here is an approach, using the approximations, where the between-finger variability estimated actually very closely approaches what would be obtained if the marks finger number and general pattern were known. This is considered the best way of estimating between-finger variability, since it takes into account that the scores obtained will be slightly higher, overall, when comparing two impressions from fingers with the same finger number / general pattern combination. This way of modelling the between-finger variability mimicks what would be obtained were the marks general pattern and finger number known (even if these two elements are not present on the mark or cannot be deduced from other marks surrounding it).

Also, in this thesis, only two cases are considered: using the whole database, or considering both the finger number and the general pattern as fixed. Either of these two characteristics can also be known on itself on the basis of the mark. To

multiply the computations did not seem useful, however. The results presented permit the assessment of the joint effect of these two factors, and it has been shown that each factor has an effect. Therefore, when only one of the two factors is known, the database used for the computation of the between-finger variability should be conditioned by this single factor.

7.4 Likelihood ratios

Tests using likelihood ratios have been carried out only for one finger of donor 2, who was not used for establishing any of the approximations used in the within- and between variability.

Generally, results show rather high rates of misleading evidence in favor of the prosecution for configurations including few minutiae. The values of these misleading likelihood ratios remain quite small: while they are misleading, they are only in the order of 100. For larger numbers of minutiae, the performance of the system as assessed here is good. Also, the examinations of whether approximated distributions yield LRs that are comparable to those obtained using data-based estimation shows that, except for low minutiae numbers (6 and 7), the approximations used are often within one order of magnitude of the LRs obtained using data-based estimation. Problems remain also for high minutiae numbers with these estimations; in LRs for 10 minutiae, the values are, in some instances, too high, due to the approximation in the denominator when compared to data-based denominators estimated on the basis of the entire database; this problem does not exist any longer when a database that is restricted to the same finger number and general pattern as that of the mark is used.

Data reduction for a data-base approach has also been successful for the between-finger variability: only 10000 fingerprints are necessary for a proper estimation of between-finger variability using the proposed parametric model.

Also, an unexpected effect of using the part of the database corresponding to the suspects' finger number and general pattern has been discovered; far from being favorable, such a selection actually increases LRs obtained under H . This is due to the fact that, when a smaller part of the database is selected, the right tail of the between finger variability is reduced, and therefore, denominator values decrease faster as scores increase, leading to higher LRs in this right tail of between-finger variability.

The approximations proposed are, finally, promising; they do yield appropriate LR values in most cases. Also, divergences have been analysed, and a remedy can easily be found; problematic deviations occur in the far left tail of the between-finger variability in some instances. These deviations may even lead to LRs above 1; they are, however, easy to recognise by verifying that the score obtained is to the left of the mode of the between-finger distribution and that therefore, the LR should be below 1. The only reason why these approximation should not necessarily be used

for casework yet is that the tests on one single different donor have shown a slight degradation of results; they are therefore not perfectly applicable to this donor, and a few further tests would allow the assessment of whether these deviations risk to be larger for other donors and finger numbers. Indeed, it is expected that now such large deviations will appear in such tests, since the finger used for testing has been chosen in order to show large differences with the finger used for the establishment of the approximations; nevertheless, if in the first few cases a within-finger variability based on 64 comparisons between 8 slaps and 8 rolled impressions could be acquired, and the self-scores obtained as well, this could add greatly to the confidence in the approximations for within-finger variability while a similar approach (using the whole between-finger database for the case itself, while checking against the approximation) would do the same for between-finger variability.

In two chapters, tail effects have been observed that are counterintuitive: in the far left tail of between- and in the far right tail of within-finger variability, LRs invert their tendency. In the far right tail of the within-finger variability, there is a point where the right tail of the between-variability is again higher than the one for the within-finger variability. A score this high would support the defense rather than the prosecution hypothesis, which may be counterintuitive at first sight. It is, however, known that among AFIS results, the highest score is not always the one matching the mark to the 'right' finger, which is why AFIS results are passed on to fingerprint examiners. While during the present work, not one such higher score from a different finger has been observed, it would be interesting to find such an observation and compute the LR, in order to verify whether the system presented here could even resist to such an event. In the far left tail of between finger variability, no such inversion between distributions has been observed, but it may be possible.

The right tail of the between-variability is heavy; this is where LRs are expected to be computed often in casework. If this tail is not heavy enough, very large LRs are obtained for scores that are in the left tail of the within-finger distribution; while this may be mathematically correct (in the case where such a light tail was used for the modelling of large values in the between-finger variability), it poses problems since such LRs may reach values such that the final decision concerning the source of the fingerprint is almost determined by the LR of the fingerprint comparison. Extremely large LRs may therefore substitute classical identification conclusions by a number so large as to lead to the same effect. This is particularly problematic when it is known that very large LRs are obtained by a system resulting in a non-negligible proportion of misleading LRs (although these misleading LRs were not very large). Substituting subjective 'identification' opinions by numbers so high as to exceed human comprehension does not seem useful, especially since these numbers are based on a certain number of hypotheses, beginning with data acquisition and ending with modeling of the distributions, that are far from indisputable (or undisputed); this is another reason why the numbers resulting from such an approach cannot be

expected to be precise to the point where judgment based on their sheer size should be passed. That is to say that the final LRs, while giving useful information, should not be so large as to be overwhelming. Here, a heavy tailed distribution is used for the between-finger variability; while this is simply due to the fact that it fitted the data well, it is considered an advantage, since very large LRs will not be obtained for observations in the left tail of the within-finger distribution. Such large LRs are still obtained for very large scores. If they are obtained, they should simply not be taken to mean something along the lines 'basically that means it's him', but still be interpreted as likelihood ratios, and integrated into a case as such. Also, the model used for obtaining such ratios should be viewed critically, and without forgetting that generally, very large (or very small) LRs are obtained in the extreme tail of one of the two distributions used, where very little (if any) data is present to inform the model. This basically that the more extreme the LR, the larger the error that is attached to it, and this is another reason why these numbers should be used with caution. It remains that LRs are extremely useful; they substitute a subjective assessment of rarity and correspondence by an assessment that is based on much more data, including rare events that may never have been observed by a particular individual. The datasets used in this thesis, for example, are probably far more extensive than what is seen by an examiner throughout his career; furthermore, the datasets used are clearly defined and of known origin, which can never be said of datasets constituting experience. The systematic use of such models can therefore be a valuable aid for the examiner and the court, simply by allowing all concerned to profit from the large datasets that are available.

More than being just an aid, the model presented here allows a transparent way of addressing two of the criteria established for scientific evidence in *Daubert v. Merrell Dow Pharmaceuticals, Inc.* (1993). Error rates are known, and the method has already been tested. Also, further testing can very easily be implemented, if this is deemed necessary.

Also, the likelihood ratios obtained here have been shown to support the hypothesis known to be true in a very large majority of cases; this model can therefore, at least using the data-based estimation approach, be implemented immediately in casework. Concerning the simplifications represented by the approximations of parameters, the results obtained here are promising, but they are not considered to be directly applicable to casework without any further testing. Since data-based estimation necessarily implies that the impressions needed for the approximations are available, and since the testing of the approximations against the data-based estimation does not imply that the ground-truth of the case be known, such validation can be carried out while casework is done using the data-based estimation techniques.

The easy application of the model established here is illustrated below, with a case example that was already used in Egli et al. (2007).

7.4.1 Case example & application of the model to cases

The mark and print used in this example are shown in figure 7.1. 9 minutiae have been annotated on these two impressions, and a score of 4192 has been obtained. The LR cited in Egli et al. (2007), obtained using a data-based estimation for between-finger variability and substituting another fingers within-variability was of $8.56 \cdot 10^7$.

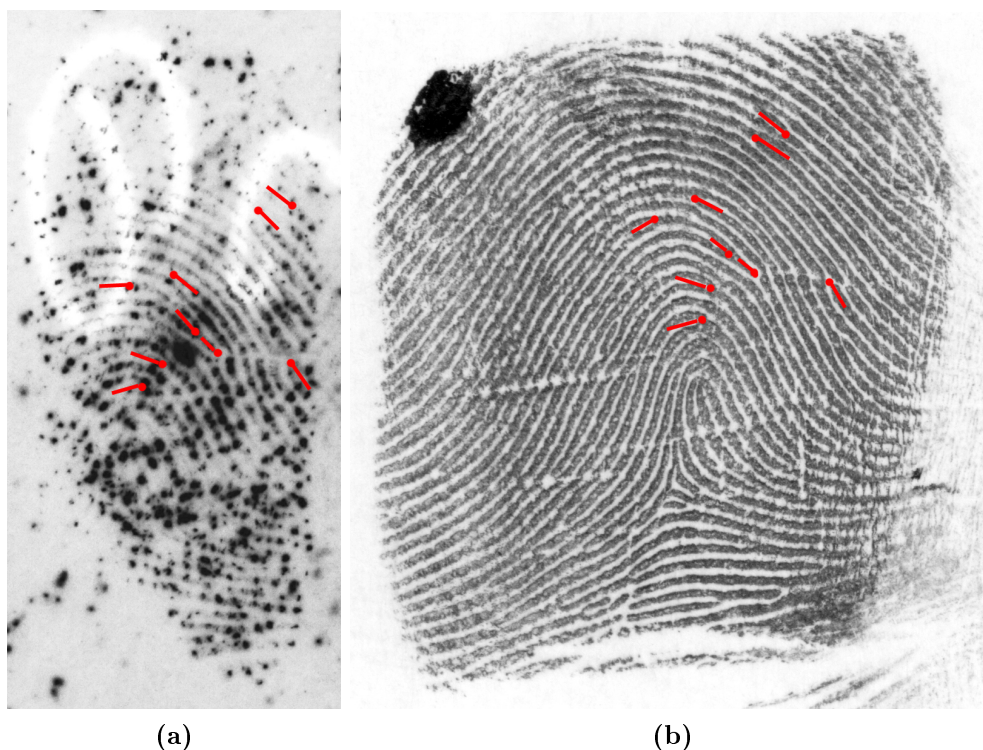


Figure 7.1: Illustration of the mark (a) and the print (b) used in the case example showing the 9 minutiae used

Now, 3 self-scores have been obtained from inked impressions of this finger; these scores are of 6250, 6273 and 6466; their mean is $6329.6\bar{6}$. Furthermore, the mark has been confronted to the whole database of non-matching prints, and the 10 highest scores are reported in table 7.1.

Table 7.1: 10 largest scores obtained when comparing the evidence mark to the database of non-matching prints

Score number	1	2	3	4	5	6	7	8	9	10
Score	3742	3736	3487	3455	3446	3408	3399	3355	3309	3268

The mean and variance of these scores obtained for the between-finger variability are 3457.6 and $37256.044\bar{4}$, respectively. The parameter α for the within-finger

variability is therefore $(s + 903.78)/1.4565 = 6329.6 + 903.78)/1.4565 = 4966.28$, which is larger than what had been used in Egli et al. (2007). The parameter β being determined by the number of minutiae (9), it can be read off from table 4.22 in chapter 4; it is of 10.4. This parameter is larger than what has been used in Egli et al. (2007). The probability to be put in the numerator is therefore the value of the Weibull probability density function with parameters (4966.28, 10.4) at a score of 4192; this value is $3.59 \cdot 10^{-4}$. For the between-finger distribution, the parameters are both computed using the equations given in chapter 5. For 9 minutiae, the equation for the first parameter is $0.2981 \cdot \log(s_{10}^-) + 5.034 = 0.2981 \cdot \log(3460.5) + 5.034 = 7.46$ and for the second parameter it is $-0.007286 \cdot (\log(s_{10}^-)/\log(\text{Var}(s_{10}))) + 0.1827 = -0.007286 \cdot (\log(3460.5)/\log(25973.61)) + 0.1827 = 0.1768$. The probability to be used in the denominator can therefore be obtained at a value of 4192 of a lognormal distribution with parameters (7.46, 0.1771). This value is $2.46 \cdot 10^{-9}$. When the numerator is divided by the denominator, an LR of $1.45 \cdot 10^5$ (rather than the LR of $8.56 \cdot 10^7$ that had been obtained in Egli et al. (2007)).

It is considered in the present thesis that the computation of LRs should, for the moment, rather be carried out using data-based estimation; this implies the following steps:

1. Obtain the score between the evidential mark and the suspects print using all minutiae visible on the mark. Ideally, only between 6 and 10 minutiae should be used, since these are the numbers examined here. Since the only results used in the following are the necessary sample size and the distributions fitted to the data (that remain the same whatever the number of minutiae), more or less minutiae could certainly also be used.
2. Obtain 8 mark substitutes and 8 rolled inked prints from the suspect. The substitutes for marks can be either the slaps from 10-print cards, simulated developed marks, or livescans acquired using distortion.
3. Annotate the minutiae used in the evidential score obtained in 1. on the (pseudo-) marks and verify their presence on the rolled inked prints.
4. Obtain the scores for the 64 comparisons between marks and prints for within-finger variability.
5. Introduce these scores into any program allowing to fit distributions (here, Matlab[®] has been used), and fit a Weibull distribution in order to obtain the parameters.
6. Introduce the evidential scores obtained in 1. and the parameters into a function allowing to obtain a Weibull function value, and obtain the numerator of the LR.
7. Obtain the scores when comparing the evidential mark to the remainder of the database, taking care to eliminate any prints from the suspect either at

this step, or clear them from the data once the scores have been obtained. This is the step that may pose the most problems; while here a custom-made algorithm directly extracted these scores as a text-file, this algorithm is not generally available.

8. Introduce these between-finger variability scores into a program allowing to fit distributions and fit a log-normal distribution. This step may or may not be preceded by a filtering step, where only scores from the same general pattern/finger number combinations as those seen on the mark are present, or a simple random subsampling step that allows the use of 10000 scores rather than all that are extracted.
9. With the parameters obtained in step 8 and the evidential score from step 1, obtain a function value from the lognormal probability density function at the value of the score; this is the denominator.
10. Divide the numerator from step 6 by the denominator obtained in step 9 in order to obtain a likelihood ratio.

The estimation of the LR based on approximation, which is not at this time the method considered optimal, requires the following steps:

1. Obtain the score between the evidential mark and the suspects print using all minutiae visible on the mark using a Sagem DMA. Only between 6 and 10 minutiae can be used here, since approximations are not available for other numbers of minutiae.
2. Obtain 3 slap impressions from the suspects finger, and insert each of them into the system twice: once as a mark, and once as an inked print. Annotate the minutiae used in the evidential mark on these slap impressions, taking care to annotate them as similarly as possible on the identical impressions used on the mark and the print side of the system. Obtain the three self-scores.
3. Compute the parameters for the within-finger distribution using the equation 4.5 given in chapter 4 for α and reading the values for β off table 4.22 in that same chapter.
4. Launch a search of the evidential mark against the database and retain the 10 highest non-mate scores.
5. Obtain the parameters for the between-finger distribution using the relevant equations from table 5.6 in chapter 5.
6. Obtain the numerator and the denominator of the LR using the evidential score and the Weibull and Lognormal distributions, using the relevant parameters computed in steps 3 and 5 above, and divide one by the other to obtain the LR.

7. Plot the within- and between variabilities as well as the evidential score obtained, in order to verify that the score is not in the extreme left tail of the between-finger variability; if this is the case, use data-based estimation. This extreme left tail is not defined as beginning at a specific score or density value. Only the comparative plot of within- and between-finger variability will allow the determination of whether a given point is within this region. This region will, on this plot, be close to the point where within-finger variability becomes greater than between-finger variability, for very low scores.

If more than 10 minutiae are visible on the mark, and only a number of minutiae tested in the present thesis should be used, these steps need to be carried out several times (if the LR is above 1 in particular) in order to see whether one of the minutiae not taken into account initially changes the LR to one that is below 1. If the LR is below 1 using 10 minutiae, it is highly unreasonable to expect to obtain an LR above 1 when exchanging one minutia; it is even more unreasonable to expect that the LR should be above 1 in this situation. While the number of steps required seems impressive in these enumerations, there are only few of these steps that take time; the annotation of the evidential mark and the control of the minutiae on the print, as well as the marking of minutiae on marks / prints used for the acquisition of within-finger variability, and the extraction of scores for data-based between-finger variability as well as its insertion into another program. While the first two items (annotation of minutiae) actually imply that a specialist is active on the system, the last two don't; they take only computer time. The computation of parameters and the numerator, denominator and LR are automated (see Appendix C); these computations do not noticeably take time.

7.5 Outlook

While the model used here performs well, there are possible improvements. These are situated in particular in the within-finger variability. In the present thesis, distortion has been taken into account in a limited way, although it has an effect on within-finger variability. While this was due to the difficulty of acquiring distorted marks, the presented results also show that livescan images are a rather good proxy in the context of AFIS scores, particularly when the minutiae noted must be clear so as to allow to place them with exactitude, to determine their direction and ideally their type.

Then, the approximation based on self-scores of the within-finger variability should be adapted to these new distributions, including distortion, obtained. The inclusion of more distortion would lead to more variance in the within-finger variability than that modelled in the present thesis, and would therefore have an impact on the equations linking the self-scores and the numbers of minutiae to the parameters of the Weibull distribution. Also, in this step, it is possible to include theoretical knowledge about within-finger variability in these approximated parameters. Such

knowledge could help to overcome problems related to the difficulty of acquiring within-variability data in the context of fingerprints.

Finally, it is possible that direct modeling of LRs based on the scores is feasible, using some indication of the score that should be obtained from the given minutiae configuration (such as the self-scores employed here) and some indication of the importance of scores in the between-finger variability. This means that within- and between-finger distributions, numerator and denominator are no longer computed; an 'LR'-distribution is estimated directly; this might greatly limit the number of parameters needed and therefore the possible imprecisions.

In figures 7.2 and 7.3, the logarithms base 10 of LRs are plotted as a function of the score obtained between mark and print for configurations of 6 to 10 minutiae, for donors 1 and 2. In these figures, clearly, there is an almost linear relationship between the scores and the logarithm base 10 of likelihood ratios (which have been obtained by data-based estimation and using the database conditioned by finger number and general pattern for between-finger variability; results are similar when all fingerprints are used). Also, the point where the LRs become greater than 1 (their logarithm base 10 becomes greater than 0) is clearly identifiable, at least for large numbers of minutiae. If the slope of the linear region and the point where the LR must be 1 can be determined from a reasonable amount of data, then direct estimation of LRs is a distinct possibility. If only four parameters must be found (the point where the LR equals 1 and the slope of the line, as well as the two end points where linearity is no longer present), it is possible that the data needed for estimation can be greatly reduced, even if a data-based approach is used. It is also quite possible that a parametric distribution could be used to model this relationship; while indeed, the LRs inverse their tendency on the left and the right of the curve plotted, this is due to the relationship of the tails of the between- and the within-finger distributions used and the relationship between their tails rather than the behaviour that should be exhibited by the LRs in these tails.

When subjectively judging the point where LRs obtained should equal 1, table 7.2 can be established on the basis of figures 7.2 and 7.3.

Table 7.2: Subjective assessment of the score where the LR should be equal to 1

Number of minutiae	6	7	8	9	10
Score D1	2240	2450	2700	2800	3200
Score D2	2500	2800	3000	3300	4000

These subjectively judged values differ between donors 1 and 2; therefore, it is expected that again, the relationship between scores and LRs depends at least on the donor, but more probably on the minutiae configuration (as within- and between-finger variability have been shown to be linked to the configuration itself). These curves could probably be linked to the configuration through the self-scores,

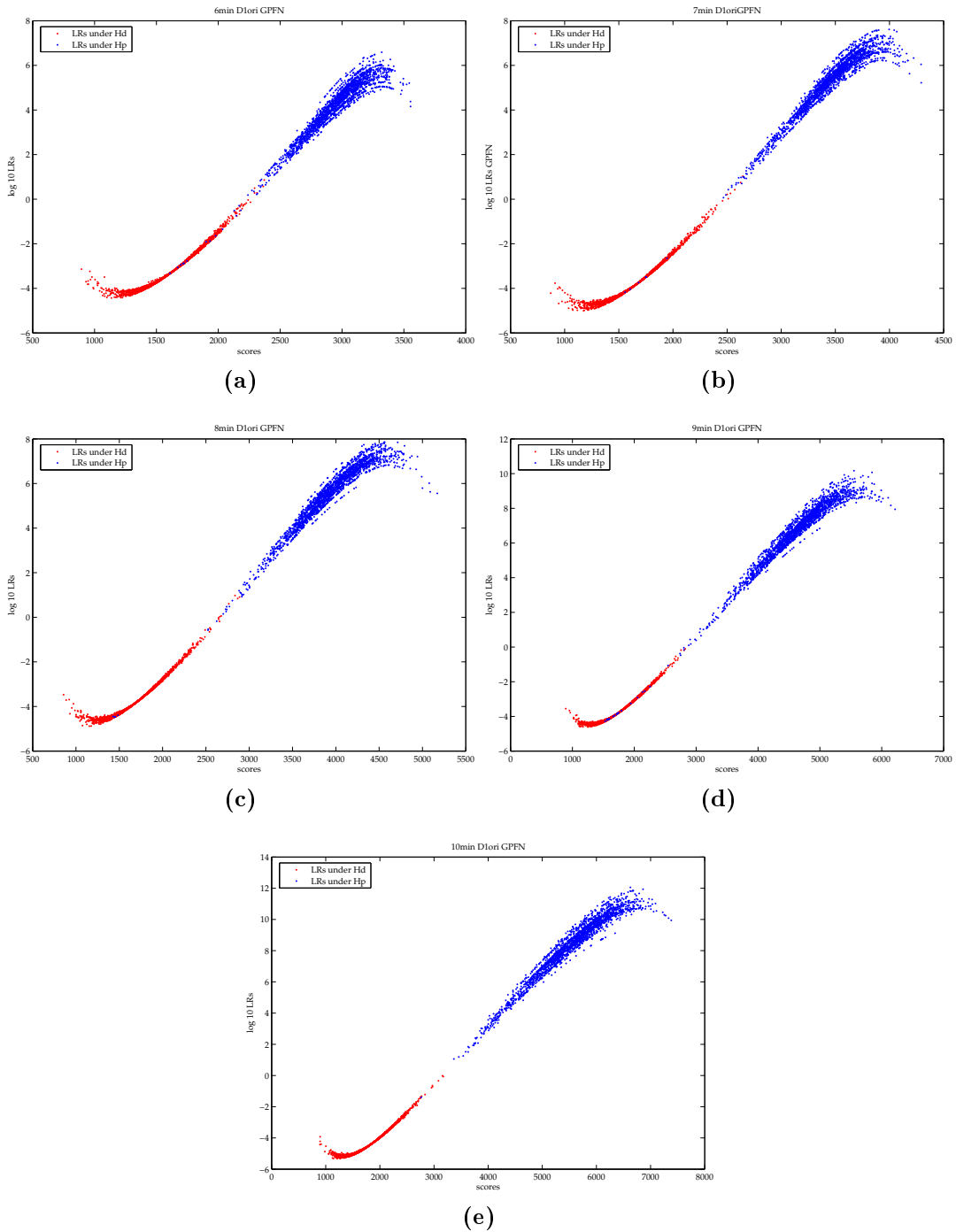


Figure 7.2: log base 10 of LRs obtained under H and \bar{H} for the configuration on the right thumb of donor 1 as a function of scores for a) 6 b) 7 c) 8 d) 9 and e) 10 minutiae. Data-based estimation is used, and the between-finger database includes only prints from right loops on right thumbs.

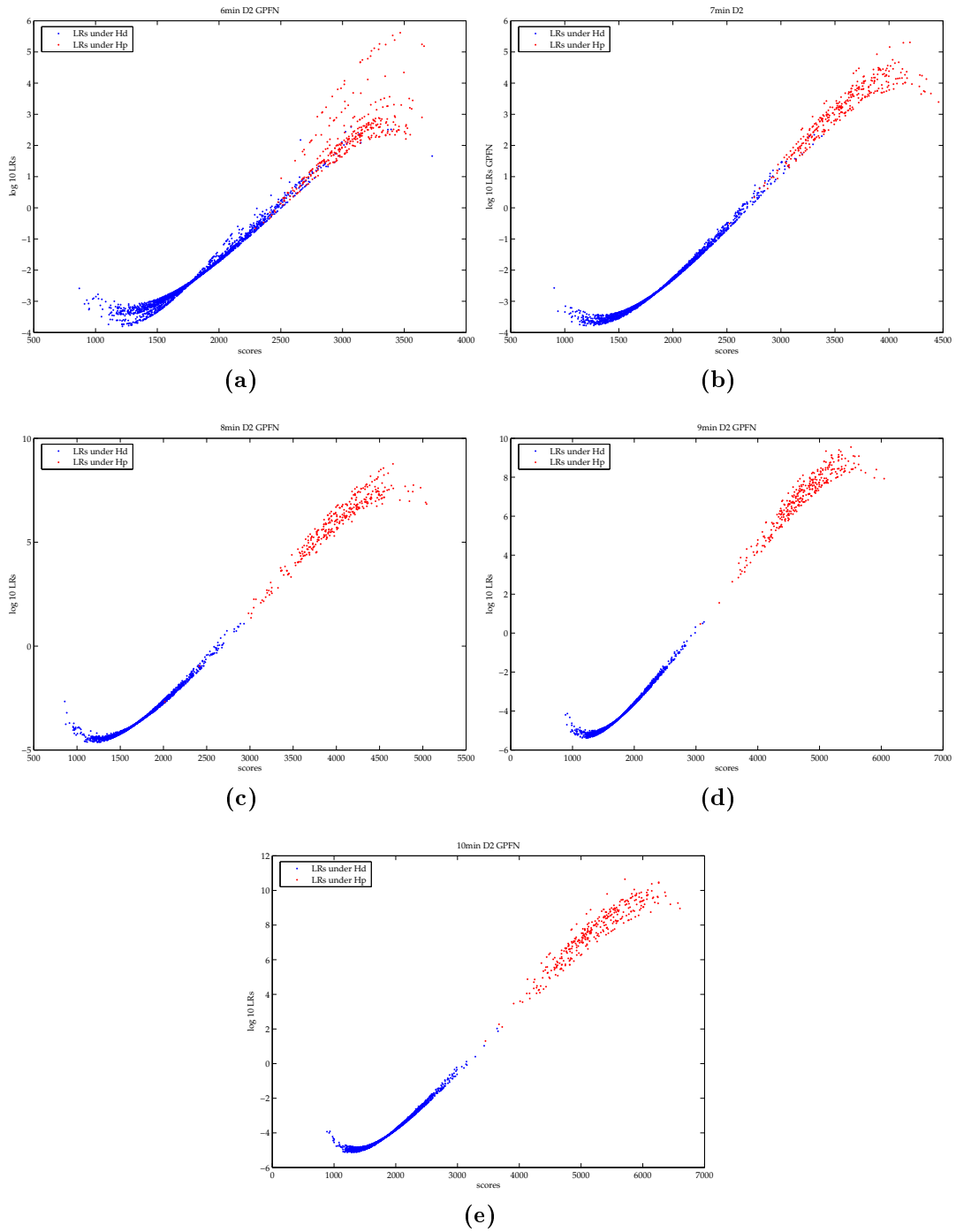


Figure 7.3: log base 10 of LR obtained under H and \bar{H} for the configuration on the left thumb of donor 2 as a function of scores for a) 6 b) 7 c) 8 d) 9 and e) 10 minutiae. Data-based estimation is used, and the between-finger database includes only prints from whorls on left thumbs.

and of course through the maximum scores obtained from a database of non-mates. This is considered here to be a very promising venue to be explored further.

Chapter 8

Conclusion

In the present thesis, a model allowing the evaluation of fingerprint comparison results using a likelihood ratio is proposed. A great advantage of this model is the use of the scores output by an Automated Fingerprint Identification System (AFIS). Such systems have a long history of development, they are optimized for the extraction of the relevant data (i.e. minutiae, in the present case), and they are used for distinguishing same source from different source fingerprints. Therefore, the proximity measure used in these systems had, a priori, a good chance of being extremely useful when employed as a measure for evaluation purposes.

Data for the description of the variability of scores when impressions from one finger are compared using this system have been acquired, employing widely used detection techniques. Then, the minimal number of repeated impressions for robust estimation of this within-finger variability has been determined, and a parametric model fitted to this distribution of scores. Also, a precise description of the data that should be used for the establishment of such a within-finger variability distribution has resulted from the work presented: rather than including only marks in this within-finger variability, the inclusion of rolled inked prints also allows to capture the variability due to the rolling process, which introduces distortion effects as well. It has been chosen here to include the same number of rolled inked prints as marks in the data used for comparisons, which leads to the use of 8 marks (or substitutes, e.g. slaps or live scan images) and 8 rolled inked prints.

Also, a background database of over 600 000 fingerprints was available and has been used. This database is far larger than any database that has been used previously for the examination of fingerprint variability in forensic science, exception made of one study (Meagher et al., 1999). On this large database, the influence of finger number and general pattern on the distribution of scores when a given mark is compared to a large amount of different prints could be explored. Also, again, the minimum number of data for robust estimation of this distribution of scores has been determined (10000 fingerprints), and then, a parametric model fitted to this distribution.

In a next step, for both within- and between-finger distributions, data reduction has been attempted. Direct approximation of parameters of the two distributions

used is proposed, based on 3 and 10 datapoints for within- and between-finger variability, respectively.

Finally, in a testing step, the results obtained on the finger used for the establishment of models have been tested on the finger of a different donor. The results of this testing step allow to determine the performance of the model as such, as well as the results of the approximations.

While the model results in rates of misleading evidence that are quite high for low numbers of minutiae (a maximum of 5.2% for 6 minutiae and 3.2% of misleading evidence in favour of the prosecution for 7 minutiae for one of the two donors used), these rates diminish as the number of minutiae included in configurations increases. It is therefore a model that yields rational results in the sense that its performance increases as the information available increases.

The second result of this testing step is that the approximations proposed yield LR's that correspond well with those estimated on the basis of empirical data. The immediate use of these approximations for casework purposes is seen as premature, however, since only two known donors have truly been investigated here. This does not preclude, in casework, to use the proposed data-based approach while acquiring the necessary data to further check the approximations. If a data-based approach is used in a given case, only 3 self-scores (based, for example, on slaps from ten-print cards) need to be acquired; this seems feasible for validation purposes.

Overall, for within-finger variability, the comparison of 8 'slap' impressions from ten-print cards to the same number of rolled inked prints has been shown to result in within-finger distributions that are close to distributions based on developed marks and inked prints acquired in the course of the present study. This remains the preferred process for the acquisition of within-finger variability. For between-finger variability, where automated extraction is possible, 10000 scores suffice for the estimation of the distribution.

Presently, a model that can be directly used in casework has been established, tested and presented. This model needs the acquisition of repeated impressions from the suspects finger (8 ten-print cards with slap and rolled inked impressions), and precise guidelines as to how LR's should be obtained are given in the discussion (on page 187). While an approach where less data needs to be acquired is proposed and yields promising results, it is not at this time considered as having been sufficiently tested. There is a limitation to the generalizability of the results obtained in the present work in the sense that they are intimately linked to a given AFIS: the Sagem DMA. They are directly applicable only to the scores issued from this precise system. The methodology and approach to the establishment and testing of this model are, however, portable to other systems. The immediate application to casework is only possible with this same system, however.

The model proposed addresses two of the issues that arise in *Daubert v. Merrell Dow Pharmaceuticals, Inc.* (1993): the necessity of testing of any method used, and the need for known error rates of this method. Also, due to the transparency of the

data used for its establishment, the modelling steps used and the testing carried out, the present model can easily be subjected to peer reviewing.

Finally, and perhaps most importantly, the presented model represents a solution to possible issues that could arise in the future, due to the increase in the size of the databases used as a pool of suspects. This increase may lead to more similar fingerprints being found than ever before. Should such problems arise, a probabilistic model based on large amounts of data would certainly become a necessity. Even if this increase in database size does not lead to any problems, the use of data to underpin the evaluative process in a probabilistic context, while taking at the same time advantage of the specific knowledge and expertise of fingerprint examiners, is in the present thesis seen as a promising future for fingerprint examination.

Of course, this approach would be the most useful if it could be implemented directly in an AFIS. This would allow for immediate modelling of between-finger variability based on the scores while at the moment, scores must be extracted from the system and modelled in another program. Also, such an implementation would make it possible to have specific tools for the acquisition of the data used for the modelling of within-finger variability. The probability of such an implementation actually being carried out by a provider of such a system is unknown to the author. It is certain, however, that it will be function of the clients' demands. At this point in time, the demand for probabilistic evaluation of fingerprint evidence is not made by the fingerprint community although mention is made of models based on AFIS scores in a report from the National Institute of Justice (McClure, 2007).

Concerning future perspectives, more distortion, such as observed on livescan images where distortion is voluntarily introduced, should be integrated into within-finger variability in order to verify the influence of such distortion on the model. A different approach is direct modelling of the likelihood ratio as a function of the scores from the system; this seems a promising subject for future research. Indeed, it is quite possible that, for a given minutiae configuration, the relationship between scores and LRs could be modelled without first modelling within- and between-finger variability separately. Such a direct approach would most certainly be easier and quite possibly could also improve the precision and exactitude of estimates, since fewer parameters would need to be estimated.

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Appendices

Appendix A

Application of the parameter estimation to a new donor

A.1 Material and Methods

Up to now, all results presented were based on a single finger. Of course, the interest of the results presented in section 4.7.2 is to be able to find a description of the within variability of another donor based on very few impressions. Impressions have therefore been acquired from a second donor. While the first donor was female, right handed and had ulnar loops on the selected fingers, the new donor is male, left handed and has whorls on the selected fingers. From this donor, two configurations, again increasing from 6 to 10 minutiae, have been selected on two different fingers, the left thumb and the left forefinger. These configurations are shown in figures A.1 and A.2, and will be referred to as LI_D2 and LT_D2 in graphics, respectively.

Since all the work on donor 1 has been carried out on images of the right thumb, a maximum of difference is thus sought. The parameters remaining similar between these two donors are, to some extent, the corpulence, age, and occupation, as well as the fact that the impressions acquired come, in both cases, from the dominant hand (left for the left-handed donor 2 and right for the right-handed donor 1).

12 ten print cards were acquired of this second donor. Marks were acquired by dusting with aluminium powder only. For the forefinger, 34 marks showed the minutiae selected, and for the thumb, 28 did.

These ten print cards and marks were compared, resulting in 408 and 336 AFIS scores. Furthermore, using three slaps from the ten print cards, 'self-scores' were again computed, for each configuration and number of minutiae. The parameters of the Weibull distributions fitted to these datasets were estimated first based on the data, and then based on the equations shown above.



Figure A.1: Minutiae configuration on the left index of donor 2 (LI_D2)



Figure A.2: Minutiae configuration on the left thumb of donor 2 (LT_D2)

A.2 Results

Both of the configurations show a progression of scores, as well as an increase in variability, as the minutia number increases (see figures A.3 and A.4).

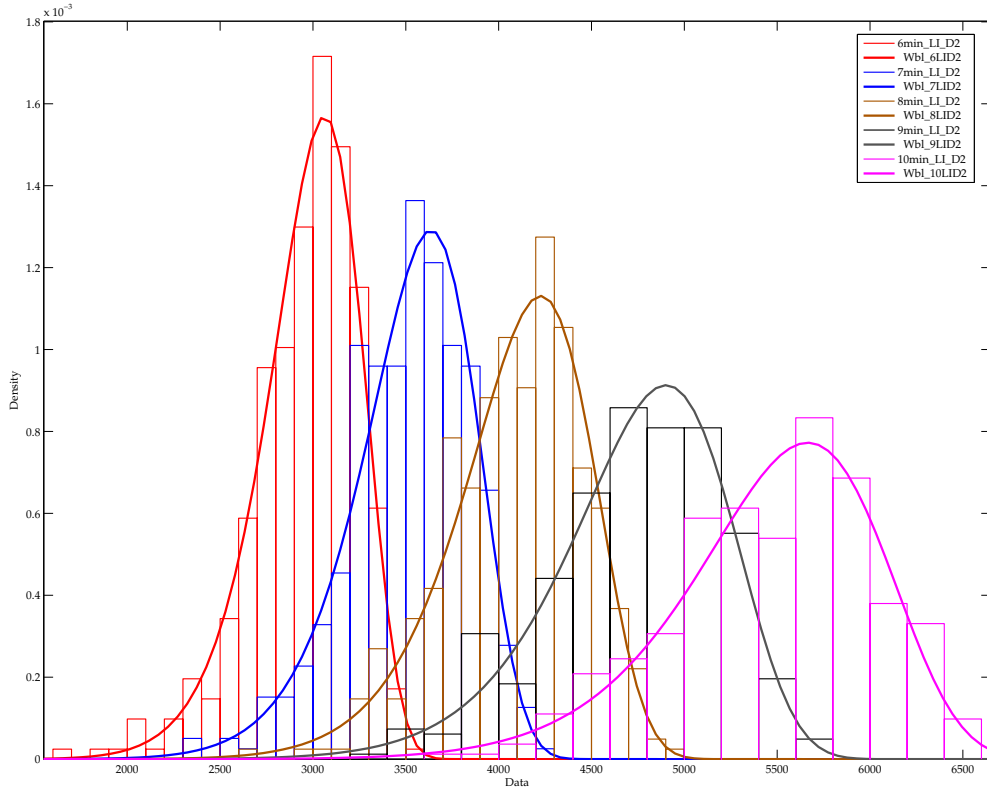


Figure A.3: Progression of the distributions on the left forefinger of Donor 2, from 6 to 10 minutiae

Estimations and confidence intervals were obtained for the Weibull parameters from 6 to 10 minutiae on the forefinger and are shown in table A.1). The self-scores obtained were, as usual, much higher than the marks' scores (see table A.2). Finally, the parameters deduced from these self-scores and the mean of the the parameters β obtained from donor 1 above are shown in table A.3.

Overall, the approximated parameters α are too low with respect to those estimated from the data, whereas the parameters β are just different, sometimes higher and sometimes lower than those based on the data. However, the approximated parameters are not very far away from the parameters estimated from the data. Furthermore, where only α influences where the distributions mode is situated, both parameters together determine the shape. Therefore, the distributions resulting from the approximations are not necessarily very different from those observed on the data.

On the thumb, the estimations and confidence intervals were also obtained for the Weibull parameters from 6 to 10 minutiae and are reported in table A.4.

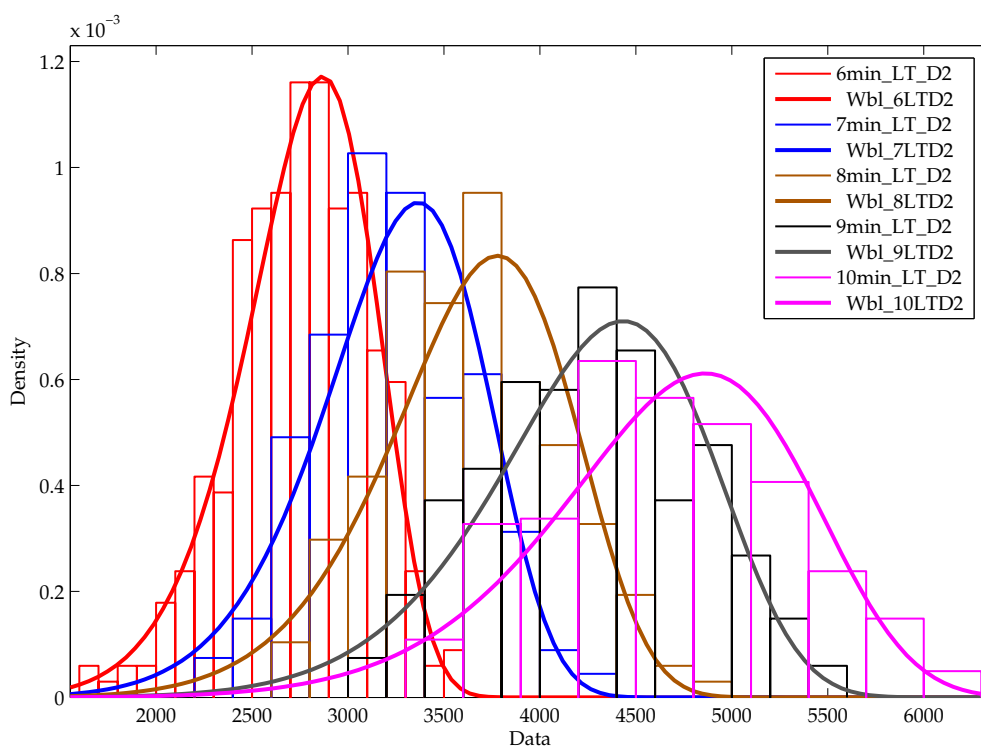


Figure A.4: Progression of the distributions on the left thumb of Donor 2

Table A.1: Parameters and confidence intervals obtained for a Weibull distribution for 6 to 10 minutiae for the left forefinger of donor 2

	α			β		
	Est	CI		Est	CI	
6	3082	3058	3106	13.1	12.1	14.2
7	3659	3629	3689	12.8	11.9	13.8
8	4253	4219	4286	13.0	12.1	14.1
9	4936	4895	4978	11.3	11.3	13.2
10	5706	5657	5755	12.0	11.1	12.9

Table A.2: Scores obtained for the comparison to themselves of 3 flat impressions of the second donors left forefinger (LI_D2) with configurations from 6 to 10 minutiae

Print	6 min	7 min	8min	9min	10 min
1	3582	4403	5317	6377	7387
2	3355	4080	4853	5775	6817
3	3591	4330	5034	6105	7284
mean	3509	4271	5068	6086	7163

Table A.3: Estimation of the parameters obtained using the self-scores for the left forefinger of donor 2 (LI_D2)

Number	α	β
6	3030	13.9
7	3553	12.7
8	4100	11.5
9	4799	10.4
10	5538	10.3

Table A.4: Parameters and confidence intervals obtained for a Weibull distribution for 6 to 10 minutiae for the left thumb of donor 2 (LT_D2)

	α			β		
	Est	CI		Est	CI	
6	3159	3131	3188	12.5	11.6	13.6
7	3724	3686	3762	11.2	10.4	12.1
8	4182	4140	4224	11.1	10.3	12.1
9	4939	4889	4989	11.3	10.4	12.2
10	5460	5401	5520	10.4	9.6	11.2

The self-scores obtained for the thumb are, overall, greater than those obtained for the forefinger (see tables A.5 for the thumb and A.2 for the forefinger).

Table A.5: Scores obtained for the comparison to themselves of 3 flat impressions of the second donors left thumb with configurations from 6 to 10 minutiae (LT_D2)

Print	6 min	7 min	8min	9min	10 min
1	3417	4101	4926	6066	7204
2	3652	4543	5461	6747	7657
3	3656	4448	5260	6433	7569
mean	3574	4364	5216	6415	7477

Finally, the parameters deduced from these self-scores and the mean of the the parameters β obtained from donor 1 above are shown in table A.6.

Here, as opposed to the forefinger, the approximated parameters α are too high with respect to those estimated from the data. The parameters β are too high for 6 and 7 minutiae, whereas they are inside the confidence interval of the parameters estimated from the data for 8, 9 and 10 minutiae.

Between these two configurations, it is furthermore clear that the approximation using the self-scores cannot work, since, in some cases, the selfscores of the thumb

Table A.6: Estimation of the parameters obtained using the self-scores for the left thumb of donor 2 (LT_D2)

Number	α	β
6	3075	13.9
7	3617	12.7
8	4202	11.5
9	5025	10.4
10	5754	10.3

are greater than those of the index finger, while the parameters α of the forefinger are greater than those of the thumb. Therefore, the application of a monotonically increasing equation will yield inverted results for this parameter of the distributions of scores issued from these two fingers.

Since the parameters (and the distributions) as well as the self-scores are quite close between the configurations of the same number of minutiae on the thumb and the forefinger of donor 2, however, it is possible that their approximations are still useful. This has been tested by comparing the distributions obtained from the approximated parameters directly to the observed data using the empirical cumulative distribution function.

When examining the empirical cumulative distribution functions (ecdf) obtained on the data acquired and the ecdf of random samples from the distributions with the approximated parameters, the results in figure A.5 are observed for the left forefinger of donor 2. On these figures are also shown the upper and lower 95 % confidence intervals for the function obtained on the data, as well as the parameter approximations when using the maximum and minimum observations from these 3 selfscores instead of the mean.

On figure A.5, the ecdf of the random sample from a Weibull distribution where the parameter α is based on the maximum of the selfscores is at least partly inside the confidence bounds from the data. For 6 minutiae (figure A.5a), the correspondence between the distributions is perfect in the sense that the approximated ecdf is inside the observed ecdf's confidence interval everywhere, even if the shapes differ slightly. The comparison between the pdfs based on approximations or on data is shown in figure A.6a) and in figure A.6b), the comparison between the logarithm base 10 of these distributions is shown. At score values of less than 125 and of more than 3553, the difference between these two distributions becomes greater than one order of magnitude; the approximation yields function values that are smaller than those estimated based on data in both tails. This difference is more troublesome in the left tail, where it is expected that most casework scores would be situated. However, not unexpectedly, the probability of observing a score issued from the comparison of two impressions from the same finger that is smaller than 125 is ex-

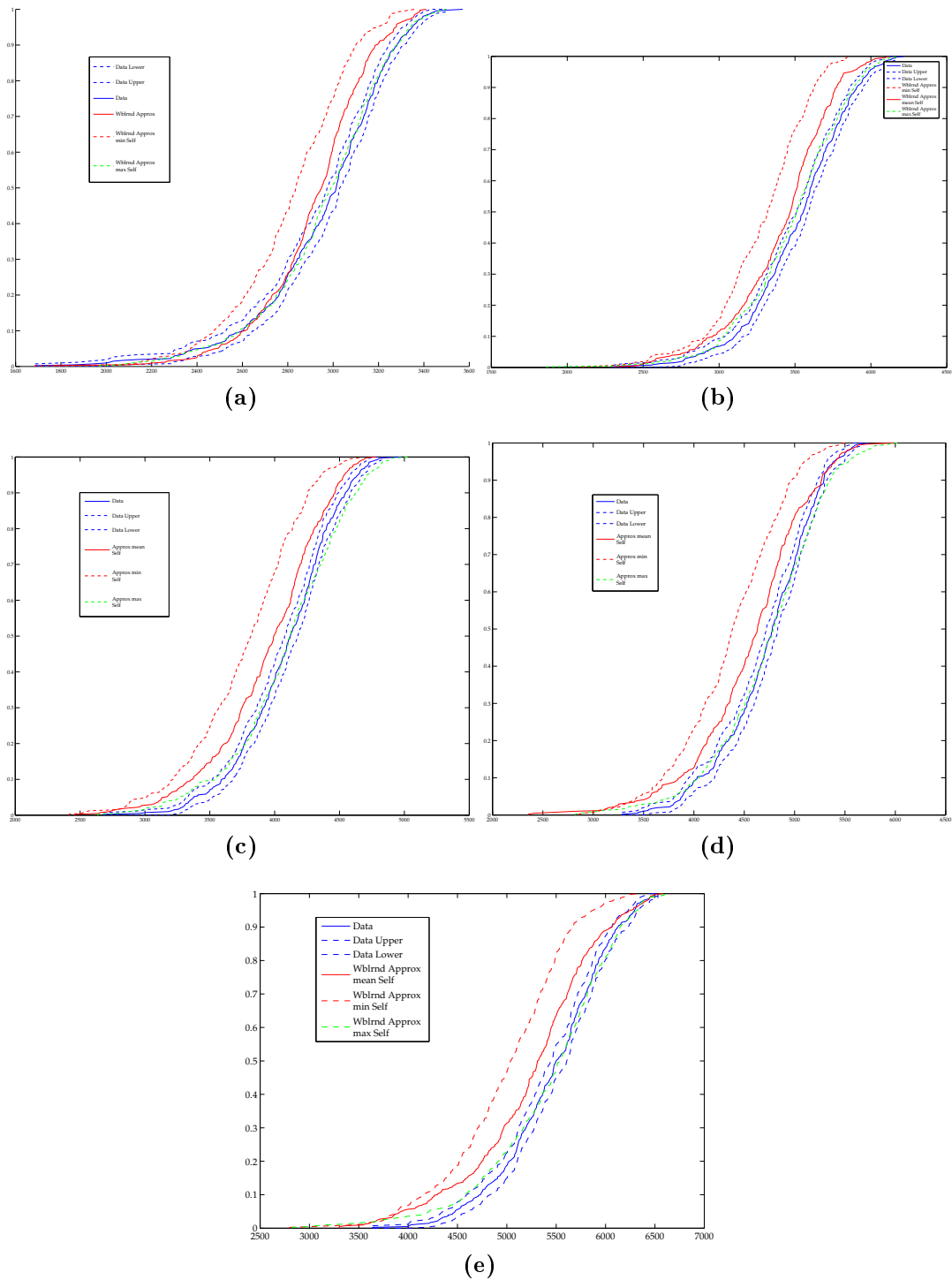


Figure A.5: Empirical cumulative distribution functions obtained on the data compared to those from random samples of the Weibull distribution using approximated parameters for the left forefinger of donor 2, for a) 6 minutiae b) 7 minutiae c) 8 minutiae d) 9 minutiae e) 10 minutiae. In red are the ecdf of the random sample from a Weibull with α based on the mean of the selfscores (-) and on the minimum of the selfscores (- -), and in green based on the maximum of the selfscores. In blue is the ecdf of the data (-) with the upper and lower bound of the 95% confidence interval (- -)

ceedingly rare. It can be found based on the cdf of the Weibull distribution fitted on the data. This is done using the fact that the cdf results in $p(X \leq 125)$. In this case, this value as given by Matlab is 0, which means that it is smaller than the smallest number that Matlab can compute, which is $2.225 * 10^{-308}$. To observe such a small score when impressions from one finger are compared is therefore very unlikely. However, since between-finger variability is on this side of the tail, LRs may be computed for such values and must therefore be precise. The probability of observing a score smaller than 125 has been computed for the between variability of one mark (compared to a database of 100000 ten print cards). The probability of a between finger comparison resulting in a score this low or lower (when this finger and 6 minutiae are used) is again very small: $1.1 * 10^{-50}$. The smallest value observed for between finger scores is 848 in this example. For the values in the right tail, similar considerations are necessary. The probability density function of the minimal score where the difference exceeds an order of magnitude (3553), based on the data, is $3.72 * 10^{-5}$. The percentage of marks exceeding a score of 3553, for comparisons between impressions of the same finger, is again computed using the cdf, except that now we are interested in observing a number greater than 3553. Therefore, the required probability is $1 - p(X \leq 3553)$; the percentage of marks from a same finger exceeding 3553 is 0.16%. One of the observations of scores from real mark to print comparisons carried out is above this limit; it is of 3571.

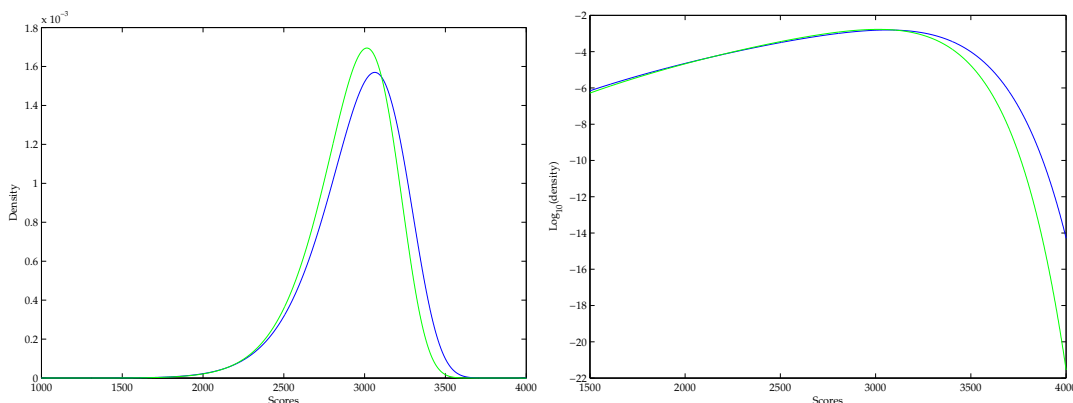


Figure A.6: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 6 minutiae on the left forefinger represented a) linear and b) using the log 10 of the pdf

For 7 minutiae (see figure A.5b), the differences between the ecdfs that are observed are more constant than was the case for 6 minutiae. Here, the approximated distribution is slightly displaced to the left with respect to the distribution fitted to the data (see also figure A.7a). Again, in figure A.7 b) the comparison between the logarithms base 10 of these distributions are shown. The differences between the distribution based on the data and the approximation shown in this figure are quite small. Only scores of 4212 or larger are expected to yield numerators that

differ by at least an order of magnitude depending on the option taken for parameter estimation. The percentage of mark-to print comparisons (where both come from the same finger) that are expected above that value of score is 0.24%; again, exactly one of the 408 comparisons used here is above this limit (the observed score is 4216).

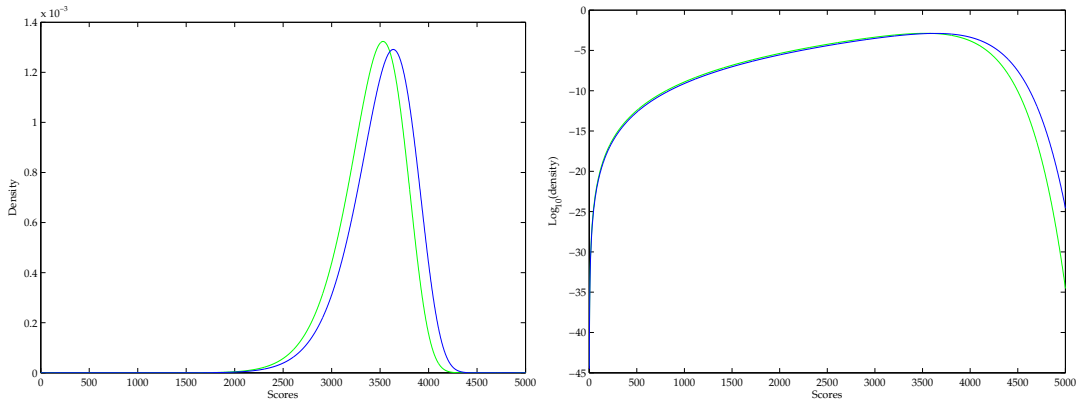


Figure A.7: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 7 minutiae on the left forefinger represented a) linear and b) using the log 10 of the pdf

For 8 minutiae (figure A.5c), the differences between the observed and approximated data are similar as for seven minutiae; the approximated distribution is slightly flatter than the one estimated on the basis of the data, however. This is shown more clearly on figure A.8a); again, in figure A.8b) the logarithm base 10 of the two distributions is shown. As in the case of 6 minutiae, both in the left and right tail there are scores for which the difference between the two distributions is larger than an order of magnitude. This is the case for scores below 1132 and for scores above 5789. Contrarily to what was the case for 6 and 7 minutiae, now the approximated distribution is heavier tailed than the observed one, and therefore yields larger numerators in the tails (which is, generally speaking, not favorable to the suspect, since it is in the tails where large differences are observed). Again, in the left tail both the probability of observing such low scores under H as well as \bar{H} must be considered. In the present case, the probability of observing a score of 1132 or less when both impressions come from the same finger is not as low as it was for 6 minutiae: it is 3.2×10^{-8} . To observe such a score when the two impressions come from different fingers is 0.045, which means that in the case of comparing this minutiae configuration to any finger, there is a very large probability of obtaining diverging numerators. In the right tail, the probability of observing a score larger than 5789 when both impressions come from a same finger is, again, approximately 0 (smaller than 10^{-308}). It is larger for impressions of different fingers 2.2×10^{-14} ; this is due to the heavier right tail of the lognormal distribution fitted on between finger data. Indeed, in this far right tail, an LR has been computed (for the score

value of 5789) and it supports the *defense hypothesis* with a value of 4.8×10^{-10} . The maximum score observed in the within finger data used here is 4981, comfortably below the score where large differences are observed; the minimum observed in that dataset is 2678. In the between finger dataset used here (as a proxy, as only one pseudo-mark with the relevant configuration is used) the minimum observed (when not including the scores of 0 due to the absence of impressions from ten print cards) is 853, inside of values that would yield large differences in the numerator, and the maximum observed is 3640.

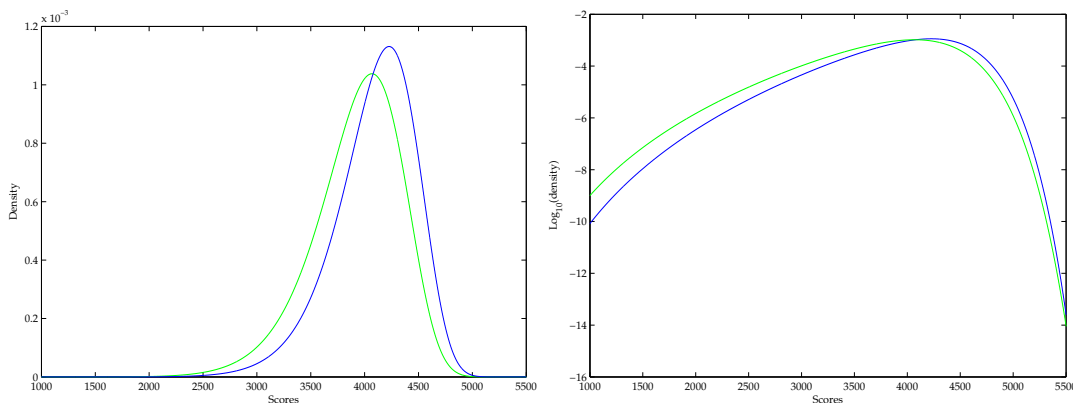


Figure A.8: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 8 minutiae on the left forefinger represented a) linear and b) using the log 10 of the pdf

For 9 minutiae (figure A.5d), the situation is very similar to the one for 8 minutiae. The two probability density functions are, again, shown, in figure A.9. Again, the approximated distribution is heavier tailed than the one based on the data.

When comparing those two pdfs, it is also visible that the modes are not superposed. But, again, the numerical differences to be expected on the numerators and therefore the LRs are quite small in the high probability density region of the probability density functions. There are quite large effects in the far right tail, however, which are clearly visible when the logarithm base 10 is represented (see figure A.9b). Again, when analyzing the two functions, there are differences larger than an order of magnitude in both tails of the within finger variability: below scores of 1475 and above scores of 6298. When both impressions come from the same finger, the probability of observing a score lower than 1475 is 3.94×10^{-7} , and the probability of observing a score above 6298 is 3.15×10^{-9} . When the two impressions do not come from the same finger, these probabilities are of 0.35 and 3.46×10^{-13} , respectively. The maximum score observed in within-finger variability is 5734, the minimum 3287, while these data are 4143 and 853 for between-finger variability.

For 10 minutiae (figure A.5e), it is the left tail which is much heavier in the approximated distribution than in the observed one. Again, the comparison of the pdfs is useful and is shown in figure A.10a) and juxtaposed with the logarithm base

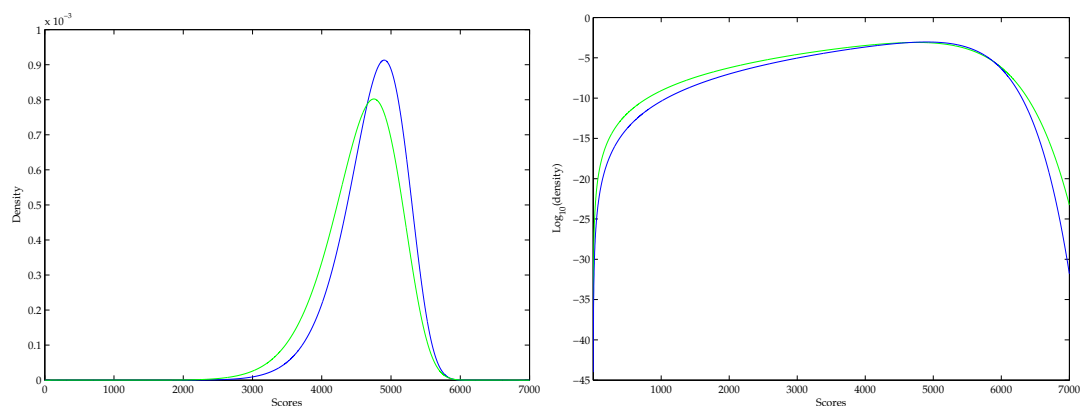


Figure A.9: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 9 minutiae on the left forefinger represented a) linear and b) using the log 10 of the pdf

10 of the same data in part b) of the same figure. Again, both tails show differences of more than the order of magnitude for this configuration; scores below 1515 and above 7427 will yield numerators that differ in this sense. Again, the probabilities of falling below or above these limits have been computed. For the within-finger comparisons the probabilities of obtaining a score lower than 1515 is 1.33×10^{-7} , and the probability of a score above 7427 is 7.75×10^{-11} . The probabilities to obtain such differences when two different fingers are compared are 0.31 and 1.99×10^{-13} , respectively. The lowest observation in the between-finger variability used here is far below the limit in the left tail, while the maximum of scores obtained is 4639 and therefore below the limit in the right tail. In the within-finger variability data, there is no observation exceeding either limit; the minimum is 3640 and the maximum 6544.

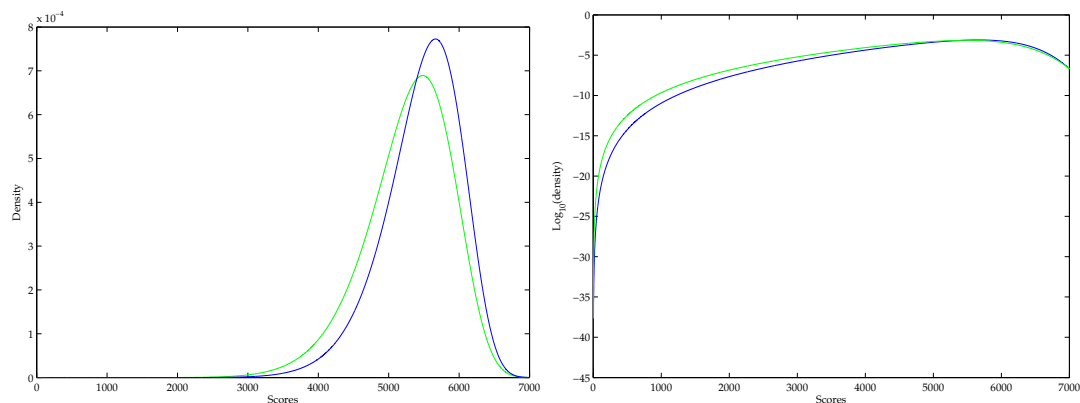


Figure A.10: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 10 minutiae on the left forefinger represented a) linear and b) using the log 10 of the pdf

For this finger, in conclusion, a good approximation can be found when using the mean of 3 'self' scores and an equation based on another donors' finger. Although there are problems with the approximation in the tails, in particular in the left tail of the within-finger variability, where large differences with respect to the data-based approach can be obtained with a high probability when the two impressions compared come from different fingers. However, these differences still occur for rather small scores; in an operational setting, impressions yielding such small scores are not expected to be frequently evaluated. As an example, if a suspect is identified using an AFIS search, the largest scores are observed first. In the examples above, in some instances, a probability of obtaining a given score (or smaller) from the between finger comparisons exceeding 0.3 was obtained. This means, however, that over 60% of the whole database when compared to the mark yields a higher score than this limit, and will therefore be higher in the list. Generally, only the fingerprints yielding the largest scores are compared to the mark in a case in order to find a suspect, not the top 70% of the available database.

The plots of the ecdfs have also been generated for the left thumb of donor 2 and are shown in figure A.11. When looking at these plots overall, the maximum of the self-scores (in green) is far removed from the observed data. The mean models the data better, but for the higher minutiae numbers, the minimum would be the best, in this case.

Of course, only the results based on the mean of the self-scores is discussed here. Again, the criterion used will be a distance of no more than one order of magnitude for observations of high probability.

For 6 minutiae on the left thumb of donor 2, results do not correspond extremely well. On figure A.11 a), it is clear that the approximation based on the selfscores is displaced to the left with respect to the function estimated on the basis of the data. The pdf and its log 10 are shown in figure A.12.

While there are differences larger than one order of magnitude between the left tails (below scores of 420) of the data-based and the approximated distributions for this 6 minutiae configuration, these have a very low probability of occurring (10^{-16} when impressions of different fingers are compared and 10^{-11} when impressions from the same finger are compared). In the right tail of within-finger variability, such differences occur for scores larger than 3541, with a probability of 0.015 for comparisons between impressions from the same finger and a probability of $4.2 \cdot 10^{-5}$ for comparisons between different fingers. Here, the probability of obtaining such a large difference in the numerator due to the use of the approximation rather than data-based parameter estimation has a rather high probability of occurring when impressions of the same finger are compared; seven out of 336 comparisons from this fingers are above the limit. The differences between the two probability density functions at the observed values remain below two orders of magnitude.

For 7 minutiae, the approximation is close to the distribution based on the data, although, in figure A.11 b) the fit is shown to be slightly less good than was the

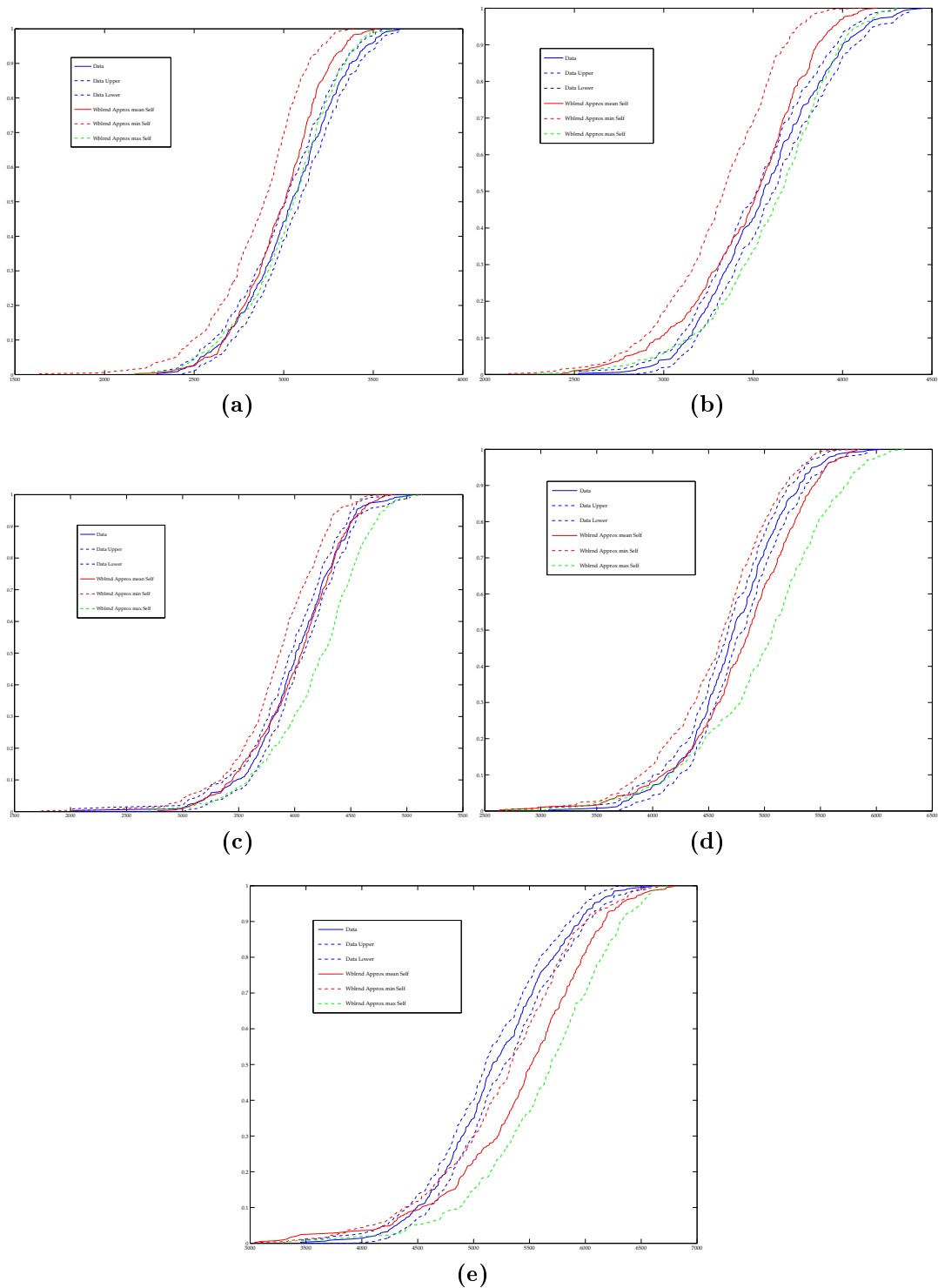


Figure A.11: Empirical cumulative distribution functions obtained on the data compared to those from random samples of the Weibull distribution using approximated parameters for the left thumb of donor 2, for a) 6 minutiae, b) 7 minutiae c) 8 minutiae d) 9 minutiae e) 10 minutiae.

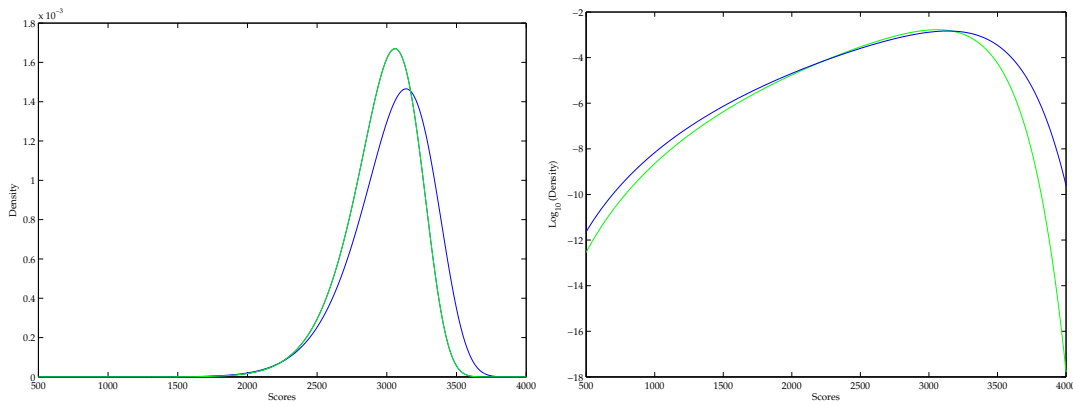


Figure A.12: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 6 minutiae on the left thumb represented a) linear and b) using the log 10 of the pdf

case for 6 minutiae. The probability density functions are quite close (see figure A.13). The order of magnitude of difference between the approximation and the data-based estimation of the distribution is exceeded for score values below 594 and above 4213. To obtain scores below the lower limit is expected to be quite rare. The probability of obtaining such values under H is $1 * 10^{-9}$, and under \bar{H} it is $6 * 10^{-9}$. The situation is, again, different in the right tail of the within-finger distribution: 1.8% of comparisons between impressions from the same finger are expected to fall into the region where the approximation differs by more than an order of magnitude from the distribution estimated on the basis of the acquired data. This probability is far lower for comparisons between impressions from different fingers; in this case, it is of $3 * 10^{-5}$. Nine values above the upper limit have been observed among the 336 observations of within-finger variability. Here, the probability of being far enough

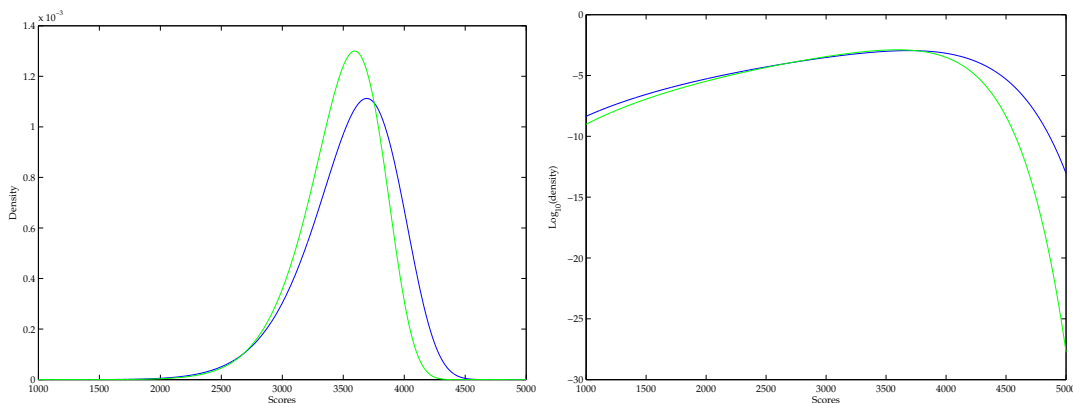


Figure A.13: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 7 minutiae on the left thumb represented a) linear and b) using the log 10 of the pdf

in the right tail to have an order of magnitude or more of difference is of 1 in 54, and the probability of being at 2 orders of magnitude or above is of 1 in 510. Again, these differences between the approximated function and the one fitted to the data, joined with the high probability of actually observing a case where this deviation is true, does not indicate that the approximation can be used. Here, as for the results obtained for 6 minutiae on this finger, these large deviations are observed in regions where the numerator computed using the approximation will be smaller than the numerator obtained when the numerator is obtained from a distribution estimated on the basis of data. This would tend to favor the suspect in the sense that the LR_s obtained in these regions where the distributions differ by more than an order of magnitude would be lower when using the approximation than when using the 'true' distribution.

For 8 minutiae, the correspondence between the approximation and the observed data is almost perfect (see figure A.14 as well as the ecdf in figure A.11 c). Here,

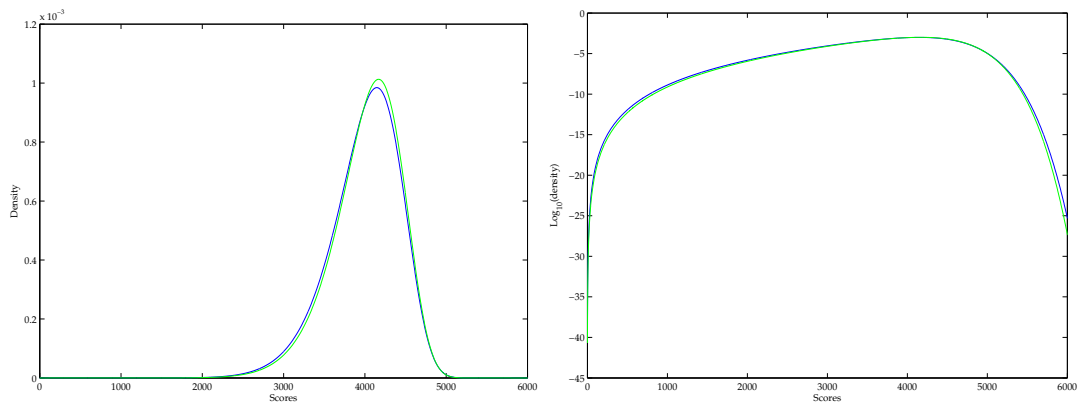


Figure A.14: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the self-scores (green), for 8 minutiae on the left thumb represented a) linear and b) using the log 10 of the pdf

the point where the two distributions differ by more than an order of magnitude in the left tail of within-finger variability is at a score of 9, while in the right tail this point is at a score of 5756. The probability of obtaining a score from the between variability of 9 or lower is $2 * 10^{-190}$, and from the within finger variability it is lower than 10^{-308} . In the right tail, the probability of obtaining a score of at least 5756 from the within-finger variability is $6 * 10^{-16}$, and from the between-variability it is $2 * 10^{-11}$. Again, we are in the region of the far right tails of within- and between-finger variability where LR_s become again smaller than 1, i.e. these scores are so high as to be of higher probability when two impressions of different fingers are compared; this is, as mentioned before, due to the heavy right tail of the distribution used here to model between-finger variability. The highest score actually obtained in the within-finger data is 5044 and in the between-finger variability this highest score is 3569.

For 9 minutiae on the left thumb of donor 2, the approximated distribution is displaced to the right with respect to the distribution of the data (figure A.11 d). On figures A.15 a) and b), again, it is highlighted that great differences between

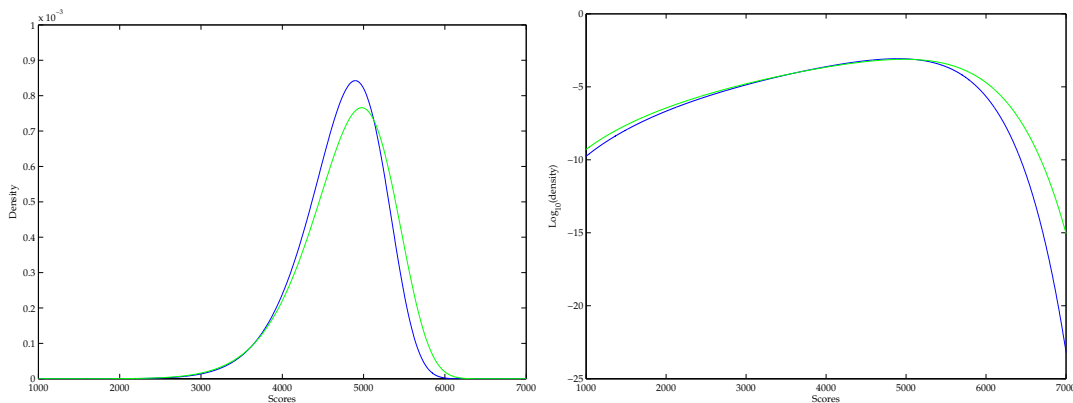


Figure A.15: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the self-scores (green), for 9 minutiae on the left thumb represented a) linear and b) using the log 10 of the pdf

these pdfs and therefore the numerator occur in the far tails, for observations that are quite unlikely. The limit below which scores will yield function values that differ by at least an order of magnitude between these two distributions is 241, while the upper limit, above which such large differences are observed, is 6019. The probability of falling below the lower limit is $3 \cdot 10^{-29}$ under \bar{H} , and it is $2 \cdot 10^{-15}$ under H . This is therefore, in the absolute, a highly unlikely event. In the right tail, however, the probabilities of obtaining scores above 6019 are $3 \cdot 10^{-10}$ under \bar{H} and $9 \cdot 10^{-5}$ under H . These probabilities, although not excessively low, are still low enough to accept the approximation as a reasonable proxy in this case of 9 minutiae, although one of the scores obtained in the data for within variability exceeds the upper limit. This observation is a score of 6047.

For 10 minutiae on the left thumb of donor 2, the displacement towards higher values of the approximated distribution is more pronounced than it was for 9 minutiae (see figures A.11 e) and A.16 a) and b). Again, these differences are great when comparing the two pdfs in figure A.16 a), but their influence on the numerator is small in the left tail (as seen in figure A.16 b); indeed, in this left tail, no difference exceeding the order of magnitude is observed for this configuration. In the right tail, the divergence between the two distributions is great, and differences of one order of magnitude or more would have to be expected frequently (with a probability of $1 \cdot 10^{-3}$ for impressions of the same finger and a probability of $2 \cdot 10^{-11}$ for impressions of different fingers) when using the approximation rather than the observed values.

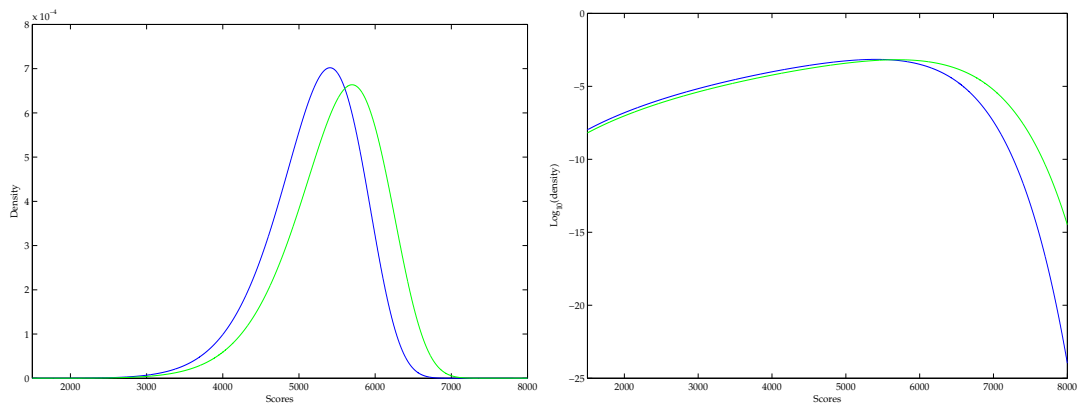


Figure A.16: Weibull probability density function fitted to the data (blue) compared to one with α based on the mean of the selfscores (green), for 10 minutiae on the left thumb represented a) linear and b) using the log 10 of the pdf

Appendix B

Commands for score extraction

B.1 Data acquisition in the system

Three different custom-made utilities have been used in the present work for the direct extraction of scores and of general patterns. The first two are `raw_dump.py` and `spec.exe`, for the extraction of scores and the third is `PatternExtractor.py`. It is important that in the casefiles (for latents) there be only *one* mark; otherwise, `spec.exe` will not be able to automatically compute a score.

B.2 Command lines for the extraction of marks or tenprints, the extraction of scores, and that of general patterns

```
python raw_dump.py -f <Filename.txt> -D <ngaAFIS_DB> -s <SearchText> -l
```

Explanation of terms:

-f : allows to define the filename under which the output will be saved

-D: definition of the database to be used; generally, this will be `ngaAFIS_DB`, the AFIS database

-s: which casenumbers / tenprints should be extracted. For tenprints, this is the Family Name. * and ? have the usual meanings in this search.

-l: must be used if marks are extracted and not used if prints are extracted.

Command line for the automated extraction of scores based on the outputs of `raw_dump`

```
spec.exe <MarksFilename.txt> <PrintsFilename.txt>
```

Command lines for the extraction of patterns

For marks:

```
python PatternExtractor.py -l -D ngaAFIS_DB -o <output_directory>
```

The output file will be called `latent_pattern.txt` and be found in the directory defined under `output_directory`.

For prints

```
python PatternExtractor.py -p -D ngaAFIS_DB -o <output_directory>
```

The output file will be called `print_pattern.txt` and be found in the directory defined under `output_directory`.

Appendix C

Matlab functions for the computations of Likelihood ratios and Tippett plots

C.1 Function importing the data from the different text-files

```
% This function lets the user manually select a directory (must not have
% the .DSSStore file inside) where the .txt files of scores output by AFIS
% are to be found. The directory needs to be put in the Matlab path before
% using this function.
% There is one file for each mark used, where the scores of this mark
% compared to all prints defined in the function extracting scores from
% AFIS are stored, along with the identifier of the ten-print card and the
% finger.
%
% Matlab version info below.
% -----
% MATLAB Version 7.0.1.24704 (R14) Service Pack 1
% -----
% MATLAB Version 7.0.1 (R14SP1)
% Curve Fitting Toolbox Version 1.1.2 (R14SP1)
% Image Processing Toolbox Version 5.0.1 (R14SP1)
% Neural Network Toolbox Version 4.0.4 (R14SP1)
% Statistics Toolbox Version 5.0.1 (R14SP1)

function results=import_files_batch
%choose the directory
repertoire=uigetdir;
%list the files in the directory
```

```
repertoire=dir(repertoire);
%number of files
taille=size(repertoire,1);
%start with the 3rd, the first two are '.' and '..'
for file=3:taille
    %get the name for the file
    fichierName=repertoire(file).name;
    nout=taille-2;
    %load the file
    savename=load(fichierName);
    %put the data in the first two columns into the first two columns of
    %the output
    results(:,1:2)=savename(:,1:2);
    %put the scores where they should go (into the fileth column of the
    %output)
    results(:,file+1)=savename(:,3);
end
results;
```

C.2 Function for putting data into a vector format

```
% This function takes an array and reorganises the data in a vector.
%
% Matlab version info below.
% -----
% MATLAB Version 7.0.1.24704 (R14) Service Pack 1
% -----
% MATLAB Version 7.0.1 (R14SP1)
% Curve Fitting Toolbox Version 1.1.2 (R14SP1)
% Image Processing Toolbox Version 5.0.1 (R14SP1)
% Neural Network Toolbox Version 4.0.4 (R14SP1)
% Statistics Toolbox Version 5.0.1 (R14SP1)

function outvect=mettre_vect(Matrix_In)

j=1;
outvect=[];
taille=size(Matrix_In,2);
while j<taille+1
    %add the current column of the array below all the data already
```

```

%stored in the vector.
outvect=[outvect;Matrix_in(:,j)];
j=j+1;
end

```

C.3 The global function for the Tippett plots

```

% The function makes tippett plots on randomly chosen comparisons in 2
% tables;
% The first table is made up of comparisons between impressions of the
% same finger and the second one of comparisons between different
% fingers.
% In both tables, rows are fingerprints, columns are fingermarks.
% The first 3 columns are not scores, but 1) the identifier of the
% ten-print card, 2) zeroes and 3) the finger number. For comparisons
% between impressions from the same finger, after
% importation, the finger number must be chosen.
% Matlab version info below.
% -----
% MATLAB Version 7.0.1.24704 (R14) Service Pack 1
% -----
% MATLAB Version 7.0.1 (R14SP1)
% Curve Fitting Toolbox Version 1.1.2 (R14SP1)
% Image Processing Toolbox Version 5.0.1 (R14SP1)
% Neural Network Toolbox Version 4.0.4 (R14SP1)
% Statistics Toolbox Version 5.0.1 (R14SP1)
% The function outputs two matrices: 1) true and 2) false. True is
% based on comparisons where the impressions come from the same
% finger and False on impressions from different fingers.
% The rows in these two tables correspond to the maximum 2000 observa-
% tions generated, while the columns are, in that order, the score,
% corresponding LR's computed using all data available (or rather, the
% database input for database_betweenALL, see inputs below) for the
% between-finger variability, LR's computed using,for the between-
% finger variability, only impressions that have the same finger num-
% ber/general pattern combination as the mark (or rather the database
% input for database_betweenFNGP, see inputs below), the numerator
% corresponding to the scores based on data, the denominator based
% on all data (database_betweenALL), the denominator based on a
% database conditioned by general pattern and finger number,LR based
% on fixed parameters for the denominator (and estimation for the

```

```
% numerator) LR based on a downsampled between-finger database of
% 10000 observations selected from database_betweenALL and estimated
% numerator LR based on approximations for both numerator and deno-
% minator,numerator and denominator obtained using approximation,
% denominator obtained using fixed parameters and denominator based
% on the randomly downssampled database.
% Inputs are:
% number_of_data: the number of LRs to be obtained under
% both hypotheses; if for the data obtained
% when comparing impressions from the same
% finger fewer observations are available,
% they will be used systematically for the
% Tippett plot (one after the other).
% 2000 have been used systematically.
% nbmin: the number of minutiae observed in the
% evidential comparison
% database_within: The database that contains all compari-
% sons between impressions from the same
% finger.
% (rows=prints, columns=marks, first 3
% columns will be eliminated by the code).
% database_betweenALL: The database of all comparisons of the
% marks to the non-matching prints
% (rows=prints,
% columns=marks, first 3 columns will be
% eliminated by the code). Here,zeroes will
% be eliminated by the code and the
% columns will be sorted at one point;
% no need to prepare data.
% database_betweenFNGP; between-finger database conditioned by
% finger number and general pattern.
% selfscores: Three scores obtained on the basis of 3
% slap impressions compared to themselves
% (where the relevant minutiae for the
% case have been annotated as identically
% as possible on a given impression used
% once as a 'mark' and once as a 'print').

function [True,False]=TippettPlotDifferent(number_of_data,nbmin,...
database_within,database_betweenALL,database_betweenFNGP,...
selfscores);
```

```

% define counter; will be used for the storing of the results.
count1 = 1;
% prepare within and between finger databases by taking out the
% first 3 columns.
database_within(:,1:3)=[];
database_betweenALL(:,1:3)=[];
database_betweenFNGP(:,1:3)=[];
%store the size of the within-finger database
sizeIn=size(database_within);
%put within-finger variability in a vector for fitting of the
%Weibull later; all data from within-finger database is used
%for the fitting of the within-finger distribution.
vector_within=mettre_vect(database_within);

% determine whether sufficient data is available in the within-
% finger database for random selection of 'number of data'
% scores. If this is not the case, each score is used in turn.
if size(vector_within)<number_of_data

    for istep = 1:sizeIn(2)
        % for each column, corresponding to the comparisons of one mark
        % to sizeIn(1) prints
        vector_betweenALL=sort(database_betweenALL(:,istep),...
        'descend');
        %select the column corresponding to the mark in the
        %between-finger database; sort it.
        vector_betweenFNGP=sort(database_betweenFNGP(:,istep),...
        'descend');
        % the same as previous line for second between-finger
        % database.
        for jstep=1:sizeIn(1)
            % systematically go through the scores for the
            % selected mark.
            withinLAT=database_within(jstep,istep);
            %select evidence score from within-finger database
            % Compute relevant elements (LRs, numerators,
            % denominators for
            % the different options) for the selected evidence.
            % COMPARISONS UNDER H
            [scoreT(count1),LR_E_APPROX_T(count1),...
            LR_E_FIX_T(count1),LR_E_RED_T(count1),...

```

```

LRD_ALL_T(count1),LRD_FNGP_T(count1),...
NumE_T(count1),DenE_App_T(count1),...
DenE_Fix_T(count1),DenE_Red_T(count1),...
NumD_T(count1),DenD_All_T(count1),...
DenD_FNGP_T(count1)] = calculLRMany(withinLAT,...
nbmin,vector_within,vector_betweenALL,...
vector_betweenFNGP,selfscores);
%increment the counter
count1=count1+1;
end
%print istep, to know where you are at.
istep
end
%put results into the 'True' matrix in order to have fewer
%variables in output.
True=[scoreT',LRD_ALL_T',LRD_FNGP_T',NumD_T',DenD_All_T',...
DenDFNGP_T',LR_E_FIX_T',LR_E_RED_T',LR_E_APPROX_T',...
NumE_T',DenE_App_T',DenE_Fix_T',DenE_Red_T'];
%say when the computation of the LRs under H is finished.

'Under H finished'
% if there are more than 'number of data' observation in the
% within (stratified random selection will be used here;
% stratification is for reducing the time it takes to
% compute).
else
% compute the number of observations that will be selected
% from each column. Notice that the 'ceil' command rounds
% up; slightly more observations than number_of_data will
% be obtained.

numberPerColumn1=ceil(number_of_data/size(database_within,2));
for istep = 1:sizeIn(2) % again, go through the columns.
vector_betweenALL=sort(database_betweenALL(:,istep),...
'descend');
%select the column corresponding to the mark in the
%between-finger database; sort it.
vector_betweenFNGP=sort(database_betweenFNGP(:,istep),...
'descend');
% the same as previous line for second between-finger
% database.
placeWithin=randperm(size(database_within,1));

```

```

%randomly permutate numbers between 1 and the length of the
% vector corresponding to the comparison of 1 mark to
% several prints.
withinLAT=database_within(placeWithin(1:numberPerColumn1),...
istep);
%withinLAT is the vector of evidential scores that will be
%used for the computations of LR's etc.
for jstep=1:max(size(withinLAT))
    % choose each of the evidential scores in turn.
    % Compute relevant elements (LRs, numerators, denominators
    % for the different options) for the selected evidence.
    %COMPARISONS UNDER H
    [scoreT(count1),LR_E_APPROX_T(count1),...
    LR_E_FIX_T(count1),LR_E_RED_T(count1),...
    LRD_ALL_T(count1),LRD_FNGP_T(count1),...
    NumE_T(count1),DenE_App_T(count1),...
    DenE_Fix_T(count1),DenE_Red_T(count1),...
    NumD_T(count1),DenD_All_T(count1),DenD_FNGP_T(count1)]...
    =calculLRMany(withinLAT,nbmin,vector_within,...
    vector_betweenALL,vector_betweenFNGP,selfscores);
    % increment the counter for storing the results.
    count1=count1+1;
end
%print istep, to know where you are at.
istep
end
end
end
True=[scoreT',LRD_ALL_T',LRD_FNGP_T',NumD_T',DenD_All_T',...
DenD_FNGP_T',LR_E_FIX_T',LR_E_RED_T',LR_E_APPROX_T',...
NumE_T',DenE_App_T',DenE_Fix_T',DenE_Red_T'];
'Under H finished'

%here begin computations under Hbar
% create a new counter for these new results.
count2=1;
%Again, stratified random sampling is used for the selection of the
%evidential score. Again, the use of ceil will yield slightly more
%observations than what is defined by number_of_data.

numberPerColumn=ceil(number_of_data/size(database_betweenALL,2));

for kstep=1:size(database_betweenALL,2)

```

```

% select each column (corresponding to a mark each) in turn.
% randomly permutate numbers between 1 and the length of the vector
% corresponding to the comparison of 1 mark to several prints.
placebetw=randperm(size(database_betweenALL,1));
% select the evidential scores under Hbar, using the indices stored
% in placebetw. betweenLAT is a vector.
betweenLAT=database_betweenALL(placebetw(1:numberPerColumn),kstep);
%choose the proper between-finger data for the latents, sort them.
vector_betweenALL=sort(database_betweenALL(:,kstep),'descend');
vector_betweenFNGP=sort(database_betweenFNGP(:,kstep),'descend');
for hstep=1:max(size(betweenLAT))
    %for each evidential score, compute LRs etc.
    [scoreF(count2),LR_E_APPROX_F(count2),LR_E_FIX_F(count2),...
    LR_E_RED_F(count2),LRD_ALL_F(count2),...
    LRD_FNGP_F(count2),NumE_F(count2),DenE_App_F(count2),...
    DenE_Fix_F(count2),DenE_Red_F(count2),NumD_F(count2),...
    DenD_All_F(count2),DenD_FNGP_F(count2)]...
    =calculLRMany(betweenLAT(hstep),nbmin,...
    vector_within,vector_betweenALL,vector_betweenFNGP,selfscores);
    %Increment the counter for the results.
    count2 = count2 + 1;
end
% print kstep to know how far it is.
kstep
end
%store results in a single variable.
False=[scoreF',LRD_ALL_F',LRD_FNGP_F',NumD_F',DenD_All_F',...
DenD_FNGP_F',LR_E_FIX_F',LR_E_RED_F',LR_E_APPROX_F',...
NumE_F',DenE_App_F',DenE_Fix_F',DenE_Red_F'];
% From now on, it's only plotting of Tippett plots using the data
% generated above.
% TAKEN AS IS FROM CEDRIC NEUMANN'S CODING FOR A PROJECT
% FUNDED BY TSWG.

% FIGURE 1: DATA-BASED ESTIMATION IS USED FOR BOTH NUMER-
ATOR
% AND DENOMINATOR,USING THE WHOLE BETWEEN-FINGER DATABASE

%FOR DENOMINATOR ESTIMATION (LRD_ALL_T AND LRD_ALL_F);
PlottingTippetts(LRD_ALL_T,LRD_ALL_F)
% FIGURE 2: DATA-BASED ESTIMATION IS USED FOR BOTH NUMERA-
TOR

```



```

% AND DENOMINATOR, USING THE BETWEEN-FINGER DATABASE
% CONDITIONED BY GENERAL PATTERN AN FINGER NUMBER
% FOR DENOMINATOR ESTIMATION
% (LRD_FNGP_T AND LRD_FNGP_F);
PlottingTippetts(LRD_FNGP_T,LRD_FNGP_F)
% FIGURE 3: APPROXIMATION IS USED FOR BOTH NUMERATOR AND
%DENOMINATOR, USING FIXED PARAMETERS FOR THE BETWEEN-
% (FINGER DISTRIBUTION. LR_E_FIX_T AND LR_E_FIX_F);
PlottingTippetts(LR_E_FIX_T,LR_E_FIX_F)
% FIGURE 4: APPROXIMATION IS USED FOR THE NUMERATOR AND A
% REDUCED DATASET IS USED FOR ESTIMATION OF THE
%DENOMINATOR (LR_E_RED_T AND LR_E_RED_F);
PlottingTippetts(LR_E_RED_T,LR_E_RED_F)
% FIGURE 5 (LAST ONE): APPROXIMATION IS USED FOR BOTH THE
% NUMERATOR AND THE DENOMINATOR
% (LR_E_APPROX_T AND LR_E_APPROX_F);
PlottingTippetts(LR_E_APPROX_T,LR_E_APPROX_F)

```

C.4 The function for computing LR_s using different options

```

% This function computes LRs (numerators and denominators) from the
% within and between data inserted. It also estimates the parameters
% for the between finger variability (approximated and databased).
% It is made for being called by TippetPlotDifferent.m.
%
% Matlab version info below.
% -----
% MATLAB Version 7.0.1.24704 (R14) Service Pack 1
% -----
% MATLAB Version 7.0.1 (R14SP1)
% Curve Fitting Toolbox Version 1.1.2 (R14SP1)
% Image Processing Toolbox Version 5.0.1 (R14SP1)
% Neural Network Toolbox Version 4.0.4 (R14SP1)
% Statistics Toolbox Version 5.0.1 (R14SP1)

%Input:
% EVIDENCE: an evidential score
% nbmin: the number of minutiae observed in the
% evidential comparison.

```

```
% vector_within: the vector of within-variability scores
% (obtained by comparing the suspects marks
% and prints using AFIS)
% database_betweenALL: the database of scores obtained when compa-
% ring the evidential mark to the whole
% database.
% database_betweenFNGP: the database (vector)of evidential scores
% obtained when comparing the evidence mark
% to a database of nonmatching prints that
% have the same finger number and general
% pattern as the mark.
% selfscores Three scores obtained on the basis of 3
% slap impressions compared to themselves
% (where the relevant minutiae for the
% case have been annotated as identically
% as possible on a given impression used
% once as a 'mark' and once as a 'print').
function [score,LR_E_APPROX,LR_E_FIX,LR_E_RED,LR_D_ALL,...
LR_D_FNGP,NumE,DenE_App,DenE_Fix,DenE_Red,NumD,...
DenD_All,DenD_FNGP]=calculLRMany(EVIDENCE,nbmin,vector_within,...
database_betweenALL,DatabaseBetweenFNGP,selfscores)
% Eliminate zeroes from between-finger databases
database_betweenALL=database_betweenALL(database_betweenALL>0);
DatabaseBetweenFNGP=DatabaseBetweenFNGP(DatabaseBetweenFNGP>0);
% fit lognormal distribution to database of all fingerprints
plognALL=lognfit(database_betweenALL);
% separate the two parameters into two variables
plogn1ALL=plognALL(1);
plogn2ALL=plognALL(2);
% fit lognormal to fngp database
plognFNGP=lognfit(DatabaseBetweenFNGP);
%separate the two parameters into two variables
plogn1FNGP=plognFNGP(1);
plogn2FNGP=plognFNGP(2);

%compute the approximated parameters for the between-finger variability
[parmhatBetween1APPROX,parmhatBetween2APPROX]=...
compute_parmhat_betweenForTippett(database_betweenALL,nbmin);
%put the fixed parameters read off elsewhere into two variables
parmhatBetween1FIX=7.50879430990458;
parmhatBetween2FIX=0.179001625332056;
% These two params are the mean of estimates obtained for 6oDFO on RTRL
```

```

%randomly select 10000 observations from the 'All' database
p=randperm(max(size(database_betweenALL)));
ParmhatBetweenRED=lognfit(database_betweenALL(p(1:10000)));
% fit the Weibull distribution to the within-finger data
estim=wblfit(vector_within);
%prepare estimated parameters for the within-finger variability
if nbmin==6
    beta=13.9208240390902;
elseif nbmin==7
    beta=12.7407795236924;
elseif nbmin==8
    beta=11.5226744918335;
elseif nbmin==9
    beta==10.4143410025036;
elseif nbmin==10
    beta=10.3284587778818;
end
alpha=(mean(selfscores)+903.78)/1.4565;

%compute the numerator using the approximation
NumE=wblpdf(EVIDENCE(1,1),alpha,beta);
%compute the numerator using the data-based estimation
NumD=wblpdf(EVIDENCE(1,1),estim(1),estim(2));
%compute the denominators
%1) using all data
DenD_All=lognpdf(EVIDENCE(1,1),plogn1ALL,plogn2ALL);
%2) using fngp data
DenD_FNGP=lognpdf(EVIDENCE(1,1),plogn1FNGP,plogn2FNGP);
%3) using the approximation
DenE_App=lognpdf(EVIDENCE(1,1),parmhatBetween1APPROX,...
parmhatBetween2APPROX);
% 4) using the fixed parameters
DenE_Fix=lognpdf(EVIDENCE(1,1),...
parmhatBetween1FIX,parmhatBetween2FIX);
% 5) using the parametrs from the randomly reduced database
DenE_Red=lognpdf(EVIDENCE(1,1),ParmhatBetweenRED(1),...
ParmhatBetweenRED(2));
% divide numerators by denominators as needed
LR_D_ALL=NumD/DenD_All;
LR_D_FNGP=NumD/DenD_FNGP;
LR_E_APPROX=NumE/DenE_App;
LR_E_FIX=NumE/DenE_Fix;

```

```
% Here, numerator from data should be used; has been done manually in
% thesis from the outputs
LR_E_RED=NumE/DenE_Red;
%output the score for further use.
    score=EVIDENCE;
```

C.5 The function for actually plotting the Tippett plots

```
% This function takes different LRH (obtained under H and
% Hbar) as input, and plots the Tippetts.
% Matlab version info below.
% -----
% MATLAB Version 7.0.1.24704 (R14) Service Pack 1
% -----
% MATLAB Version 7.0.1 (R14SP1)
% Curve Fitting Toolbox Version 1.1.2 (R14SP1)
% Image Processing Toolbox Version 5.0.1 (R14SP1)
% Neural Network Toolbox Version 4.0.4 (R14SP1)
% Statistics Toolbox Version 5.0.1 (R14SP1)
```

```
function PlottingTippetts(LRH,LRHbar)
```

```
% UNDER H
```

```
figure
```

```
[yy,xx,n,msg] = cdfcalc(log10(LRH));
```

```
k = length(xx);
```

```
n = reshape(repmat(1:k, 2, 1), 2*k, 1);
```

```
xCDF_true = [-Inf; xx(n); Inf];
```

```
yCDF_true = [0; 0; yy(1+n)];
```

```
% INVERSION OF THE CDF
```

```
yCDF_true = 1-yCDF_true;
```

```
plot(xCDF_true,yCDF_true,'g');
```

```
hold on;
```

```
% UNDER HBAR
```

```
[yy,xx,n,msg] = cdfcalc(log10(LRHbar));
```

```
k = length(xx);
```

```
n = reshape(repmat(1:k, 2, 1), 2*k, 1);
```

```
xCDF_false = [-Inf; xx(n); Inf];
```

```
yCDF_false = [0; 0; yy(1+n)];
```

```
% INVERSION OF THE CDF
```

```

yCDF_false = 1-yCDF_false;
plot(xCDF_false,yCDF_false,'r');
title('Data based parameters: ALL data')
% rescale X axis
xlim_value=get(gca,'xlim');
tmp_xlim = max(abs(xlim_value(1)),xlim_value(2));
set(gca,'xlim',[-tmp_xlim, tmp_xlim]);
% LEGEND UNDER H
b=find(xCDF_true<=0);
text(0.8,0.93, ['\fontsize{12}\fontname{times}\it{LR true min =}'...
num2str(10^xCDF_true(2))],'horizontalalignment','left',...
'verticalalignment','middle','unit','norm');
text(0.8,0.88, ['\fontsize{12}\fontname{times}\it{LR true max =}'...
sprintf('%8.2o',10^(xCDF_true(size(xCDF_true,1)-1)))],...
'horizontalalignment','left','verticalalignment','middle',...
'unit','norm');
text(0.8,0.83, ['\fontsize{12}\fontname{times}\it{LR true < 1}' ...
sprintf('%8.2f',(100-100*yCDF_true(b(size(b,1)))) ' %')],...
'horizontalalignment','left','verticalalignment','middle',...
'unit','norm');

% put the legend into the graph
position_text = findobj(gca,'type','text');
s = get(position_text,'extent');
max_extent = max([s{1}(3),s{2}(3),s{3}(3)]);
t = get(position_text,'position');
if max_extent > 0.2
    set(position_text(1),'position',[1-max_extent-0.01, t{1}(2), 0]);
    set(position_text(2),'position',[1-max_extent-0.01, t{2}(2), 0]);
    set(position_text(3),'position',[1-max_extent-0.01, t{3}(2), 0]);
end
% legend under Hbar
c=find(xCDF_false>=0);

text(0.05,0.12, ['\fontsize{12}\fontname{times}\it{LR false max =}'...
sprintf('%8.2o',10^(xCDF_false(size(xCDF_false,1)-1)))],...
'horizontalalignment','left','verticalalignment','middle',...
'unit','norm');
text(0.05,0.17, ['\fontsize{12}\fontname{times}\it{LR false min =}'...
num2str(10^xCDF_false(2))],'horizontalalignment','left',...
'verticalalignment','middle','unit','norm');
text(0.05,0.07, ['\fontsize{12}\fontname{times}\it{LR false > 1}' ...

```

```
sprintf('%8.2f',(100*yCDF_false(c(1)))) ' %',...
'horizontalalignment','left','verticalalignment','middle',...
'unit','norm');

b=yCDF_true(b(size(b,1)));
line([0,0],[yCDF_false(c(1))+0.05,b-0.05],'color',[0 0 0],...
'linestyle','-');
text(0.49,0.49,['\fontsize{12}\fontname{times}\it{LR = 1}'],...
'horizontalalignment','left','verticalalignment','middle',...
'unit','norm','rotation',90);
```

C.6 Computing the approximated parameters for the between-finger variability

```
%Takes the the ordered vector (without zeroes) of between-finger data as
%input, as well as the number of minutiae in the evidential comparison, and
%computes the approximated parameters of the between-finger distribution
% Matlab version info below.
% -----
% MATLAB Version 7.0.1.24704 (R14) Service Pack 1
% -----
% MATLAB Version 7.0.1 (R14SP1)
% Curve Fitting Toolbox Version 1.1.2 (R14SP1)
% Image Processing Toolbox Version 5.0.1 (R14SP1)
% Neural Network Toolbox Version 4.0.4 (R14SP1)
% Statistics Toolbox Version 5.0.1 (R14SP1)
function [parmhat1,parmhat2]...
=compute_parmhat_betweenForTippett(between_data,nbmin)
%Choose the first ten observations (the ten highest)
Datasorted=between_data(1:10);
%compute their mean
MeanDataS=mean(Datasorted);
%compute their variance
VarDataS=var(Datasorted);
%use the equations to obtain approximated parameters.
if nbmin==6
    parmhat1=0.6246*log(MeanDataS)+2.422;
    parmhat2=0.01199*(log(MeanDataS)./log(VarDataS))+0.1282;
elseif nbmin==7
    parmhat1=0.8113*log(MeanDataS)+ 0.9021;
```

```
    parmhat2=0.009652*(log(MeanDataS)./log(VarDataS))+0.1415;
elseif nbmin==8
    parmhat1=0.819*log(MeanDataS)+0.8089 ;
    parmhat2=-0.01174*(log(MeanDataS)./log(VarDataS))+0.1772;
elseif nbmin==9
    parmhat1=0.2981*log(MeanDataS)+ 5.034;
    parmhat2=-0.007286*(log(MeanDataS)./log(VarDataS))+0.1827;
elseif nbmin==10
    parmhat1=0.3947*log(MeanDataS)+ 4.248;
    parmhat2=-0.002005*(log(MeanDataS)./log(VarDataS))+0.1817;
end
```

