

# AGEING EFFECTS IN FINGERPRINT RECOGNITION

## Masterthesis

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# Table of Contents

1	Abstract	4
2	Introduction	5
	2.1 Biometrics and Ageing	6
	2.2 Goals	12
	2.3 Terminology	12
3	Fingerprints and Fingerprint Recognition Systems	16
	3.1 Fingerprint Recognition Methodologies	16
	3.2 Fingerprint Recognition Systems	19
	3.3 NIST Biometric Image Software (NBIS)	20
	3.4 VeriFinger	23
	3.5 Finger-Code	23
	3.6 Phase-Only-Correlation	25
4	Data Sets and Ground Truth Search	27
	4.1 CASIA 2009	27
	4.2 CASIA 2013	29
	4.3 Ground Truth Search	30
	4.4 Acquisition Conditions	36
	4.5 Comments on Notation and Experimental Settings	39
	4.6 Test Procedure	44
5	Ageing Experiments	48
	5.1 General Information	48
	5.2 NBIS	53
	5.3 NEURO	73
	5.4 FC	88
	5.5 POC	92
	5.6 Variability of data sets and 2. non minutiae experiments	93
	5.7 2. FC Experiments:	97
	5.8 2. POC Experiments:	114
6	Doddington's Zoo and Menagerie Analysis	131
	6.1 Doddington Zoo	131

6.2	Menagerie Analysis - Pre-Information and Assumptions . . . . .	132
6.3	Menagerie Analysis - Experiments and Results . . . . .	133
6.4	User-defined Menagerie Analysis Results . . . . .	136
6.5	Mean scores and System errors . . . . .	179
6.6	Menagerie Analysis and Ageing Effects detected in Section 5 . . . . .	186
7	Fingerprint Ageing and Quality . . . . .	190
7.1	NIST Fingerprint Image Quality (NFIQ) . . . . .	192
7.2	Image Quality of Fingerprint (IQF) . . . . .	194
7.3	Gabor Filter Image Quality of Fingerprint (GFIQF) . . . . .	197
7.4	Average False Accepted and Rejected Quality Analysis . . . . .	200
7.5	Refined Quality Analysis . . . . .	210
8	Conclusion . . . . .	235

## 1 Abstract

The aim of the present master thesis is investigations concerning different influences in fingerprint recognition that can be caused probably by so called 'ageing effects'. 'Ageing' is one of the biggest natural process controlling daily life. For this purpose it seems natural to have a closer look at the biometric aspects of ageing in fingerprint recognition. Using a variety of different fingerprint data bases provided by a biometrics research team at the Chinese Academy of Sciences, Institute of Automation (CASIA) and different fingerprint matching methods, including minutiae and non minutiae based based implementations, three main tasks including performance, menagerie and quality analysis have been fulfilled.

In order to focus on the performance and matching related effects the first experiments have been designed to discover and compare ageing abnormalities related to the matching score distributions. The number of different data bases, including diverse acquisition conditions for example caused by three sensor types, usage of two minutiae based and two non minutiae fingerprint recognition software solutions provided a broad spectrum of information which was also used in the other two experimental setups. Due to this, the second experiments have been used to have a look at the theoretical concept of 'Doddington's Zoo'. The theory, originally introduced in speech recognition, is focusing on different characteristics depending on the user behavior with respect to automatic recognition systems. After performing experiments that are mainly related to the matching score distributions and the user behavior, a final goal was to investigate the impact of the imprint quality. This aspect is a crucial one because the interferences caused by low quality could be higher than probably detectable ageing effects.

## 2 Introduction

*'Personal traits of humans that can be somehow measured (sampled, acquired) from a person in the form of a biometric identifier and that uniquely distinguish a person from the rest of the world population. [11]'*

That is one possible definition of what biometrics are and one reason why biometric systems have become an important aspect by modern standards. The possibility to identify a person because of some certain distinctive characteristics provides various capabilities. Access control systems like immigration screening at airports, prison visitor systems, user authentication for convenience human computer interaction like the fingerprint scanner built into consumer notebooks and mobile phones are just a few areas of application.

According to the different applications and human characteristics there are various types of biometric methodologies. Fingerprint, palm print, hand and finger geometry, finger veins geometry, iris and retina scans, voice and signature and also face, ear and gait recognition are the most well known techniques. Nevertheless not all of the quoted methods are that familiar.

*'Fingerprints are perhaps what the majority of people immediately associate with biometrics. [8]'* According to [9] the knowledge of the individuality of fingerprints has been discovered by the Chinese about 6000 years ago. During the late 17. and beginning of the 18. century the first studies of the human skin have been published. At the end of the 19. century the most important research outcomes for fingerprint recognition of today were published. Sir William J. Herschel (1833-1917) studied the persistence of friction ridge skin [9] and Henry Fauld (1843-1930) published about the value of friction ridge skin for individualization [9]. During the same time the first book 'Finger Prints' (1892) about fingerprints was written by Sir Francis Galton (1822-1911). Starting *'The palms of the hands and the soles of the feet are covered with two totally distinct classes of marks. [15]'* he set forth that the friction ridge skin is unique and persistent. This major knowledge combined with the relative simple possibility of capturing the fingerprints and the technological development in computer sciences led to biometric recognition systems which can be used for a lot of purposes. In chapter 3 there will be a more detailed discussion on fingerprints

and fingerprint recognition systems.

But not only fingerprints can be used to determine a persons identity. As displayed in [20] there are four requirements that a biometric characteristic must fulfill to be suited to be used in a biometric recognition system. Without *universality*, *distinctiveness*, *permanence* and *collectability* even a fingerprint recognition system would not work.

## 2.1 Biometrics and Ageing

In biometric processing there are different types of age factor or ageing effects. Looking at the before described four requirements the properties of distinctiveness and permanence are those that can be influenced by ageing as discussed in [14]. Apart from the later on introduced aspect of loss of collagen [24], other physiological effects of ageing on fingerprints are discussed in chapter 12 of [14]. As readable in [29], ageing introduces following four effects on the fingerprint ridge structure:

- Fine wrinkle tend to appear in the skin ridge structure.
- The skin gets thinner and more transparent for older people compared to younger ones.
- Loss of fat below the first level skin layer, reducing the firmness of the skin.
- Loosing osseous matter reduces the elastic behavior, which is also effected by the aforementioned loss of fat.

They can be summarized to so called intrinsic age factors. Extrinsic age factors like for example working conditions and injuries are based to certain individuals. So of course ageing is an aspect that needs to be discussed in terms of biometric recognition.

As introduced in [22] the most important characteristics affected by ageing are face, fingerprints, hand biometrics, voice, behavior (like signature) and iris. For each of those biometric characteristics ageing based research is performed. There are a few difficulties to solve. The most prominent one is the task of acquiring a suitable data base. It is obvious that before talking about ageing effects the most important precondition is the need of a data set including a time span. This requirement can be fulfilled, but there is an additional problem. The number of non-ageing based variability within the data set should be as low as possible. These fluctuations are based

on the different acquisition conditions in the majority of the cases. Another aspect concerning the data acquisition is the very important issue of choosing a sensor. If the same sensor is used in the different acquisition sessions the influence of sensor ageing must be discussed. If different sensors are chosen, cross-sensor matching must be taken into account as well. Those mentioned acquisition conditions are also a problem in this master thesis and there will be a discussion about the topic in Section 4 and Section 6. But it can be stated that it is nearly impossible to collect data which is free of ageing based influences because this biological process is present in each part of human life. Especially if different extrinsic and intrinsic factors are taken into account. Due to these circumstances there are only a few suitable data sets available, which are discussed in [22].

In [14] different approaches concerning face, online signature, iris, fingerprints and speech recognition are collected and presented in detail. All of those characteristics seem to be influenced by ageing. In fingerprint and speech recognition those effects are clearly observable. In online signature the detectable ageing impact depends on the used matching system due to robustness to the passing of time. According to Anil K. Jain it is commonly agreed that the reliability of facial recognition systems is lowered if the time span between two facial images of the same person is more or less 10 years [33]. In iris based research there are different results available and the outcomes are focus of several discussions. In the following the focus will be on fingerprint related aspects from now on.

During the time the first book about fingerprints was published the scientists had no exact idea what ageing is in relation to biometric changes. Even today there are various hypothesis but no real comprehensive description for this biological circumstance. In terms of skin ageing this biological process effects in loss of collagen [24]. This structural protein is responsible that elderly skin is loose and dry compared to young skin. Shimon K. Modi and his colleagues confirmed a difference in the quality of fingerprint images and in the matching performance using Detection Error Tradeoff (DET) curves [24]. They tried to evaluate the impact of different age on the imprint quality. So they constructed four data sets containing fingerprint images of different age groups. Those four age groups are from 18 to 25, from 26 to 39, from 40 to 60 and the last one containing imprints from volunteers which are 62 or older. This last age group and the first one are the same that have been used in [35]. Therefore they have

been acquired in 2005, while the remaining two age group data sets were collected in 2006. So there is not only a high variability concerning the different age groups and the acquisition conditions - for example different sensor types used for the acquisition process - but also a high fluctuation based on the volunteers because there are no imprints which belong to the same person in every age group. Besides the total number of imprints in the single groups is also not similar. In the 18 to 25 and the 62+ set much more fingerprints are contained compared to the other two sets. For sure it is very difficult - nearly impossible - to gather a data set, where for each acquisition period and for each age group always the same volunteers are available. After extracting the minutiae and quality information of each imprint, using unspecified tools, it was possible to gather following results. Looking at the different age groups it is clearly observable that on the one hand the quality is not the same across the single data sets and on the other hand a fluctuation concerning the number of extracted minutiae can be detected as well. So the results from [24] confirmed the results from [35] that it is possible to find variances between different age groups. Especially in [35] it is confirmed that young fingerprints exhibit more moisture compared to adult imprints. Another aspect of ageing was discussed in [10]. Basically it was possible to determine a skin ageing effect analyzing topography structures of fingerprint skin. Using watershed analysis the cell area distribution of the used imprints was generated. Looking at the distribution a linear correlation due to ageing is displayed. This can be stated because ageing is directly affecting the cell structure by enlarging the cell area. The used data set was collected using a so called TouchChip sensor developed by ST Microelectronics. In total 30 volunteers have been included in this research, but there is no information about how many imprints have been used.

The mutational effects of fingerprint ageing are discussed in [13]. Of course the main issue of this research is not directly related to the topic of this master thesis. But nevertheless, why shouldn't it be realistic that mutation effecting cell ageing in general, is responsible for fingerprint ageing as well.

Another ageing related point of view is based on the individuality of the volunteers, different age groups and other biometric characteristics. In [27], [37], [38] and [41] those topics have been discussed. The impact of individuality to a fingerprint recognition system is discussed in [27]. The aspect of individuality is one of the two most important fundamentals of fingerprint recognition - the other basic condition is persistence. But individuality is only accepted to be true based on empirical results and



therefore the formal point of view was the issue of [27]. They used a data set including fingerprint images of 167 volunteers and four imprints for each volunteer acquired by an optical sensor developed by Digital Biometrics, Inc. The acquisition process was repeated once again 6 weeks later to generate a second data base using the same acquisition modalities. After extracting the minutiae information using a self-made Automatic Fingerprint Matching System (AFMS), designed to perform fingerprint verification on a given data set following results could be obtained. To provide a stable amount of individuality a so called 12-point guideline was introduced. This guideline is using exactly 12 minutiae in both prints that shall be matched against each other to reduce possible matching errors as good as possible and to preserve the aspect of fingerprint individuality. They have been able to show that using this small number of minutiae is sufficient high enough to ensure that 'the likelihood of an adversary guessing someone's fingerprint pattern is significantly lower than a hacker being able to guess a six character alpha-numerical case-sensitive password . . . . [27]' So individuality of a fingerprint is a important issue due its high amount of biometric secureness. Another important aspect regarding the quality of the imprints was not taken into account.

For this master thesis the remaining three research results named before, [37], [38] and [41], are mainly interesting and important. Comparing the verification performance of kids and adults for fingerprint, palmprint, hand-geometry and digitprint biometrics was described in [37]. Due to the circumstance that the performance behavior of children and adults should be compared, two data sets have been constructed using a flatbed scanner (HP 3500c), at 500dpi resolution. To control the environmental light the scanner was placed in a box. The adult data set consists of 172 templates of 86 volunteers, all older than 18 years. The second data set includes 498 templates of 301 children which are aged from 3 to 18. Five different geometric and texture-based algorithms, including the NIST minutiae extraction software (NBIS) are employed to gather minutiae, palmprint, eigenpalms and eigenfingers, shape and geometry information of the full hand images. Using equal error rate (EER), false match rate (FMR), false non match rate (FNMR) and receiver operating characteristics (ROC) information following results could be determined. In case of the minutiae and palmprint features the adult data base performed better than the children data set. Eigenpalms and eigenfingers seem to be nearly not influenced by ageing. The adult data set performed a little bit better compared to the second set. Using the

geometry information the children data set, especially the volunteers from 3 to 10 performed much better than the other age groups. The 11 to 18 age group was performing best in terms of shape information. Based on the results the aspect of ageing in fingerprint recognition is also discussed in [38]. The same sensor device as in [37] was used to acquire 127 full hand imprints of 28 volunteers in 2007 and a second set including the same volunteers and 135 hand images in 2012. So the two data sets exhibit a time span of 5 years. All volunteers have been older than 18 years. Performing the experiments minutiae, eigenhand, palmprint, silhouette, shape and length based features were extracted from the full hand images. It was possible to disprove that there is no statistical ageing impact comparing both data sets using EER and ROC. The assumption that ageing has a detectable effect on the used features as well could be disclaimed. Further the hypothesis that short-time intra-personal variability increases with age too. The fourth main task is very interesting for this master thesis. This issue is using the goats concept of 'Doddington's Zoo', [12], to represent the tendency observable in the genuine and impostor matching scores. The three outcomes for this experiment are:

- There exist users with low matching scores across all used features.
- Users labeled as goats in 2007 are prone to be labeled in 2012 as well.
- Features of different users are causing problems and for this purpose they are suggested for combining them to one feature.

In Section 6 the concept of 'Doddington's Zoo' will be discussed in detail on the used data sets of this master thesis.

A totally different type of data set was taken into account in [41]. It is a longitudinal data set of fingerprints of 15597 people. Those people have been arrested by Michigan State Police (MSP) and the data includes a time span from 5 up to 12 years for each person. For each person a so called ten-print card is acquired. That means that each of the ten fingers is acquired at least five times. If taking the time span into account, 122685 ten-print cards are contained in this data set in total. Additionally it is necessary to mention that those ten-print cards probably must be scanned before they can be used in the computational recognition process. To perform the experiments two commercial off-the-shelf (COTS) fingerprint matchers are used to compute the needed matching scores. Basically the longitudinal study of fingerprint recognition that was performed in [41] used a multilevel statistical model based on different se-

tups. Those models have been tested how well they fit to the data sets. According to the fact that there are different parameters included in each model setup, it was possible to find the best fitting parameter setting that describes the data base. The most interesting effects that can be observed are:

- Concerning the genuine match distributions a decrease of the score values can be observed while the time interval between the data is increased. Besides there is not only a relationship between ageing and the genuine score decrease, the imprints quality impacts the decrease as well. So if the quality of the imprints is decreased than the matching score too.
- On the other hand the impostor scores seems to be more or less stable. There is not a real important change observable.
- The third important result is related to the ageing and the quality parameter of the used statistical models including the NFIQ measurement. The experiments showed that the quality parameter has a higher impact on the imprints than the ageing one.

As presented in [33] it can be summarized that the recognition accuracy according to the used data set does not degrade. This effect can be detected looking at the almost stable impostor scores. So the number of false accepted users is not raising. It indicates that the security aspect is not influenced by ageing in this point of view. But based on the three most important parameters, time span, age and quality another conclusion can be made. It seems that the effect of the selected variables is prone to genuine scores. Especially the quality and the ageing aspect seems to have a very high impact on those matching results. According to this information it will be interesting to have a closer look on this aspect. Especially the use of NFIQ, which is based on using minutiae information could lead to not distinct results. NFIQ indicates a low quality if there is low minutiae information contained in the fingerprint. But it is mandatory to mention that if there is less minutiae information caused by skin ageing, the NFIQ value will be low as well. So it is not clear if a low NFIQ value is just influenced by quality based aspects or also/only by ageing itself.

In this master thesis in Section 5 there will be a general discussion based on the matching performance and accuracy. Besides, the distinction between ageing and quality effects is a complicated task because they might influence each other. So in Section 7 the quality aspect of the given data will be taken into account as well.

It will be interesting to compare the results of those experiments and the outcomes presented in [41].

## 2.2 Goals

Within this master thesis the main goal will be the investigation on ageing aspects in terms of fingerprint recognition. Looking at the purposes in detail they can be defined as follows:

- After performing the fingerprint matching using different fingerprint recognition systems, an evaluation based on the genuine and impostor score distributions will be taken into account. Probably it is possible to find particular irregularities that , can be named ageing effects.
- In the next step there will be an investigation if such ageing related effects have an influence in fingerprint recognition performance. Basically this task will be focusing on special characteristics that are included in the so called 'Doddington's Zoo'.
- The third part of the thesis will focus on the quality impact of the different data bases. For this purpose the focus lies on several quality measurements, including NIST Fingerprint Image Quality (NFIQ), to separate ageing effects from quality effects.
- Because different sensor types are used it will be of general interest, if possible, to have a look on abnormalities that are probably related to cross sensor usage.

In Section 5 the first and last issue will be discussed in detail. The second task, including the search for 'Doddington's Zoo', will be described in Section 6. Finally the experiments concerning the quality impact of the given data are presented in Section 7.

## 2.3 Terminology

There are a few terms and definitions which will be used in this master thesis. The most important ones are described in the following part. Especially the definitions of *Zero FRR*, *Zero FAR*,  $FAR_{100}$  and  $FAR_{1000}$  are introduced as described in [1].

***Gallery Image:*** In most fingerprint applications different data bases of imprints are used. Those imprints contain the distinctive information that allow an identification. All images within such a data base will be named gallery image.

***Probe Image:*** In the present work the term probe image will be used to nominate the image to be tested against the gallery image(s). In many scenarios probe images are not enrolled in the data bases. In this work all gallery images will be a probe image once during their testing. Therefore the same time a gallery image is the probe image as well, it will be excluded from the gallery image set.

***Fingerprint Verification and Identification:*** In verification applications the identity of a fingerprint is claimed. So this image will be tested against a specific gallery image to determine if the claim is correct or not. Due to that, verification systems perform a 1 to 1 comparisons. In identification systems, 1 to  $n$  comparisons are conducted, to determine the corresponding identity of the probe image. In this master thesis only verification tasks have been performed.

***Matching Scores:*** During the comparison of two fingerprint images the similarity or difference of them is computed. The calculated value describes the correspondence. All the used matcher in the present work, that are discussed in part 3.2, generate a similarity score. The similarity scores can be divided into two groups, the genuine and impostor scores. If there is no explicit distinction between genuine and impostor scores, the total number of calculated similarity scores will be named matching scores.

***Genuine Scores:*** Those values are generated when the probe image corresponds to the gallery image. So if there are, for example, another 4 images apart from the probe image of the same finger included in the gallery image set, than for this particular probe image 4 genuine match scores can be derived. So those scores always belong to a specific user within the data bases.

***Impostor Scores:*** If the probe image is not corresponding to the gallery image of claimed identity, a so called impostor score can be calculated.

***False Acceptance Rate (FAR):*** When two different fingerprints are declared to be from the same finger and they are not, then the probe imprint will be incorrectly accepted. So the *false acceptance rate* denotes the number of false acceptances that occur among the total number of impostor matching tests.

**False Rejection Rate (FRR):** When two same fingerprints are declared to be from different fingers and they are not, then the probe imprint will be incorrectly rejected. Due to that, the *false rejection rate* denotes the number of false rejections that occur among the total number of genuine matching tests.

**Zero Acceptance Rate (ZeroFAR):** The *zero acceptance rate* denotes the lowest FRR for FAR equals zero.

**Zero Rejection Rate (ZeroFRR):** The *zero rejection match rate* denotes the lowest FAR for FRR equals zero.

**Genuine Acceptance Rate (GAR):** The *genuine acceptance rate* can be calculated using the FRR values:  $GAR = 1 - FRR$ . It will be used for plotting the ROC.

**$FAR_{100}$ :** The  $FAR_{100}$  denotes the lowest FRR for FAR less or equal to 0.1%.

**$FAR_{1000}$ :** The  $FAR_{1000}$  denotes the lowest FRR for FAR less or equal to 0.01%.

**Equal Error Rate (EER):** The *equal error rate* denotes a specific point of the biometric recognition system, where corresponding FAR and FRR are equal. So this value indicates that the number of false accepts is equal to the number of false rejects. Due to this fact the operating threshold is important because the comparison of the matching scores is depending on thresholds. The threshold indicating the *EER*, the so called EER-threshold, is also indicating at which point the same amount of false accepts and rejects are detected.

**Receiver Operating Curve (ROC):** The *receiver operating curve* is a special curve that can be used to display the performance of a recognition system. Because the ROC curve is threshold independent it is possible to compare the performance of different systems under similar conditions. In the present work the GAR is plotted against the FAR.

**Area Under Curve (AUC):** The *area under curve* is defined as the area that can be obtained by calculating the integral of the ROC.

The following graphical example Figure 1 shows a possible situation looking at genuine and impostor score distribution, EER and false non match and false match probabilities of a biometric recognition system. In Figure 2 an example for the ROC and AUC based on FAR and GAR is displayed.

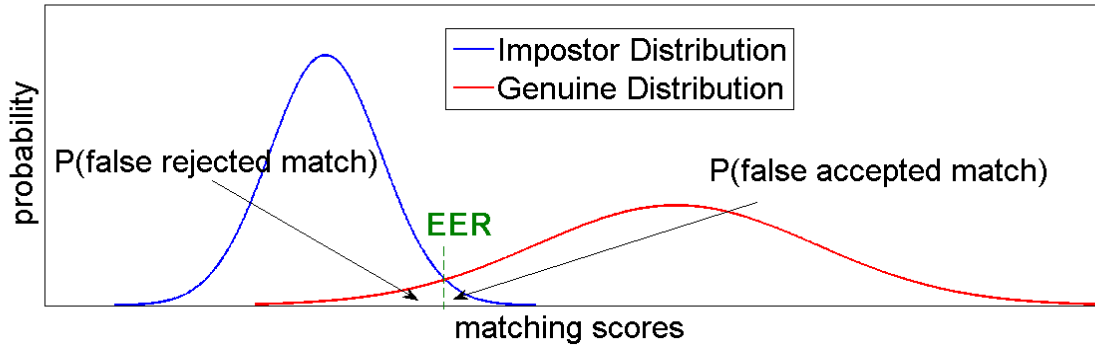


Fig. 1: Genuine and impostor score distribution example.

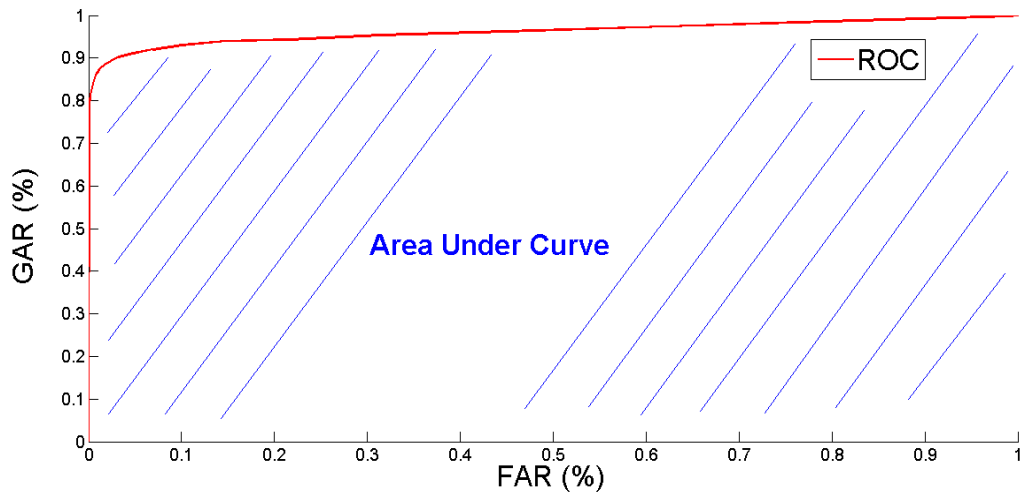


Fig. 2: ROC plot example based on FAR and GAR.

### 3 Fingerprints and Fingerprint Recognition Systems

To fulfill the main goals of this thesis the need for automatic fingerprint recognition systems is mandatory. Otherwise it would not be possible to achieve the wanted tasks. In this regard it is especially interesting to compare different matching methodologies. During the experiments it will be rewarding to have a look at the following questions: If there are ageing effects, does a certain method have special weaknesses or strong points? Does this technique maybe have advantages over other methods? But before that, there will be a detailed discussion on the used recognitions systems and the associated theoretical background.

#### 3.1 Fingerprint Recognition Methodologies

There are different approaches in fingerprint recognition systems. The most important parts in those systems are the feature extraction and matching score calculation. Basically there are certain methods to capture designated and discriminative features which represent a specific fingerprint. So as described for example in [28] the basic fingerprint recognition pipeline can be divided into imprint acquisition, pre-processing, feature extraction, matching and match score calculation.

The most obvious characteristic in terms of a fingerprint is a special model that consists of overlapping ridges and valleys. Those darker and brighter areas in a fingerprint image (looking at Fig.3) can be described in a hierarchical ordering according to [23]:

- The first level, the global level or Level 1, describes the ridge flow pattern in the image. Most of the time the mountainous region are running parallel to each other. Sometimes they reach distinct regions. These regions are called singularities or singular points and can be classified into three types: *Loop*, *Delta* and *Whorl* [23]. Loops and whorls are areas of high curvature and deltas can be characterized as regions of triangle-shaped patterns. In Figure: 4 and 5 they are marked in images of one data set.
- Having a closer look at the first level it is possible to capture some additional properties. At this more localized point of view the orientation and the frequency information of the ridge and valley structure is observable. The orientation represents the overall tendency of the ridge pattern. The frequency can be derived as



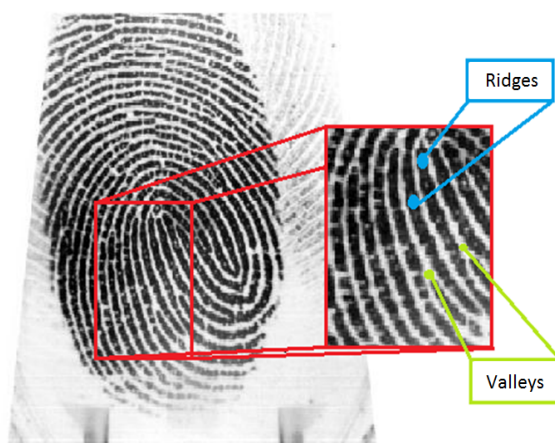


Fig. 3: Ridge and valley structure in a fingerprint image.

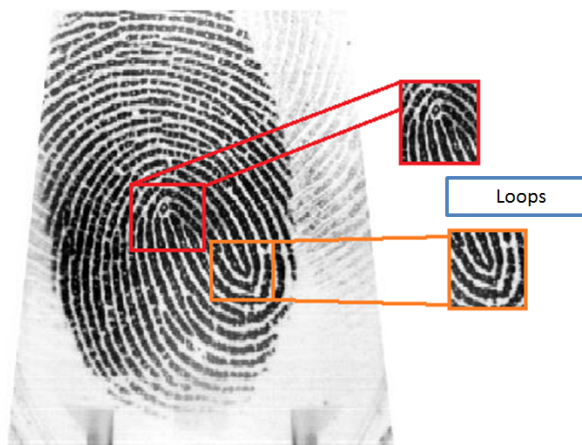


Fig. 4: Two Loops visible in a fingerprint.



Fig. 5: Delta and whorl in a fingerprint image.

inter-ridge space information. This level is a kind of level between level one and two. For this purpose it will be named as Level 1a.

- At the second level the minutiae feature information can be found. According to the fact that this level is focusing on a local point of view it seems natural that minutiae means small detail [23]. Those small details are the most important features that are used in state-of-art fingerprint recognition systems. Francis Galton was the first person to realize that these very local areas remain unchanged over an individual's lifetime [15,23]. All in all the seven most common minutiae types are *Ridge ending*, *Bifurcation*, *Lake*, *Independent ridge*, *Point or Island*, *Spur* and *Crossover* as mentioned in [23]. Ridge endings are patterns, as its name implies where a ridge terminates. Bifurcations can be compared to a junction of two ridges that looks like a Y-shaped illustration. Another pattern that is related to a bifurcation is called lake. There is a second special case of a bifurcation. After leaving the splitting point it is possible that one of the arms terminates. This event is a spur. Independent ridges are an interesting kind of minutiae because it seems they start at some point and end after some time but they never have contact to one of the neighboring ridges. If an independent ridge is a very short one it is named as Point or Island. The last minutiae type is a crossover. It can be characterized by combining four ridge parts into a single point creating a pattern that looks like a X- junction.
- The third level of fingerprint details requires high resolution fingerprint scanners of 1000 dpi and higher. At this very local level it is possible to gather attributes of certain ridges. Those include width, shape, edge contour, sweat pores, incipient ridges, breaks, creases and scars like mentioned in [23]. Due to the fact that the images in the data bases used in this master thesis have been captured with 512 and 508 dpi resolution certain algorithm using the sweat pore information are not further taken into account.

Based on the described types of features different fingerprint recognition systems are considered in this master thesis. A fingerprint matching algorithm compares two given fingerprints and returns either a degree of similarity (without loss of generality, a score between 0 and 1) or a binary decision (mated/non-mated) [23].

## 3.2 Fingerprint Recognition Systems

There is a wide spectrum of different fingerprint matcher implementations. Finding the same fingerprints is a quite difficult assignment. Due to the differences within an imprint there are a few main factors that result in intra-class variability. The most important forms of those are *displacement, rotation, partial overlap, non-linear distortion, pressure and skin distortion* and *noise* [23]. As mentioned above the used matchers are related to the described levels of imprints. Each of these methods is trying to compensate the variability. So structuring them into classes it is possible to drain 3 types:

**Minutiae based recognition systems:** The most widely used implementations extract the various types of minutiae for one imprint. This set is determined and stored in a list. But not only the exact type also the position and orientation information is saved. Regarding to the fingerprint this list is not always of the same size. During the matching process the feature set of the input image and the template are aligned. During this alignment step the best conformity of the both minutiae pairings is calculated. The higher the number of compliant pairings the better the match. The number of aligned pairs is characterized by a similarity score. The higher the score is the better is the match between those imprints.

**Ridge feature based recognition systems:** A fingerprint recognition system that belongs to that category uses the ridge and valley structure. But not level 1 is used. The before mentioned level 1a is taken into account. That means that the orientation and the frequency information of the ridges and valleys is necessary to perform the matching results. The idea is to apply those two characteristics and construct a specific feature set of the imprints and compare them afterwards resulting again in a score value.

**Correlation based recognition systems:** Those recognition system types make use of the entire, global information that can be extracted at level 1. So the global ridge and valley structure of an image itself is rotated and translated to another imprint. After using different transformations the score matching value is generated via

cross correlation.

In the present thesis four different fingerprint recognition systems will be used. Two of them will follow the common minutiae based approach. The other two are both non minutiae based. One is a correlation based and one is focusing on the detail information of the ridges and valleys within a fingerprint. As a matter of course there are a lot of different recognition system variations available. For example one special aspect of a method refers to the imprint enhancement that is performed before starting to extract the feature information. Apart from the techniques to follow, in [16] the enhancement is performed using a combination of Fast Fourier Transform (FFT) and Gabor Filters. Another concept is based on a hierarchical matching strategy. As explained in [42] it belongs to ridge feature based implementations. Based on [19] the invariant texture information of an imprint is extracted using a Gabor Filter bank once more. After this first process a two step based hierarchical matching, including the coarse and the fine matching, is performed to generate transformation parameters. The congruence of those parameters is used to calculate the matching score between two fingerprints.

### 3.3 NIST Biometric Image Software (NBIS)

The first recognition system is a minutiae based matching implementation. The *National Institute of Standards and Technology (NIST) Biometric Image Software package*, short *NBIS* is an open source algorithm<sup>1</sup>. It was implemented by *NIST* for the Federal Bureau of Investigation (FBI) and Department of Homeland Security (DHS) of the United States of America [3]. Basically it consists of two different parts. The first one is *mindtct*, the feature extractor, and the second one is *bozorth3*, the fingerprint matcher. *Bozorth3* is a matcher that is based on an implementation by Allen S. Bozorth, but is a strong modified version of it. The package that was used for this thesis is the 5.0.0 release of the NBIS setup. In the present work all experiments using this software have been performed using lossless JPEG. There are also other input types provided but the non-minutiae methods use TIFF files as input. To ensure final comparisons both minutiae based recognition systems utilize lossless JPEG as input.

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<sup>1</sup> <http://www.nist.gov/itl/iad/ig/nbis.cfm>

All following information can be looked up at [3] and the user guide that can be downloaded from the web page [2].

**Mindtct:** *Mindtct* algorithm of the *NBIS* package was used to extract the minutiae information of the input images. This program can be structured into different steps that can be looked up at [2]. The following part will give a short overview of which steps are included:

- **Generate Image Quality Maps:** Due to the fact that the input imprints may be of different quality it is necessary to analyze the input detecting degraded parts to use them later on. According to the different problems that can occur several methods have been implemented:
  - *Direction Map:* This first step is used to represent the ridge structure agreeable to the directional ridge flow. The aim is to analyze areas within the imprints that are sufficiently displaying the most significant ridges to find well describing minutiae.
  - *Low Contrast Map:* It is likely that not necessary background information is captured in an fingerprint image as well and not only the wanted ridge structure. For this purpose the second step is used to distinguish areas where too much background is pictured. In those so called low contrast blocks no minutiae detection will be performed later on.
  - *Low Flow Map:* Corresponding to low quality areas in an imprint it is possible to detect blocks where no dominant ridge flow can be found. These parts are marked as less reliable.
  - *High Curve Map:* Looking at the core and areas assigned to be a delta the curvature is higher compared to other parts of a fingerprint image. Those are also tagged as not meaningful in terms of feature extraction.
  - *Quality Map:* This map can be called the final image quality map since the quality information of the maps mentioned above are combined into one single map. Each region within the imprint is dedicated to one of five quality values. So zero is the lowest value and four the best.
- **Binarize Image:** A pixel is assigned a binary value based on the ridge flow direction associated with the block the pixel is within. If there was no detectable ridge flow for the current pixel's block, then the pixel is set to white. If there is

detected ridge flow, then the pixel intensities surrounding the current pixel are analyzed within a rotated grid [2].

- **Detect Minutiae:** During this step the binarized imprint is analyzed and ridge endings or splittings are detected.
- **Remove False Minutiae:** There are a lot of minutiae that can not be used during the matching process and due to that they must be removed. The most important ones are lakes, islands, overlaps, minutiae that are too wide or narrow and minutiae which are detected in areas of too low quality.
- **Count Neighbor Ridges:** The five nearest minutiae of each found minutia from below and the right side are detected and stored in a list.
- **Assess Minutia Quality:** Although a lot of low quality minutiae have been removed it is possible that there are quality differences within the final feature list. To enhance the robustness of the matching results the features are organized according to a dynamic threshold.
- **Output Minutiae File:** This file will be used in the following bozorth3 algorithm to perform the matching. It contains a list of all detected minutiae. Each included feature is characterized by its location in the imprint and the orientation as well as the corresponding quality information.

**Bozorth3:** The main concept of this algorithm is to read in two minutiae files constructed by mindtct, compare them and calculate a score value. The higher the match score the better the fingerprints fit together. According to [39] there are three key steps. Those provide an implementation that is rotation and translation invariant:

- **Construct Intra-Fingerprint Minutia Comparison Tables:** The first step of the matcher is responsible to calculate relative measurements for each minutia to all other minutiae in the same imprint. This computation is responsible for the invariance to rotation and translation of the algorithm.
- **Construct an Inter-Fingerprint Compatibility Table:** The comparison tables of the input fingerprints are compared to each other during this step. The idea is to find features which are fitting together according to their distances and orientation angles.
- **Traverse the Inter-Fingerprint Compatibility Table:** As its name implies, this step uses the compatibility table entries and interprets them as a graph. This graph is now traversed. The goal is to find the longest path of linked feature

entries. The length of this specific path will represent the match score. Obviously it is clear that a long path means that there are a lot of features that are shared in both fingerprints and that they are quite similar.

### 3.4 VeriFinger

VeriFinger developed by Neurotechnology [5] is the second minutiae based fingerprint recognition system in the present work. To be more precise the current available version is the *VeriFinger SDK 7.1*<sup>2</sup> that is based on the *MegaMatcher SDK* algorithm. The latest release includes algorithmic solutions that enhance the performance of the environment focusing on rolled and flat fingerprints matching, tolerance to fingerprint translation, rotation and deformation as well as adaptive image filtration [4]. So the basic concept of this recognition system is quite similar to the NBIS package. The major difference in terms of use is that this implementation is a commercial one. There is just a 30 days trial version free for download.

There are some additional information about the company and the algorithm. First of all, the company's name was changed to Neurotechnology in 2008. Before known as Neurotechnologija, founded 1990 and based in Vilnius, Lithuania, they released their first fingerprint recognition software in 1998. Basically the company is developing biometric fingerprint, face, iris, palm-print and voice identification algorithms and object recognition technology.

The fingerprint software was submitted to several international competitions. For example the *FVC2000*, *FVC2002*, *FVC2004*, *FVC2006* as well as *Fingerprint Vendor Technology Evaluation (FpVTE)* from 2003 and 2012 are well known. They received good results each time.

### 3.5 Finger-Code

The Finger-Code matcher is the first non minutiae based fingerprint recognition system applied in the current thesis. The basic concept was presented in 2002 by Ross et al. in [32] and [30]. This concept and the following Phase-Only Correlation methodology was implemented by Michael Pober during his master thesis 'Comparing performance of different fingerprint matchers by using StirMark distorted images'. The corresponding results have been presented in [17]. In this section there will be a short

<sup>2</sup> <http://www.neurotechnology.com/verifinger.html>

discussion about the main ideas and algorithmic steps.

The overall idea behind this software is to use Gabor filters, to be precise exactly 8, to derive the ridge overall orientation and frequency information. Due to that principle the implementation can be categorized as matcher belonging to feature level 1a as introduced in subsection 3.1. The most important steps are enhancement and segmentation, determine localized feature information and combine all values for one imprint in a special map, the *Ridge Feature Map* (RFM) and the final step, the matching.

**Finger-Code Enhancement and Segmentation:** The fingerprint enhancement and segmentation process contains five steps, that are accomplished one after the other satisfying a specific ordering:

- *Normalization:* This pre-processing step must be a method that does not manipulate the overall ridge and valley structure. For this purpose the variation within the gray level values is adapted using predefined mean and variance values.
- *Orientation Image Estimation:* After calculating the gradient information per pixel a least square estimate of the ridge orientation is derived. Due to the circumstance that there may be some estimation error a correction must be established as well.
- *Frequency Image Estimation:* The normalized and orientation estimated image is divided into a set of blocks. Using a window within each block the so called x-signature is derived. That means that the gray level values of the imprint are projected to the length 1. Those projection entries are used to calculate the average distances between the peaks in the x-signature. Taking the reciprocal leads to the local estimated frequency information.
- *Region Mask Generation:* This step is responsible to separate the background and the foreground information of the fingerprints applying for example a nearest neighbor classifier to achieve this task.
- *Filtering:* This final step is performed to remove noise and distortion using a Gabor filter.

**Ridge Feature Map and Matching:** As before a set of Gabor filters is applied to the fingerprint image. The big difference to the enhancement and segmentation step is a preset filter bank consisting of 8 different filter configurations. So there is a set of



8 angles starting from  $0^\circ$  to  $180^\circ$  that are applied to the enhanced image constructing a so called *Standard Deviation Map* each. Those maps are finally combined to one single map: the *Ridge Feature Map*.

The local orientation and frequency information in these ridge feature maps can be compared in the matching step. All in all a translation vector is determined to express the offset between the input images. After this vector is derived two ridge feature maps can be compared by computing the correlation value. Due to speed concerns the correlation calculation is performed in the Fourier space. Subsequently to deriving the inverse Fourier transformation the correlation result is weighted due to the overlap of the imprints.

The final score can be established by calculating the Euclidean distances between the ridge feature values of the gallery imprint and the standard deviation values of the query image. Due to the fact that the gallery imprint is rotated during the correlation process finding the best fitting position there are lists of scores available. The lower a value in the list, the better is the alignment of the two fingerprints. Thus the lowest is assigned to be the final match score.

### 3.6 Phase-Only-Correlation

Based on [25] and [18] the last recognition system is again a non minutiae based. As well as the Finger-Code basics the idea behind this implementation is also quite simple at the first look. Basically the Fourier transformation of the imprints is generated, the normalized cross spectrum is calculated and the output is transformed back and named *Phase Only Correlation Function (POC Function)*. The last step is the calculation of the band limited phase only correlation function and a specific set of highest peaks within this function are summed up generating the matching score [17].

There are a few properties of the POC function that are appealing for fingerprint matching. High discrimination capability, shift invariance, brightness invariance and high immunity to noise are the most important ones. Using those characteristics the matching process of the POC implementation can be divided into the following main steps:

- *Rotation alignment*: Due to the high sensitivity to rotation, the rotation alignment is a very crucial step. So from  $-20^\circ$  up to  $+20^\circ$  each rotated gallery image is

used for the correlation calculation. The gallery imprint that delivers the highest correlation peak will be selected for the ensuing determinations.

- *Displacement alignment:* Because of the knowledge of the correlation peak the imprints can be aligned easily and the translation displacement is corrected.
- *Common region extraction:* The third step calculates the fingerprint information that is shared by the gallery and the query image. Thus the images have been aligned if due to rotation and translation they have only necessary fingerprint information in common. Those parts that are not shared will not be necessary anymore and can be deleted.
- *Fingerprint matching:* After extracting the shared imprint parts of both input images the band limited phase only correlation function can be determined. The highest peaks are summed up to the final matching score value.

After introducing the used fingerprint recognition systems and their corresponding theoretical background there will be a detailed discussion on the investigated data bases in the following Chapter 4.

## 4 Data Sets and Ground Truth Search

For the fingerprint ageing experiments we will be using two data bases provided by the biometrics research team headed by Tieniu Tan at the Center for Biometrics and Security Research (CBSR) at the National Laboratory of Pattern Recognition (NLPR), Chinese Academy of Sciences, Institute of Automation (CASIA). Because of the necessary time gap for the research there are two data sets used and described in the following part of this chapter.

In the present work the data bases will be named:

- CASIA Fingerprint Image Database 2009 and
- CASIA Fingerprint Image Database 2013

In short terms they will be called CASIA 2009 and CASIA 2013. The first one is part of the online available CASIA fingerprint image database version 5.0 (CASIA-FingerprintV5)<sup>3</sup>. The CASIA 2013 data base includes several sub sets which have been acquired for this particular study. For this purpose some volunteers of CASIA-FingerprintV5 were chosen once more to get their fingerprint images again. The scans of both data sets have been stored in the same way, but there are some differences observable.

### 4.1 CASIA 2009

The first data set contains 1960 fingerprint images of 49 volunteers. For each volunteer, always 40 images of 8 fingers have been acquired. In total for both hands there are fingerprint scans of thumb, forefinger, second finger and third finger, 5 prints per finger.

All images have been captured by an U.are.U 4000 scanner produced by DigitalPersona. This is an optical sensor with 512 dots per inch (dpi) resolution. All fingerprint images are 8-bit per pixel gray scale images and have a resolution of 328x356 pixel. The scans are saved as bitmap image (BMP) files and are looking like shown in Figure 6.

The images of CASIA 2009 have been stored using the strategy given below:

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<sup>3</sup> <http://biometrics.idealtest.org/dbDetailForUser.do?id=7>



Fig. 6: Example image CASIA 2009 named 0403\_00030\_0003\_3\_S.bmp.

– `XXXX_YYYYA_ZZZB_B_S.bmp`

1. `XXXX`:

This first number denotes the type of sensor that has been used. In the case of CASIA 2009 an U.are.U 4000 scanner is signed as 0403. So each image in this data set starts with this number combination.

2. `YYYYA`:

These five numbers are responsible for assigning each scan to the true person the print belongs to. For example, 00230 provides the information that this image belongs to volunteer 23. It is necessary to know that the last number of the combination `A` contains important information too. This entry is in between  $\{0, 1, 2, 3, 5, 6, 7, 8\}$  and assigns the finger of the test person. So  $\{0, 5\}$  represents the thumbs,  $\{1, 6\}$  the forefingers,  $\{2, 7\}$  the second fingers and  $\{3, 8\}$  the third fingers. There is no information available if the numbering  $\{0, 1, 2, 3\}$  denotes the left hand or  $\{5, 6, 7, 8\}$  is fulfilling this task.

3. `ZZZB_B`:

The third part of the image names count the number of prints of the same finger. The `ZZZ` part is always 0 and `B_B` represents how often the finger was scanned.

4. `S`:

This character is always added to the image name but delivers no information that can be used.

## 4.2 CASIA 2013

The second data set contains 1000 fingerprint images of 50 volunteers. There are always 20 images of 4 fingers included. In total, that are for both hands fingerprint scans of forefinger and second finger, 5 prints per finger. Due to the fact that there is one additional volunteer this one will be not taken into account during the research because there is no counterpart in the CASIA 2009. So we have 980 images of 49 volunteers.

The first interesting given condition is the number of used sensors. 3 different sensor types are used to acquire the finger prints in this data set. The acquired scans are stored in 5 folders. 2 folders belong to the U.are.U 4000 and the U.are.U 4500 sensor because of two independent imprint acquisition sessions each and one folder for the fingerprints scanned by the *TCS2* (short *T2*) sensor. Each of the sensor types is produced by DigitalPersona.

The U.are.U 4000 is the same sensor type as in 2009. The U.are.U 4500 is a quite similar optical sensor with 512 dots per inch (dpi) resolution as well. The *T2* sensor is a silicon fingerprint sensor with 508 dots per inch (dpi) resolution and the imprints acquired by this sensor have a resolution of 256x360 pixel. All other characteristics of the imprints from U.are.U 4500 and *TCS2* are identical to the U.are.U 4000 from 2009. Since three types of sensors are used it is possible to see differences between the sensors looking at the following sample images represented in Figure 7.



(a) CASIA 2013 image captured by *T2* sensor.



(b) CASIA 2013 image captured by U.are.U 4000 sensor.



(c) CASIA 2013 image captured by U.are.U 4500 sensor.

Fig. 7: Some image impressions from the second data set.

Storing the images in the volunteer specific folders the same strategy as described in the CASIA 2009 section was used. There are two slight differences. On the one hand this is the total number of images for each volunteer and on the other hand the first combination  $XXXX$ . For the U.are.U 4500 it remains the same as for the U.are.U 4000 but for the T2 it is changed to 0413.

The total number of images is not the same number as in 2009 because the thumbs and third fingers are not included anymore. So only the forefingers and second fingers remain.

Actually the reduction itself of test images is not a big problem, but there is another one. It turned out that during the storing and denominations process there must be some failure.

Looking at the images within the data sets CASIA 2009 and CASIA 2013 it is not possible to find similarities between the imprints when accepting the given nomination. In fact the first slight problem is that in 2009 twice as much fingerprints have been acquired as in the younger data set 2013. This circumstance can be solved, realizing that just the images recorded from fingers 1, 2, 6, 7 remain the same in both years as mentioned at the end of section 4.2. This can be figured out looking at the data first-hand and without any computational assistance.

During the engagement with the data it was also possible to observe a second, much bigger problem: It seems that for example the imprints assigned to be from finger 1 are not identical in CASIA 2009 and 2013. So finger 1 was not the same finger 1, finger 2 not finger 2, finger 6 not finger 6 and finger 7 not finger 7 in both years. Verifying the ground truth would become the first mandatory task in this master thesis. The so called *ground truth search* fixing the described problem setting will be discussed in the following Section 4.3.

### 4.3 Ground Truth Search

According to the used name giving strategy described ahead it should not be a problem to find the images of volunteers that belong together. It became apparent that this was not that simple.

First have a look at the following Figure 8. It is named 0403\_00031\_0004\_4\_S and was gathered in 2009 representing one forefinger of volunteer 0003.



Fig. 8: CASIA 2009 image 0403\_00031\_0004\_4\_S

Now search for the same image name in the second data set. If everything fits together as presumed then it should be possible to find an image that was captured from the same finger four years later. The images using 0403\_00031\_0004\_4\_S as search keyword found in 2013 database are displayed in Figure 9.



(a) CASIA 2013 image captured by T2 sensor.



(b) CASIA 2013 image captured by U.are.U 4000 sensor.



(c) CASIA 2013 image captured by U.are.U 4500 sensor.

Fig. 9: CASIA 2013 reference images for 0403\_00031\_0004\_4\_S

Looking at the reference imprints from 2013 it seems that those are not captured from the same finger. The main reason why the images from CASIA 2009 and 2013 can not correspond together is visible in the central part of the fingerprints like displayed in Figures 10 and 11. It is obvious that the loop and delta structure is not

the same in both years. But such a huge change is not possible to occur for one and the same person and therefore the conclusion that there must be a mistake included holds. Furthermore the chosen example is not the exception but it is the common case.

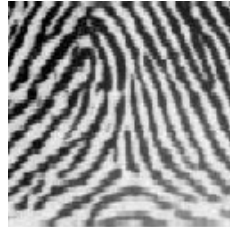
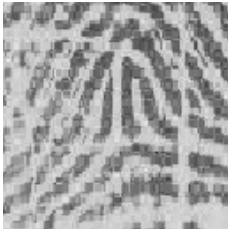
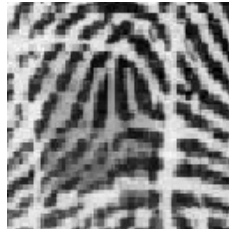


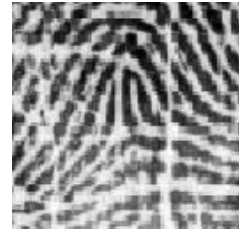
Fig. 10: CASIA 2009 image 0403\_00031\_0004\_4\_S central characteristic.



(a) CASIA 2013 image central characteristic captured by T2 sensor.



(b) CASIA 2013 image central characteristic captured by U.are.U 4000 sensor.



(c) CASIA 2013 image characteristic captured captured by U.are.U 4500 sensor.

Fig. 11: CASIA 2013 reference images for 0403\_00031\_0004\_4\_S central characteristic.

But for the experiments and ageing analysis the knowledge of the exact conformation is mandatory. Due to that fact the first part of this thesis was the ground truth search. The approach behind this step was a quite simple one:

1. Look through the images of 2013 and find the corresponding images.
2. Think about a methodology behind the sorting.
3. Use the gathered information from step 2 and validate this idea using the NBIS implementation.

It was possible to gather the information that there must have been a rearrangement of the data during the acquisition process. That means that the true corresponding



images are stored in the same volunteer folder but the naming was a different one as in 2009. So the imprints denoted as finger 1 and 2 in 2009 are saved as finger 6 and 7 in 2013, respectively vice versa. Based on this information the correct reference images for 0403\_00031\_0004\_4\_S from 2009 are stored as 0403\_00036\_... in 2013 as displayed in Figure 12. The before mentioned central characteristic is now corresponding.



(a) CASIA 2013 image captured by T2 sensor.



(b) CASIA 2013 image captured by U.are.U 4000 sensor.



(c) CASIA 2013 image captured by U.are.U 4500 sensor.

Fig. 12: CASIA 2013 true reference images for 0403\_00031\_0004\_4\_S

This new data organization will be taken into account during all following experiments and will not be named explicitly. That means imprints denoted to be acquired from finger 1 will be from this finger in all data sets no matter what year it was recorded.

The correctness of this assumption was verified in the following way. At first, for each volunteer, 2 separate test data bases have been constructed. Both contained images from 2009 and 2013. In case of the CASIA 2013 the used data base for the ground truth search is the second set acquired by the uru4000 sensor. It was randomly selected from the five data sets existing for this imprint acquisition process.

So for each of the volunteers included in the data sets the following test set composition was built. The images from CASIA 2009 were split up into fingers signed with  $\{0, 3, 5, 8\}$  and  $\{1, 2, 6, 7\}$ . There is a certain reason for performing this splitting step. While looking through the imprints within the data sets from 2009 and 2013 it became clear that the imprints labeled with  $\{0, 3, 5, 8\}$  are not included in the newer

data bases. Only the fingerprints which have been signed as  $\{1, 2, 6, 7\}$  can be found in both years. According to this information two different ground truth test setups have been constructed. In the first setup the imprints with label  $\{1, 2, 6, 7\}$  of both years are included and in the second one the fingerprints with labels  $\{0, 3, 5, 8\}$  from 2009 and the imprints from 2013 are used. The reason for constructing two different setups was to avoid to loose information that probably fingers  $\{0, 3, 5, 8\}$  have been captured in 2013 by mistake too.

It is important to mention that the ground truth calculation was performed for each volunteer independently. Because there are 49 volunteers and as explained before two basic setups, in total two time 49 single ground truth data sets are taken into account. Both will be explained into detail in the following.

The first ground truth data set will be called 'hypothesis set(s)' and the second one will be named as 'alternative set(s)'. Looking at the result Tables 2 and 3 each row is representing the results for one volunteer and the main columns are displaying the affiliation to hypothesis set(s) or alternative set(s).

According to the fact that in 2009 for each volunteer 40 imprints have been acquired and in 2013 the half number it is necessary to describe the single ground truth data sets more detailed. Splitting the older data base leads to the effect that for each volunteer 20 imprints are included in the hypothesis sets and 20 are contained in the alternatives sets. To be able to compare the fingerprint information from both years it is obvious that the imprints from 2013 are used too. So those fingerprint images are added to the hypothesis sets and the alternative sets as well. Due to the fact that in the newer data base for each volunteer 20 imprints are included, it is clear that after adding these data to the hypothesis and alternative sets, 40 images for each user are available. So summarizing the ground truth experimental setup the following situation can be stated:

– 2 **Basic setups:**

- *Hypothesis sets for each volunteer:*
  - \* 20 imprints from 2009 denoted as  $\{1, 2, 6, 7\}$  in the original 2009 data base
  - \* 20 imprints from 2013 denoted as  $\{1, 2, 6, 7\}$  in the original 2013 data base
- *Alternative sets for each volunteer:*
  - \* 20 imprints from 2009 denoted as  $\{0, 3, 5, 8\}$  in the original 2009 data base
  - \* 20 imprints from 2013 denoted as  $\{1, 2, 6, 7\}$  in the original 2013 data base

Basically the main idea to verify the assumption is quite intuitive. After calculating the match scores for each of the 98 data sets the values are split into two different parts. The first one are the genuine scores and the other one are the impostor scores. Then the average genuine and impostor values are derived. The reason for this step is that the inter-class and intra-class variability are used to gather the final solution. So looking at one of those sets that contains images which belong together the following result should be obtainable. The average genuine score should be significantly higher than the average impostor scores. It is necessary that the average scores are calculated for each finger and not only for the total number of scores. Otherwise a comparison with the corresponding alternative data set is not correct using the inter-class and intra-class variability.

For example we will focus on one specific finger to explain in more detail what exactly is done. So the finger will be finger number 7 of volunteer 0003. The averaged matching scores are displayed in Table 1.

<b>data set</b>	<b>av. gen. score</b>	<b>av. imp. score</b>
hypothesis set	99.5	9.4
alternative set	79.8	10.73

Table 1: Average genuine and impostor scores calculated from volunteer 0003.

In Table 1 the relationship between inter- and intra-class variability is clearly observable. First, due to the higher impostor score for the alternative set it can be stated that the inter-class variability is slightly higher than in the hypothesis case. The fact that the intra-class variability is lower at the same time, observable in the lower average genuine score, confirms the assumption that the finger names must have been switched.

In the following Tables 2 and 3 the evaluation of the genuine and impostor scores as described above and the difference in inter-class and intra-class variability between the hypothesis and alternative set is displayed. To be able to display the results combined for each volunteer the average genuine and impostor score of each finger was

used to calculate a mean average genuine and impostor score. The terms mean average genuine and impostor score will not be used explicitly. These mean values will be simply named average genuine and impostor scores in Tables 2 and 3.

So looking at Tables 2 and 3 it seems clear that for most volunteer sets the same outcome can be shown as for the single finger before. The genuine scores are always higher in the before described hypothesis sets. So the hypothesis, that there has been a failure during naming the imprints of 2013, can be verified in the expected manner. Besides, the average impostor scores for the alternative data sets are not always higher than in the hypothesis test sets. The reason for this circumstance is the different acquisition conditions. There are a few very important distortions included that will be discussed in the following Section 4.4 in more detail.

#### 4.4 Acquisition Conditions

Beyond the described mixture of the imprint naming, different acquisition conditions have been given during the data acquisition process. The most important differences will be discussed in the following list:

- Rotated imprints displayed in Figures 13 and 14.



Fig. 13: Different rotated positions.

- Different vertical and horizontal positions displayed in Figure 15.
- Different pressure during the acquisition and no sensor platens cleaning displayed in Figure 16.

volunteer	hypothesis sets		alternative sets	
	av. gen. score	av. imp. score	av. gen. score	av. imp. score
0000	16.24	7.66	16.10	7.86
0003	88.48	8.40	49.70	8.86
0007	26.88	6.61	25.58	6.60
0011	53.08	7.59	27.69	7.78
0023	25.05	7.63	24.99	8.19
0025	55.06	6.29	34.81	6.25
0052	74.34	8.54	44.98	7.89
0069	18.89	6.57	16.48	6.66
0097	29.13	8.24	24.60	8.53
0128	28.80	8.05	21.17	8.01
0130	44.61	7.38	34.07	7.59
0131	21.23	7.25	16.65	7.47
0149	54.33	6.68	25.89	7.02
0161	30.15	6.80	24.93	6.74
0174	37.32	6.72	28.17	7.64
0178	41.35	7.73	24.74	7.75
0189	32.96	6.80	28.26	6.89
0198	30.46	6.81	15.33	6.41
0200	30.23	7.41	23.94	7.20
0210	78.50	9.37	39.68	8.98
0211	42.81	7.22	22.98	7.01
0217	28.16	4.92	22.04	6.25
0227	22.40	6.48	15.52	6.23
0305	36.06	7.56	24.88	7.26
0357	27.79	4.74	20.00	5.73
0872	48.01	6.25	31.91	6.40

Table 2: First part of the round truth verification of all volunteer data sets.

volunteer	hypothesis sets		alternative sets	
	av. gen. score	av. imp. score	av. gen. score	av. imp. score
0890	38.98	7.32	38.81	7.11
0944	29.50	6.99	28.95	6.73
0952	56.17	7.90	37.51	8.27
1004	51.39	7.69	31.46	7.48
1006	65.19	7.40	27.38	7.09
1014	69.31	8.53	38.43	8.11
1019	54.69	8.10	38.11	7.59
1025	55.02	6.8	36.05	6.73
1036	45.03	8.79	34.06	8.11
1049	48.33	7.56	33.98	8.01
1052	40.80	6.50	33.33	6.16
1053	78.34	8.18	43.96	7.00
1054	28.07	8.65	24.37	8.49
1062	42.60	8.94	32.20	8.51

Table 3: Second part of the round truth verification of all volunteer data sets

- Imprints with skin distortion displayed in Figure 17.
- Moistened fingerprints displayed in Figure 18.
- Dried fingerprints displayed in Figure 19.
- Imprints with certain artifacts displayed in Figure 20. In particular the interest lies on block based (ir)regularities located in the center of the acquired fingerprints. Those artifacts can be observed in nearly all images using an *U.are.U* sensor. The results are displayed in the following Table 4. The percentages have been retrieved counting the number of imprints containing those blocks and dividing these values by the total number of imprints in each data set.

It seems that not in all images the artifacts are contained. In fact because of high pressure, low quality or dried finger imprints it was not possible to find those blocks visible to the naked eye. But it can be said that it must be a sensor specific characteristic because in the *T2* images the same feature could not be observed.



Fig. 14: Different rotated positions.



Fig. 15: Different vertical and horizontal positions.

- Other characteristics are displayed in Figure 21. These special tees can be observed at specific volunteers that are about 2.8% of all images in CASIA 2009. In CASIA 2013 the same effects appear in  $T2$  in 3.6%, in *uru4000\_1* in 3.77%, in *uru4000\_2* in 3.97%, in *uru4500\_1* in 3.57% and in *uru4500\_2* in 2.85% of the imprints. To be more precise, those characteristics can be assigned to certain volunteers. For example, the structure that can be observed in the right image in Figure 21 appears just for one volunteer, namely 0944.

#### 4.5 Comments on Notation and Experimental Settings

Based on the before described data sets it is necessary to introduce some shortcuts and designations that will be used during the ageing experiments. So as mentioned above 49 volunteers will be taken into account. For each volunteer images of 4 fingers

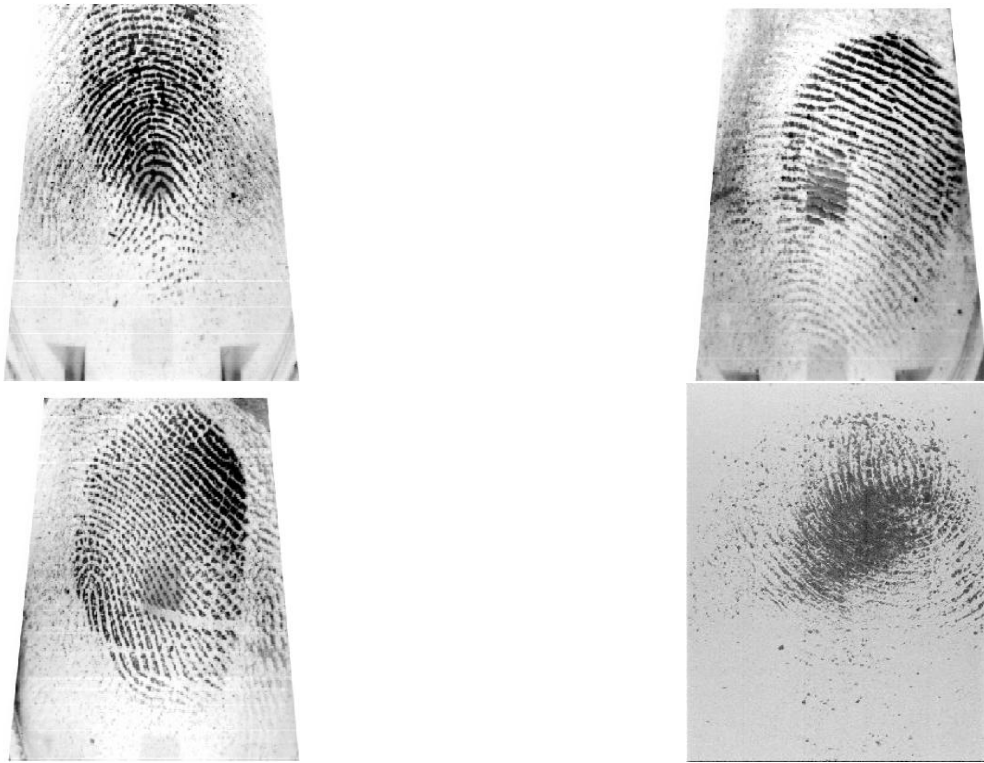


Fig. 16: Different pressure and no sensor platens cleaning.

have been acquired. That is why 196 fingers are taken into account in total. Displaying the data sets it is possible to characterize them as follows:

- **Single Data Sets:** Those sets are including 196 fingers and 5 images each. The imprints are corresponding to the sensor types used during the acquisition process. So each single set is containing 980 images. They will be called
  - *finger1267*: That is the data set from 2009 which only contains the fingers signed as 1, 2, 6, 7 because of the information gathered in the previous section 4.3.
  - *T2*,
  - *uru4000*<sub>1</sub>,
  - *uru4000*<sub>2</sub>,
  - *uru4500*<sub>1</sub> and
  - *uru4500*<sub>2</sub> representing the 5 single sets from 2013.
- **Crossed Data Sets:** Those contain 196 fingers again, but 10 imprints from each finger because the images from 2009 and 2013 are included. The first five images





Fig. 17: Skin distortion.

data set	block artifacts (in %)
CASIA 2009	88.82%
CASIA 2013 T2	—
CASIA 2013 uru4000 <sub>1</sub>	80.52%
CASIA 2013 uru4000 <sub>2</sub>	77.65%
CASIA 2013 uru4500 <sub>1</sub>	81.02%
CASIA 2013 uru4500 <sub>2</sub>	66.93%

Table 4: User exhibiting block artifacts.

are always from the older data set and the remaining are from 2013. As described in Section 4.3 a manually denomination adjustment has been performed to ensure that the imprints from both years belong to the same finger. Due to the fact that in 2013 5 sets are existing, also 5 crossed sets have been established. Those data sets will be called

- *finger1267 T2*,
- *finger1267 uru4000<sub>1</sub>*,
- *finger1267 uru4000<sub>2</sub>*,
- *finger1267 uru4500<sub>1</sub>* and
- *finger1267 uru4500<sub>2</sub>*.

Overall, there are 6 single data sets including 980 imprints and 5 crossed ones containing 1960 images.

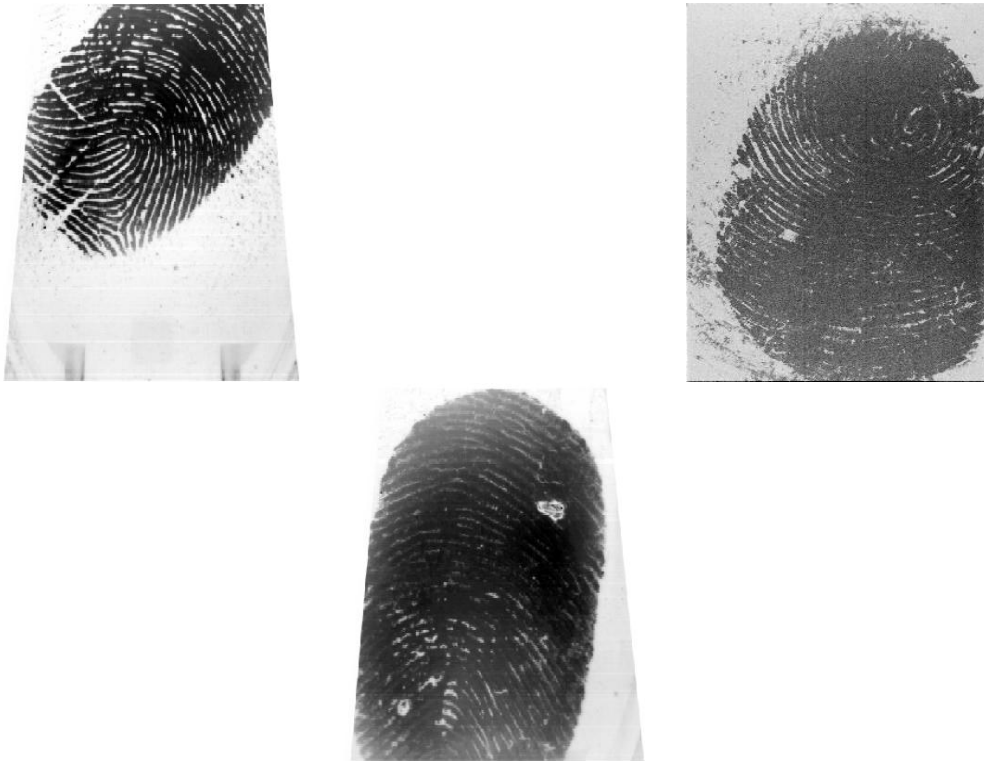


Fig. 18: Moistened fingerprints.

According to the described denomination in Section 4.1, an adaptation will be used during this master thesis. The new notation is based on the total number of used fingers and the number of how much imprints are given for each finger. Therefore the imprint names are constructed using the following scheme  $X\_X$ . The first part denotes the name of the finger. It will be a number from 1 to 196 because in total 196 fingers will be used. The second part describes the number of the imprint. This index value can be a number from 1 to 5 in the single data sets or from 1 to 10 in the crossed data sets. In case of the crossed data sets the index numbers from 1 to 5 are used for the single data set imprints from 2009 and those from 6 to 10 for the corresponding fingerprint images from 2013. So for example the image 0403\_00031\_0004\_4\_S from 4.3 will be denoted as 5\_5.

Besides, the following abbreviations will be used for the different fingerprint recognition systems from now on.

- **NBIS** - for the NIST Biometric Image Software (mindtct and bozorth3)



Fig. 19: Dried fingerprints.



Fig. 20: Imprints with block artifacts located in the center.

- **NEURO** - for the VeriFinger matcher
- **FC** - for the Finger-Code implementation
- **POC** - for the Phase-Only-Correlation matcher

The same applies to the specific data set names that have been introduced above. To minimize the space that is needed to describe the following tables and figures, abbreviations have to be introduced. They will be used from now on during the whole thesis.

- 2009 *data set*:
  - **A**: finger1267
- 2013 *data sets*:
  - **B1**: T2
  - **B2**: uru4000<sub>1</sub>



Fig. 21: Other characteristics.

- B3: uru4000<sub>2</sub>
- B4: uru4500<sub>1</sub>
- B5: uru4500<sub>2</sub>
- *crossed data sets*:
  - C1: finger1267 T2
  - C2: finger1267 uru4000<sub>1</sub>
  - C3: finger1267 uru4000<sub>2</sub>
  - C4: finger1267 uru4500<sub>1</sub>
  - C5: finger1267 uru4500<sub>2</sub>

So each time when an 'A' is used as description the data set from 2009 is discussed. 'B' denotes always a data base from 2013 and 'C' one of the crossed data sets.

#### 4.6 Test Procedure

At the end of this Chapter 4 there will be a short discussion on the used test procedure.

In the first case the question was about the ground truth search. As described in Section 4.3, the abnormality within the data sets could be corrected. The second important test procedure based on the match score calculation is the analysis regarding to ageing effects. The results of this analysis will be discussed in the next Chapter 5, but before it is necessary to display the methodology of the used match score calculation.

**Ageing experiments procedure:** The main procedure for the performance evaluation of the data sets 2009, 2013 and 2009 vs. 2013 is based on the procedure used in all four Fingerprint Verification Contests (FVC). This international competition is focused on fingerprint verification software and was changed to FVC-onGoing, a web-based online evaluation campaign. In this thesis the reference competition was the FVC-2004 [1].

Basically can the matches be partitioned into the genuine and the impostor matches. As described in [1] there are two different methods that are used to calculate the necessary number of genuine and impostor match scores.

*Genuine Tests:* Performing the genuine matches calculations corresponds to the *False Rejection Rate (FRR)*. For computing these matching scores each sample image in a data base is matched against each remaining imprint of the same finger. It is important to mention that the symmetric match calculations have not been performed to avoid correlation within the overall score information.

The total number of computed genuine values is dependent to the specific data set:

- In the 2009 and the 2013 data set there are 196 fingers included. Each finger has been captures 5 times. Therefore the number of genuine scores can be derived as follows:

$$\frac{5 * 4}{2} * 196 = 1960.$$

- In the combined data set 2009 vs. 2013 there are 10 imprints per finger. So the number of performed genuine matches can be calculated using the same formula and achieve the following result:

$$\frac{10 * 9}{2} * 196 = 8820.$$

*Impostor Test:* Those calculations have been performed to compute the *False Acceptance Rate (FAR)*. Basically the first imprint of each finger is matched against the other first imprints of the other fingers. Once again to avoid correlation the symmetric calculations are not executed. Looking at the data and the description of the data sets in part 4 the low quality of the input data must be taken into account. Therefore, there have been additional impostor score calculations. That means that not only the first image of each finger was matched against the other first imprints. The same

procedure was used several times but instead of the first imprints, also the second, the third and so on imprints were used during this calculation. So for each calculation the index part of the image names is fixed and the part denoting the finger passes from 1 to 196. The number of all impostor matches can be derived like follows:

- The 2009 and 2013 data sets provided the following total number of impostor scores:

$$\frac{196 * 195}{2} * 5 = 19110 * 5 = 95550.$$

- The combined data set 2009 vs. 2013 yielded in a total number of

$$\frac{196 * 195}{2} * 10 = 19110 * 10 = 191100.$$

impostor scores.

It is important to mention that the 19110 impostor matches are calculated for one imprint. Due to the fact that there are 5 imprints each in the single data sets and 10 imprints each in the crossed ones, the total number of impostor scores can be derived by multiplication with factor 5 or 10. Regardless of whether genuine or impostor score calculation is performed, the used methods are also designed to avoid symmetric matches as mentioned before. So for example when imprint 4 of finger 1 is matched against imprint 3 of finger 2 then it is not possible to perform the match image 3 of finger 2 against image 4 of finger 1 later on. Apart from avoiding correlation the computation time can also be reduced because the number of matches that must be calculated is decreased as well.

The FVC matching score calculation concept is valid to calculate all wanted genuine scores, but in terms of the impostor scores it is necessary to update the scheme for some additional score values concerning the crossed data sets. The reason therefore was introduced in the aforementioned Section 4.5. The indices used in the crossed data set - index 1 to 5 for the 2009 fingerprint images and 6 to 10 for the 2013 imprints - ensure a well structured organization of the the data. Despite that fact, this organization also is responsible therefore that according to the before introduced impostor score calculation scheme it is not possible to gather any information about matching from imprints from 2009 against 2013 fingerprints. For example there will be never a matching from images marked with index 2 against imprints signed with index 9.

But these impostor scores including the time span information are very important for the ageing analysis. For this purpose there are additional impostor scores that have to be calculated for the crossed data sets.

Basically the goal will be to calculate the same amount of impostor scores as can be derived using the FVC concept. As displayed in Equation 1 above it is possible to derive 191100 impostor matches using the FVC scheme. With respect to the calculation time - especially for the non-minutiae methods - and the needed ageing match information, the same number of impostor scores including the time span is sufficient enough to prove or disprove the tasks of this master thesis. For each imprint signed with index 1 the impostor matching score against those images marked with 6 will be calculated. The same procedure is performed for index tuple 2/7, 3/8, 4/9 and 5/10. So in total for 196 imprints the matching scores against 195 images were calculated five times:

$$196 * 195 * 5 = 38220 * 5 = 191100.$$

All in all 382200 impostor scores are derived for each crossed data set. Due to the circumstance that in the crossed data sets the size of imprints per finger is doubled compared to the single sets, it is necessary to take this difference into account during the evaluation of the experiments. Additionally it is important to take care that the number of ageing including matching scores and those which are not is balanced as well. This will be described in Section 5 in more detail.

## 5 Ageing Experiments

### 5.1 General Information

Within this chapter the experimental settings and results concerning performance and ageing evaluation of the fingerprint recognition systems described in Chapter 3.2 will be presented. The following experiments have been necessary to be able to compare the different fingerprint recognition systems and methodologies based on the specific used data sets. Basically the main conceptual idea displayed in Section 4.6 can be summarized shortly as follows. Computing the genuine and impostor scores of the data sets leads to different characteristic values like *EER* or the *ROC* based on each input data base.

The consideration of the results enables some first interpretations regarding the main question, the search for possibly existing observations called ageing effects. For this purpose the results of each matching method will be displayed at first one after the other and at the end of this chapter there will be a comparison based on inter-matcher abnormality if detectable.

Before the results will be displayed it is mandatory to talk about a very important fact regarding the different sizes of the data bases that have to be taken into account. As mentioned in the previous Chapter 4 there are data sets that contain 980 imprints, the so called single data sets and the crossed data bases that contain 1960 images. Due to the different number of fingerprints the impostor and genuine match score distributions are also of a different size. Therefore the behavior of the distributions may be different in the single and crossed data sets. So the exact comparison in case of the *EER* values might not be possible as well.

Apart from the mentioned imbalance in terms of the score amount variability it is very interesting to have a first look at the average genuine and impostor scores. If there are some fluctuations detectable this could indicate some measurable effect, which have to be discussed in the following investigations. Furthermore some information can probably be gathered, in order to refine the study based on the score distributions. That means that if for example a low difference in the average values is present then more detailed experiments will be performed to retrieve additional knowledge. The average genuine and impostor score calculation is based on the crossed data sets because those include the 4 year time span. For this purpose a separation between time span including and excluding average scores will be done. The results are displayed



in Tables 5 and 6. The names of the columns are abbreviations which are explained in the following:

- *AGW* - *average genuine scores without time span information*: As the name implies only genuine scores from matches of 2009 and 2013 to the same years are used.
- *AGI* - *average genuine scores including time span information*: Genuine scores from matches which have been derived using 2009 data against 2013 imprints are taken into account.
- *AIW* - *average impostor scores without time span information*: Only impostor scores from matches of 2009 and 2013 to the same years are applied.
- *AII* - *average impostor scores including time span information*: Impostor scores derived by using 2009 data and matching them against 2013 imprints are taken into account.

<b>crossed data set</b>	<b>AGW</b>	<b>AGI</b>	<b>AIW</b>	<b>AII</b>
NBIS				
<i>C1</i>	64.44	34.14	6.71	6.46
<i>C2</i>	64.28	29.06	6.64	6.38
<i>C3</i>	58.80	31.81	6.80	6.63
<i>C4</i>	67.22	34.53	6.57	6.46
<i>C5</i>	65.69	35.02	6.55	6.45
NEURO				
<i>C1</i>	504.14	238.40	0.0037	0.0020
<i>C2</i>	534.21	219.20	0.0060	0.0050
<i>C3</i>	486.68	242.24	0.0173	0.0129
<i>C4</i>	530.97	238.39	0.0090	0.0036
<i>C5</i>	497.49	236.06	0.0134	0.0044

Table 5: Average genuine and impostor scores of the crossed data sets using the minutiae based fingerprint recognition systems.

<b>crossed data set</b>	<b>AGW</b>	<b>AGI</b>	<b>AIW</b>	<b>AII</b>
FC				
<i>C1</i>	113.34	112.38	102.19	102.08
<i>C2</i>	110.98	106.90	103.29	102.03
<i>C3</i>	109.36	107.36	102.83	102.07
<i>C4</i>	110.02	107.02	102.33	102.06
<i>C5</i>	109.91	106.68	101.94	102.06
POC				
<i>C1</i>	0.2659	0.1118	0.1096	0.1087
<i>C2</i>	0.2737	0.1535	0.1105	0.1103
<i>C3</i>	0.2677	0.1648	0.1101	0.1104
<i>C4</i>	0.2920	0.1727	0.1109	0.1112
<i>C5</i>	0.2713	0.1697	0.1127	0.1119

Table 6: Average genuine and impostor scores of the crossed data sets using the non minutiae based fingerprint recognition systems.

In Tables 5 and 6 it is clearly observable that the time span excluding genuine scores and most of the time span excluding impostor scores are higher compared to the other case. This indicates a probably existing ageing effect. Especially for the genuine scores a high difference between time span in- and excluding consideration is present for all data sets and fingerprint recognition methods. The similar observation for the impostor scores is not that distinctive. Based on these first results it is possible to introduce some expectations concerning the following analysis for the different fingerprint recognition systems. Because there is a very clear fluctuation between the average genuine scores and almost stability for the impostor scores there must be some measurable variance in  $EER$ ,  $AUC$ ,  $FAR_{100}$ ,  $FAR_{1000}$  and  $Zero FAR$  comparing single and crossed data sets. Regarding the fact that for the minutiae based recognition systems the described average score differences are larger as for the non-minutiae based ones it is also assumable that the measurable effects will be more distinct for the first class. According to the fact that the amount of impostor scores for the crossed data sets is much bigger compared to the single data sets and because there

was hardly no variance looking at the average scores, it is necessary to use different analysis methods to get more detailed information on the security based aspect. For the genuine scores no special investigations are taken into account because it is very likely that the degradation of the scores is an explicit evidence of a present effect which is caused by their distributions. Basically there will be four different ways to analyze the score information for the crossed data:

- **All Scores (AS):** For the first method all scores are used. Getting a first impression of how the fingerprint recognition systems behave on the given data is the aim. The other methods will be used for a more detailed discussion.
- **Without Ageing related Information (WA):** For this method the used scores are restricted to those impostor ones which are not containing any matching information from 2009 to 2013.
- **Only Ageing influenced Scores (OA):** Here the opposite of method WA will be performed. So only impostor scores which are including any time span information are taken into account.
- **Half ageing influenced and Half not (HH):** As its name implies is this analysis method a combination out of WA and OA. How the used scores are chosen will be described below.

**Without Ageing related Information (WA):** To perform a comparable analysis of the varying values, the impostor results of the crossed data sets are split. For the following method the impostor matches including ageing related information are not taken into account. So only those scores containing matching information from 2009 against 2009 and 2013 against 2013 are used.

At first the performance measures are then calculated for the 2old3new and 3old2new data sets. That means that on the one hand, 2 imprints of original 2009 data and 3 out of the newer 2013 imprints are used, and on the other hand, 3 from 2009 and just 2 images from 2013. To be more precise, in 2old3new the images marked with index 1, 2, 8, 9, 10 are considered to calculate the  $EER$ ,  $FAR_{100}$ ,  $FAR_{1000}$ , average genuine scores and so on. In the 3old2new case the remaining imprints 3, 4, 5, 6 and 7 are deployed. There will be separate result tables for those special calculation outcomes in the following Sections 5.2, 5.3, 5.4 and 5.5.

In addition to the fixed split analysis a randomized method will be used. The randomized method in this case is quite similar to the method above. The idea is once

again to construct a set of matching scores for 980 images included. Therefore a random generator picks 5 index numbers out of 10. Those imprints that are signed with those indices are then used to calculate *EER* and all other values. The selection of the 980 images is performed 252 times because that is the number of possibilities to pick 5 values out of 10. This randomization is performed for the genuine and impostor scores. For each sampling the calculated *EER* and other characteristic performance values are stored and after all numbers have been derived they are averaged to get one representative. They will be presented in tables in the following sections of this master thesis, which are used to discuss the results for each fingerprint recognition system.

**Only Ageing influenced Scores (OA):** As introduced before the second analysis method is basically using only those impostor scores which include matches from 2009 images against imprints acquired in 2013. Therefore it is clear that the single data sets and the calculated results are the same as for the WA and for the HH method. But for the crossed data sets it was also mandatory to perform a size adaptation to be able to derive comparable performance measures like the *EER*.

The 2old3new and 3old2new idea that was used to get a first impression of how the score distributions and characteristic values will probably behave, was not performed for this method. Just the randomized split analysis was taken into account. There were a few differences compared to the randomization as used for the WA case. Because the imprint indices are mixed much more as explained in Section 4.6 the random selection of the matching scores had to be adapted. So the random generator was not picking a special set of 5 index numbers out of 10 as before in Section 5.1. This time the random generator was used to take care that the same number of genuine and impostor scores are selected as used in the single data sets. Therefore the entire sets of genuine and impostor scores were shuffled and the first 1960 genuine and 9550 impostor scores were selected for the following calculation of the performance indicators. So always a fifth of genuine and half of the impostor scores were taken into account. This random selection was performed repeatedly 252 times to ensure the same number of values which are used to derive the mean characteristic values as in the WA case.

Of course it is possible that there could occur some weaknesses. For example it could be that the number of images included in the selected set of scores is not exactly 980.

For sure this possibility is a valid one. But it is not very likely that the deviation is a significant one. Especially the outcomes of the calculations reveal that the differences between the splitted data values and complete crossed ones is not very big. This observation can be looked up in the Sections 5.2, 5.3, 5.4 and 5.5.

**Half ageing influenced and Half not (HH):** The third method is using the half number of ageing related impostor scores on the one hand. On the other hand the second half is based on scores which are not including any time span information. So the set up is basically very similar to the WA and OA case.

First of all 95550 ageing related and 95550 non ageing related impostor scores are needed. For this purpose the scores used in WA and OA are split into two halves according to the randomized selection, described in Section 5.1. The first halves of those splitted matching sets are combined to get the required number of 191100 impostor and 8820 genuine scores. After this step the calculation procedure for the characteristic values is performed using those 191100 values and the selected genuine values. It is important to mention that the calculation is repeated 252 times to use differently selected score sets. So 252 *EER* values, average impostor scores and so on are available. The final performance values for each set are the mean values of those 252 single outcomes.

Of course it is necessary to perform a size adaptation as well. For this purpose only 95550 impostor scores are needed. That means only a quarter of the ageing related and a quarter of the non ageing related scores is selected. The selection process is the same as before apart from the fact that as mentioned before just a quarter of both types of impostor scores is chosen. The genuine scores are also split using 1960 of the entire genuine values randomly. As before this selection was repeated 252 times. The mean values of the different characteristic values will be displayed in the following Sections 5.2, 5.3, 5.4 and 5.5 as final results.

## 5.2 NBIS

As introduced in Section 5.1 there are three analysis methods included for each fingerprint matcher. The corresponding results will be displayed in the same order as they have been described above.

For this purpose all derived matching scores will be used at first for the AS analysis. In the following Tables 7 and 8 the corresponding results are displayed. It is clearly

observable that there are some interesting effects. Comparing the results for single and crossed data sets several increasing and decreasing tendencies can be described. The crossed data bases' *EER* is between 3.68% and 7.22% higher as for those data bases including imprints from one specific year. For  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* it is certainly possible to detect an increase. This increase is conforming the overall *EER* tendency. Furthermore, the average genuine scores and the *AUC* values indicate an decrease for the crossed data sets whereas the average impostor scores and the *Zero FRR* remain stable. Those observations are indicating that the genuine scores are mainly responsible for a detectable shift of the genuine scores. There will be some more precise discussion on this issue in the following WA, OA and HH analysis cases. Because the impostor scores are corresponding to the security aspect of biometric systems there will be some further experiments to get some more detailed information about their behavior. The results of those experiments will be discussed and displayed in the present Section 5.2.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
<i>A</i>	7.42	0.9622	64.03	6.78
<i>B1</i>	8.95	0.9559	64.87	6.64
<i>B2</i>	8.17	0.9662	64.63	6.53
<i>B3</i>	9.07	0.9617	53.69	6.83
<i>B4</i>	5.96	0.9768	70.56	6.37
<i>B5</i>	7.30	0.9604	67.30	6.34
<b>crossed sets</b>				
<i>C1</i>	12.63	0.9243	47.61	6.58
<i>C2</i>	14.76	0.9146	44.71	6.51
<i>C3</i>	14.37	0.9230	43.81	6.71
<i>C4</i>	13.18	0.9291	49.06	6.52
<i>C5</i>	13.46	0.9252	48.65	6.50

Table 7: Characteristic individual performance values of NBIS matching including EER, AUC, average genuine score and average impostor score using all scores.

data set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>single sets</b>				
<i>A</i>	0.1341	0.2066	0.3382	1.0
<i>B1</i>	0.1520	0.2188	0.3892	1.0
<i>B2</i>	0.1336	0.1877	0.3535	1.0
<i>B3</i>	0.1882	0.2586	0.8112	1.0
<i>B4</i>	0.1071	0.1571	0.9178	1.0
<i>B5</i>	0.1367	0.1887	0.9719	1.0
<b>crossed sets</b>				
<i>C1</i>	0.2591	0.3547	0.5717	1.0
<i>C2</i>	0.2918	0.3782	0.5886	1.0
<i>C3</i>	0.2916	0.3764	0.8701	1.0
<i>C4</i>	0.2507	0.3459	0.9726	1.0
<i>C5</i>	0.2497	0.3426	0.9912	1.0

Table 8: Characteristic individual performance values of NBIS matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR using all scores.

**NBIS WA Method:** At first the individual results for the *NBIS* matching scores are displayed in Tables 9 and 10 for the WA method. The first impression which is observable in Table 9 is on the one hand the fact that the *EER* for the single data sets varies between 5.96% and 9.07%. On the other hand, within the crossed data bases, the fluctuation is around 2% from 13.01% to 15.35%. So in absolute terms an increase of about 4% to 7.5% can be detected. If the increase is considered relatively then it can be measured between 145.36% (B1 and C1) and 226.00% (B4 and C4). Furthermore it is possible to detect interesting effects in Table 10. The *Zero FRR* outcomes are always located at 1.0 for all NBIS results. The *Zero FAR* values for the single sets B3, B4 and B5 are much higher compared to the other three single data bases. This is an interesting observation because the trend from  $FAR_{100}$  to *Zero FAR* values is uniquely increasing. That the *Zero FAR* values for the single sets B3, B4 and B5 are much higher can also be detected looking at the corresponding crossed data

sets. For the crossed sets another important cross-sensor effect is valid. The  $FAR_{100}$  and  $FAR_{1000}$  values are higher for crossed data including the same sensor compared to those data sets which contain cross-sensor acquired imprints. All in all an identical trend for all calculated values can be stated as introduced in Table 7 and 8. So the assumption that for EER, AUC,  $FAR_{100}$ ,  $FAR_{1000}$  and Zero FAR a clearly measurable fluctuation is present can be verified in this first analysis method. The same is valid for the stability of average impostor scores and the Zero FRR.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	13.01	0.9221	47.61	6.78
<i>C2</i>	15.35	0.9119	44.71	6.64
<i>C3</i>	13.51	0.9212	43.81	6.80
<i>C4</i>	13.47	0.9281	49.06	6.57
<i>C5</i>	13.69	0.9242	48.65	6.55

Table 9: Characteristic individual performance values of NBIS matching including EER, AUC, average genuine score and average impostor score using the WA method.

Because of the circumstance that the number of images is doubled in those crossed data sets it is necessary to take the different number of imprints into account. So as mentioned in the introduction of this method in Section 5.1 two different methods are used. The split method using 2 fixed split strategies and the randomized methodology.

So, it is interesting to observe that the influence of the doubled number of imprints contained in the year crossed data is not that outstanding in the fixed split data sets. These results can be looked up in Tables 11, 12 and Tables 13 and 14. At first there will be a discussion about the 2old3new results. The *EER* varies between 12.40% and 14.88% in this case. The average impostor score and the *AUC* values remain almost



data set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	0.2591	0.3547	0.5611	1.0
<i>C2</i>	0.2918	0.3909	0.5815	1.0
<i>C3</i>	0.2916	0.3905	0.8701	1.0
<i>C4</i>	0.2507	0.3459	0.9726	1.0
<i>C5</i>	0.2642	0.3426	0.9912	1.0

Table 10: Characteristic individual performance values of NBIS matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR using the WA method.

stable but the average genuine score is a little bit higher as displayed in Table 11. In Table 12 can be looked up that the changes in case of  $FAR_{1000}$ , *Zero FAR* and *Zero FRR* can be neglected because they are very small. But the cross-sensor related effect concerning the  $FAR_{100}$  and  $FAR_{1000}$  values like described above can be confirmed. It seems that this could be an impact of the sensor type, but it must be verified using the other recognitions implementations as well. All in all, there is no big difference between the 2old3new results and the original crossed data set results. It is possible to detect small variances depending on the data sets but this is the only change. However the overall results of 2old3new seem to be a little bit better because for example the *EER* is lower and the average genuine score is higher then in the not splitted data sets.

The same comparison as before can be done for the second split set 3old2new. In Table 13 it is clearly visible that *EER* values vary from 13.59% to 15.77%. Hence, those values are all slightly higher than in the complete crossed sets. The average impostor scores are slightly higher for all data sets. The average genuine scores for C1, C2 are a little bit lower and for C3, C4 and C5 a little bit higher than displayed in Table 13. As for the *AUC* values from 2old3new are the outcomes for 3old2new lower as well compared to the complete data sets. In Table 14 it is possible to observe that the *Zero FAR* is revealing a slightly different situation as detectable for the entire crossed

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>crossed sets 2old3new</b>				
<i>C1</i>	12.40	0.9247	49.19	6.53
<i>C2</i>	14.88	0.9146	45.71	6.54
<i>C3</i>	13.95	0.9250	42.48	6.66
<i>C4</i>	12.41	0.9346	51.57	6.45
<i>C5</i>	12.93	0.9276	50.65	6.42

Table 11: Characteristic individual performance values of NBIS matching including EER, AUC, average genuine score and average impostor score concerning the splitted data 2old3new.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>crossed sets 2old3new</b>				
<i>C1</i>	0.2515	0.3280	0.5528	1.0
<i>C2</i>	0.2887	0.3673	0.5640	1.0
<i>C3</i>	0.2969	0.3811	0.8831	1.0
<i>C4</i>	0.2354	0.3140	0.9655	1.0
<i>C5</i>	0.2428	0.3306	0.9864	1.0

Table 12: Characteristic individual performance values of NBIS matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 2old3new.

data bases and the 2old3new outcomes. That means that in the 3old2new case the very high *Zero FAR* in data sets C3, C4 and C5 cannot be detected. The supposed cross-sensor observation detectable in *FAR*<sub>100</sub> and *FAR*<sub>1000</sub> values can confirmed for the second fixed splitting method again.

In the following part the randomized averaging method will be discussed. In Table 15 and 16 the most important characteristic values of the randomized comparison method are displayed. The *EER* values are distributed between 13.03% and 15.22%. So compared to the *EER* of the original data displayed in Table 9 it seems that there

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>crossed sets 3old2new</b>				
<i>C1</i>	13.59	0.9190	46.34	6.88
<i>C2</i>	15.77	0.9088	43.92	6.75
<i>C3</i>	14.07	0.9172	44.87	6.93
<i>C4</i>	14.42	0.9218	47.05	6.70
<i>C5</i>	14.39	0.9204	47.05	6.68

Table 13: Characteristic individual performance values of NBIS matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 3old2new.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>crossed sets 3old2new</b>				
<i>C1</i>	0.2812	0.3895	0.5326	1.0
<i>C2</i>	0.2942	0.4130	0.5761	1.0
<i>C3</i>	0.2873	0.3983	0.5542	1.0
<i>C4</i>	0.2761	0.3757	0.5363	1.0
<i>C5</i>	0.2693	0.3673	0.5287	1.0

Table 14: Characteristic individual performance values of NBIS matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 3old2new.

is no big difference. The lower *EER* bound for the crossed sets seems to be around 13.00% and the upper bound around 15.00%. The number of 1960 imprints included in the crossed data set is not effecting a big problem in case of *EER*, *AUC* or any other characteristic value comparison.

So it is valid to conclude that a raise of this value between the single and crossed data sets can be clearly detected. Regarding to the information in Tables 9, 11, 13 and 15 the *EER* varies between 7.30% and around 15.00%. Hence, it is possible to observe nearly a doubling of this most important comparison value for the NBIS matcher method. In Figures 26, 27 and 28 the graphical interpretation can looked up. The

data set	EER	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	13.03	0.9218	47.58	6.71
<i>C2</i>	15.22	0.9113	44.68	6.64
<i>C3</i>	13.86	0.9206	43.76	6.80
<i>C4</i>	13.26	0.9276	49.14	6.57
<i>C5</i>	13.43	0.9238	48.71	6.55

Table 15: Characteristic individual performance values of NBIS matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the WA method.

degradation of the time span including genuine scores like mentioned before in the introduction of the present chapter, in Section 5.1, is responsible for the following effect: Basically the number of low genuine scores is higher using those matches which are biased by the 4 year time span. For this purpose a shift in the score distribution to the left can be displayed. This shift causes that the genuine distribution tends to approximate the impostor one which can be observed in the graphical examples. There is also no difference between the data set and the used sensor types. The effect is verifiable for each possible setting. As opposed to this, the tendency of the AUC is displaying more or less the same point of view. The decrease of the AUC values can be located around 4.00% between single and crossed data sets.

There are a few more observations detectable. The *av. impostor scores* remain quite stable in all calculation outputs as readable in the tables in this subsection. More or less the same outcomes can be described for the *Zero FRR*, which remains 1.0 for each set.

On the one hand a clear difference looking at  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* outcomes between the single sets and the crossed sets is observable. This means that quite similar to the *EER* results, the  $FAR_{100}$  and  $FAR_{1000}$  values are twice as high for the crossed data bases as for the single ones. The *Zero FAR* for the larger data sets is significantly higher. In particular they are nearly doubled as well, except for those values which are nearly 1.0 - the highest possible value. On the other hand the

data set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
$C1$	0.2616	0.3604	0.5406	1.0
$C2$	0.2924	0.3925	0.5672	1.0
$C3$	0.2918	0.3899	0.8058	1.0
$C4$	0.2555	0.3461	0.7133	1.0
$C5$	0.2637	0.3457	0.8209	1.0

Table 16: Characteristic individual performance values of NBIS matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the WA method.

$FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* tend to follow a certain trend. So regardless which data base is considered the  $FAR_{100}$  is always the lowest and *Zero FAR* the highest of those three values. All those observed tendencies correspond to the expectation of the results and to the definition, which was introduced in Section 2.3. According to the increase of the crossed data sets' *EER* a different observation for  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* could only occur if some failure would be included in the calculation process.

Despite those facts, according to the *EER* values is data set *A* performing better than all the others. There is only one exception, which is the performance of the *B4* data base. So all in all, it can be said that the results for 2009 are delivering the best outcomes in terms of *EER*, then the results for the younger 2013 data sets are next and at last the crossed data results can be ranked. This tendency is displayed in the following graphics 22, 23, 24 and 25. Nevertheless it is very hard to detect a difference between the graphics because the tendency is the same for all of them. Probably this effect can only be observed for the NBIS matcher so a comparison to the same values of the other matching methods will be worthwhile. This effect could be caused by the different used sensor types or other irregularities introduced in Section 4.4.

The last information that can be gathered from the performance results are concerning the genuine and impostor score distribution. First it is not possible to detect abnormalities comparing the results for the average genuine and impostor scores. But

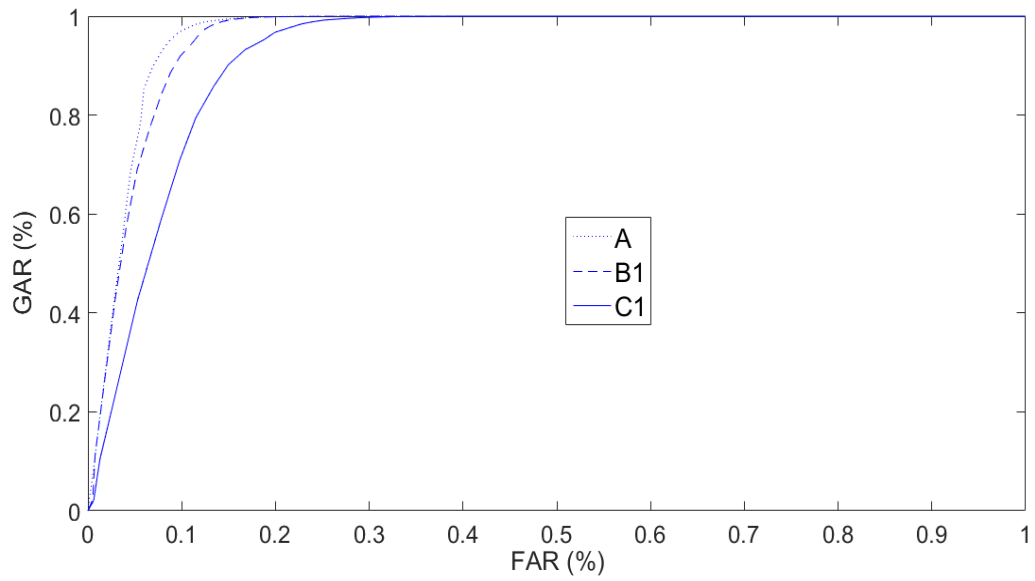


Fig. 22: ROC curves for single data sets A, B1 and crossed C1 in the 2old3new case using NBIS.

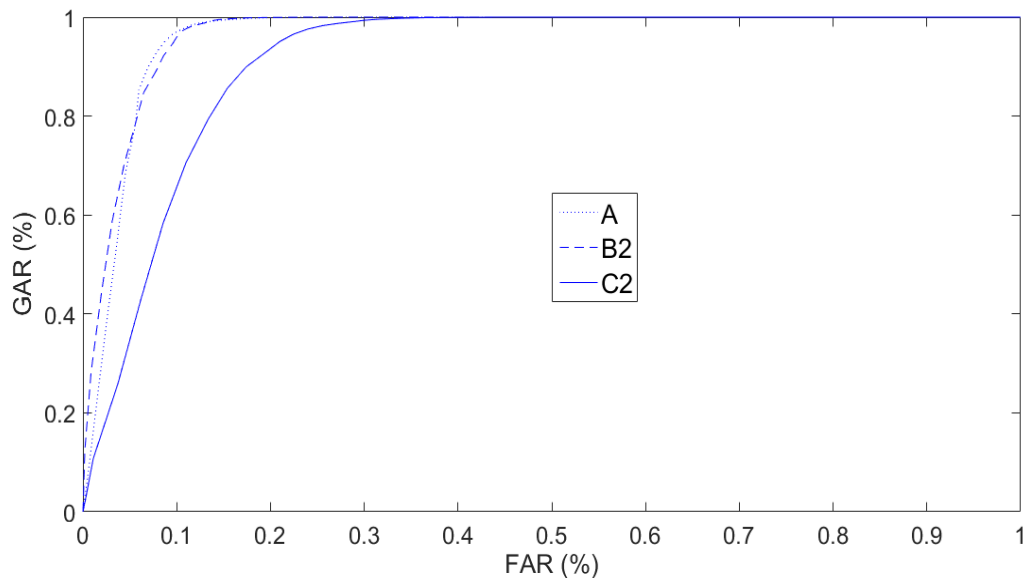


Fig. 23: ROC curves for single data sets A, B2 and crossed C2 in the 2old3new case using NBIS.

comparing the single and the crossed values there is a difference. The average impostor scores remain quite stable, even when performing the splitting into the 2old3new

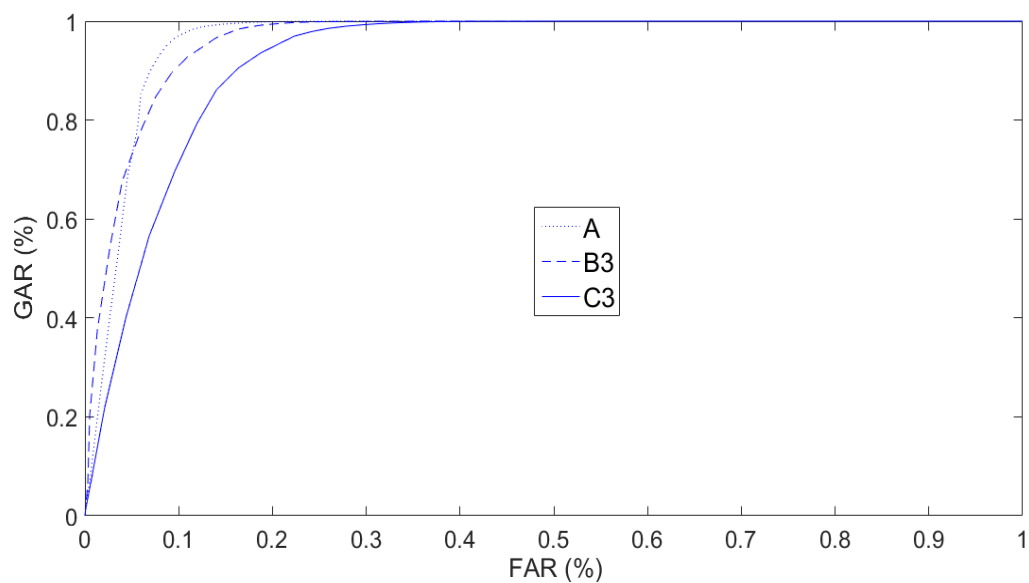


Fig. 24: ROC curves for single data sets A, B3 and crossed C3 in the 2old3new case using NBIS.

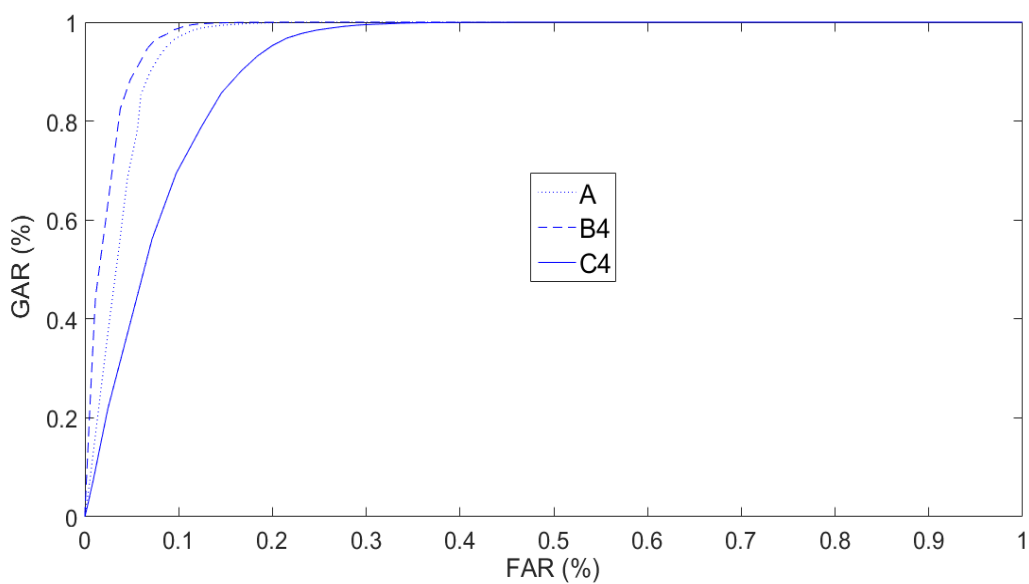


Fig. 25: ROC curves for single data sets A, B4 and crossed C4 in the 3old2new case using NBIS.

and 3old2new data sets or using the randomized selection. As opposed to this, the change in the genuine scores is remarkable. In the graphical representations below,

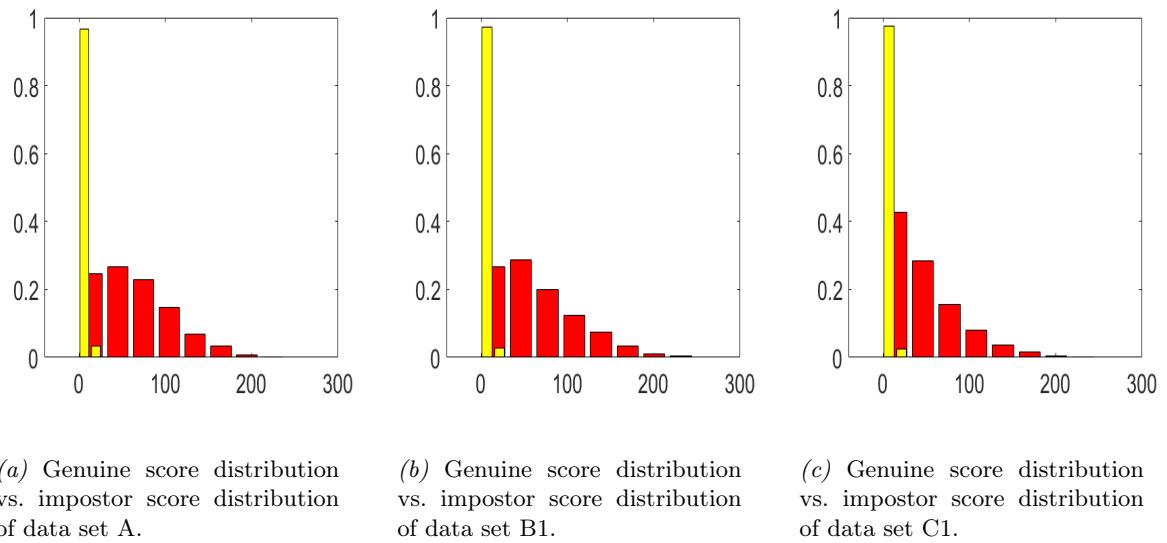


Fig. 26: Genuine (colored red) and Impostor (colored yellow) score distribution of the NBIS A, B1 and C1 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).

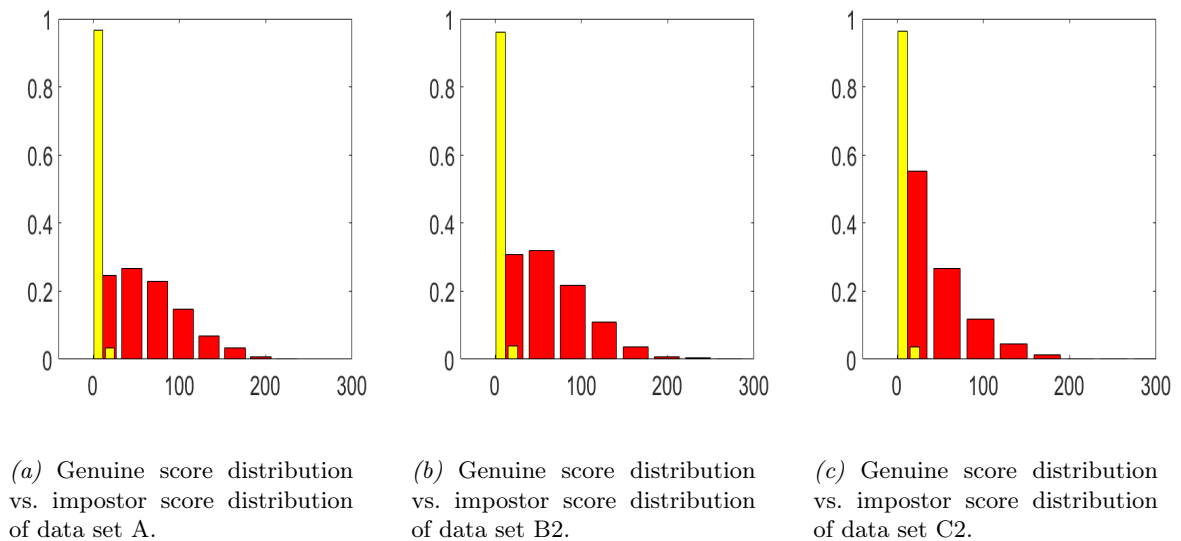


Fig. 27: Genuine (colored red) and Impostor (colored yellow) score distribution of the NBIS A, B2 and C2 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).

Figures 26, 27 and 28, the effect has been visualized. In those figures a shift in the genuine score distribution is observable. While the values remain more or less stable



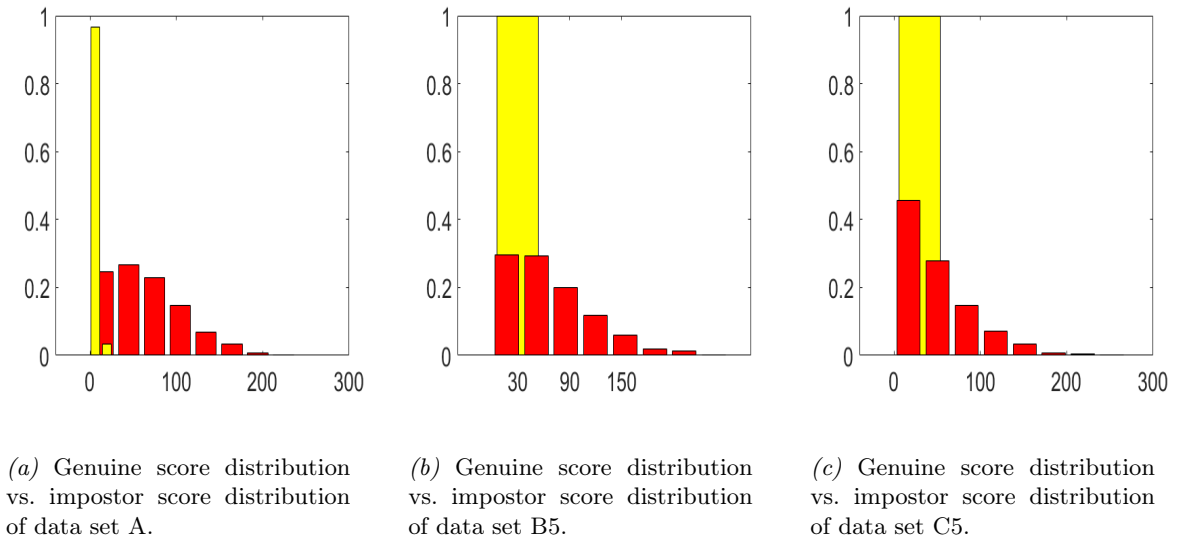


Fig. 28: Genuine (colored red) and Impostor (colored yellow) score distribution of the NBIS A, B5 and C5 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).

between 2009 and 2013, for the crossed data sets independently of the used sensor type, the genuine scores are shifted to the left, the distributions are skewed to the right. So the number of lower genuine match scores raises and the change within the average genuine scores between the non crossed and crossed data sets can be quoted to be around 30%. This value can be observed using the average genuine scores in Table 9 and calculate the fraction between, for example, the average genuine score of *C2* and *A*. Due to the circumstance that in the crossed data set imprints of different years are included, the matching scores with respect to the intra-class values get lower. That means that fingerprints which belong to the same finger can not be distinguished that well. Especially the difference between high impostor scores and low genuine scores is lowered. It seems that the genuine score distribution is approximating the impostor ones. That could lead to problems in terms of finger distinction. This degradation can be called ageing effect but due to the fact that no ageing related impostor scores have been taken into account for this method it will be interesting to compare the just described results with the following ones, which will be presented in the following Sections concerning OA and HH method.

**NBIS OA Method:** In Section 5.2 the matching results without using any information about the included time span of 5 years in the impostor scores have been presented. In the following Section 5.2 the time span will be taken into account. As before the basic information can be looked up in Tables 17 and 18. That means that in those tables the characteristic values are displayed with no regard to any size adaptation or randomized score selection. For sure the results for the single data sets are the same as in Tables 9 and 10 but they are included to have reference values for the crossed data sets where the time span correlation of the used imprints is covered.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
single sets				
	<i>same results as in the all scores case</i>			
crossed sets				
<i>C1</i>	13.60	0.9221	47.61	6.46
<i>C2</i>	14.17	0.9118	44.71	6.38
<i>C3</i>	13.97	0.9211	43.81	6.63
<i>C4</i>	12.89	0.9281	49.06	6.46
<i>C5</i>	13.24	0.9242	48.65	6.45

Table 17: Characteristic individual performance values of NBIS matching including EER, AUC, average genuine score and average impostor score using the OA method.

As presented in Table 17 varies the *EER* for the crossed data sets between 12.89% and 14.17%. Comparing those values with the outcomes of the WA method it is clearly observable that the OA *EER* is a bit lower. Especially the upper bound for the second method can be detected about 1.00% less high. So in terms of this performance value it seems to make a difference which kind of impostor scores are taken into account. *AUC*, *average genuine and impostor scores*, which are also readable in Table 17 are displaying more or less the same behavior as in the WA case. A decrease of *AUC* and *average genuine scores* compared to the single data sets and also stability in terms of *average impostor scores* can be stated.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	0.2451	0.3413	0.5717	1.0
<i>C2</i>	0.2751	0.3649	0.5886	1.0
<i>C3</i>	0.2743	0.3764	0.7608	1.0
<i>C4</i>	0.2507	0.3320	0.5146	1.0
<i>C5</i>	0.2497	0.3426	0.8001	1.0

Table 18: Characteristic individual performance values of NBIS matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using the OA method.

In case of the other Table 18 each value for the crossed sets, except for the *Zero FRR*, is lower compared to the corresponding values in Table 10. Apart from the *Zero FRR* which seems to be fixed at 1.0 there are two other irregularities mentionable. It seems that the *Zero FAR* of data set C1 and C4 is displaying an interesting effect. The value of C1 is the only one which is slightly higher compared to the WA method. This fluctuation could probably be caused by the different sensory used during fingerprint acquisition. But to a greater degree it is much more likely that some other factor is responsible. The second special case is caused by the *Zero FAR* of data set C4. As mentioned in the WA method a trend could be observed with respect to data set C3, C4 and C5. The *Zero FAR* for those three values was much higher than the results for the remaining data sets C1 and C2. First of all the same trend is also detectable for the OA method. It seems that this could be based on the matcher or on the data sets for example. Apart from the reoccurrence a second aspect must be mentioned. The value of C4 is much lower compared to the outcomes from the WA method and the other two results of the same method. It will be interesting to have a look on these effects in the results of the other matchers.

Closing the OA analysis for the NBIS matcher it is necessary to mention also the outcomes presented in Table 19 and 20. The randomly performed size adaption of the crossed data sets just confirms the outcomes described before. There is not really

data set	EER	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
$C1$	12.93	0.9263	47.62	6.46
$C2$	14.17	0.9169	44.69	6.38
$C3$	13.86	0.9251	43.80	6.63
$C4$	13.26	0.9297	49.05	6.46
$C5$	13.43	0.9255	48.58	6.45

Table 19: Characteristic individual performance values of NBIS matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the OA method.

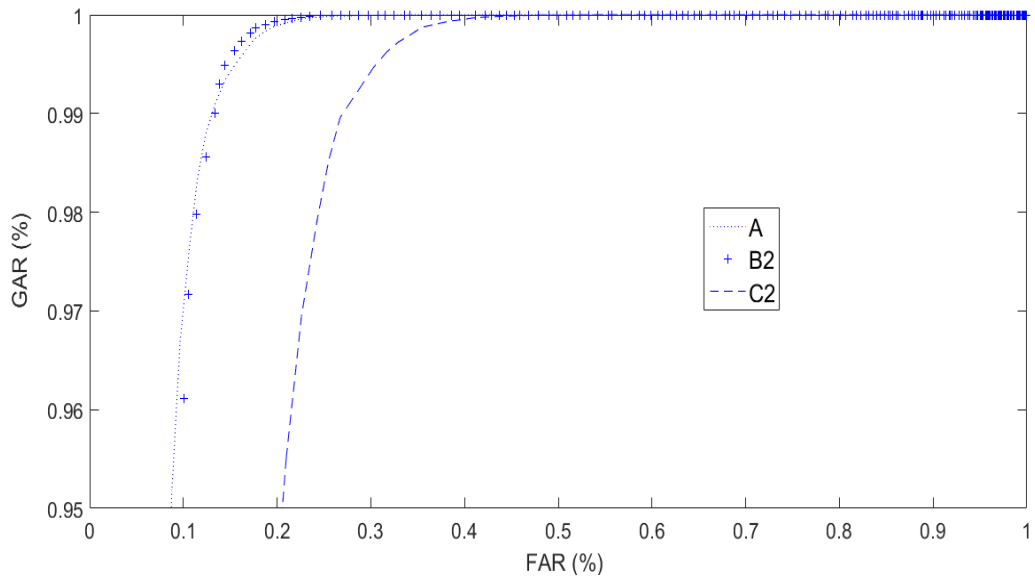


Fig. 29: ROC curves for single data sets A, B2 and crossed C2 of the OA analysis case using NBIS.

a surprising aspect that needs to be discussed in detail. The same can be stated for Figure 29, 30 and 31 as well. Both are confirming the outcomes of analysis method WA. Especially the genuine score shift to the left can be observed once more looking at Figure 30 and 31. It is very interesting that basically the same trends can be verified,

data set	$\text{FAR}_{100}$	$\text{FAR}_{1000}$	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
$C1$	0.2450	0.3372	0.5307	1.0
$C2$	0.2749	0.3657	0.5674	1.0
$C3$	0.2737	0.3735	0.6603	1.0
$C4$	0.2511	0.3363	0.4977	1.0
$C5$	0.2506	0.3385	0.6348	1.0

Table 20: Characteristic individual performance values of NBIS matching including  $\text{FAR}_{100}$ ,  $\text{FAR}_{1000}$ , Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the OA method.

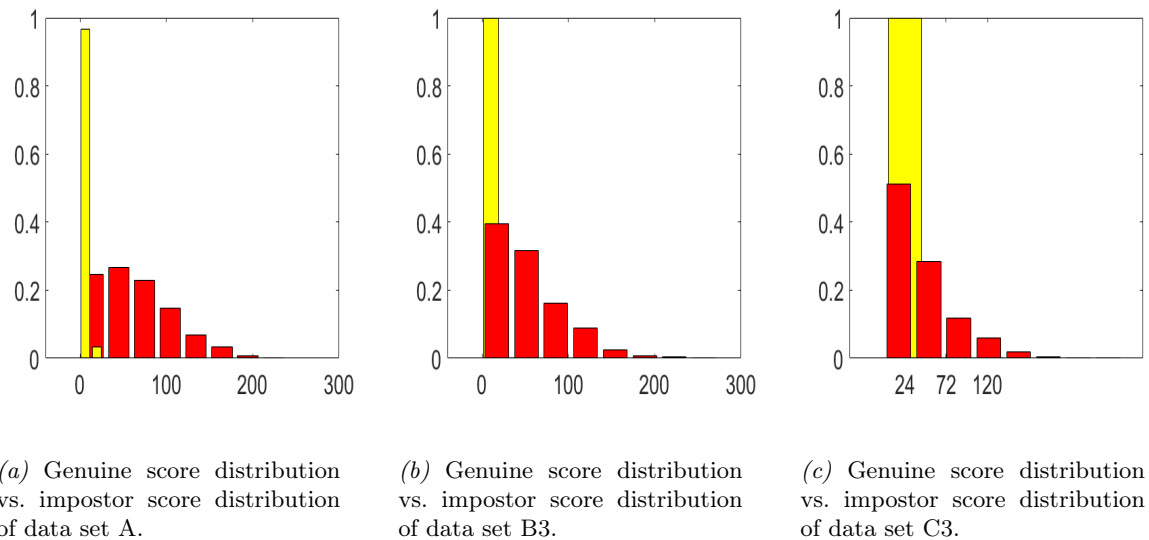


Fig. 30: Genuine (colored red) and Impostor (colored yellow) score distribution of the NBIS A, B3 and C3 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).

independently of which impostor score sets is used. According to this information the situation for the following HH analysis seems quite obvious.

**NBIS HH Method:** In the present section the results for the HH Method and the corresponding matching scores of the NBIS matcher will be presented. In Tables 21 and 22 the different characteristic values without any randomized size adaptation can

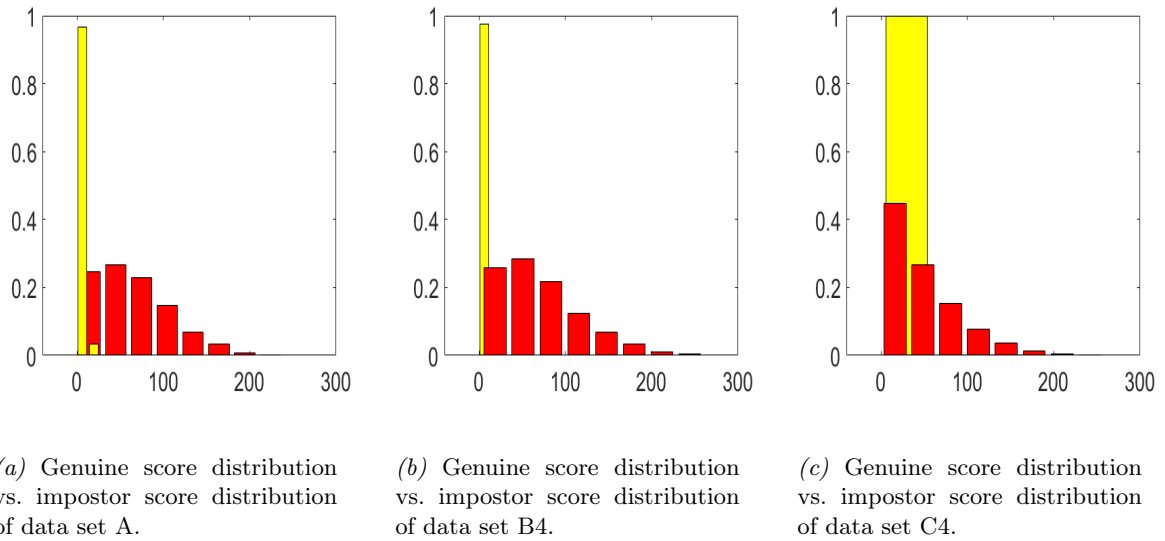


Fig. 31: Genuine (colored red) and Impostor (colored yellow) score distribution of the NBIS A, B4 and C4 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).

be looked up.

As introduced in Section 5.1 are the results of this third analysis method average values. Those values are calculated using 252 genuine and impostor score sets which have been randomized selected. Impostor scores neglecting any ageing related affiliation as well as time span including ones are taken into account. In Tables 23 and 24 the results for the size adaptation of the crossed data bases are presented.

As readable in Table 21 is it possible to locate the *EER* between 13.01% and 15.35%. In fact the used randomized selection process for the ageing including and neglecting impostor scores selection and the calculation of the mean values for each performance measure seems to equalize the single outcomes. So after this averaging process basically the same values as detected in WA case can be observed for the entire crossed data sets. In fact it seems that neither the random selection nor the inclusion of time-separated impostor scores has any impact on the overall observation regardless which value is considered.

In Table 22 very small differences are present comparing the HH results to the WA ones. The same appears for the results presented in Tables 23 and 24. The observable trends are the same as introduced in the other two analysis cases before.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	13.01	0.9239	47.61	6.71
<i>C2</i>	15.35	0.9141	44.71	6.64
<i>C3</i>	13.52	0.9225	43.81	6.80
<i>C4</i>	13.47	0.9285	49.06	6.57
<i>C5</i>	13.69	0.9242	48.65	6.55

Table 21: Characteristic individual performance values of NBIS matching including EER, AUC, average genuine score and average impostor score using the HH method.

Even the *Zero FAR* decrease for data set *C4* can be detected again. On the one hand this could be caused by the fact that ageing has no impact on the performed impostor matches. On the other hand it is also possible to conclude a relationship to the used matcher. As described in the previous WA and OA analysis are the matching scores provided by the used NBIS matcher more or less equal in each possible case and quite low as well. For this purpose it could be that the performance of the matcher is also an important aspect in terms of ageing effects in fingerprint recognition. Suggesting the assumption a better performing fingerprint matcher can not be influenced by ageing that much as a worse one could be. This will be verified in the following sections discussing the other recognition results.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	0.2593	0.3598	0.5524	1.0
<i>C2</i>	0.2918	0.3911	0.5762	1.0
<i>C3</i>	0.2916	0.3903	0.8533	1.0
<i>C4</i>	0.2556	0.3460	0.8684	1.0
<i>C5</i>	0.2642	0.3447	0.9242	1.0

Table 22: Characteristic individual performance values of NBIS matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using the HH method.

data set	EER	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	12.82	0.9239	47.56	6.58
<i>C2</i>	14.79	0.9141	44.69	6.51
<i>C3</i>	14.10	0.9225	43.84	6.71
<i>C4</i>	13.15	0.9285	49.07	6.52
<i>C5</i>	13.38	0.9246	48.74	6.50

Table 23: Characteristic individual performance values of NBIS matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the HH method.



data set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
$C1$	0.2592	0.3509	0.5345	1.0
$C2$	0.2931	0.3812	0.5667	1.0
$C3$	0.2912	0.3793	0.7544	1.0
$C4$	0.2509	0.3448	0.6076	1.0
$C5$	0.2505	0.3422	0.7130	1.0

Table 24: Characteristic individual performance values of NBIS matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the HH method.

### 5.3 NEURO

Regarding the WA, OA and HH analysis method for the matching results the presentation of the NEURO related outcomes is splitted into four parts like it was done in the NBIS related part above. For this purpose all scores will be used for the first calculations. The results are presented in Table 25 and 26 and reveal more or less the same genuine score degradation like introduced in the first minutiae based method. Furthermore the  $EER$  is increasing comparing single and crossed data sets and also  $AUC$ ,  $FAR_{100}$ ,  $FAR_{1000}$  and  $Zero\ FAR$  reveal an identical tendency as in the NBIS case. For the *average impostor* and  $Zero\ FRR$  the same stability can be measured as well. It seems that the same assumption ageing is influencing the genuine scores' behavior can be verified once more. But after getting an first impression about the performance of the NEURO software the other analysis strategies WA, OA and HH will be taken into account and a detailed discussion is performed.

**NEURO WA Method:** Regarding the results presented in the following Tables 27, 28, 29, 30, 31 and 32, the overall tendency of outcomes is quite similar to the NBIS analysis displayed in the previous Section 5.2.

Looking at the matching performance in detail those results clearly show the best measurements of all used matchers. For the single data sets the values can be be-

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
<i>A</i>	2.07	0.9787	508.56	0.0055
<i>B1</i>	3.17	0.9677	499.66	0.0019
<i>B2</i>	1.96	0.9798	562.11	0.0054
<i>B3</i>	4.00	0.9595	464.01	0.0296
<i>B4</i>	2.04	0.9791	553.72	0.0134
<i>B5</i>	3.69	0.9626	484.50	0.0213
<b>crossed sets</b>				
<i>C1</i>	5.32	0.9466	356.57	0.0028
<i>C2</i>	5.97	0.9402	359.21	0.0057
<i>C3</i>	6.16	0.9382	350.87	0.0151
<i>C4</i>	5.81	0.9418	368.43	0.0065
<i>C5</i>	6.72	0.9326	352.25	0.0087

Table 25: Characteristic individual performance values of NEURO matching including EER, AUC, Average Genuine Score and Average Impostor Score using all scores.

tween 1.96% and 4.00%. So the variation is nearly the same as in the NBIS results. For the crossed data bases outcomes an *EER* of 5.32% to 6.73% can be measured. As well as in the previous presented matcher performance it is also necessary to split the input results to gather information that is able to be suitable compared to the single sets. Therefore the *EER* for the 2old3new split can be confirmed as 5.31% to 6.75% again. Nearly identical results can be posed in the 3old2new case. The interesting information beyond that is the fact that it seems that the *EER* is more stable as in the NBIS performance looking at the single results. The absolute difference can be measured between 2.15% and 4.01%. Looking at the relative increase of B1/C1 and B2/C2 which are between 167.82% and 304.59% it gets clear that the first impression of the stability is a matter of the chosen point of view. The single values and the absolute difference of the *EER* values for the NEURO results are indeed lower compared to the NBIS outcomes. Nevertheless the fluctuation concerning the relative increase of this performance characteristic is much higher compared to the results of

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>single sets</b>				
<i>A</i>	0.0414	0.0414	0.0824	1.0
<i>B1</i>	0.0635	0.0635	0.0790	1.0
<i>B2</i>	0.0392	0.0392	0.0563	1.0
<i>B3</i>	0.0799	0.0799	0.8084	1.0
<i>B4</i>	0.0408	0.0408	0.7341	1.0
<i>B5</i>	0.0737	0.0737	0.9825	1.0
<b>crossed sets</b>				
<i>C1</i>	0.1064	0.1064	0.2215	1.0
<i>C2</i>	0.1193	0.1193	0.2582	1.0
<i>C3</i>	0.1232	0.1232	0.9026	1.0
<i>C4</i>	0.1162	0.1162	0.9064	1.0
<i>C5</i>	0.1345	0.1345	0.9956	1.0

Table 26: Characteristic individual performance values of NEURO matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using all scores.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
<i>same results as in the all scores case</i>				
<b>crossed sets</b>				
<i>C1</i>	5.32	0.9466	356.57	0.0037
<i>C2</i>	5.97	0.9402	359.21	0.0059
<i>C3</i>	6.16	0.9382	350.87	0.0173
<i>C4</i>	5.81	0.9418	368.43	0.0095
<i>C5</i>	6.73	0.9326	352.25	0.0131

Table 27: Characteristic individual performance values of NEURO matching including EER, AUC, Average Genuine Score and Average Impostor Score using the WA method.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as as in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	0.1064	0.1064	0.2215	1.0
<i>C2</i>	0.1193	0.1193	0.2582	1.0
<i>C3</i>	0.1232	0.1232	0.9026	1.0
<i>C4</i>	0.1162	0.1162	0.9064	1.0
<i>C5</i>	0.1345	0.1345	0.9956	1.0

Table 28: Characteristic individual performance values of NEURO matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using the WA method.

the other minutiae based fingerprint matcher.

The information given in Tables 29, 30, 31 and 32 are confirming the outcomes provided by the aforementioned tables. It can be detected that the decrease of the *average genuine scores* and the stability of the *average impostor scores* is present as in the other cases before. This identical tendency of those two measurements, like in the NBIS experimental results, can be confirmed basically for all considered characteristic values.

Focusing on the random selected and averaged data sets it is possible to verify the overall performance as described. Looking at the outcomes displayed in Tables 33 and 34, the following observation is detectable: In fact, there is not really a difference to the original crossed data sets observable. It seems that apart from varied values the same tendency is given. The most interesting observation which can be made is the confirmation of the drop of the *Zero FAR* value for data set *C4* like described in the NBIS case as well. Compared to the NBIS results the same tendency for *AUC*, *FAR<sub>100</sub>*, *FAR<sub>1000</sub>*, *Zero FAR* and *Zero FRR* is observable. The *Zero FRR* seems to be fixed at 1.0 once more, confirming the expected behavior. The only difference for *FAR<sub>100</sub>* and *FAR<sub>1000</sub>*, which can be measured, is that the difference between the values is not that high compared to NBIS.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>crossed sets 2old3new</b>				
<i>C1</i>	5.31	0.9467	367.79	0.0044
<i>C2</i>	5.88	0.9409	378.48	0.0068
<i>C3</i>	6.25	0.9372	351.54	0.0312
<i>C4</i>	5.41	0.9456	391.22	0.0143
<i>C5</i>	6.75	0.9322	360.96	0.0223

Table 29: Characteristic individual performance values of NEURO matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 2old3new using the WA method.

Nevertheless a short discussion about the average genuine and impostor scores will be done in the following. The average genuine score for the single data sets is much higher than in the crossed data bases no matter taking the values of all imprints into account or the splitted ones. Due to that fact the Figures 35 and 34 help to gather some more information.

The genuine score distribution for the 2009 imprints are delivering higher scores and can be compared to something like a normal distribution. For the images from 2013 it is not possible to find a distribution the matching values look like. But for the crossed set there can be the clear description that the distribution is similar to the NBIS case skewed to the right. So all in all there is the same tendency as in the other minutiae based matcher. A shift to the left of the matching scores can be detected, caused by a reduction of the genuine scores of about 30 to 38 percent. This percentage can be calculated using the genuine scores in Table 27 and divide for example the average genuine score of C1 by the average genuine score of the single data set A. The *AUC* results are also displaying the same tendency as detected in the NBIS case. So a decrease for the crossed data bases compared to the single sets can be measured. In general it can be stated that there is hardly no difference in the tendency of the used characteristic values of NBIS and NEURO. The crossed data sets' *EER* is increasing, the same can be measured for *FAR*<sub>100</sub>, *FAR*<sub>1000</sub> and *Zero FAR*. The *average genuine scores* are decreasing if the values from the single and crossed data bases are compared and the *average impostor scores* and *Zero FRR* remain more or less stable.

Data Set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>crossed sets 2old3new</b>				
<i>C1</i>	0.1061	0.1061	0.1417	1.0
<i>C2</i>	0.1176	0.1176	0.1537	1.0
<i>C3</i>	0.1249	0.1249	0.8922	1.0
<i>C4</i>	0.1082	0.1082	0.8753	1.0
<i>C5</i>	0.1350	0.1350	0.9917	1.0

Table 30: Characteristic individual performance values of NEURO matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR concerning the splitted data 2old3new using the WA method.

Completing the analysis of the NEURO results the following Figures 32, 33, 34 and 35 give a graphical visualization of the before described results.

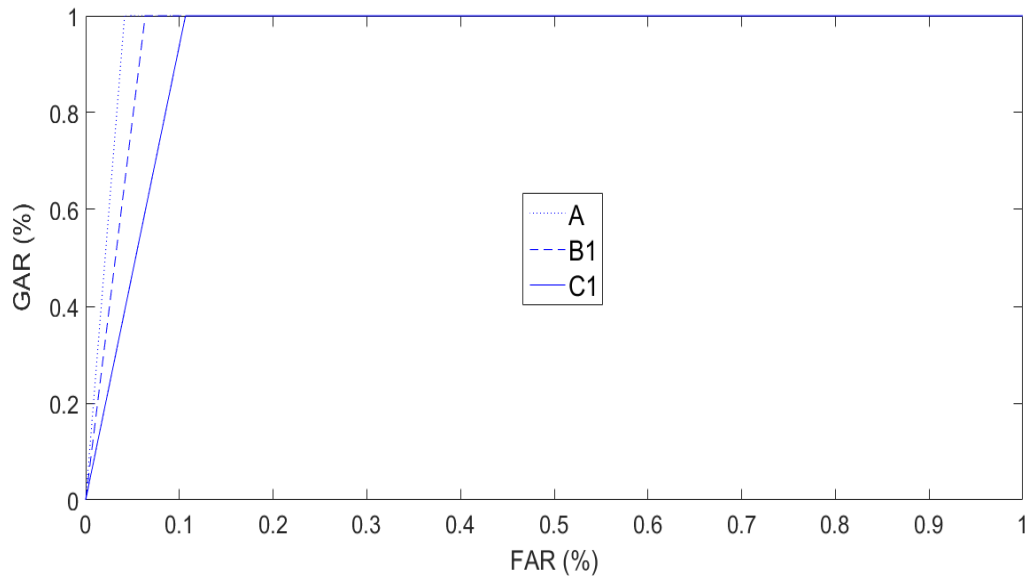


Fig. 32: ROC curves for single data sets A, B1 and crossed C1 using NEURO.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>crossed sets 3old2new</b>				
<i>C1</i>	5.33	0.9464	347.66	0.0029
<i>C2</i>	6.03	0.9395	343.88	0.0051
<i>C3</i>	6.10	0.9388	350.34	0.0034
<i>C4</i>	6.13	0.9385	350.22	0.0046
<i>C5</i>	6.71	0.9327	345.32	0.0041

Table 31: Characteristic individual performance values of NEURO matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 3old2new using the WA method.

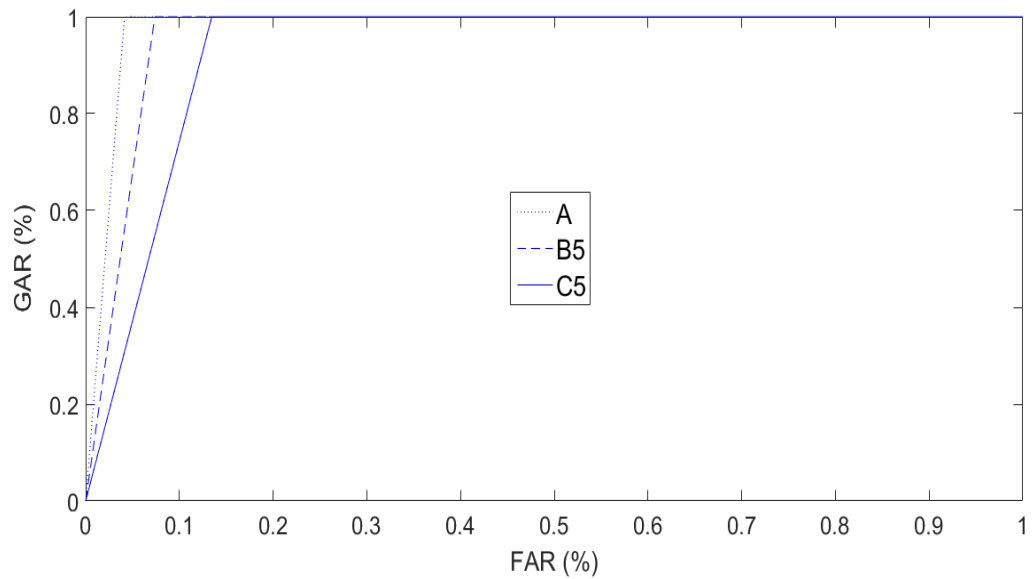


Fig. 33: ROC curves for single data sets A, B5 and crossed C5 using NEURO.

<b>Data Set</b>	<b>FAR<sub>100</sub></b>	<b>FAR<sub>1000</sub></b>	<b>Zero FAR</b>	<b>Zero FRR</b>
<b>crossed sets 3old2new</b>				
<i>C1</i>	0.1067	0.1067	0.2266	1.0
<i>C2</i>	0.1206	0.1206	0.2581	1.0
<i>C3</i>	0.1219	0.1219	0.2435	1.0
<i>C4</i>	0.1225	0.1225	0.2335	1.0
<i>C5</i>	0.1342	0.1342	0.2420	1.0

Table 32: Characteristic individual performance values of NEURO matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 3old2new using the WA method.

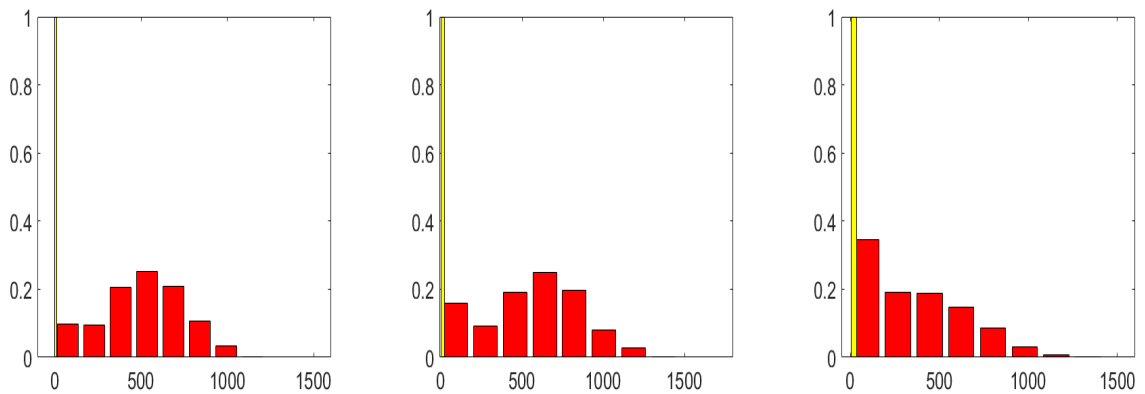
<b>data set</b>	<b>EER (%)</b>	<b>AUC</b>	<b>Av. Gen. Score</b>	<b>Av. Imp. Score</b>
<b>randomized crossed sets</b>				
<i>C1</i>	5.29	0.9465	356.93	0.0038
<i>C2</i>	5.98	0.9397	359.12	0.0060
<i>C3</i>	6.21	0.9373	350.21	0.0175
<i>C4</i>	5.75	0.9420	368.78	0.0095
<i>C5</i>	6.73	0.9321	352.36	0.0131

Table 33: Characteristic individual performance values of NEURO matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the WA method.



data set	$\text{FAR}_{100}$	$\text{FAR}_{1000}$	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
$C1$	0.1058	0.1058	0.1805	1.0
$C2$	0.1195	0.1195	0.2102	1.0
$C3$	0.1242	0.1242	0.8267	1.0
$C4$	0.1150	0.1150	0.5589	1.0
$C5$	0.1346	0.1346	0.7737	1.0

Table 34: Characteristic individual performance values of NEURO matching including  $\text{FAR}_{100}$ ,  $\text{FAR}_{1000}$ , Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the WA method.

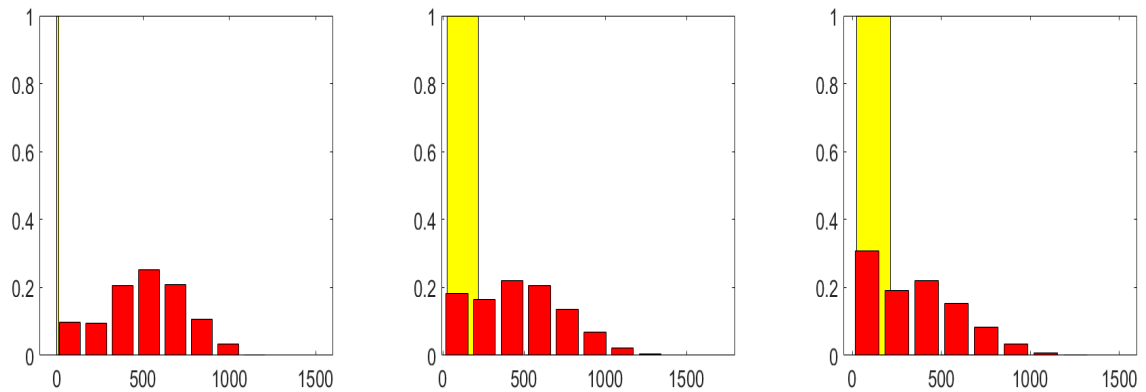


(a) Genuine score distribution vs. impostor score distribution of data set A.

(b) Genuine score distribution vs. impostor score distribution of data set B2.

(c) Genuine score distribution vs. impostor score distribution of data set C2.

Fig. 34: Genuine (colored red) and Impostor (colored yellow) score distribution of the NEURO A, B2 and C2 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1) using WA analysis.



(a) Genuine score distribution vs. impostor score distribution of data set A.

(b) Genuine score distribution vs. impostor score distribution of data set B3.

(c) Genuine score distribution vs. impostor score distribution of data set C3.

Fig. 35: Genuine (colored red) and Impostor (colored yellow) score distribution of the NEURO A, B3 and C3 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1) using WA analysis.

**NEURO OA Method:** In the following Section 5.3 the results of using only impostor scores including the 4 year time span are presented. In Tables 35 and 36 the characteristic values without any data set size adaption can be looked up.

In fact there is not really a difference measurable comparing the characteristic values of the OA analysis and those from the WA analysis of the previous section. The only difference is a small change in the average impostor scores. The average scores are a little bit lower as for the corresponding ones in the WA case. Despite an interesting observation can be made looking at data set C4 and the *Zero FAR*. As introduced in the OA analysis of the NBIS results the reduction of this value can be detected once more. So the assumption that the drop could be a matter of the used matcher can be devitalized. It remains to be seen if the same effect occurs for the non-minutiae matchers as well. It could be that it is based on the used minutiae strategy. Because there was not really a difference to the results of the WA method it is likely that for the following randomly size adapted analysis also the same stability can be detected. The calculated values of the size adaption are presented in Tables 37 and 38.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	5.32	0.9466	356.57	0.0019
<i>C2</i>	5.97	0.9402	359.21	0.0055
<i>C3</i>	6.16	0.9382	350.87	0.0128
<i>C4</i>	5.81	0.9418	368.43	0.0036
<i>C5</i>	6.72	0.9326	352.25	0.0044

Table 35: Characteristic individual performance values of NEURO matching including EER, AUC, Average Genuine Score and Average Impostor Score using the OA method.

Looking at the results the presumption of almost no changes can be verified. Especially for *EER*, *AUC*, *average genuine scores* *average impostor scores* and *Zero FRR* a high amount of similarity is present. The probably most interesting aspect is that *FAR<sub>100</sub>* and *FAR<sub>1000</sub>* outcomes tend to stay identical whereas the *Zero FAR* is the most fluctuating value of the whole OA analysis for the NEURO results. These specific results for the randomized crossed sets are lowest for all considered *Zero FAR* values so far. Therefore it could be worthwhile to have a look on this trend in the following HH analysis part.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed sets</b>				
<i>C1</i>	0.1064	0.1064	0.1816	1.0
<i>C2</i>	0.1193	0.1193	0.1873	1.0
<i>C3</i>	0.1232	0.1232	0.6909	1.0
<i>C4</i>	0.1162	0.1162	0.5736	1.0
<i>C5</i>	0.1345	0.1345	0.7346	1.0

Table 36: Characteristic individual performance values of NEURO matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using the OA method.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	5.31	0.9463	356.94	0.0001
<i>C2</i>	5.98	0.9397	359.34	0.0055
<i>C3</i>	6.18	0.9377	351.02	0.0132
<i>C4</i>	5.83	0.9412	368.42	0.0036
<i>C5</i>	6.73	0.9321	351.94	0.0040

Table 37: Characteristic individual performance values of NEURO matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the OA method.

data set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
$C1$	0.1062	0.1062	0.1521	1.0
$C2$	0.1195	0.1195	0.1648	1.0
$C3$	0.1235	0.1235	0.5773	1.0
$C4$	0.1165	0.1165	0.3592	1.0
$C5$	0.1346	0.1346	0.4475	1.0

Table 38: Characteristic individual performance values of NEURO matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the OA method.

**NEURO HH Method:** The final presentation of the missing third part of the NEURO matching score analysis will be displayed in this section of the master thesis. The results described in Tables 39 and 40 are representing the performance characteristics of the entire used data set, while the size adapted analysis can be looked up in Tables 41 and 42.

Basically all results which can be looked up in Tables 39, 40, 41 and 42 are more or less same as before in OA and WA analysis. So once more a clear observable stability of *average impostor scores* and a decrease in terms of *AUC*, *average genuine scores*,  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* can be described comparing the single and crossed data sets' results. An identical increase of the *EER* is detectable as well. The variety of all NEURO based results is more similar to each other compared to the outcomes presented in Section 5.3. There will not be a detailed description of the single values because this has been done in the aforementioned WA analysis and there are no real differences to those outcomes. Basically it seems that neither the random selection nor the inclusion of time-separated imposter scores has any impact on the overall observation. The shift of the genuine score distribution based on an approximation toward the impostor score distribution can be detected in WA, OA and HH analysis independently.

In Figure 36 it can be verified that the difference between this figure and Figure 34

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed Sets</b>				
$C1$	5.32	0.9466	356.57	0.0038
$C2$	5.97	0.9402	359.21	0.0061
$C3$	6.16	0.9382	350.87	0.0173
$C4$	5.81	0.9418	368.43	0.0091
$C5$	6.73	0.9326	352.25	0.0129

Table 39: Characteristic individual performance values of NEURO matching including EER, AUC, Average Genuine Score and Average Impostor Score using the HH method.

using the same data base can hardly be seen except for one bar of the histogram in the right column.

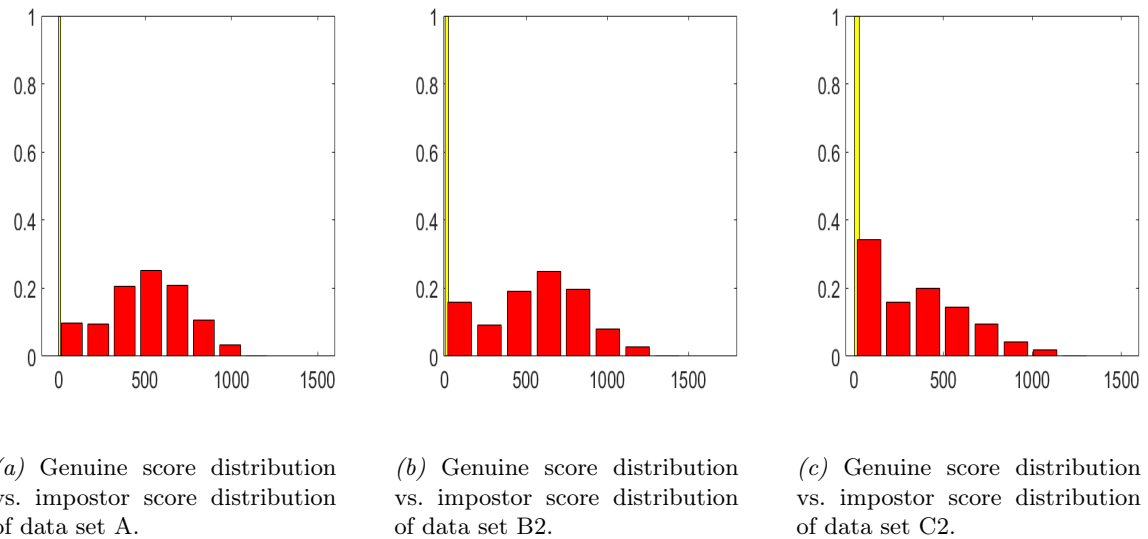


Fig. 36: Genuine (colored red) and Impostor (colored yellow) score distribution of the NEURO A, B2 and C2 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1) using HH analysis.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>crossed Sets</b>				
<i>C1</i>	0.1064	0.1064	0.2050	1.0
<i>C2</i>	0.1193	0.1193	0.2321	1.0
<i>C3</i>	0.1232	0.1232	0.8798	1.0
<i>C4</i>	0.1162	0.1162	0.7179	1.0
<i>C5</i>	0.1345	0.1345	0.9301	1.0

Table 40: Characteristic individual performance values of NEURO matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using the HH method.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	5.33	0.9462	356.95	0.0029
<i>C2</i>	6.00	0.9394	359.12	0.0058
<i>C3</i>	6.16	0.9379	350.82	0.0151
<i>C4</i>	5.80	0.9414	368.33	0.0066
<i>C5</i>	6.71	0.9323	352.39	0.0092

Table 41: Characteristic individual performance values of NEURO matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the HH method.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
<i>C1</i>	0.1066	0.1066	0.1713	1.0
<i>C2</i>	0.1200	0.1200	0.1874	1.0
<i>C3</i>	0.1231	0.1231	0.7153	1.0
<i>C4</i>	0.1160	0.1160	0.4452	1.0
<i>C5</i>	0.1342	0.1342	0.6410	1.0

Table 42: Characteristic individual performance values of NEURO matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the HH method.

#### 5.4 FC

The following results represent the performance of the first non minutiae based fingerprint matcher. The calculated matching scores differ from the before described minutiae based outcomes. The described outcomes are based on the WA analysis method. In Tables 43 and 44 the most important performance values can be looked up. It seems that there must be a failure each time when the 2009 data set is involved in the matching process. In fact the *EER* of the single 2009 and crossed 2009 calculations are the worst of all performed. So for example an *EER* of 55.68% is even worse than bet on tossing a coin.

Based on the results there is a second effect observable. The *EER* of the 2013 single data sets is located around 12% for the B2 and B4 data set and respectively between 16% and 18% for the other three data bases. Those are interesting outcomes because the impression of the first results could be that there is something wrong with the implementation or with the used method itself. But it seems that there must be another reason why the matcher is delivering such bad results on the one hand and on the other hand *EER* values that are more or less in a realistic range.

Looking at the performance values more precisely there is a tendency within the splitted crossed data bases. The 2old3new data sets gather the worst results. The



Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Single Sets</b>				
<i>A</i>	55.68	0.4532	101.01	100.53
<i>B1</i>	17.92	0.9029	111.89	103.97
<i>B2</i>	11.85	0.9456	113.10	104.56
<i>B3</i>	17.09	0.9023	111.06	103.29
<i>B4</i>	11.82	0.9423	112.76	103.15
<i>B5</i>	16.15	0.918	111.31	101.72
<b>Crossed Sets</b>				
<i>C1</i>	42.59	0.6329	105.56	102.18
<i>C2</i>	53.50	0.5019	103.00	102.22
<i>C3</i>	53.58	0.5142	102.60	101.91
<i>C4</i>	51.22	0.5312	103.15	101.84
<i>C5</i>	49.05	0.5511	102.78	101.72

Table 43: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score.

3old2new *EER* for the crossed data is delivering the best values compared to the others. Meaning that the *EER* of 3old2new is about 5% lower than the crossed data sets of 2009 and 2013 as displayed in Tables 45, 46, 47 and 48. Due to the used imprints there must be a reason behind this situation based on the input quality of the images. This will be discussed after the next subsection in subsection 5.6.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Single Sets</b>				
<i>A</i>	0.9436	0.9976	1.0	0.9862
<i>B1</i>	0.3617	0.9083	1.0	0.7342
<i>B2</i>	0.1547	0.8402	1.0	0.6816
<i>B3</i>	0.3664	0.9281	1.0	0.7362
<i>B4</i>	0.1599	0.8581	1.0	0.6296
<i>B5</i>	0.2886	0.8524	1.0	0.9383
<b>Crossed Sets</b>				
<i>C1</i>	0.8939	0.9914	1.0	0.9136
<i>C2</i>	0.9562	0.9978	1.0	0.9395
<i>C3</i>	0.9488	0.9965	1.0	0.9679
<i>C4</i>	0.9444	0.9962	1.0	0.9337
<i>C5</i>	0.9350	0.9960	1.0	0.9949

Table 44: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 2old3new</b>				
<i>C1</i>	45.66	0.5938	104.42	102.14
<i>C2</i>	58.83	0.4298	101.61	102.75
<i>C3</i>	56.93	0.4578	101.41	101.89
<i>C4</i>	55.38	0.4732	101.83	101.79
<i>C5</i>	51.95	0.5074	101.61	100.94

Table 45: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 2old3new.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Crossed Sets 2old3new</b>				
<i>C1</i>	0.9039	0.9912	1.0	0.9480
<i>C2</i>	0.9639	0.9975	1.0	0.9665
<i>C3</i>	0.9576	0.9968	1.0	0.9800
<i>C4</i>	0.9511	0.9967	1.0	0.9627
<i>C5</i>	0.9401	0.9961	1.0	0.9965

Table 46: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 2old3new.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 3old2new</b>				
<i>C1</i>	38.27	0.6825	106.99	102.22
<i>C2</i>	46.24	0.5886	104.73	102.34
<i>C3</i>	46.26	0.5849	104.09	101.93
<i>C4</i>	45.14	0.6042	104.81	101.89
<i>C5</i>	44.46	0.6090	104.24	101.32

Table 47: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 3old2new.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Crossed Sets 3old2new</b>				
<i>C1</i>	0.8708	0.9911	1.0	0.8270
<i>C2</i>	0.9453	0.9980	1.0	0.8783
<i>C3</i>	0.9342	0.9963	1.0	0.9270
<i>C4</i>	0.9345	0.9957	1.0	0.8668
<i>C5</i>	0.9227	0.9962	1.0	0.9056

Table 48: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 3old2new.

## 5.5 POC

Regarding to the second non minutiae based matching results there is a huge difference between the minutiae based outcomes once again using the WA analysis strategy. First of all it is very interesting to consider the *EER* values of the data bases. Roughly spoken, similar to the minutiae matcher results a correlation between the non minutiae matcher results can be spotted. That means that for the POC the *EER* results are quite similar to the values from FC. The *EER* for the single data sets from 2013 is allocated between 22 and 26 percent. But each time imprints from 2009 are included in a data base they are distributed from 40 to 46. The difference of the worst results, delivered by the A again, is even larger than before. Here the gap between the crossed sets and the single set from 2009 is almost 3%. The overall calculated values can be looked up in the following Tables 49, 50, 51, 52, 53 and 54.

For this purpose the *EER* values for the split data sets are rather diverse. For the 2old3new case the results are oscillating between 29 and 35 percent whereas in 3old2new they get even worse than the 2009 single *EER* namely 46% to nearly 49%. Because of this situation it is not sure to argue if there is a similar shift to the left within the genuine score distribution like in the minutiae based matcher results. Furthermore the outcomes confirm the unexpected jump in the *Zero FRR* values located in the minutiae based matchers to be an abnormality related to those matcher

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Single Sets</b>				
<i>A</i>	46.11	0.5665	0.1119	0.0812
<i>B1</i>	26.06	0.7842	0.2365	0.0810
<i>B2</i>	22.66	0.8082	0.2567	0.0828
<i>B3</i>	25.03	0.7911	0.2449	0.0820
<i>B4</i>	22.61	0.8077	0.2875	0.0838
<i>B5</i>	24.87	0.7919	0.2532	0.0858
<b>Crossed Sets</b>				
<i>C1</i>	40.11	0.6626	0.1442	0.0812
<i>C2</i>	41.74	0.6570	0.1527	0.0820
<i>C3</i>	43.12	0.6427	0.1489	0.0816
<i>C4</i>	40.68	0.6688	0.1641	0.0825
<i>C5</i>	40.49	0.6674	0.1552	0.0835

Table 49: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score.

types and the data. But there is another interesting fact concerning the *Zero FAR*. It seems that this value is stable over all data sets and more or less fixed at 0.7614 without any detectable reason. It is also necessary to discuss the  $FAR_{100}$  and  $FAR_{1000}$  outcomes because at the chosen observation values it was not possible to gather any information because the lowest FAR values that can be taken into account are greater than those values.

Finally it is clear that there must be the same problem included as in the FC matching results. In the following Section 5.6 this situation will be discussed into more detail.

## 5.6 Variability of data sets and 2. non minutiae experiments

Regarding the displayed results in Section 5.2 there are a few interesting observations that need to be discussed. The most important one is the quite bad performance of the non minutiae based matchers *FC* and *POC*.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Single Sets</b>				
<i>A</i>	-	-	0.7614	0.9413
<i>B1</i>	-	-	0.7613	0.7031
<i>B2</i>	-	-	0.7614	0.6332
<i>B3</i>	-	-	0.7614	0.6097
<i>B4</i>	-	-	0.7614	0.6995
<i>B5</i>	-	-	0.7614	0.6760
<b>Crossed Sets</b>				
<i>C1</i>	0.7602	0.7614	0.7614	0.9083
<i>C2</i>	0.7606	0.7614	0.7614	0.8909
<i>C3</i>	0.7602	0.7614	0.7614	0.8742
<i>C4</i>	0.7602	0.7614	0.7614	0.9125
<i>C5</i>	0.7614	0.7614	0.7614	0.9023

Table 50: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 2old3new</b>				
<i>C1</i>	31.24	0.7910	0.1916	0.0801
<i>C2</i>	33.79	0.7723	0.2013	0.0816
<i>C3</i>	35.31	0.7518	0.1937	0.0810
<i>C4</i>	28.48	0.8237	0.2312	0.0820
<i>C5</i>	29.72	0.8102	0.2112	0.0832

Table 51: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 2old3new.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Crossed Sets 2old3new</b>				
<i>C1</i>	0.5974	0.7494	0.7614	0.8245
<i>C2</i>	0.6632	0.7551	0.7614	0.8398
<i>C3</i>	0.6862	0.7544	0.7614	0.7888
<i>C4</i>	0.6077	0.7490	0.7614	0.7638
<i>C5</i>	0.6251	0.7612	0.7614	0.8163

Table 52: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 2old3new.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 3old2new</b>				
<i>C1</i>	46.45	0.5559	0.1064	0.0822
<i>C2</i>	47.28	0.5638	0.1137	0.0824
<i>C3</i>	48.61	0.5533	0.1130	0.0823
<i>C4</i>	48.31	0.5421	0.1103	0.0830
<i>C5</i>	47.80	0.5514	0.1105	0.0838

Table 53: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 3old2new.

On the one hand the results in terms of *EER* and average genuine and impostor scores seems to be realistic in case of looking at the CASIA 2013 data sets. For sure, for example the *EER* is not that good compared to the minutiae based methods but the values range in the same area as in [17].

On the other hand each data set where the CASIA 2009 images are included is performing bad for those two matcher methodologies. There is not a big difference between tossing a coin and finding the corresponding imprints because the *EER* can be located around 40% in case of the POC method and around 55% for the FC matcher.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Crossed Sets 3old2new</b>				
<i>C1</i>	-	-	0.7614	0.9649
<i>C2</i>	-	-	0.7614	0.9557
<i>C3</i>	-	-	0.7614	0.9267
<i>C4</i>	-	-	0.7614	0.9453
<i>C5</i>	-	-	0.7614	0.9482

Table 54: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 3old2new.

The first idea concerning the bad performance reason was that there must be a certain problem with the 2009 data set. But in fact it is a circumstance that has been discussed in the Section 2.1 - non-ageing related variability during data acquisition. The failure occurs because of the main idea behind the matching algorithms and the imprints included in the older data set. Each part for itself is causing no problem, the composition is providing it.

Therefore the second idea was to look at the matcher methodologies and the data sets once more. The non minutiae based methods have one specific common idea during the match score calculation. Both are using a kind of rotation during the comparison step. So the imprints are rotated against each other. In case of the FC matcher using Gabor filter banks for each imprint a so called ridge feature map is constructed. As described in Section 3.5 the local orientation and frequency information is stored within those maps. During the matching process, the maps are rotated against each other to find the best fitting position. So the rotation step is very crucial. But not only for the FC matcher. The rotation alignment is one of the main steps during the POC matching as well. So to guarantee a good matching performance the imprints must be orientated always in roughly the same way. But this orientation condition is not given in the 2009 data set. There is a broad variety included as displayed in Section 4.4. As displayed in the aforementioned section it is possible to detect different positioned imprints. Based on this information a manual rotation adjustment was performed. This method compensated rotational differences from 45°, 90°, 180° and 270°. Each imprint was rotated to be nearly in the same position using 45° rotating



steps. To be on the safe side the same adaption was also performed for some images in the 2013 data sets too. The rotated imprints can be located after this rotation step within a angle of  $40^\circ$ . This specific area is the rotation range that is covered by the rotation step of the non minutiae matching methods.

So after the adjustment step the matching calculation for POC and FC were performed once again. For the non minutiae based matcher there was no need to repeat the experiments due to the fact that the this method is, due to the minutiae features, rotation independent.

During the calculation step another failure occurred for the FC method. As described in Chapter 4 the image width is 328 pixel and the height 356 pixel. According to the manual rotation not all imprints have a resolution of 328x356 anymore. There are a lot of images the measurement of which have been flipped to 356x328. Therefore the implementation is not able to compare both kinds of images. All imprints must have the same dimensions to provide a correct ridge feature map comparison. To ensure perfect functioning, all images dimensions have been equalized to 328x328. This is possible because each imprint contains a lot of information that is not useful for the comparison because the surface of the sensor is acquired. Those parts were cut off.

In the following two Sections 5.7 and 5.8 the results of the second experiments concerning the FC and POC fingerprint recognition system will be described. Basically an identical analysis was performed as introduced in Section 5.1. So for both experiments AS, WA, OA and HH analysis method are used to describe the results into more detail.

## 5.7 2. FC Experiments:

The presentation of the 2. FC and POC experiments will be done in the same manner as the results for the minutiae based matcher has been performed. So at first there will be the discussion based on the results without using the ageing influenced impostor scores and afterward those scores were added and the OA and HH analysis will be described. But before the corresponding outcomes of the entire data sets are presented in Tables 55 and 56. Similar to the minutiae based outcomes a degradation of the *average genuine scores* of the crossed sets is observable. Furthermore there is one

variation included as well. The difference between the *average genuine scores* of the single and crossed data bases is smaller as for NBIS and NEURO. Looking at the other results basically a very similar situation as for the minutiae based fingerprint recognition systems can be described. Nevertheless it is possible to observe that the manual rotation alignment improved the performance a lot comparing the values with the first experiments. But a clear difference between data set A and the other single sets remains. This effect is present for nearly all measurements. It is based on the circumstance that much more rotational displacement was included in the imprints contained in data base A. Furthermore this will certainly have an impact on the crossed data measurements as well. So all results are biased by this rotation caused effect which influences a precise comparison with the minutiae based recognition systems as well. In general the same *average genuine score* degradation is causing the *EER* increase comparing single data bases and crossed ones. *AUC* decreases, *FAR*<sub>100</sub>, *FAR*<sub>1000</sub> and *Zero FAR* tend to increase. Additionally is the stability of the *average impostor scores* and *Zero FRR* confirming as well that the second experiments behave like expected. The detailed discussion can be looked up in the following descriptions of WA, OA and HH analysis.

**FC WA Method:** The results for the second FC experiments and in particular the corresponding without ageing impostor score analysis will be displayed in the following Tables 57 and 58. It is clearly observable that the manual rotation adjustment caused a much better performance then during the first experiments. The *EER* of the 2013 data sets remain almost stable. Due to a few rotation adjustments within those data sets a slight difference is detectable but not crucial. The *EER* of the beforehand worse performing data bases was more than halved. The outcomes are now located between 20.17% and 29.24% in the data sets containing imprints from 2009.

According to the *EER* results of the 2. FC experiments it is necessary to discuss those values into more detail. At first view only the same tendency as detected in the minutiae based matching results can be observed. But, it is decisive that the impact of the high non-ageing related variability within the given data sets is influencing the matching results, even after performing the rotation alignment step discussed before. Therefore lets have a look at for example data set B2 and data set C2. The relative increase of the *EER* in the NBIS results for these two data bases is around 188%. The relative increase based on the NEURO outcomes is around 304%. The relative

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Single Sets</b>				
<i>A</i>	23.86	0.8192	110.24	102.03
<i>B1</i>	17.13	0.8928	113.18	104.62
<i>B2</i>	12.20	0.9427	113.10	104.67
<i>B3</i>	17.32	0.8987	111.06	103.50
<i>B4</i>	11.72	0.9450	112.56	102.80
<i>B5</i>	16.73	0.9086	111.11	102.21
<b>Crossed Sets</b>				
<i>C1</i>	20.15	0.8329	112.81	102.13
<i>C2</i>	27.23	0.8073	108.72	102.67
<i>C3</i>	25.70	0.8219	108.52	102.44
<i>C4</i>	25.66	0.8233	108.62	102.19
<i>C5</i>	27.21	0.8071	108.12	102.00

Table 55: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score using all matching scores.

values for the FC matcher is around 239%. So depending on this data set the relative increase of the *EER* in FC is higher compared to the results from NBIS but even lower as for the NEURO case. It will be interesting to see if in the POC outcomes the same effect can be displayed. Especially because the absolute increase for the first non-minutiae matcher is located between 3.04% and 17.04%. So a much higher variability can be detected as for the minutiae based approaches.

While the *EER* is higher for the crossed data bases, the *AUC* is decreasing compared to the single data sets. The same increase as for the *EER* can be observed for  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* as well. During the 2old3new, 3old2new and also the randomized averaging size adaptation computations the same tendencies could be confirmed. Especially looking at the average genuine score tendency leads to the assumption that also the shift in the genuine and impostor score distribution like observed in the

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Single Sets</b>				
<i>A</i>	0.5331	0.6551	0.8352	1.0
<i>B1</i>	0.3698	0.4948	0.6592	1.0
<i>B2</i>	0.3326	0.4801	0.6612	1.0
<i>B3</i>	0.4091	0.5969	0.7376	1.0
<i>B4</i>	0.2637	0.4071	0.7071	1.0
<i>B5</i>	0.3785	0.5285	0.9663	1.0
<b>Crossed Sets</b>				
<i>C1</i>	0.4317	0.5321	0.6861	1.0
<i>C2</i>	0.6539	0.7741	0.9191	1.0
<i>C3</i>	0.6488	0.7873	0.9496	1.0
<i>C4</i>	0.6252	0.7555	0.9223	1.0
<i>C5</i>	0.6522	0.7761	0.9984	1.0

Table 56: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using all matching scores.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
<i>same results as in the all scores case</i>				
<b>Crossed Sets</b>				
<i>C1</i>	20.17	0.8319	112.81	102.19
<i>C2</i>	29.24	0.7849	108.72	103.29
<i>C3</i>	26.91	0.8097	108.52	102.83
<i>C4</i>	25.92	0.8204	108.62	102.33
<i>C5</i>	27.07	0.8088	108.12	101.94

Table 57: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score using WA analysis.

Data Set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
$C1$	0.4253	0.5285	0.6613	1.0
$C2$	0.6750	0.7890	0.9191	1.0
$C3$	0.6518	0.7860	0.9496	1.0
$C4$	0.6238	0.7551	0.9223	1.0
$C5$	0.6454	0.7727	0.9984	1.0

Table 58: Characteristic individual performance values of FC matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR using WA analysis.

minutiae based matcher results can be stated as well in the FC case. The results of the 2old3new, 3old2new and the averaging computations can be looked up in Tables 59, 60, 61, 62, 63 and 64.

Looking at the average impostor and genuine scores the difference between the results of the first experiments is also detectable. While the outcomes for the impostor scores did not change significantly, the genuine scores raised in those data bases where imprints from 2009 are included. The same tendency is observable for the AUC values as well. So the AUC is now almost stable comparing the single data sets with each other. Additionally a more detailed information concerning the  $FAR_{100}$  and  $FAR_{1000}$  can be described. Two examples of ROC, also displaying AUC, can be looked up in Figures 37 and 38.

Similar like in the NBIS and NEURO results it seems that the growing process from  $FAR_{100}$  to *Zero FAR* can be compared with the tendency observable in the minutiae matching processes. Of course the difference between  $FAR_{100}$  and  $FAR_{1000}$  is much higher and the deviation between  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* is much lower for this FC case compared to NBIS or NEURO. The increase of the  $FAR_{100}$  values from single to crossed data sets is also much bigger, but all in all the same tendency can be stated. Besides, a cross-sensor effect concerning the T2 sensor data sets B1 and

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 2old3new</b>				
$C1$	21.20	0.8281	112.41	102.28
$C2$	32.03	0.7518	108.14	103.52
$C3$	27.76	0.7973	108.24	102.90
$C4$	27.78	0.7994	108.20	102.53
$C5$	27.75	0.8020	107.84	101.85

Table 59: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 2old3new using WA analysis.

$C1$  displayed in Table 57 is detectable. Especially looking at the *EER* outcomes it is clearly visible that there must be an impact because the values are definitely lower compared to the other data sets. It is interesting that this cross-sensor effect exists for the FC outcomes. For the minutiae based matcher the same did not occur. So probably it is matcher based and therefore just detectable for the FC results. Additionally it must be mentioned that the described drop of the *Zero FAR* for data set  $C4$  seems to be based on NBIS and NEURO results. For the remaining analysis of the second non-minutiae matcher these aspects will be discussed as well.

As displayed in Figures 39 and 40 a similar shift of the genuine score distribution to the left can be detected. It is clear that this shift is not that large as in the minutiae based results but nevertheless it is clearly visible. The difference to the uniqueness of the minutiae based method can be explained looking at the average genuine and impostor score values. They are much more similar to each other compared to the NBIS and NEURO matching results. The difference between the impostor scores and genuine scores for the crossed data sets is smaller than in the single data sets. This effect can be explained due to the not so clear distinctive matching results. It will be interesting to see how far these circumstances will be important in the OA and HH analysis and also in Chapter 6.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Crossed Sets 2old3new</b>				
<i>C1</i>	0.4300	0.5424	0.6320	1.0
<i>C2</i>	0.7228	0.8322	0.9414	1.0
<i>C3</i>	0.6669	0.8032	0.9559	1.0
<i>C4</i>	0.6389	0.7734	0.9430	1.0
<i>C5</i>	0.6579	0.7910	0.9991	1.0

Table 60: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning the splitted data 2old3new using WA analysis.

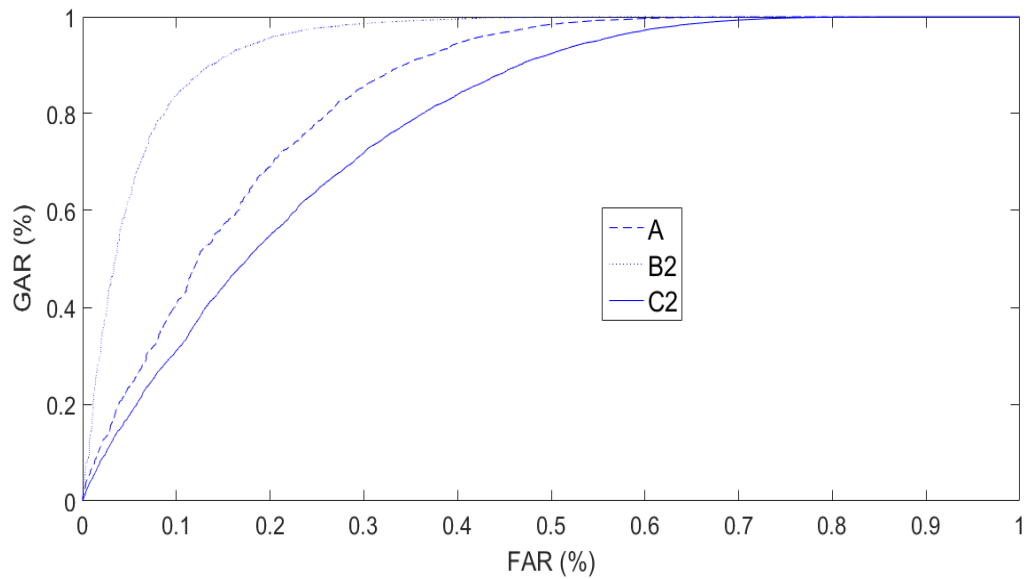


Fig. 37: ROC curves for single data sets A, B2 and crossed C2 using FC WA analysis.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 3old2new</b>				
$C_1$	19.33	0.8361	113.31	102.11
$C_2$	25.91	0.8225	109.44	103.05
$C_3$	25.74	0.8243	108.86	102.75
$C_4$	23.71	0.8435	109.15	102.17
$C_5$	26.06	0.8182	108.46	102.04

Table 61: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 3old2new using WA analysis.

Data Set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>Crossed Sets 3old2new</b>				
$C_1$	0.4158	0.5061	0.6321	1.0
$C_2$	0.6165	0.7329	0.8612	1.0
$C_3$	0.6293	0.7650	0.9107	1.0
$C_4$	0.6012	0.7252	0.8772	1.0
$C_5$	0.6308	0.7505	0.8989	1.0

Table 62: Characteristic individual performance values of FC matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR concerning the splitted data 3old2new using WA analysis.



data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	20.25	0.8321	112.83	102.20
<i>C2</i>	29.21	0.7853	108.73	103.29
<i>C3</i>	26.88	0.8093	108.52	102.83
<i>C4</i>	25.86	0.8203	108.63	102.33
<i>C5</i>	27.10	0.8080	108.11	101.94

Table 63: Characteristic individual performance values of FC matching including EER, average genuine and impostor scores concerning the randomized splitted data sets.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
<i>C1</i>	0.4242	0.5280	0.6534	1.0
<i>C2</i>	0.6751	0.7883	0.9073	1.0
<i>C3</i>	0.6510	0.7865	0.9347	1.0
<i>C4</i>	0.6232	0.7543	0.9169	1.0
<i>C5</i>	0.6474	0.7732	0.9528	1.0

Table 64: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the WA method.

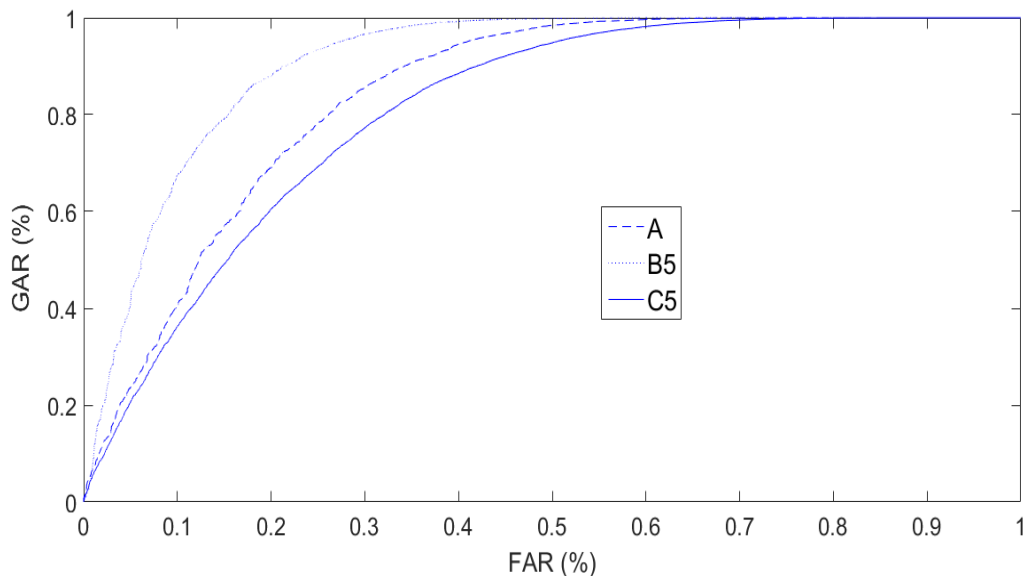
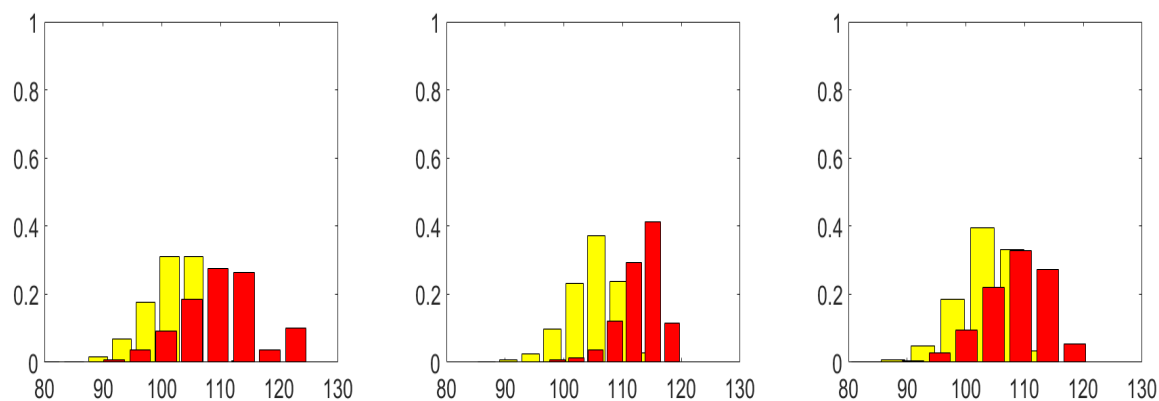


Fig. 38: ROC curves for single data sets A, B5 and crossed C5 using FC WA analysis.

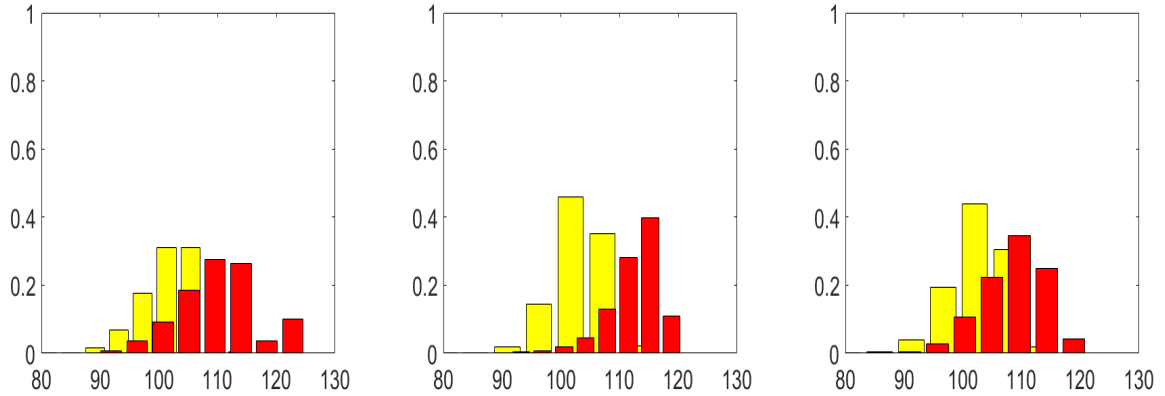


(a) Genuine score distribution vs. impostor score distribution of the rotated data set A using WA analysis.

(b) Genuine score distribution vs. impostor score distribution of the rotated data set B2 using WA analysis.

(c) Genuine score distribution vs. impostor score distribution of the rotated data set C2 using WA analysis.

Fig. 39: Genuine (colored red) and Impostor (colored yellow) score distribution of the FC rotated A, B2 and C2 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).



(a) Genuine score distribution vs. impostor score distribution of the rotated data set A using WA analysis.

(b) Genuine score distribution vs. impostor score distribution of the rotated data set B4 using WA analysis.

(c) Genuine score distribution vs. impostor score distribution of the rotated data set C4 using WA analysis.

Fig. 40: Genuine (colored red) and Impostor (colored yellow) score distribution of the FC rotated A, B4 and C4 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	20.15	0.8340	112.81	102.06
<i>C2</i>	25.07	0.8297	108.72	102.06
<i>C3</i>	24.49	0.8340	108.52	102.06
<i>C4</i>	25.41	0.8262	108.62	102.06
<i>C5</i>	27.32	0.8054	108.12	102.06

Table 65: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score using OA analysis.

**FC OA Method:** After the results of the WA analysis for the FC matcher have been presented in the previous Section 5.7 of this master thesis the second analysis focusing on the time span including impostor scores will be discussed. In Tables 65, 67, 66 and 68 the performance values for the first non-minutiae matcher can be observed.

Data Set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	0.4325	0.5325	0.6861	1.0
<i>C2</i>	0.6183	0.7441	0.9191	1.0
<i>C3</i>	0.6460	0.7879	0.9496	1.0
<i>C4</i>	0.6272	0.7564	0.9223	1.0
<i>C5</i>	0.6557	0.7789	0.9409	1.0

Table 66: Characteristic individual performance values of FC matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR using OA analysis.

Basically there is not really a difference between the outcomes for the without ageing impostor score analysis (WA) and the present one using only time span including impostor scores. The  $EER$ ,  $FAR_{100}$ ,  $FAR_{1000}$  and  $Zero FAR$  are higher for the crossed data bases. The  $AUC$  and *average genuine scores* are lower as in the single data sets. Of course there are small fluctuations, but except one special case no abnormal behavior can be described. This special observation could be caused by the used sensor. Looking at the  $EER$  values the aspect is clearly visible. In Table 65 are the results for data set C2 at 25.07% and for C3 at 24.49%. Both are those crossed data sets where the sensor types used during the fingerprint image acquisition in 2009 and 2013 have been the same - the uru4000<sub>1</sub>. As readable in Table 57, the  $EER$  for C2 in the WA analysis is located at 29.24% and for the C3 at 26.91%. So a clear reduction is observable using different types of impostor scores.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
$C1$	20.08	0.8343	112.83	102.06
$C2$	25.11	0.8289	108.71	102.06
$C3$	24.60	0.8331	108.51	102.06
$C4$	25.39	0.8261	108.63	102.06
$C5$	27.32	0.8050	108.12	102.06

Table 67: Characteristic individual performance values of FC matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using OA analysis method.

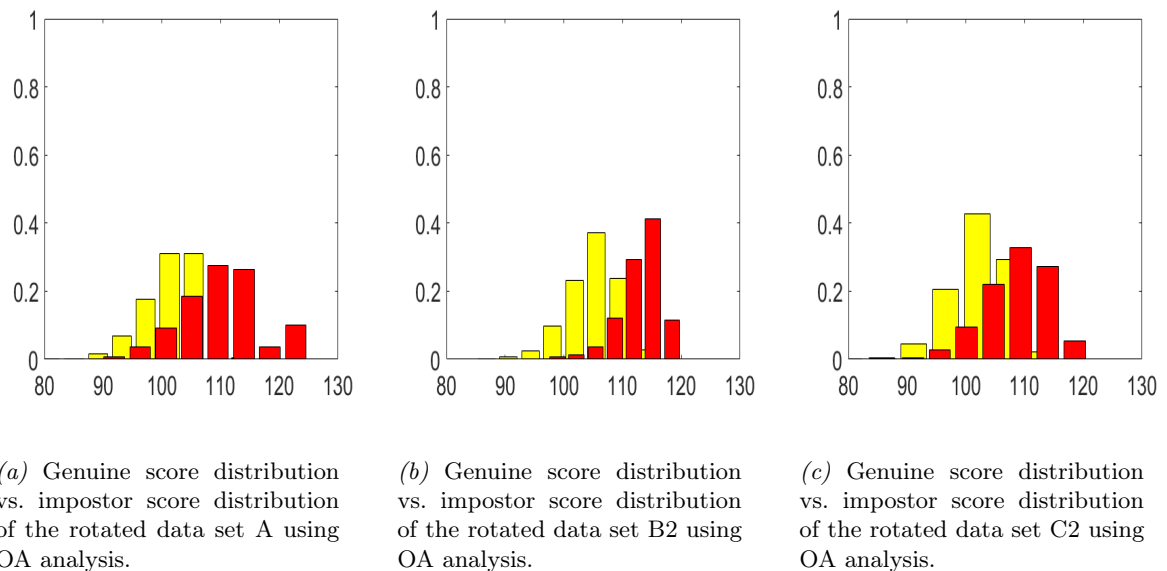


Fig. 41: Genuine (colored red) and Impostor (colored yellow) score distribution of the FC rotated A, B2 and C2 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1).

Looking at the average impostor scores it can be detected that the slight decrease of the average from WA to OA analysis will be the reason for this effect. The reduction can be caused by different aspects. The two most important are quality and included ageing. But based on the average scores this can not be classified. Probably the quality analysis described in Chapter 7 may help to find a valid answer for this circumstance.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
<i>C1</i>	0.4316	0.5329	0.6798	1.0
<i>C2</i>	0.6183	0.7442	0.9098	1.0
<i>C3</i>	0.6462	0.7880	0.9423	1.0
<i>C4</i>	0.6267	0.7563	0.9145	1.0
<i>C5</i>	0.6557	0.7789	0.9340	1.0

Table 68: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the OA method.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>single sets</b>				
<i>same results as in the all scores case</i>				
<b>Crossed Sets</b>				
<i>C1</i>	20.19	0.8319	112.81	102.19
<i>C2</i>	29.24	0.7849	108.72	103.29
<i>C3</i>	26.91	0.8097	108.52	102.83
<i>C4</i>	25.91	0.8204	108.62	102.33
<i>C5</i>	27.07	0.8088	108.12	101.94

Table 69: Characteristic individual performance values of FC matching including EER, AUC, Average Genuine Score and Average Impostor Score using HH analysis.

Despite, the same effect can be verified looking at Table 63 and 67 as well, but for a detection in a figure the differences are not high enough. It remains to be seen if the same observation can be made for the following HH analysis.

**FC HH Method:** In the present section the results of the FC HH analysis will be discussed. The outcomes, which can be looked up in Tables 69, 71, 70 and 72 are more or less equal to the values presented in the WA analysis using the FC fingerprint recognition system.

The only difference is the sensor impact like introduced in Section 5.7. Because there are also impostor scores used, where no time span is included, the detectable effect on the *EER* of data sets C2 and C3 is not that strong compared to the OA analysis. Nevertheless the same tendency is clearly measurable. According to this it must be considered that this effect could also be matcher dependent because for the minutiae based ones the same circumstance was not present. Therefore a further investigation will be taken into account while discussing the results of the second non-minutiae matcher, the POC matcher.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>single sets</b>				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	0.4250	0.5291	0.6596	1.0
<i>C2</i>	0.6752	0.7883	0.9142	1.0
<i>C3</i>	0.6517	0.7860	0.9428	1.0
<i>C4</i>	0.6237	0.7547	0.9209	1.0
<i>C5</i>	0.6463	0.7728	0.9834	1.0

Table 70: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using HH analysis.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	20.23	0.8321	112.81	102.13
<i>C2</i>	27.24	0.8046	108.71	102.67
<i>C3</i>	25.73	0.8165	108.51	102.44
<i>C4</i>	25.69	0.8204	108.62	102.19
<i>C5</i>	27.20	0.8081	108.12	102.00

Table 71: Characteristic individual performance values of FC matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using HH analysis.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
<i>C1</i>	0.4297	0.5312	0.6686	1.0
<i>C2</i>	0.6538	0.7746	0.9076	1.0
<i>C3</i>	0.6485	0.7878	0.9354	1.0
<i>C4</i>	0.6250	0.7555	0.9140	1.0
<i>C5</i>	0.6519	0.7765	0.9445	1.0

Table 72: Characteristic individual performance values of FC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the HH method.



As mentioned earlier this aspect is the most interesting one of the HH analysis for the FC results. All the other characteristic performance values seem to be equal to the WA and OA case. This leads to the assumption that ageing is not influencing the performance of the fingerprint matching regarding the different types of impostor scores. For the used fingerprint recognition system the impostor scores are always more or less stable for each matcher and distinctively lower compared to the genuine ones so far. So once more it seems that neither the randomized score selection process nor the impostor score split has an impact on the overall observed behavior of the used fingerprint recognition system. The genuine score shift to the left caused by either the imprints' quality or fingerprint ageing can be verified for the first non-minutiae based approach regardless which analysis method is used.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Single Sets</b>				
<i>A</i>	25.39	0.8218	0.2366	0.1121
<i>B1</i>	11.67	0.9376	0.2951	0.1070
<i>B2</i>	8.00	0.9635	0.3107	0.1088
<i>B3</i>	10.90	0.9408	0.2987	0.1080
<i>B4</i>	6.87	0.9672	0.3473	0.1096
<i>B5</i>	10.04	0.9415	0.3059	0.1131
<b>Crossed Sets</b>				
<i>C1</i>	37.75	0.6892	0.1802	0.1091
<i>C2</i>	27.58	0.7958	0.2069	0.1103
<i>C3</i>	26.12	0.8080	0.2105	0.1106
<i>C4</i>	24.62	0.8273	0.2257	0.1110
<i>C5</i>	25.63	0.8164	0.2148	0.1122

Table 73: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score using WA analysis.

## 5.8 2. POC Experiments:

Completing the presentation of the performance experiment results, the outcomes of the second experiments concerning the second non minutiae based matcher, the POC matcher, will be described. As described before the result presentation starts with the AS results to get an overview impression for the performance of fingerprint recognition system. The most interesting observation is based on the difference between the average genuine and impostor scores of FC and POC.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>Single Sets</b>				
<i>A</i>	0.4428	0.5260	0.7698	1.0
<i>B1</i>	0.2005	0.3178	0.6959	1.0
<i>B2</i>	0.1494	0.2479	0.5739	1.0
<i>B3</i>	0.1933	0.2882	0.5326	1.0
<i>B4</i>	0.1137	0.1862	0.6408	1.0
<i>B5</i>	0.1979	0.3107	0.7275	1.0
<b>Crossed Sets</b>				
<i>C1</i>	0.6942	0.7418	0.8900	1.0
<i>C2</i>	0.5241	0.6354	0.8502	1.0
<i>C3</i>	0.5026	0.6167	0.8487	1.0
<i>C4</i>	0.4675	0.5766	0.8765	1.0
<i>C5</i>	0.4935	0.6179	0.8975	1.0

Table 74: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using WA analysis.

Although both methods are non minutiae based it seems that the second recognition system is delivering more distinct outcomes in terms of clear separable average matching scores. Of course using *EER* and considering the crossed data sets FC performs better, but for the single data sets from 2013 POC is performing much better. The results for the AS interpretation are available in Tables 73 and 74. Basically an identical overall performance of POC like described for NBIS, NEURO and FC is

present. At the first sight it seems that there is no difference. But a few fluctuations can be detected if the FC and POC results are compared. As mentioned before POC is performing better in terms of *EER* using the data bases B1 till B5. According to this aspect a overall better performance of POC can be observed for all data sets considering  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR*. Apart from this the *AUC* and the *average genuine scores* are decreasing comparing single and crossed data bases. Whereas *EER*,  $FAR_{100}$ ,  $FAR_{1000}$  and *Zero FAR* are increasing once more. In the following the WA analysis is taken into account and the investigations will end with the HH analysis like for the other fingerprint recognition systems before.

**POC WA Method:** In the following Tables 75, 76, 77, 78, 79, 80, 81 and 82 the WA analysis' results of the POC fingerprint recognition system are displayed.

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
single sets				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	38.24	0.6831	0.1802	0.1096
<i>C2</i>	27.71	0.7950	0.2069	0.1105
<i>C3</i>	25.99	0.8110	0.2105	0.1100
<i>C4</i>	24.59	0.8282	0.2257	0.1109
<i>C5</i>	28.98	0.7944	0.2148	0.1126

Table 75: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score using WA analysis.

In fact the main tendency is quite similar compared to the FC matching results. The rotation adjustment effected a decreasing of the *EER* of about 10% to 19%. So the matching performance of the last non minutiae based fingerprint recognition system could be improved as well. Comparing the outcomes with the characteristic values of the other it is distinct that the minutiae based ones are performing better in all possible absolute values. The comparison with the FC fingerprint recognition system

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
single sets				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	0.6895	0.7405	0.8900	1.0
<i>C2</i>	0.5230	0.6342	0.8502	1.0
<i>C3</i>	0.5007	0.6109	0.8487	1.0
<i>C4</i>	0.4673	0.5750	0.8765	1.0
<i>C5</i>	0.4954	0.6221	0.8975	1.0

Table 76: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using WA analysis.

is not as clear. For the single data set of 2013 the POC fingerprint recognition system is delivering better matching results. The same is true for data sets C2, C3 and C4. In the other data sets it would be better to use the first non-minutiae based fingerprint recognition system instead. So it is not that easy to set up a unique ranking which gives a complete overview of the performance of the used fingerprint recognition system of this master thesis. Especially it is not possible to assign the worst of the four used fingerprint recognition implementations because it depends which data set is taken into account.

The *EER* of the POC fingerprint recognition system using WA analysis of the single data sets varies from 6.87% to 25.39%. For the crossed data sets the *EER* can be located between 24.59% and 38.24%. Having a look at the absolute differences between the single and crossed data bases a fluctuation from 15.09% to 26.57% can be observed. If the same comparison will be performed for the relative differences the variation is in the range of 238.44% to 357.93%. Depending on this relative consideration of the *EER* it is possible to state that the POC is the most unstable fingerprint recognition system of the used ones.

All other characteristics like *AUC*, *FAR*<sub>100</sub>, *FAR*<sub>1000</sub>, *Zero FAR* and *Zero FRR* support the *EER* outcomes because they exhibit an identical trend, which is displayed in the FC characteristic values. First and foremost the detected drop of the *Zero*

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 2old3new</b>				
<i>C1</i>	33.78	0.7375	0.1989	0.1083
<i>C2</i>	23.02	0.8391	0.2276	0.1100
<i>C3</i>	21.82	0.8487	0.2277	0.1092
<i>C4</i>	20.07	0.8709	0.2534	0.1100
<i>C5</i>	21.71	0.8523	0.2336	0.1122

Table 77: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 2old3new using WA analysis.

*FAR* in data set *C4* in the minutiae based fingerprint recognition systems can not be confirmed in the POC. Both, the FC and POC results are supporting the assumption that this effect is an interesting observation caused by NBIS and NEURO. The same is valid for the trend from  $FAR_{100}$  to *Zero FAR*. NBIS and NEURO are displaying a different one as for the non minutiae fingerprint recognition system.

The performance of the WA analysis of the POC fingerprint recognition system is also displayed in Figures 42 and 43 where two example ROC can be looked up. These two graphical representations are confirming once more that in the data set from 2009 there must be a lot of rotation and other positional variances within the fingerprint images. Those fluctuations are the reason for the big differences between the performance of the single data sets from 2009 and 2013.

Based on the average genuine and impostor score distributions it is possible to detect quite the same effect as before looking at the other matching score distributions. So the genuine score distribution is also skewed to the left. There is a higher number of low genuine scores in the crossed data set looking at Figures 45 and 44. But there is also a difference. The number of impostor scores is also lower. In the following Chapter 6 it will be interesting to have a look at this effect.

In Figures 44 and 45 the shift in the genuine score distribution to the left can be detected like in all other cases before. Additional to the genuine shift it can also

Data Set	$\text{FAR}_{100}$	$\text{FAR}_{1000}$	Zero FAR	Zero FRR
<b>Crossed Sets 2old3new</b>				
$C1$	0.6035	0.6681	0.8308	1.0
$C2$	0.4375	0.5637	0.8058	1.0
$C3$	0.4260	0.5433	0.8112	1.0
$C4$	0.3670	0.4750	0.8298	1.0
$C5$	0.4186	0.5568	0.8668	1.0

Table 78: Characteristic individual performance values of POC matching including  $\text{FAR}_{100}$ ,  $\text{FAR}_{1000}$ , Zero FAR and Zero FRR concerning the splitted data 2old3new using WA analysis.

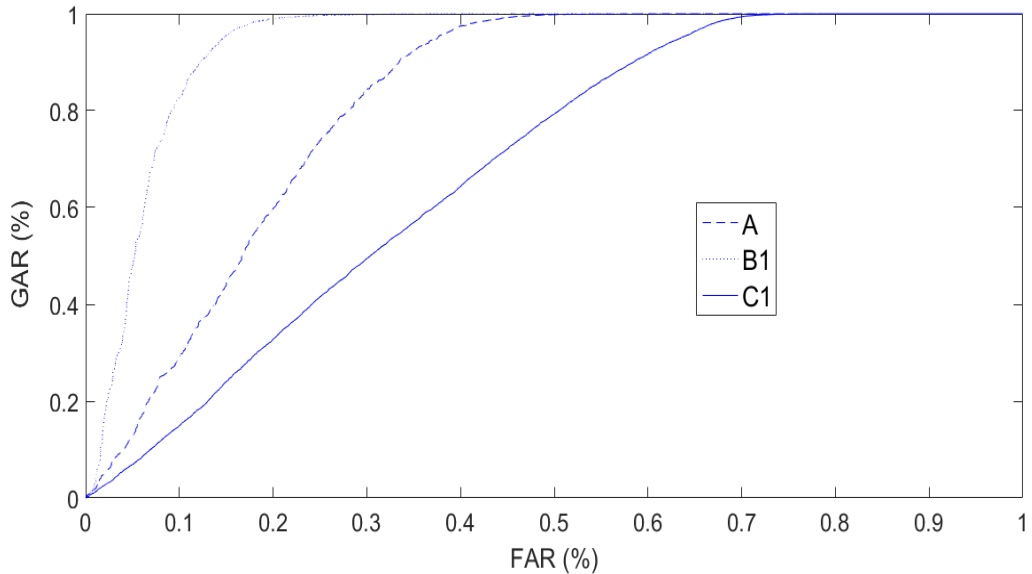


Fig. 42: ROC curves for single data sets A, B1 and crossed C1 using POC and WA analysis.

be detected that there is a higher variability within the total number of impostor scores. The reason for the impostor fluctuation probably is caused by the fingerprint recognition system because it has not been observed in the other matching results. Therefore it will be necessary to have a more detailed look on this abnormality in OA and HH analysis of this fingerprint recognition system. Nevertheless the shift for

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>Crossed Sets 3old2new</b>				
<i>C1</i>	41.83	0.6344	0.1653	0.1108
<i>C2</i>	31.22	0.7582	0.1903	0.1109
<i>C3</i>	29.32	0.7785	0.1967	0.1108
<i>C4</i>	27.97	0.7914	0.2035	0.1117
<i>C5</i>	28.82	0.7826	0.1997	0.1130

Table 79: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score concerning the splitted data 3old2new using WA analysis.

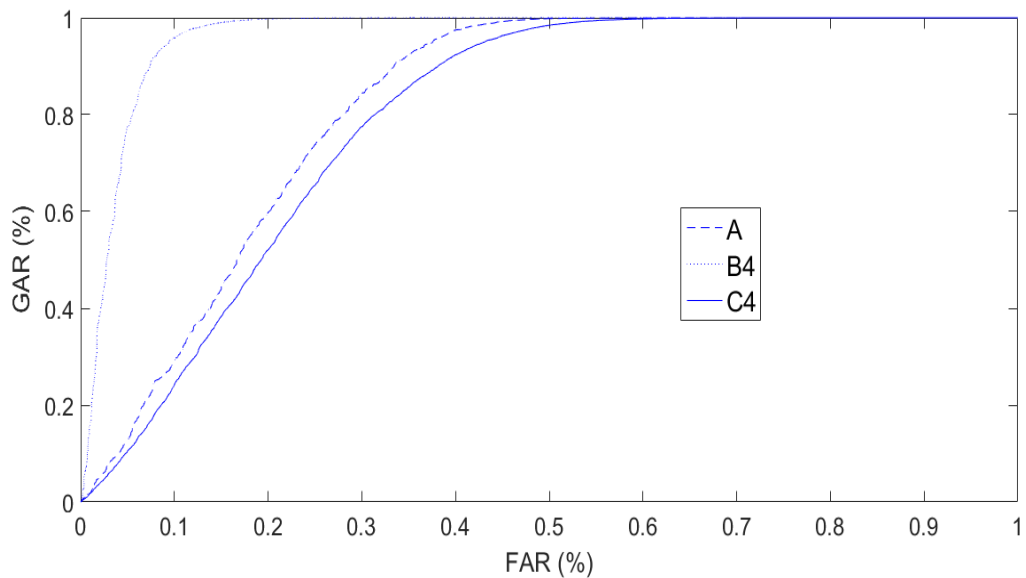
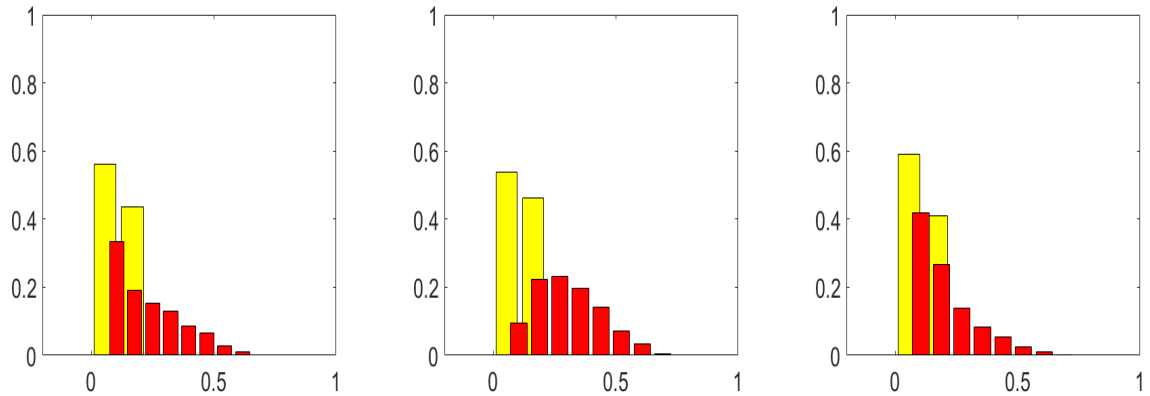


Fig. 43: ROC curves for single data sets A, B4 and crossed C4 using POC and WA analysis.

the genuine scores and the more or less stability of the impostor scores for all cases leads to the confirmation of a first ageing effect.

Data Set	$FAR_{100}$	$FAR_{1000}$	Zero FAR	Zero FRR
<b>Crossed Sets 3old2new</b>				
$C1$	0.7577	0.7975	0.9157	1.0
$C2$	0.5924	0.6904	0.8702	1.0
$C3$	0.5630	0.6618	0.8583	1.0
$C4$	0.5444	0.6571	0.8422	1.0
$C5$	0.5571	0.6738	0.8746	1.0

Table 80: Characteristic individual performance values of POC matching including  $FAR_{100}$ ,  $FAR_{1000}$ , Zero FAR and Zero FRR concerning the splitted data 3old2new using WA analysis.



(a) Genuine score distribution vs. impostor score distribution of the rotated data set A using WA analysis.

(b) Genuine score distribution vs. impostor score distribution of the rotated data set B2 using WA analysis.

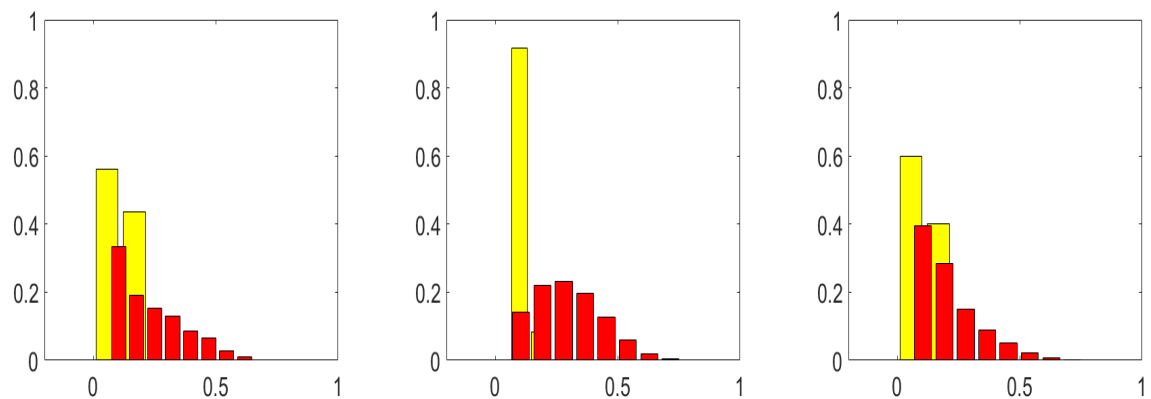
(c) Genuine score distribution vs. impostor score distribution of the rotated data set C2 using WA analysis.

Fig. 44: Genuine (colored red) and Impostor (colored yellow) score distribution of the POC rotated A, B2 and C2 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1) using WA analysis.



data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
$C1$	38.28	0.6824	0.1803	0.1096
$C2$	27.75	0.7941	0.2065	0.1105
$C3$	25.98	0.8108	0.2106	0.1100
$C4$	24.50	0.8284	0.2257	0.1109
$C5$	25.81	0.8146	0.2148	0.1126

Table 81: Characteristic individual performance values of POC matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using WA analysis..



(a) Genuine score distribution vs. impostor score distribution of the rotated data set A using WA analysis.

(b) Genuine score distribution vs. impostor score distribution of the rotated data set B3 using WA analysis.

(c) Genuine score distribution vs. impostor score distribution of the rotated data set C3 using WA analysis.

Fig. 45: Genuine (colored red) and Impostor (colored yellow) score distribution of the POC rotated A, B3 and C3 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1) using WA analysis.

data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
<i>C1</i>	0.6895	0.7401	0.8730	1.0
<i>C2</i>	0.5239	0.6348	0.8382	1.0
<i>C3</i>	0.5009	0.6104	0.8330	1.0
<i>C4</i>	0.4668	0.5742	0.8372	1.0
<i>C5</i>	0.4951	0.6213	0.8751	1.0

Table 82: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the WA method.

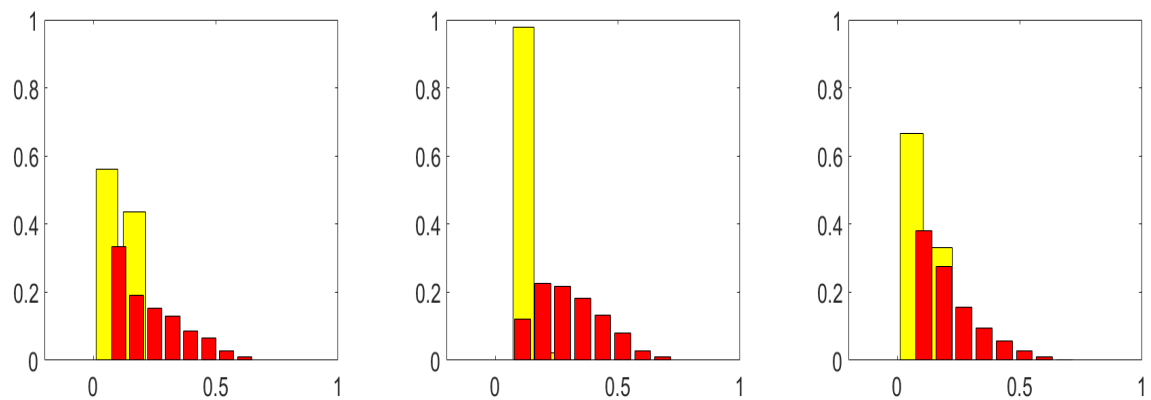
**POC OA Method:** In the present section the results for OA analysis of the POC fingerprint recognition system will be discussed. As for the other three fingerprint recognition system there are mainly four tables which are representing the results of the performance analysis. Those Tables were 83, 85, 84 and 86. In Table 83 and 84 the outcomes without size adaption for the crossed data sets are displayed. The performance characteristics for the randomized size adaption were presented in Table 85 and 86.

Examination of the results of the present POC based OA analysis leads to the conclusion that there is not a significant difference between this analysis and the previous WA one. Even having a closer look at the outcomes only reveals two slightly higher fluctuations. The first one can be located concerning the *EER* values. For data set *C1* in Table 83 the deviation is around 1.00% and for data set *C5* around 3.50%. Both values for the OA analysis are lower compared to the results of the without ageing impostor (WA) analysis. It seems that the quite significant difference for the *C5* data base is caused by some random circumstance. Because for the randomly generated size adaption just the fluctuation of the *C1* *EER* can be detected again looking at Table 81 and 85.

The second variation is observable in the *Zero FAR* values which can be looked up in Table 84 and 86. As readable in Table 76 and 82 those *Zero FAR* outcomes are higher compared to the same results for the corresponding data sets in the OA analysis. It

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
single sets				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
$C1$	37.20	0.6952	0.1802	0.1087
$C2$	27.40	0.7965	0.2069	0.1102
$C3$	26.26	0.8050	0.2105	0.1111
$C4$	24.62	0.8282	0.2257	0.1112
$C5$	25.39	0.8185	0.2148	0.1119

Table 83: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score using OA analysis.



(a) Genuine score distribution vs. impostor score distribution of the rotated data set A using OA analysis.

(b) Genuine score distribution vs. impostor score distribution of the rotated data set B5 using OA analysis.

(c) Genuine score distribution vs. impostor score distribution of the rotated data set C5 using OA analysis.

Fig. 46: Genuine (colored red) and Impostor (colored yellow) score distribution of the POC rotated A, B5 and C5 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1) using OA analysis.

is interesting that the  $FAR_{100}$  and  $FAR_{1000}$  on the contrary seem to be more or less stable.

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
single sets				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	0.6980	0.7425	0.8214	1.0
<i>C2</i>	0.5255	0.6358	0.7926	1.0
<i>C3</i>	0.5039	0.6197	0.8414	1.0
<i>C4</i>	0.4676	0.5786	0.8437	1.0
<i>C5</i>	0.4917	0.6141	0.8640	1.0

Table 84: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using OA analysis.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	37.19	0.6948	0.1801	0.1087
<i>C2</i>	27.46	0.7959	0.2067	0.1102
<i>C3</i>	26.23	0.8051	0.2107	0.1111
<i>C4</i>	24.60	0.8261	0.2258	0.1112
<i>C5</i>	25.38	0.8181	0.2146	0.1119

Table 85: Characteristic individual performance values of POC matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the OA method.

In Figure 46 it is also detectable that the genuine score distribution shift to the left and the overall stability of the impostor scores occur like in all other cases before. Especially the very high number of low impostor scores like displayed in the middle graphic of Figure 45 is also visible in the middle image of Figure 46 which was introduced before. Furthermore the clear trend that the genuine score distributions tend to adapt the impostor one is present in the right sub image of Figure 46.

data set	$\text{FAR}_{100}$	$\text{FAR}_{1000}$	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
<i>C1</i>	0.6982	0.7427	0.8194	1.0
<i>C2</i>	0.5258	0.6366	0.7841	1.0
<i>C3</i>	0.5031	0.6196	0.8123	1.0
<i>C4</i>	0.4678	0.5781	0.8249	1.0
<i>C5</i>	0.4920	0.6148	0.8279	1.0

Table 86: Characteristic individual performance values of POC matching including  $\text{FAR}_{100}$ ,  $\text{FAR}_{1000}$ , Zero FAR and Zero FRR concerning the randomized splitted data sets using the OA method.

**POC HH Method:** In the last section of Chapter 5 the results for the outstanding HH analysis of the fourth fingerprint recognition system will be presented. Additionally the general information gained from this chapter will be discussed at the end of the present Section 5.8.

First of all the performance characteristics for the HH analysis of the POC fingerprint recognition system can be looked up in Tables 87, 89, 88 and 90. The first impression is that the outcomes are basically similar to the other two analysis methods presented in the previous sections. This impression is true for many calculated values. Despite, it is also possible to gather an additional information. For the other fingerprint recognition systems discussed in this chapter the HH analysis was always a mixture of WA and OA. Of course that is probably the logical assumption, but for the POC this

Data Set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
single sets				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	38.24	0.6831	0.1802	0.1096
<i>C2</i>	27.71	0.7950	0.2069	0.1105
<i>C3</i>	25.99	0.8110	0.2105	0.1100
<i>C4</i>	24.58	0.8282	0.2257	0.1109
<i>C5</i>	25.84	0.8144	0.2148	0.1126

Table 87: Characteristic individual performance values of POC matching including EER, AUC, Average Genuine Score and Average Impostor Score using HH analysis.

assumption can be verified much better. The reason for this is a higher variation in the single values. That means that there are certain characteristics which are shared in a more distinct way either with the WA case or with the OA one.

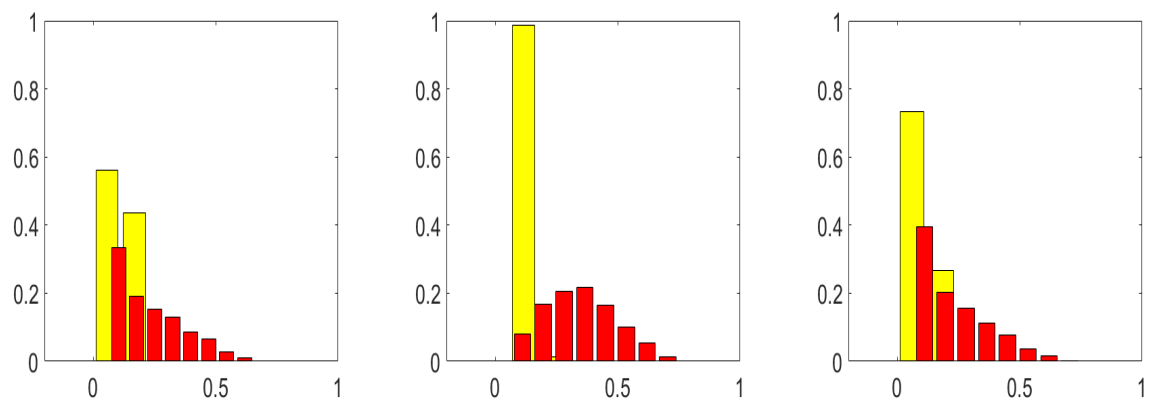
The most prominent examples are the *EER* values for data sets C1. For the entire data set analysis displayed in Tables 75, 83 and 87 the *EER* value is similar for each of the cases. On the contrary for the randomly size adapted analysis presented in Tables 81, 85 and 89 it is clearly observable that the equal error rate of the HH analysis corresponds more to the outcome of the WA case. Another example can be detected looking at the *Zero FAR*. There is no doubt that the derived values of WA and HH analysis are more similar than for comparing OA and the HH case.

Apart from this information there is no specific unexpected abnormality included in the results of the HH analysis. Therefore it is also not a surprise that the genuine score distribution shift appears once more. Additionally an increase in the *EER*, *FAR*<sub>100</sub>, *FAR*<sub>1000</sub> and *Zero FAR* for the crossed data sets is detectable. According to this information stability in *average impostor scores* and *Zero FRR* can be described. The *AUC* decreases similar to the *average genuine scores*. In Figure 47 one example for data set A, B4 and C4 is displayed. It is interesting to observe that the shift of the genuine scores from the single 2009 set to the crossed C4 data base is not

Data Set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
single sets				
	<i>same results as in the all scores case</i>			
<b>Crossed Sets</b>				
<i>C1</i>	0.6895	0.7404	0.8845	1.0
<i>C2</i>	0.5228	0.6343	0.8461	1.0
<i>C3</i>	0.5010	0.6111	0.8424	1.0
<i>C4</i>	0.4673	0.5746	0.8574	1.0
<i>C5</i>	0.4953	0.6215	0.8905	1.0

Table 88: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR using HH analysis.

very big. So a clear difference to the very distinct outcomes of for example NEURO can be detected.



(a) Genuine score distribution vs. impostor score distribution of the rotated data set A using HH analysis.

(b) Genuine score distribution vs. impostor score distribution of the rotated data set B4 using HH analysis.

(c) Genuine score distribution vs. impostor score distribution of the rotated data set C4 using HH analysis.

Fig. 47: Genuine (colored red) and Impostor (colored yellow) score distribution of the POC rotated A, B4 and C4 data set (x-axis denotes the matching scores and y-axis the percentage scaled from 0 to 1) using HH analysis.

data set	EER (%)	AUC	Av. Gen. Score	Av. Imp. Score
<b>randomized crossed sets</b>				
<i>C1</i>	25.56	0.8161	0.2106	0.1091
<i>C2</i>	27.66	0.7945	0.2066	0.1103
<i>C3</i>	26.13	0.8077	0.2106	0.1106
<i>C4</i>	24.57	0.8271	0.2257	0.1110
<i>C5</i>	25.63	0.8160	0.2147	0.1122

Table 89: Characteristic individual performance values of POC matching including EER, average genuine and impostor scores concerning the randomized splitted data sets using the HH method.

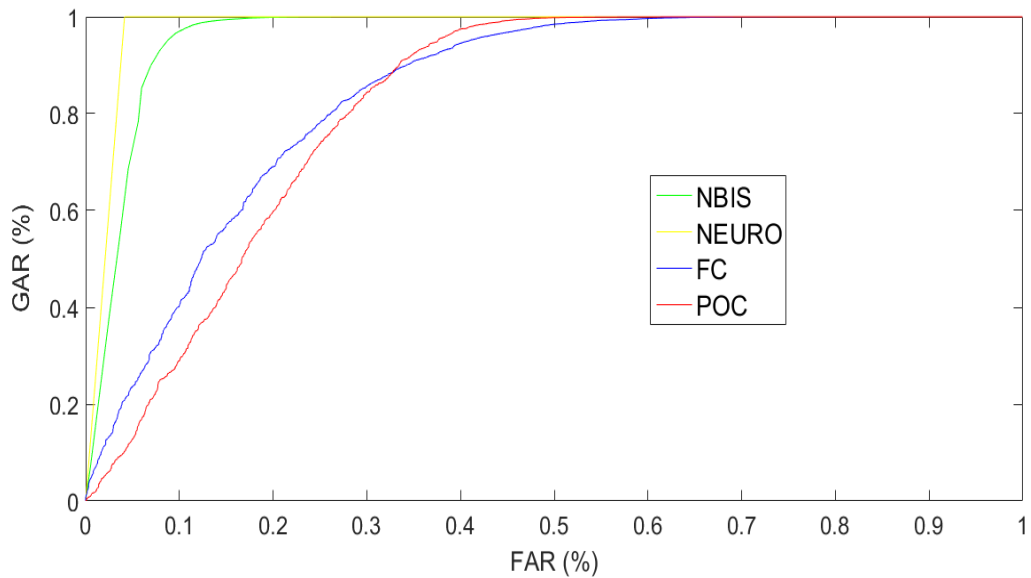


Fig. 48: ROC curves of data set A using results from all used fingerprint recognition system types using HH analysis.

Based on the knowledge about each fingerprint recognition systems' performance it is possible to summarize and compare the results. First there can be a comparison in terms of the ROC curves. In Figures 48 and 49 this is displayed. In Figure 48 data set 2009 is pictured. In the second Figure 49 the crossed data set C2 is depicted. For



data set	FAR <sub>100</sub>	FAR <sub>1000</sub>	Zero FAR	Zero FRR
<b>randomized crossed sets</b>				
<i>C1</i>	0.5080	0.6190	0.8325	1.0
<i>C2</i>	0.5253	0.6365	0.8283	1.0
<i>C3</i>	0.5025	0.6170	0.8217	1.0
<i>C4</i>	0.4668	0.5756	0.8257	1.0
<i>C5</i>	0.4937	0.6187	0.8571	1.0

Table 90: Characteristic individual performance values of POC matching including FAR<sub>100</sub>, FAR<sub>1000</sub>, Zero FAR and Zero FRR concerning concerning the randomized splitted data sets using the HH method.

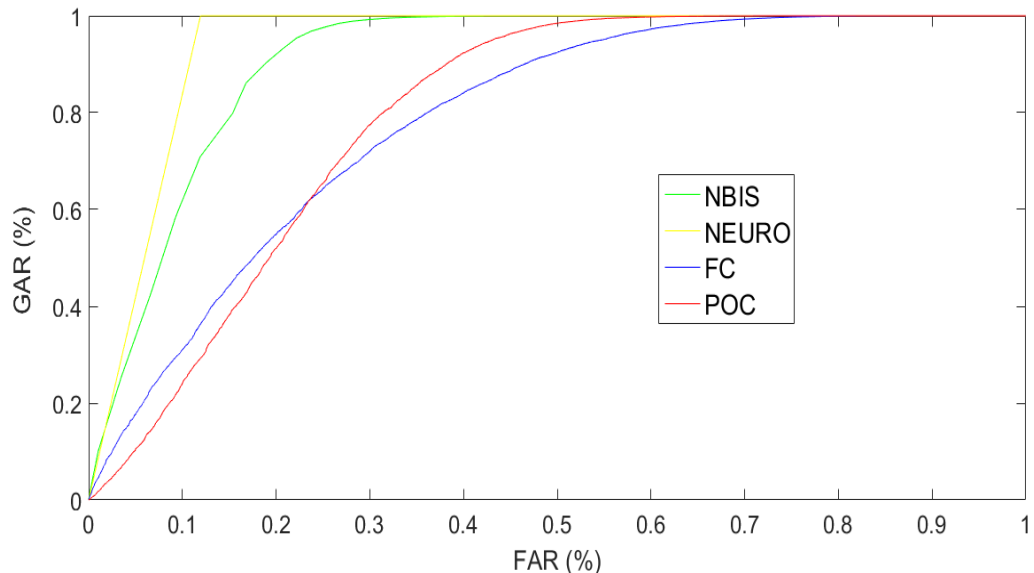


Fig. 49: ROC curves of data set C2 using results from all used fingerprint recognition system types using HH analysis.

both figures mentioned above data calculated by using the HH analysis was taken into account. The obvious distinction between the minutiae and non minutiae based recognition approaches can be detected easily.

As displayed in the tables in this Chapter 5 it is clear that the NEURO fingerprint recognition system is always providing the best results. The second best outcomes

are provided by the NBIS fingerprint recognition system. Furthermore, the minutiae based fingerprint recognition systems are performing better than the non minutiae ones. In Figure 49 it is displayed that sometimes the FC performance and sometimes the POC performance is slightly worse compared with the other non-minutiae based fingerprint recognition system in a limited area of the ROC. According to the information that two different data sets have been used to construct those visualizations a data set dependent variation is present as well. It remains an open question whether the used sensor types are responsible for this or probably the user behavior during imprint acquisition. In general there is no doubt that the performance of both non minutiae based fingerprint recognition system is not anything like as good as NEURO and NBIS. Judging from the fact that not only the overall performance is not the best, it is also observable that the ageing effect is not that high as for the NEURO fingerprint recognition system. Especially for the FC recognition system the equalization trend of both score distributions is much lower compared to the remaining three methods. The shift in the genuine score distribution to the left is much lower because of the anyway present high similarity of the matching scores. This circumstance can be observed looking at Figures 35 and 39. Those two figures are just representatives. The situation is always identical for each used data base. The ageing effect, the genuine score shift to the left, can be detected in each data set and for every fingerprint recognition system. The only variance can be observed in the intensity. For example, comparing both minutiae based fingerprint recognition systems a distinct difference is available. In Figures 27 and 34 this is clearly recognizable. For this purpose as a final statement for this chapter it is realistic to state the following conclusion: 'Ageing effects in terms of shifted score distributions can be detected for each fingerprint recognition system and sensor type independently how good the matching accuracy looks like.'

## 6 Doddington's Zoo and Menagerie Analysis

Before talking about ageing effects in detail it is necessary to focus on the topic concerning the fingerprint image quality. As discussed in Sections 4.4 and 5.6 the quality respectively the variety during the acquisition process of the imprints are important and deliver a huge impact in the recognition performance of used matcher techniques. Independently, there are a lot of different effects that can occur and eventually affect matching results. In Section 4 those that can be detected in the used data sets are represented. There are a lot of reasons why such degradations emerge. Aside from the fact that there are medical reasons like arthritis or injuries like cuts reducing the imprints' quality also natural human ageing must be taken into account. So the loss of collagen impacts the texture of the skin and effects for example dry skin [24].

In the following Section 6.1 there will be a short discussion how to characterize the different properties of people within a recognition system. There will be two different parts. On the one hand a pure statistical analysis using two hypothesis testing methods are applied to verify that those types of characterizations exist. On the other hand a distinct search for so called animal behavior using a combination of empirical and statistical methods is performed. The different methods are based on [12], [31] and [40].

### 6.1 Doddington Zoo

The idea of characterizing differences in recognition systems based on the individuality of the user was first presented in 1998 by George Doddington et al. [12]. They performed a speaker analysis searching for different types of speaker behavior within automatic recognition systems. It was possible to describe four different types so called 'animals'. Each of them shows a specific behavior and users can be labeled to a specific animal type, due to the fact that the match score distribution will exhibit high as well low genuine and impostor values. According to the similarity scores it is possible to detail the basic animal types as follows.

- *Sheep*: Those types are the so called default users. They are dominant within the population and perform well on recognition systems. Based on the genuine scores they receive high scores while matching against themselves and low values

if compared to other individuals. Therefore they tend to imply a low FRR because their features are separating them well from all the other inputs.

- *Goats*: As opposed to the first class, the second type based on genuine scores are those who are awkward to recognize. Because they are gathering low genuine scores they are affecting false rejections.
- *Lambs*: The interesting characteristic of them is the feature set that produces an overlap with other individuals within the data base. It is quite easy to imitate them and effecting an increase of the FAR. 'Lambs, on average, tend to produce high match scores when being matched against by another user [40].'
- *Wolves*: Wolves are those users who are gaining high match scores when matched against other individuals in the data set. So they can be found while looking at the impostor scores again and are very similar to lambs. They can cause false accepts and according to [12] finding wolves represents a possible system weakness. In Section 6.2 there will be a short discussion about the similarity between lambs and wolves.

Beyond the before mentioned basic types of user behavior there are some other animals that can be found as well. In the present work they will not be covered but for the sake of completeness they will be introduced shortly. They have been introduced by Neil Yager and Ted Dunstone in 2010 [40]. As opposed to sheep, goats, lambs and wolves they are not based only on the genuine and impostor scores. Worms, chameleons, phantoms, and doves are defined using the relationship between the matching values. So, for example, doves are the best user type that can be found within any data base. They retrieve high scores when matched against themselves and also low values when matched against others. Whereas worms are causing the biggest problems that can occur. They are gathering low genuine as well high impostor scores increasing the recognition system errors.

## 6.2 Menagerie Analysis - Pre-Information and Assumptions

Performing the menagerie calculation and proving the existence of sheep, goats, lambs and wolves a set of different methods will be applied. Due to the fact that sheep are the so called default user there will not be a specific investigation on those more theoretical types. The second important clarification is about lambs and wolves. Since

during the matching the symmetric calculations have not been executed to avoid correlation it is not possible to distinguish between those two types. In the lambs case the user of interest is already contained in the gallery. For the wolves calculation the person of interest is the so called probe user. For this purpose both definitions are equivalent for the used performance experiments. In the following lambs and wolves will be treated as one combined class. Actually the menagerie analysis will be focused on two classes. On the one hand the goat class and on the other hand the lambs/wolves class.

Furthermore it is necessary to set up a few assumptions which will be considered in the menagerie investigations. According to the performance analysis, displayed in Chapter 5, the degradation of genuine scores and stability of impostor scores leads to the following two hypotheses. The fluctuation's amount among the number of different users signed as a goat in the crossed data sets will be quite high. Based on the genuine scores degradation there won't be a lot of volunteers who can be marked as goat-like in data sets from 2009, 2013 and in the crossed ones. As opposed to this a high amount of stability in terms of different lamb-/wolf-like users is assumed due to the stability of the impostor scores. Apart from those two main hypothesis it is also interesting to have a look on the comparison between minutiae based and non-minutiae based fingerprint recognition systems. Probably there are no differences based on the menagerie analysis detectable. Furthermore, the impact of the used analysis methods (mean, variance, mean2 and minimum/maximum) will be a crucial one too. Those methods will be introduced in the following Section 6.3.

### 6.3 Menagerie Analysis - Experiments and Results

In the following subsection there will be a discussion on the analysis of the performed experiments concerning the different animal types. At first, an existence analysis was performed to verify if they are available. After this calculation a specific search for single users characterized as an animal type was executed.

**Existence Analysis** In [12] there are three methods used to perform a statistical existence analysis of goats, lambs and wolves. F-Test, Kruskal-Wallis Test and Durbin Test have been chosen. In the present thesis two of them have been used as well. On the one hand the F-Test and on the other the Kruskal-Wallis Test are executed. In

both cases the null hypothesis was said to be that there are no such special characterizations in the data sets. That means that it is not possible to find differences between the individual score distributions. For both tests a significance level of 0.01 was taken.

*F-Test:* Each statistical test respectively the test statistic that follows the F-distribution can be assigned to be an F-Test. In the present work a classical one-way analysis of variance (ANOVA) test has been used in the same way as described in [12]. As mentioned in [40] there is a slight problem. Due to the fact that the well known standard F-Test expects a normal distributed data set it is clear that this cannot be guaranteed. Looking at the genuine and impostor distributions pictured in Section 5 it seems that the scores approximate in some way a normal distribution. Therefore the hypothesis test has been performed on the given matching data. Regarding the beforehand null hypothesis and significance level on each data set there was the same result no matter if looking for goats or for lambs/wolves. The null hypothesis must be rejected for all data bases and matching results. Even when performing the same testing on another significance level of 0.05.

*Kruskal-Wallis Test:* The Kruskal-Wallis Test or also called H-Test is a non-parametric one-way analysis of variance by ranks test that does not need a normal distributed data set. Therefore, this test is well suited for the given data situation. The big difference to the before used F-Test is the replacement of the matching scores. This implies that the matching values are replaced by ranks. There is also a limitation of the test as well, it is mandatory to have at least five samples from each finger. Apart from this the null hypothesis and the significance level remain same as before. For the goats and lambs/wolves calculations that have been performed according to [12], the null hypothesis must be rejected once again. So at a significance level of 0.01 the alternative hypothesis that there are goats, lambs and wolves within the data sets could be accepted.

**User Analysis Theory** The user analysis refers to the effective search for users that can be characterized as a certain animal type. Regarding to the previous part of the thesis the existence of goats and lambs/wolves is confirmed. In the following paragraph four different methods will be used to identify these individuals:

- *mean scores method*: The first method is based on the mean scores like presented in [12]. The idea is to describe the behavior of each user by the expected value of their associated match score distribution. So the mean of all match scores belonging to a person is calculated. After performing this step for all people within the data set the list of all mean scores is sorted. Based on the paper of Doddington from 1998 the lowest and highest 2.5% of those values are assigned to represent an animal behavior. The related user is signed to be a goat or lamb/wolf. Concerning the two different types of characteristics there must be a distinction between the calculation details. In the goat case simply all matching scores are used. Looking at the lamb/wolf case there is a small difference due to the calculated scores. According to the methodology the impostor scores have been derived with, there are 5 or 10 sets of independent values. For each set and for each user the maximum impostor score is evaluated. That means that for each individual the mean impostor score is derived out of 5 or 10 maximum values before sorting them and calculating the goat-like or lamb-/wolf-like users.
- *variance scores method*: This method is also presented in [12]. Basically the same calculation is performed as mentioned before. The only difference is the use of variance instead of the expected value.
- *mean2 scores method*: The third alternative is based on [31]. That means that originally after deriving the mean values as before and sorting them, the users whose mean values is lower than the 30-th percentile are labeled as goats. In the lamb/wolf case those are assigned to be a lamb/wolf whose mean score is below the 10-th percentile. During the first experiments it becomes apparent that the chosen percentiles are much too high compared to the other values. Therefore they have been adapted. So in both cases the 5-th percentile will be taken into account.
- *minimum/maximum scores method*: This method is using an empirical idea. For the goats calculation the lowest value of each user distribution is chosen. Those genuine score values are sorted afterwards and the user who are assigned to the lowest 5-th percentile are labeled as goat. The calculation in the lamb/wolf case is quite similar except for the fact that not the lowest impostor scores of the user distributions have been taken, but the maximum values.

Based on those methodologies there are some weaknesses that must be discussed as well. The problem concerning the last menagerie analysis method is the quite high

sensitivity to outliers. Especially looking at the genuine and impostor scores of the NEURO matching it is clear that those can cause some problems in the further analysis. The majority or to be more precise almost all matching scores using the NEURO implementation are 0 across all data sets. For sure that is not only a problem for the minimum/maximum method.

The mean, mean2 and variance (var) method are robust to those outliers. That is the biggest advantage. But apart from this there is also a slight weakness to be covered later on. The disadvantage is the not confirmed relationship between the mean scores and the contribution to possible system errors. According to [40] this participation must be considered in a separate experimental setting. The results of this experiments will be presented at the end of the chapter in Section 6.5. But before the results of the performed investigations will be presented.

#### **6.4 User-defined Menagerie Analysis Results**

In this Section of the master thesis the detailed menagerie user analysis results will be presented. At first there will be a discussion about the goat-like behavior of different users within the data sets. In the second part the analysis results for the lambs/wolves experiments are taken into account. The user-defined menagerie analysis can be summarized by means of plotting the user's average genuine scores against the user's average impostor scores. So to get a general overview, Figure 50 can be used to get an impression of where the different animal types can be found. The plots displayed in Figures 51, 52, 53 and 54 visualize the existence of goats and lamb/wolves, but also the other 'animal'-like characteristics described before. To be more precise in the first figure, Figure 51, the different animal types and their position according to Figure 50 are marked. The signed goat-like (red colour) and lamb/wolf-like (green colour) volunteers have been calculated using the mean method. The dark blue colored users are displaying no special behavior and those who are signed in cyan represent the sheep case. Those sheep-like volunteers have been selected using a rectangle shaped area around the center of the mean scores according to their assumed location.

In the before mentioned figures the presence of goats is detectable looking at the low user's genuine scores indicated at the x-axis. The higher values shown on the y-axis are representing the lamb/wolf-like users. It is clearly observable that all animal types



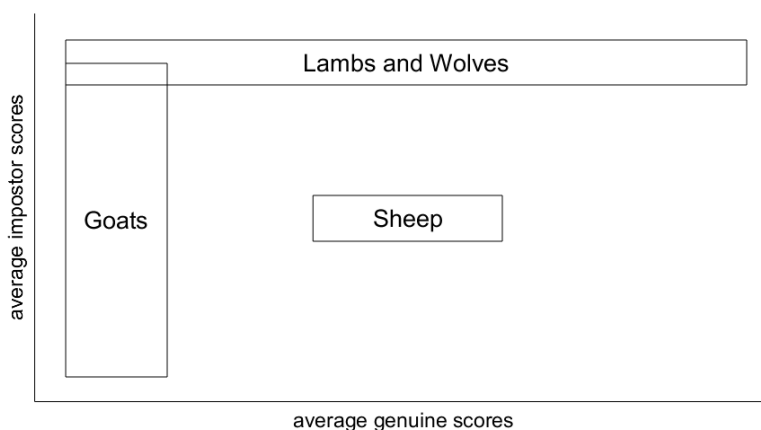


Fig. 50: General overview of the position of the different animal types according to their definition introduced in subsection 6.1.

can be detected in each data set and across all used recognition systems looking for example at the marked entries in Figure 51. But those four figures are just representing the situation using the mean menagerie analysis method. Using the user's average variance scores the distinction between the animal types is not always so clear, but nevertheless the existence of goats and lambs/wolves can be verified once again. This situation is displayed in Figure 55.

Basically, the most important information about the menagerie analysis is the fact that not single imprints are labeled as an animal type rather users are labeled. Each data sets contains 196 users as introduced in Section 4. Due to the described menagerie analyzing methods always a fixed number of volunteers will be labeled as goats or lambs/wolves. The reason for this is that depending on the matching results for example the users with a mean matching score value less than the 5 percentile score value are signed. So the higher number of imprints in the crossed data sets is not directly influencing this analysis. There is just a small impact. For example think about the mean score calculation used in the mean method. The higher number of imprints guarantee a higher number of matching values. For this purpose, within the mean score calculation, more values are taken into account but this is the only difference between the crossed and the single data sets. For each user the mean score value is used to perform the animal type labeling.

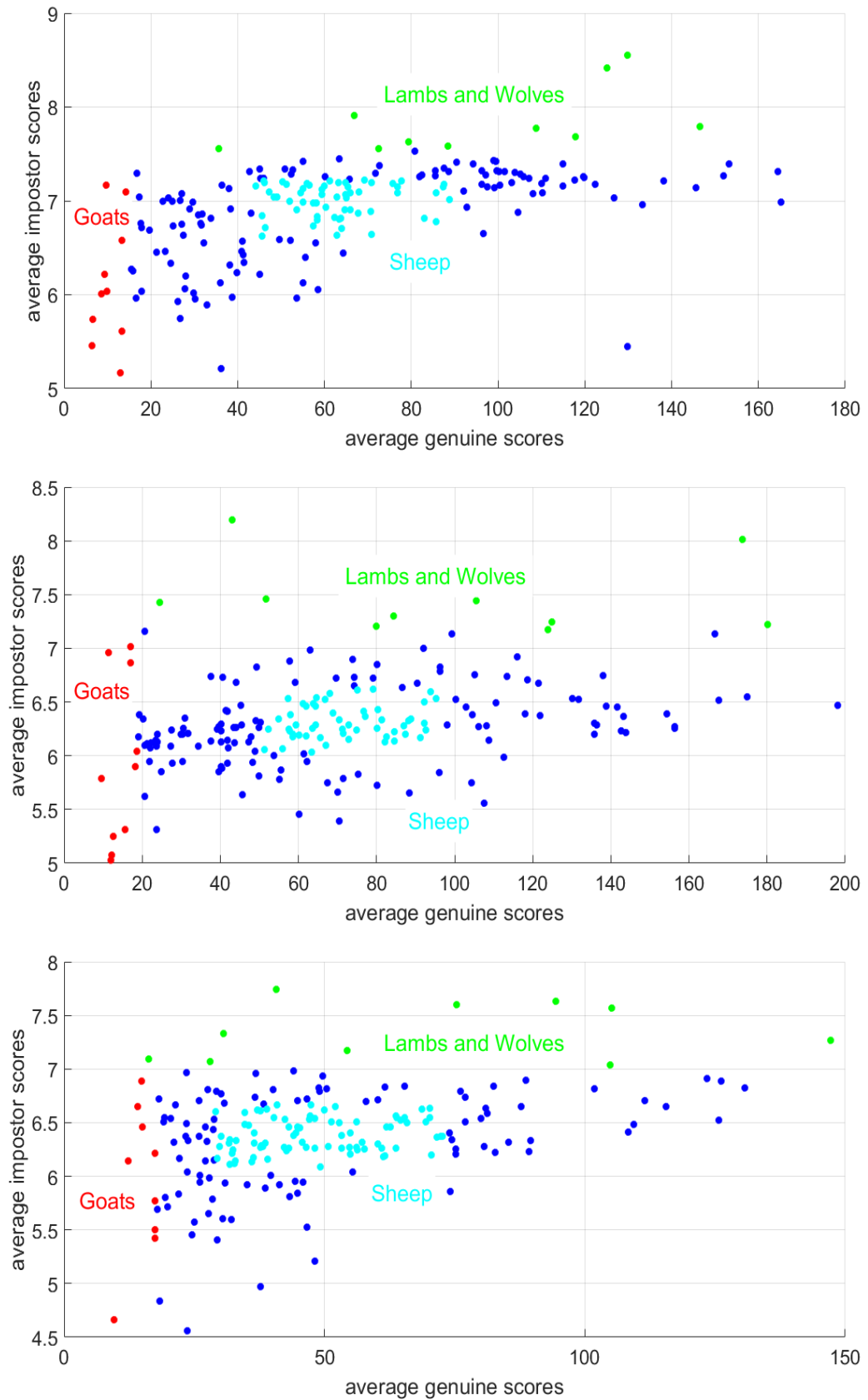


Fig. 51: User's average mean genuine scores (x-axis) and user's average mean impostor scores (y-axis) using NBIS and data A in the first graphic, B4 in the second one and C4 in the last one.

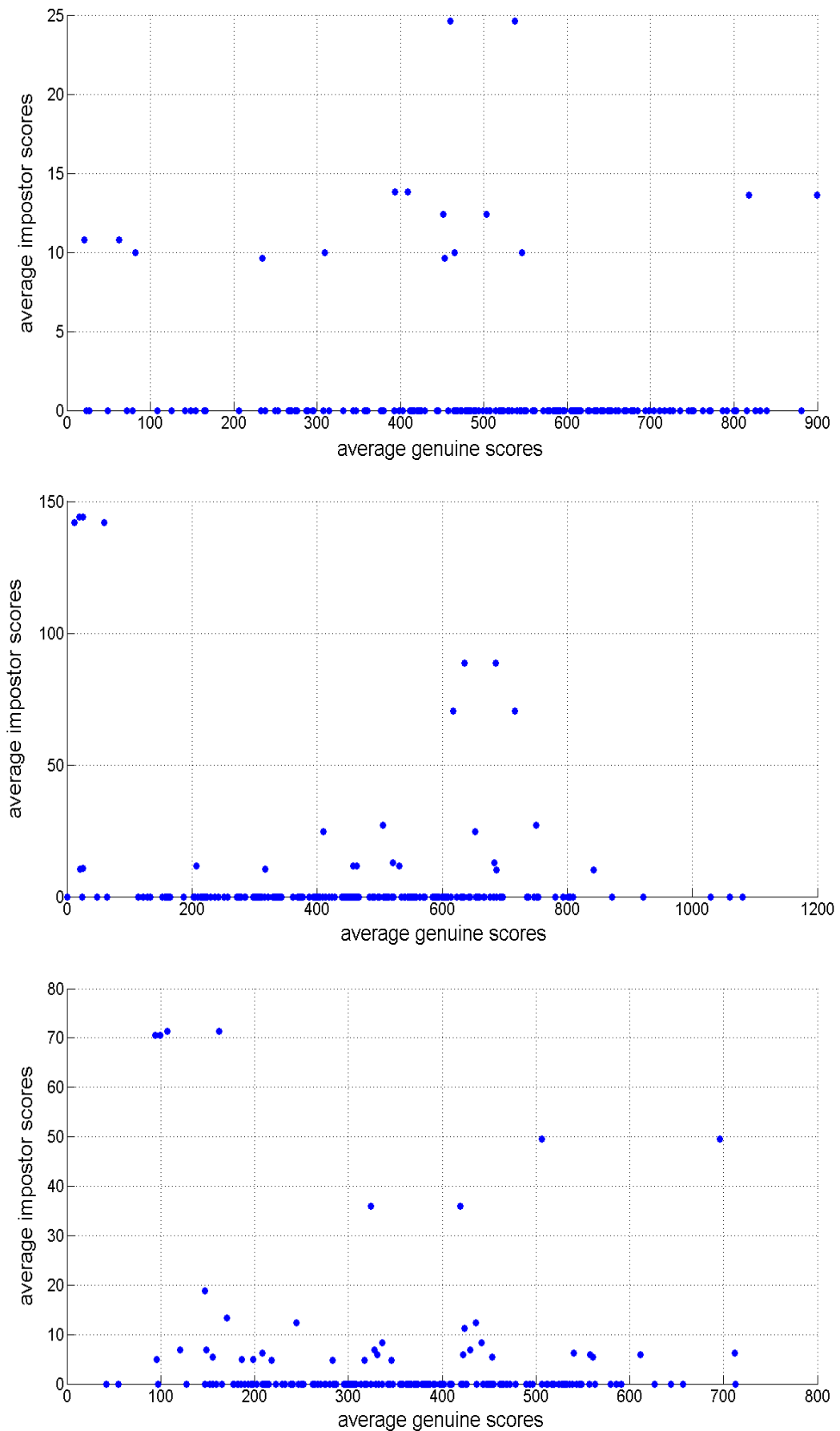


Fig. 52: User's average mean genuine scores (x-axis) and user's average mean impostor scores (y-axis) using NEURO and data set A in the first graphic, B3 in the second one and C3 in the last one.

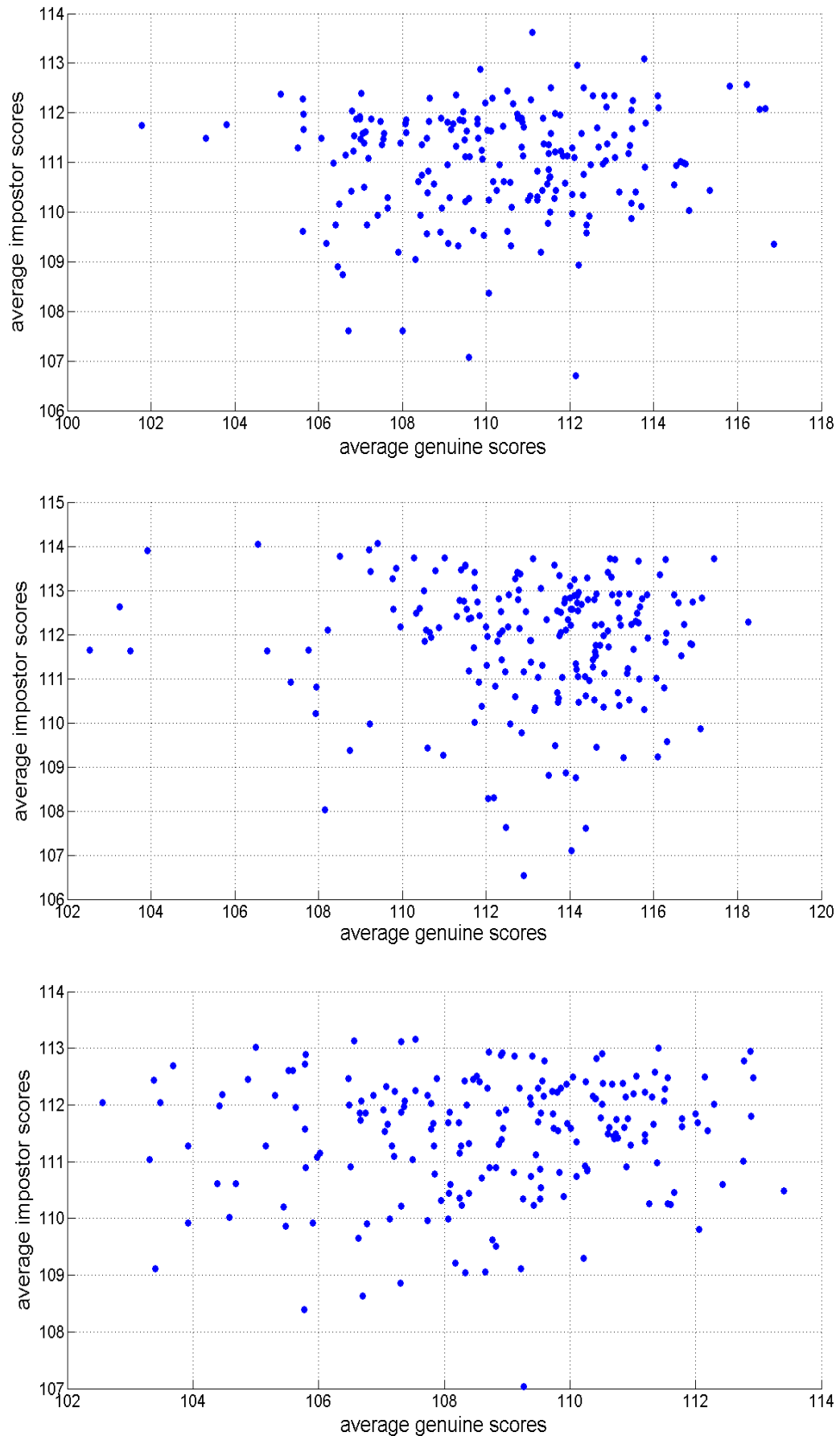


Fig. 53: User's average mean genuine scores (x-axis) and user's average mean impostor scores (y-axis) using FC and data set A in the first graphic, B2 in the second one and C2 in the last one.

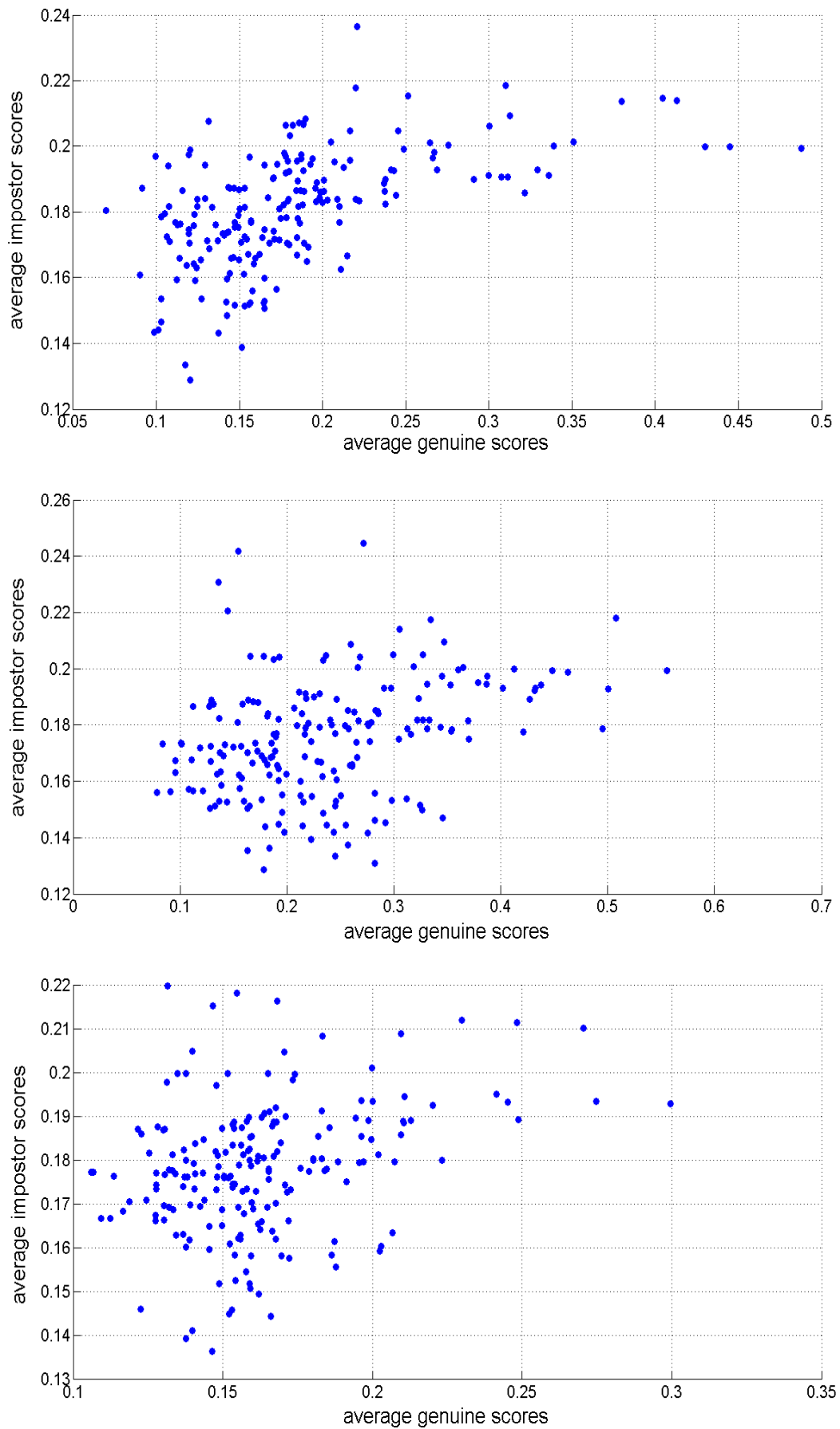


Fig. 54: User's average mean genuine scores (x-axis) and user's average mean impostor scores (y-axis) using POC and data set A in the first graphic, B1 in the second one and C1 in the last one.

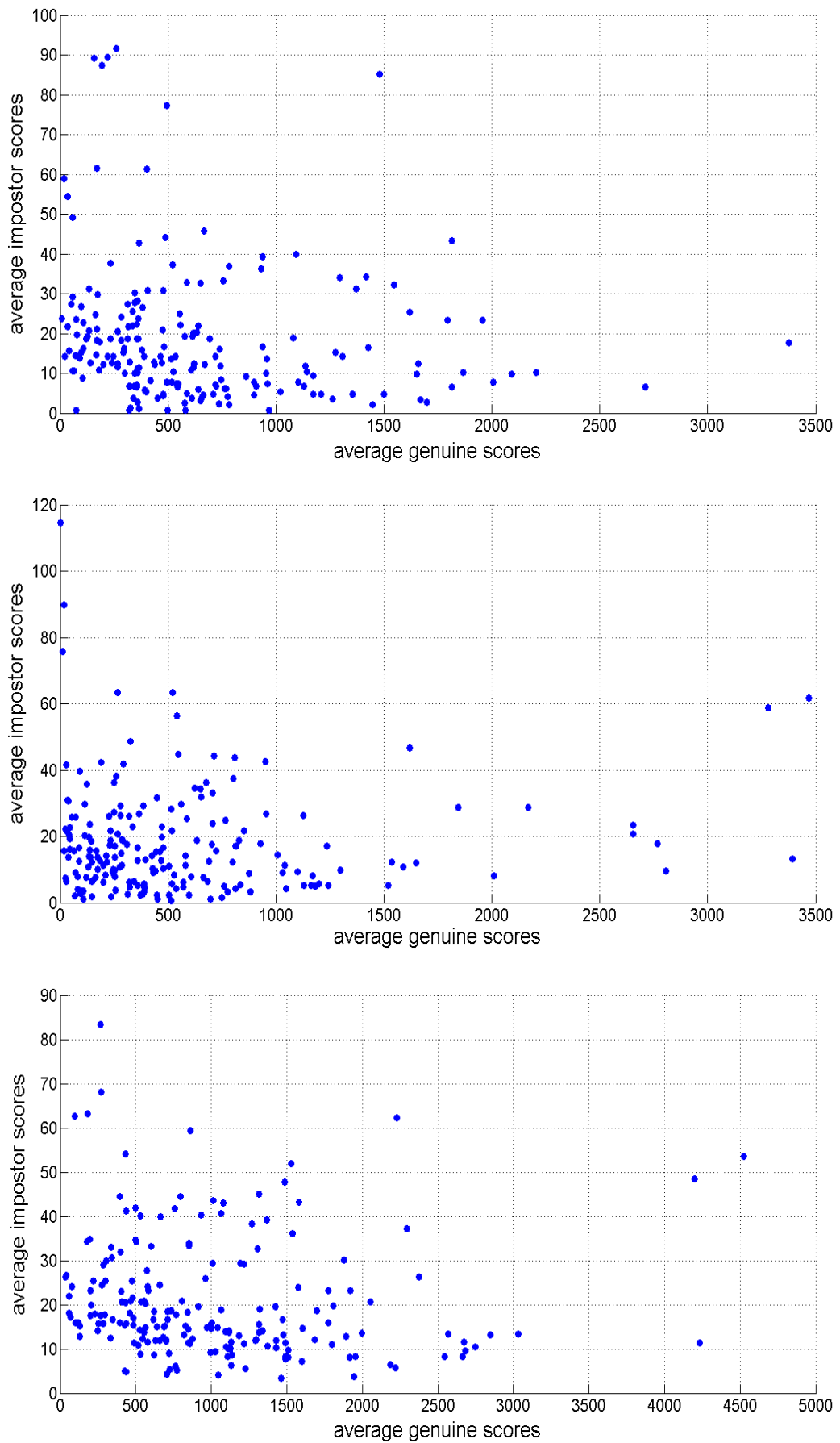


Fig. 55: User's average variance genuine scores (x-axis) and user's average variance impostor scores (y-axis) using NBIS and data set A in the first graphic, B2 in the second one and C2 in the last one.

Before talking about goats there is a short part about sheep. For sure there was not an experimental setting to verify sheep-like users, but nevertheless during the goats analysis the question, which users are never signed to be goat-like, occurred. So the non goat-like term 'never occur' must be explained. In this context it means that all those were signed to be non goat-like if they are never included in the goats analysis no matter what data base is looked at. So in Table 91 the number of those users is listed.

Due to that fact there are always 11 users labeled for the mean and variance method and 10 for the mean2 method. The minimum/maximum method is the sole exception. There is a specific reason for this effect. After looking at the for example 5 percentile score value, not only the lower score values are taken into account. There is also a comparison to those score values that are next in the value ordering. All following values that are of the same size as the 5 percentile score value, are also labeled as a specific animal type. This is done because the score values are the same but due to the ordering they would not be taken into account, but in fact they have to. The ordering is performed according to the users ID and it would not be correct to ignore them because they have the same low score value as the threshold percentile.

**Goats Analysis:** Due to the definition of sheep, the so called 'default user type', it is clear that the users displayed in Table 91 could be signed as sheep. But they will be signed as not goat-like and not as sheep-like because no explicit sheep experiments have been performed. For each matching method there are some users that are always included in the non goat-like list. Those volunteers could be determined with no respect to a specific data set/sensor type.

Looking at Table 91 it is necessary to remember that the maximum number of enrolled users is 196. According to this, it is important to look at the amount of non goat-like users in more detail. That means, that the number of non goat-like users is varying between 73.98% in the mean2 method for NBIS and POC matcher and 13.78% in the minimum method for the NEURO matcher. Especially remarkable is the circumstance that the three numbers that are far below the 50% line are all for the minimum analysis method. Apart from this there is no other analysis method that seems to be very sensitive to the matching scores. But as discussed in Section 6.3 it was very likely

	<b>number of no goat-like users</b>			
	<b>NBIS</b>	<b>NEURO</b>	<b>FC</b>	<b>POC</b>
<b>mean method</b>	138	133	123	122
<b>variance method</b>	126	119	125	118
<b>mean2 method</b>	145	129	131	145
<b>minimum sore method</b>	86	27	137	91

Table 91: Number of users exhibiting no goat-like behavior in the data sets including all sensors.

to observe this situation. The minimum method is not very robust against outliers. On the other hand this method's weakness delivers an interesting information about the matching scores of the FC algorithm. It seems that there are not many outliers contained because the number of non goat-like users is high compared to the other values of the same menagerie analysis method. This effect can be observed because there was no distinction between the different sensor types. A further reason can also be the low distinctiveness of the results of this matcher. That means that the difference between genuine scores and impostor score values is not so high compared to the results of the other matching methods. So as for example displayed in Table 63 that aspect can be looked up.

Another impression is that in the NEURO and POC results the smallest number of non goat-like users are included but actually they are only providing the highest variance within the found users. That means that those numbers of users who are listed in Table 91 are those that are marked as non goat-like in all menagerie analysis methods for each matching method. So in the NEURO and POC results there must be a quite high number of users that are signed to be non goat-like either in 2009 or 2013 or in the crossed data sets but not in all three types of data sets at the same time. Therefore the goat-like users are also not 'stable' with respect to the year of the data sets or even not with respect to the sensors and additionally the number of goat-like users must be higher compared to the other menagerie analyzing methods. There will be a discussion based on this information within this section later on. But it is very interesting to see that it seems that one minutiae based matcher and



one non-minutiae based matcher are delivering 'stable' results in terms of goat-like menagerie analysis.

Based on the non goat-like experiments the more interesting task is the search for users characterized as animal type 'goat'. In the following Tables 92, 93, 94 and 95 the results for the goat experiments are displayed. For each matcher type and data set the same experiment was performed, gathering the results as depicted in the before mentioned four tables. For each menagerie analyzing method the investigation was performed year dependent. So in the first step for each data set the data base dependent goat-like volunteers have been marked. To get an overall description of all those special users which occur, the single results are combined. So the volunteers effecting a goat-like behavior are clustered to three centers. In the Tables 92 till 95 the data set from 2009 will be called 'old'. The data sets from 2013 are called 'new' altogether and finally the crossed data sets from 2009 and 2013 will be named 'crossed'. Looking at the results the first important fact is the poor performance of the minimum method. While there is a long list for the NBIS results, there would have been too many users marked as a goat in the NEURO and POC results. This circumstance proves the results from the non goat results for those two matchers. So there are a lot of users signed as goat-like in the NEURO and POC results. Apart from this information it is clearly observable that there are differences between the goat-like users. That means that there are a lot of 'goats' which are occurring just in the 'old' data set or in one of the 'crossed' one for example. So in fact it is possible to differentiate between five classes of occurrence:

- **Class 1:** Those volunteers are labeled as goat only once in 2009, 2013 or in the crossed data sets. Looking at the NBIS results for the mean menagerie analysis method user 154 belongs to this class.
- **Class 2:** There are some users which are signed to have a goat-like behavior in all of the different years, like volunteer 100 as displayed using mean method and the corresponding NBIS results.
- **Class 3:** The volunteers assigned to this class are labeled in 2009 and 2013. So using the same analysis set as in the classes before, user 21 is detected in 2009 and in the T2 data set from 2013.

Data Set	User ID
<b>matcher</b>	<b>NBIS</b>
	<b>mean method</b>
<b>old</b>	21, 25, 47, 56, 64, 86, 98, 100, 131, 134, 154
<b>new</b>	1, 2, 3, 4, 6, 12, 13, 14, 20, 21, 25, 27, 30, 33, 36, 37, 38, 44, 45, 50, 54, 55, 62, 64, 69, 74, 78, 82, 85, 88, 90, 98, 100, 103, 129, 136
<b>crossed</b>	3, 4, 5, 6, 27, 29, 32, 47, 52, 53, 56, 80, 86, 87, 91, 100, 112, 119, 123, 124, 129, 131, 134, 159, 162, 170, 187
	<b>variance method</b>
<b>old</b>	9, 10, 47, 49, 56, 78, 100, 129, 134, 142, 158
<b>new</b>	1, 2, 3, 4, 6, 7, 8, 14, 18, 29, 30, 35, 36, 41, 48, 51, 52, 55, 64, 66, 74, 77, 78, 79, 82, 86, 90, 92, 96, 103, 104, 114, 121, 129, 130, 132, 139, 148, 156, 157, 185
<b>crossed</b>	4, 5, 8, 10, 16, 27, 29, 35, 46, 47, 48, 56, 61, 62, 64, 76, 78, 80, 86, 92, 98, 100, 101, 113, 123, 124, 130, 133, 134, 137, 154, 163, 168, 178, 187
	<b>mean2 method</b>
<b>old</b>	5, 21, 25, 129, 130, 131, 134, 154, 159, 163
<b>new</b>	6, 11, 12, 13, 14, 16, 20, 25, 27, 33, 36, 38, 41, 44, 48, 51, 63, 64, 69, 70, 74, 78, 82, 83, 89, 103, 129, 136, 163, 164, 185
<b>crossed</b>	5, 16, 21, 22, 25, 26, 27, 72, 80, 119, 129, 131, 132, 134, 154, 158, 159, 160, 161, 162, 163, 170, 178, 187
	<b>minimum sore method</b>
<b>old</b>	9, 10, 11, 32, 36, 55, 56, 69, 71, 75, 86, 87, 112
<b>new</b>	1, 2, 3, 4, 11, 19, 21, 29, 30, 37, 40, 45, 46, 49, 50, 52, 54, 55, 57, 62, 65, 66, 69, 72, 76, 81, 85, 88, 89, 90, 91, 98, 100, 106, 109, 110, 117, 118, 121, 122, 125, 126, 127, 128, 134, 140, 145, 147, 148, 153, 156, 158, 173, 182, 183
<b>crossed</b>	1, 2, 3, 4, 9, 10, 11, 12, 15, 17, 18, 19, 23, 29, 30, 31, 32, 34, 36, 38, 39, 44, 47, 48, 50, 52, 53, 54, 55, 56, 57, 58, 60, 64, 68, 71, 74, 75, 77, 78, 83, 84, 86, 87, 88, 91, 92, 93, 97, 98, 100, 105, 107, 108, 112, 115, 119, 120, 125, 126, 127, 128, 129, 136, 137, 138, 139, 145, 146, 148, 154, 155, 156, 157, 174, 175, 180, 185, 195

Table 92: User exhibiting a goat-like behavior in the NBIS data sets including all sensors.

Data Set	User ID
<b>matcher</b>	<b>NEURO</b>
	<b>mean method</b>
<b>old</b>	6, 9, 10, 25, 26, 47, 56, 64, 122, 124, 176
<b>new</b>	1, 2, 3, 4, 10, 18, 19, 20, 25, 38, 39, 53, 54, 55, 57, 60, 66, 76, 78, 86, 92, 98, 117, 119, 129, 133, 153, 156, 163, 166, 169, 171, 177, 179, 180, 185, 192, 194
<b>crossed</b>	1, 3, 4, 6, 21, 24, 29, 32, 47, 53, 56, 56, 64, 74, 80, 88, 110, 122, 123, 124, 131, 132, 140, 153, 154, 162, 169, 170, 176, 187
	<b>variance method</b>
<b>old</b>	10, 14, 44, 47, 58, 66, 88, 113, 122, 124, 129
<b>new</b>	1, 2, 3, 4, 6, 12, 18, 19, 20, 30, 35, 38, 51, 52, 54, 55, 56, 59, 66, 71, 74, 76, 78, 88, 91, 92, 108, 115, 120, 121, 122, 125, 126, 146, 150, 153, 157, 163, 175, 176, 188, 192
<b>crossed</b>	9, 10, 29, 30, 32, 35, 45, 46, 47, 48, 51, 53, 55, 56, 58, 60, 61, 69, 74, 79, 84, 86, 87, 97, 98, 100, 101, 110, 122, 123, 124, 136, 146, 154, 156, 160, 176, 178, 179, 180
	<b>mean2 method</b>
<b>old</b>	5, 6, 25, 26, 64, 135, 146, 165, 176, 193
<b>new</b>	10, 12, 23, 25, 27, 34, 38, 39, 47, 48, 53, 54, 58, 60, 61, 70, 78, 86, 92, 97, 117, 119, 129, 133, 138, 140, 156, 163, 164, 166, 169, 171, 177, 179, 180, 185, 186, 187
<b>crossed</b>	6, 21, 24, 25, 27, 63, 64, 72, 79, 80, 84, 88, 110, 118, 129, 131, 132, 139, 140, 154, 158, 159, 161, 162, 169, 170, 171, 172, 176, 187
	<b>minimum sore method</b>
<b>old</b>	9, 10, 11, 15, 29, 32, 47, 49, 55, 56, 58, 69, 71, 74, 75, 77, 78, 87, 112, 123, 124, 127, 128, 128, 140, 153, 155, 156, 157, 168, 192
<b>new</b>	too many entries due to outliers
<b>crossed</b>	too many entries due to outliers

Table 93: User exhibiting a goat-like behavior in the NEURO data sets including all sensors.

Data Set	User ID
<b>matcher</b>	<b>FC</b>
	<b>mean method</b>
<b>old</b>	107, 109, 115, 124, 151, 153, 154, 156, 163, 174, 196
<b>new</b>	1, 6, 38, 44, 65, 66, 67, 68, 70, 72, 76, 86, 125, 126, 128, 129, 135, 137, 138, 144, 149, 151, 152, 153, 154, 155, 157, 170, 173, 175, 179, 181, 182, 183, 185, 187, 188, 190, 192, 194, 195
<b>crossed</b>	4, 5, 6, 11, 15, 16, 17, 18, 20, 21, 24, 26, 27, 32, 41, 44, 55, 56, 62, 65, 67, 68, 88, 111, 131, 136, 137, 139, 140, 159, 163, 183, 190, 191
	<b>variance method</b>
<b>old</b>	26, 27, 75, 79, 113, 114, 167, 171, 172, 183, 193
<b>new</b>	3, 15, 17, 25, 27, 30, 32, 34, 41, 44, 48, 50, 52, 56, 59, 72, 74, 75, 85, 102, 107, 113, 114, 115, 117, 119, 120, 122, 127, 128, 133, 128, 133, 138, 139, 145, 153, 156, 159, 160, 168, 181, 195
<b>crossed</b>	2, 6, 14, 15, 16, 21, 24, 26, 27, 32, 39, 44, 47, 48, 56, 59, 60, 61, 62, 68, 72, 75, 79, 102, 107, 108, 111, 115, 119, 121, 124, 125, 134, 136, 139, 153, 159, 171, 172, 179, 183, 195, 196
	<b>mean2 method</b>
<b>old</b>	107, 109, 111, 115, 120, 121, 124, 136, 139, 151
<b>new</b>	1, 3, 16, 38, 46, 69, 70, 72, 86, 129, 131, 137, 138, 142, 144, 149, 151, 161, 168, 173, 175, 179, 180, 181, 183, 184, 185, 187, 190, 193, 195
<b>crossed</b>	5, 6, 7, 16, 21, 22, 24, 25, 26, 27, 28, 37, 49, 50, 57, 60, 64, 76, 79, 82, 83, 84, 86, 99, 164, 169
	<b>minimum sore method</b>
<b>old</b>	55, 56, 67, 75, 108, 158, 167, 175, 182, 193
<b>new</b>	1, 2, 3, 4, 7, 18, 22, 23, 37, 50, 52, 58, 65, 66, 67, 68, 91, 99, 112, 117, 119, 122, 125, 126, 127, 128, 134, 153, 156, 157, 159, 160, 168, 173
<b>crossed</b>	17, 35, 48, 50, 55, 56, 61, 62, 66, 67, 68, 70, 75, 93, 102, 108, 125, 126, 154, 158, 161, 163, 164, 167, 174, 179, 182, 190, 193, 195

Table 94: User exhibiting a goat-like behavior in the FC data sets including all sensors.

Data Set	User ID
<b>matcher</b>	<b>POC</b>
	<b>mean method</b>
<b>old</b>	16, 17, 22, 25, 27, 108, 172, 180, 190, 191, 192
<b>new</b>	6, 8, 10, 11, 12, 13, 14, 23, 25, 27, 36, 38, 44, 74, 78, 82, 103, 104, 108, 109, 110, 113, 117, 118, 119, 125, 127, 128, 131, 140, 153, 155, 156, 158, 174, 176, 178, 182, 183, 184, 190, 194
<b>crossed</b>	1, 3, 6, 7, 16, 18, 19, 20, 21, 24, 25, 26, 27, 37, 50, 64, 70, 83, 84, 99, 105, 106, 108, 112, 125, 150, 153, 154, 155, 164, 175, 180, 182, 190, 192, 195, 196
	<b>variance method</b>
<b>old</b>	35, 48, 71, 77, 100, 120, 121, 151, 152, 156, 169
<b>new</b>	3, 4, 17, 18, 21, 29, 30, 31, 43, 46, 49, 53, 55, 56, 57, 58, 63, 66, 79, 94, 98, 99, 114, 115, 116, 119, 120, 124, 133, 138, 140, 148, 156, 157, 162, 164, 166, 169, 170, 171, 176, 179, 185, 186, 191
<b>crossed</b>	13, 14, 19, 27, 33, 35, 36, 44, 48, 53, 55, 66, 70, 71, 74, 75, 77, 80, 94, 100, 113, 114, 116, 118, 121, 122, 135, 139, 140, 146, 153, 154, 164, 169, 171, 172, 174, 177, 187, 188, 189
	<b>mean2 method</b>
<b>old</b>	16, 17, 19, 22, 25, 27, 30, 50, 54, 80
<b>new</b>	5, 6, 8, 9, 10, 11, 12, 13, 14, 21, 23, 24, 25, 27, 33, 34, 35, 36, 38, 39, 42, 43, 44, 52, 60, 62, 64, 74, 75, 78, 82, 83, 84
<b>crossed</b>	5, 6, 7, 8, 11, 12, 15, 16, 21, 22, 23, 24, 25, 26, 27, 28, 37, 61, 64, 76, 80, 89, 99
	<b>minimum sore method</b>
<b>old</b>	too many entries due to outliers
<b>new</b>	too many entries due to outliers
<b>crossed</b>	too many entries due to outliers

Table 95: User exhibiting a goat-like behavior in the POC data sets including all sensors.

- **Class 4:** This class is displaying those users assigned to be a goat in 2009 and the crossed data sets. Looking at the menagerie results using the uru4500 data sets volunteer 134 belongs to this class.
- **Class 5:** In the last class the goat-like volunteer of 2013 and the crossed data sets are collected. So in the POC results for the mean2 menagerie analysis using the uru4000 data sets user 6 can be assigned to this class.

In fact it seems that there is no certain observable structure behind the occurrence and no tendency can be specified. But nevertheless it is possible to have a look which users are signed as goat in some particular settings. Those settings are which 'goats' can be labeled in 2009 and a 2013 data set or in 2009 and a crossed data set or in 2013 and a crossed data set. So which are those users that are kind of 'stable goats'. Tables 96, 97, 98 and 99 are used to display the 'stable goats'.

Looking at the results in Table 96, 97 and 98, it is observable that there are not many users that are kind of stable goat-like across the data sets and matcher types. Also a big difference between the menagerie analyzing methods is detectable. In particular the results of the minimum method are highly scattered therefore they will not be considered any longer for the goats analysis calculations.

The first interesting fact is that the number of goat-like users which are marked in 2009 and 2013 or 2009 and crossed data sets or 2013 and crossed data sets is not a constant one, despite that the total number of detected goats is always the same for mean, variance and mean2 method. The smallest number of identical labeled users can be found comparing the results from data set A and the data sets from 2013. It does not make a difference which matcher or menagerie analysis method is taken into account. That means that there not many volunteers which have been labeled in 2009 and in the single sets from 2013 as well. The second lowest number can be observed looking at the result from the 2013 data sets and the crossed data ones. This aspect indicates that there are just a few goat-like user who reoccur in the crossed data if they have been marked in the single 2013 bases. For this purpose it is very interesting to detect the highest number of same goats-like users when finger1267 is compared to the crossed data bases. On the one hand this leads to the conclusion that the data set from 2009 has an higher impact as the newer data sets from 2013 in case of searching for goats. The chance to label those users in the crossed data as goats,

	menagerie analyzing method			
data set	mean method	variance method	mean2 method	minimum method
	<b>NBIS</b>			
<b>A vs B1</b>	25, 98	78	24	55
<b>A vs B2</b>	64	129		
<b>A vs B3</b>	21			
<b>A vs B4</b>	21, 98, 100		129, 163	69
<b>A vs B5</b>	21, 98			11
	<b>NEURO</b>			
<b>A vs B1</b>	25	122	25	too many outliers
<b>A vs B2</b>		88		too many outliers
<b>A vs B3</b>	66			too many outliers
<b>A vs B4</b>				too many outliers
<b>A vs B5</b>	10	66		too many outliers
	<b>FC</b>			
<b>A vs B1</b>	154			
<b>A vs B2</b>		27, 75		
<b>A vs B3</b>	151	27, 75	67	67
<b>A vs B4</b>	151, 153, 154			
<b>A vs B5</b>		113		
	<b>POC</b>			
<b>A vs B1</b>	27, 108		27	too many outliers
<b>A vs B2</b>	25	120, 169	25	too many outliers
<b>A vs B3</b>		156		too many outliers
<b>A vs B4</b>				too many outliers
<b>A vs B5</b>	190	169		too many outliers

Table 96: Displaying the 'stable goats' which can be detected comparing data set A and the data sets from 2013.

<b>menagerie analyzing method</b>				
<b>data set</b>	<b>mean method</b>	<b>variance method</b>	<b>mean2 method</b>	<b>minimum method</b>
<b>NBIS</b>				
<b>A vs C1</b>	47, 56, 100, 131	56, 100, 134	5, 131, 159, 163	10, 11, 32, 55, 56, 71, 75, 86, 87
<b>A vs C2</b>	47, 56, 86	10, 47, 134	5, 25, 159	10, 11, 32, 55, 56, 75, 86, 87, 112
<b>A vs C3</b>	47, 86, 131	47, 134	5, 25, 159	9, 11, 32, 55, 56, 71, 75, 86, 87
<b>A vs C4</b>	100, 131, 134	78, 100, 134	5, 21, 25, 129, 131, 134, 154	11, 32, 36, 55, 56, 71, 75, 86, 87
<b>A vs C5</b>	47, 86, 100, 131, 134	100	5, 129, 131, 134,	11, 36, 55, 56, 75, 86, 87, 112
<b>NEURO</b>				
<b>A vs C1</b>	6, 56, 176		6, 176	too many outliers
<b>A vs C2</b>	6, 47, 64	10, 47, 122, 124	6, 64	too many outliers
<b>A vs C3</b>	6, 47, 124	47, 58	6, 25, 64	too many outliers
<b>A vs C4</b>	124	47, 124	25, 176	too many outliers
<b>A vs C5</b>	6, 122	10	6, 25	too many outliers
<b>FC</b>				
<b>A vs C1</b>		26, 27, 79, 158, 167, 182, 193	55, 56, 67, 75, 158, 167, 182, 193	55, 56, 67, 75,
<b>A vs C2</b>		75	56, 75, 108	56, 75, 108
<b>A vs C3</b>		75	56, 67, 75	56, 67, 75
<b>A vs C4</b>	124, 153, 154, 156		56, 75	56, 75
<b>A vs C5</b>	124, 151, 154, 196		56, 158	56, 158
<b>POC</b>				
<b>A vs C1</b>	25, 27	48, 100, 121	22, 25, 27	too many outliers
<b>A vs C2</b>	25, 27, 180, 190	35, 77, 100, 169	22, 25, 27	too many outliers
<b>A vs C3</b>	25, 180, 190		25, 27	too many outliers
<b>A vs C4</b>	16, 108	35, 100, 121	16, 22, 25, 27, 80	too many outliers
<b>A vs C5</b>	25, 27, 108, 190, 192	70	22, 25, 27	too many outliers

Table 97: Displaying the 'stable goats' which can be detected comparing data set A and the crossed data sets.



<b>menagerie analyzing method</b>				
<b>data set</b>	<b>mean method</b>	<b>variance method</b>	<b>mean2 method</b>	<b>minimum method</b>
<b>NBIS</b>				
<b>B1 vs C1</b>			27	3, 4, 30, 55, 57, 125, 126, 127, 128
<b>B2 vs C2</b>	6		6	3, 30, 100, 125, 156
<b>B3 vs C3</b>	6		6	91, 100
<b>B4 vs C4</b>	100	29	163	29, 50, 52, 98, 100, 148, 156
<b>B5 vs C5</b>		4	6	11, 100, 127
<b>NEURO</b>				
<b>B1 vs C1</b>		146		too many outliers
<b>B2 vs C2</b>			169,171	too many outliers
<b>B3 vs C3</b>	3	167	169,187	too many outliers
<b>B4 vs C4</b>	1, 3, 4			too many outliers
<b>B5 vs C5</b>	169		169, 171	too many outliers
<b>FC</b>				
<b>B1 vs C1</b>				
<b>B2 vs C2</b>	6, 67	15, 48, 75	125	125
<b>B3 vs C3</b>	44, 65, 67, 68	15, 48, 56, 75, 139	66, 67, 68	66, 67, 68
<b>B4 vs C4</b>	153, 154		50	50
<b>B5 vs C5</b>				
<b>POC</b>				
<b>B1 vs C1</b>	27	53, 55, 164	6, 27	too many outliers
<b>B2 vs C2</b>	25	169, 171	5, 21, 25	too many outliers
<b>B3 vs C3</b>			12	too many outliers
<b>B4 vs C4</b>		140		too many outliers
<b>B5 vs C5</b>	190			too many outliers

Table 98: Displaying the 'stable goats' which can be detected comparing data sets from 2013 and the crossed data sets.

<b>menagerie analyzing method</b>				
<b>data set</b>	<b>mean method</b>	<b>variance method</b>	<b>mean2 method</b>	<b>minimum method</b>
<b>NBIS</b>				
A vs B1 vs C1				55
A vs B2 vs C2				
A vs B3 vs C3				
A vs B4 vs C4	100		163	
A vs B5 vs C5				11
<b>NEURO</b>				
A vs B1 vs C1				too many outliers
A vs B2 vs C2				too many outliers
A vs B3 vs C3				too many outliers
A vs B4 vs C4				too many outliers
A vs B5 vs C5				too many outliers
<b>FC</b>				
A vs B1 vs C1				
A vs B2 vs C2		75		
A vs B3 vs C3		75		67
A vs B4 vs C4	153, 154			
A vs B5 vs C5				
<b>POC</b>				
A vs B1 vs C1	27		27	too many outliers
A vs B2 vs C2	25	169	25	too many outliers
A vs B3 vs C3				too many outliers
A vs B4 vs C4				too many outliers
A vs B5 vs C5	190			too many outliers

Table 99: Displaying the 'stable goats' which can be detected in 2009, 2013 and in the crossed data sets.

that have been labeled as goats in the old data set, is higher than the chance that a goat-like user labeled in 2013 is labeled again in the crossed set. In general there are only a few goat-like users which are labeled in 2009, 2013 and the crossed data. They are displayed in Table 99. As readable a high dependence to certain analysis methods and fingerprint recognition systems can be stated.

On the other hand there is another interesting fact. Due to the circumstance that there are only a few goat-like users identical in data set A and the data sets from 2013 it is clear that there is a high fluctuation between those two year independent data bases. Additionally the also quite small variance between 2013 data sets and the crossed data bases leads to a similar statement. Combined with the high number of shared goat-like users between data set A and the crossed data sets and using the information displayed in Tables 92 till 95 and the information from Tables 96, 97 and 98, the following conclusion can be stated.

If the same goat-like users would be found in each data set, than the total number would be stable, but according to Tables 96, 97 and 98 there must be a very high number of different users being goat-like in the used data sets. This high variability can be detected as well looking at the following Table 100.

There are 10 different categories displayed: The number of different users labeled in 2009, 2013 and in the crossed sets (column 2 to 4), the total amount of different goat-like volunteers in the 2013 and crossed sets excluding those which have been labeled in 2009 before (column 5 and 7) and those which are signed the first time only in the crossed bases (column 9). The remaining columns 6, 8 and 10 were used to display the relative information of column 5, 7 and 9. For this purpose the relative value calculation will be performed by dividing the results from column 5, 7 and 9 by the outcomes of 3, 4 and 4. For each column an abbreviation will be used: Column 2 is named 'Old' (O), column 3 'New' (N), column 4 'Crossed' (C), column 5 is named 'New without Old' (NwO), column 7 is called 'Crossed without Old' (CwO) and finally column 9 'OC' which is the short form of 'Only Crossed'. The columns representing the relative values where always be named by the short names of those columns which information was used to derive the results.

Basically Table 100 is another representation of the described goats situation. For example, in the last two columns which are dedicated to those volunteers who are only signed as goat-like in the crossed sets, the chance to be labeled only in the crossed data bases can be retrieved. Most of the time the probability is ranged be-

matcher	number of goat-like users								
	O	N	C	NwO	NwO/N	CwO	CwO/C	OC	OC/C
	<b>mean method</b>								
<b>NBIS</b>	11	36	27	31	86.11%	21	77.77%	16	59.25%
<b>NEURO</b>	11	38	29	36	94.73%	22	75.86%	16	55.17%
<b>FC</b>	11	42	40	39	92.85%	34	87.17%	23	57.50%
<b>POC</b>	11	42	37	38	90.47%	30	81.08%	25	67.56%
	<b>variance method</b>								
<b>NBIS</b>	11	41	35	39	95.12%	29	82.85%	20	57.14%
<b>NEURO</b>	11	42	40	39	92.85%	35	87.50%	27	67.50%
<b>FC</b>	11	43	42	38	88.37%	36	85.71%	22	52.38%
<b>POC</b>	11	45	41	42	93.33%	34	82.92%	25	60.97%
	<b>mean2 method</b>								
<b>NBIS</b>	10	31	25	28	90.32%	16	64%	13	52%
<b>NEURO</b>	10	38	30	37	97.36%	26	86.66%	20	66.67%
<b>FC</b>	10	33	26	31	93.93%	26	100%	24	92.30%
<b>POC</b>	10	34	23	32	94.11%	18	78.26%	9	39.13%

Table 100: Number of users exhibiting a goat-like behavior in the data sets including all sensors.

tween 50% and 70%. So if a user has been signed before in one of the single sets, it is not implausible that this volunteer is detected once more in the crossed bases. Of course there is a lot of influence in the given results observable which can be caused by the recognition systems or by the data sets themselves. Comparing column NwO and CwO it is also clear that the users who have been labeled in 2009 are detected in the crossed sets more likely.

Based on the performed analysis of the goats case it can be summarized that there are goats-like users observable. There are only a few who stay 'stable' comparing the data bases from 2009, 2013 and the crossed ones. So a high amount of fluctuation is included which makes it impossible to conclude a specific tendency if, when and

probably why a volunteer can be marked as goat. But nevertheless the chances to sign a volunteer more than once is likely. Apart from these information it also can be stated that not all assumptions introduced in this Chapter 6 are confirmed. First of all, the amount of fluctuation between the different goat-like volunteers is not that high as expected. Nevertheless it was possible to confirm that it is not unrealistic to detect a goat-like user once again in crossed data bases after marking this person in one of the single data sets before. Of course there is no certain answer if fingerprint ageing or quality influences or even user dependent behavior are responsible for the detected tendencies. But it was possible to prove that neither minutiae based fingerprint recognition systems nor non-minutiae ones are outperforming the others in most of the cases. All recognition systems display basically the same tendencies. For the used analysis methods an identical tendency can not be confirmed for all of them. As assumed the minimum/maximum method is not suited for the goats analysis due to their sensitivity to outliers. For the remaining methods (mean, variance and mean2) no crucial abnormalities are detected.

**Lambs/Wolves analysis for time span excluding impostor scores:** As the title of this section implies, two different analysis steps for the lambs/wolves analysis are discussed in the present thesis. According to the outcomes of Chapter 5 there is a very high amount of stability corresponding to the impostor scores. Therefore only two cases were presented in more detail. The first one is excluding impostor scores which could be influenced by fingerprint ageing. So in fact this analysis is the equivalent to the WA method of the previous Chapter. The second one will be very similar to the HH analysis. The difference between the investigations presented in Section 6.4 and the HH method is the number of impostor scores which were taken into account. That means that for the second lambs/wolves discussion all calculated impostor matching scores will be included and no repeated randomized selection of the scores performed. The reason for the chance is based on the before mentioned stability of the impostor scores.

Basically the lambs/wolves analysis was performed similarly compared to the goats analysis. With respect to the matching results, excluding correlation as described in Section 4.6, there will be no distinction between lambs and wolves in this master the-

	number of no lambs/wolves-like users			
	NBIS	NEURO	FC	POC
<b>mean method</b>	123	147	130	139
<b>variance method</b>	106	150	132	121
<b>mean2 method</b>	127	121	141	145
<b>maximum score method</b>	148	122	146	150

Table 101: Number of users exhibiting no lambs/wolves-like behavior in the data sets including all sensors but using just impostor scores without time span information.

sis. So looking at the first result table, Table 101, it is clearly observable that there is a difference to the results from the goats analysis. The big difference comparing the first three methods and the maximum method can not be observed once again. Actually it seems that the maximum method is displaying similar or even a better tendency. This enhancement is caused by the stability of the impostor scores. The present fluctuations within the matching scores are not so high as for the genuine results. So the lowest detectable number of users labeled as lamb or wolf can be derived using the NEURO matching results and the variance method. The displayed 106 users correspond to 54.08% of all volunteers within the data sets. The highest number of users which are never signed as lamb or wolf is 150 in the variance case using the NEURO and using POC for the maximum score method. For this purpose the margin between those who are never labeled as lamb or wolf in any data set, analysis and matcher method is 22.45%. Compared to the goat margin it is much lower. So the high fluctuation in the goat case is also not detectable for lambs/wolves. It could be that the characteristics of a lamb- or wolf-like user are more distinctive on the one hand. The assumption seems to be a realistic one because of the stability of the impostor scores which has been detected in Chapter 5. On the other hand it is also possible that the similarity of the impostor results causes some problems for the recognition of lamb/wolf-like users. The distinction between lamb/wolf or not lamb/wolf could be influenced because the outcomes of the analysis methods are related too much. For this purpose a low margin can also indicate that it is hard to distinguish between true lambs/wolves and those who are normal in the sense of those animal types. Both

introduced interpretation are valid and there will be no further investigation based on these hypothesis.

As performed in the goat analysis, in Tables 102, 103, 104 and 105 those lamb/wolf-like users which can be detected are displayed. The 'old' data set corresponds again to the 2009 data set. The 'new' data is the same as the data bases from 2013 and finally the 'crossed' set is based on the the crossing data bases from 2013 and 2009. It is easy to see that there were overlaps between the goats and lambs/wolf results. Nevertheless the first big difference to be mentioned between the goats and lambs/wolves set is the number of in totally labeled users. In most of the cases comparing the information from Tables 91 and 101 there are more volunteers signed as lamb or wolf than as goat. To be more precise, in 12 of the displayed 16 cases, the number of goats is lower than lambs/wolves. Especially interesting is that in 3 of the 4 cases where more goats are labeled the variance analysis method has been used. That could be a coincidence, but on the other hand this method could also be more suitable for detecting goats or lambs/wolves. The main reason why this circumstance occurs will be hard to detect because there are too many variables. The most important are the imprints contained in the data sets, the used sensor types, the fingerprint matcher systems and as a matter of course the variance method itself.

Another interesting effect is the performance of the maximum analysis method. In the goat analysis this method performs very bad due to the sensitivity to outliers within the matching scores. At first sight the same problem is not detectable in the lambs/wolves analysis. In fact there are no big problems using this method during the further procedure because there is not such a high amount of fluctuations in the used matching scores compared to the goats case.

In opposition to the goats analysis in Tables 102, 103, 104 and 105 no specific abnormality can be observed. None of the four used analyzing methods was gathering an extremely low or high number of lambs/wolves. The only interesting observation can be detected for the maximums method using NBIS and POC results.

For both experiments the lamb/wolf-like volunteers in the all crossed, which have been detected, the users where the same as in 2009. This is possible of course, but was not expected to be present. 3 volunteers, respectively 4, could be signed for the data sets from 2013 as well. It seems that their score values were extraordinary unique to mark them more than once.

Data Set	User ID
<b>matcher</b>	<b>NBIS</b>
	<b>mean method</b>
<b>old</b>	8, 47, 65, 86, 92, 98, 100, 130, 165, 166, 182
<b>new</b>	2, 10, 11, 13, 20, 24, 26, 27, 28, 30, 37, 38, 50, 51, 52, 54, 55, 56, 59, 62, 63, 64, 69, 78, 79, 80, 85, 88, 90, 98, 100, 101, 104, 110, 111, 114, 118, 159, 167, 178, 179, 180, 181, 187, 189, 194
<b>crossed</b>	6, 8, 9, 12, 23, 25, 39, 47, 49, 50, 52, 53, 56, 57, 64, 75, 77, 78, 86, 87, 92, 98, 100, 109, 114, 139, 142, 144, 148, 162, 165, 166, 177, 178, 182
	<b>variance method</b>
<b>old</b>	26, 39, 54, 71, 88, 129, 143, 158, 160, 165, 188
<b>new</b>	1, 2, 6, 10, 11, 13, 18, 22, 27, 28, 33, 35, 39, 40, 43, 45, 51, 52, 54, 55, 56, 59, 60, 61, 79, 80, 81, 85, 88, 108, 113 120, 128, 135, 138, 141, 146, 148, 154, 155, 158, 159, 171, 175, 181, 183, 185, 187, 193, 194, 195
<b>crossed</b>	5, 16, 21, 22, 25, 26, 27, 72, 80, 119, 129, 131, 132, 134, 154, 158, 159, 160, 161, 162, 163, 170, 178, 187
	<b>mean2 method</b>
<b>old</b>	8, 21, 25, 130, 131, 134, 162, 165, 166, 182
<b>new</b>	6, 10, 11, 13, 20, 27, 28, 38, 51, 52, 54, 55, 56, 64, 69, 71, 74, 75, 78, 79, 80, 83, 89, 103, 104, 111, 112, 115, 116, 122, 129, 136, 142, 146, 162, 164, 166, 167, 179, 180, 184, 185, 187, 194
<b>crossed</b>	8, 9, 12, 25, 49, 50, 53, 77, 78, 80, 81, 109, 110, 114, 129, 130, 131, 134, 142, 144, 148, 160, 162, 165, 166, 177, 178, 182, 185, 186, 196
	<b>maximum sore method</b>
<b>old</b>	8, 54, 109, 129, 160, 162, 165, 166, 182, 188
<b>new</b>	1, 6, 10, 11, 13, 19, 20, 22, 27, 28, 35, 38, 41, 51, 52, 54, 56, 64, 69, 71, 74, 78, 79, 80, 85, 93, 111, 115, 116, 120, 130, 141, 142, 146, 155, 161, 162, 163, 166, 167, 179, 180, 187, 193, 194
<b>crossed</b>	8, 54, 109, 129, 160, 162, 165, 166, 182, 188

Table 102: User exhibiting a lamb/wolf-like behavior in the NBIS data sets including all sensors but using just impostor scores without time span information.



Data Set	User ID
<b>matcher</b>	<b>NEURO</b>
	<b>mean method</b>
<b>old</b>	54, 73, 74, 95, 130, 191, 192, 193, 194, 195, 196
<b>new</b>	10, 11, 27, 28, 34, 46, 51, 52, 54, 55, 62, 79, 80, 97, 104, 138, 141, 165, 168, 178, 181, 185, 191, 192, 193, 194, 195, 196
<b>crossed</b>	9, 12, 25, 26, 36, 48, 49, 50, 53, 54, 56, 73, 74, 77, 78, 95, 140, 143, 167, 180, 183, 191, 192, 193, 194, 195, 196
	<b>variance method</b>
<b>old</b>	54, 73, 74, 95, 130, 191, 192, 193, 194, 195, 196
<b>new</b>	10, 11, 27, 28, 34, 46, 51, 52, 54, 55, 62, 79, 80, 97, 104, 141, 165, 168, 178, 181, 185, 191, 192, 193, 194, 195, 196
<b>crossed</b>	9, 12, 25, 26, 49, 50, 53, 54, 56, 73, 74, 77, 78, 95, 99, 143, 167, 180, 183, 191, 192, 193, 194, 195, 196
	<b>mean2 method</b>
<b>old</b>	40, 45, 54, 69, 73, 74, 75, 91, 95, 130
<b>new</b>	1, 2, 3, 4, 5, 10, 11, 16, 23, 27, 28, 33, 34, 37, 38, 46, 51, 52, 54, 55, 62, 65, 70, 79, 80, 89, 97, 104, 110, 112, 118, 138, 141, 142, 161, 162, 165, 168 175, 178, 181, 185, 187, 192, 193, 194, 195, 196
<b>crossed</b>	9, 12, 25, 26, 36, 39, 40, 45, 48, 49, 50, 53, 54,56, 64, 69, 73, 74, 75, 77, 78, 91, 95, 99, 130, 140, 143, 144, 163, 164, 167, 180, 183, 192, 193, 194, 195, 196
	<b>maximum sore method</b>
<b>old</b>	40, 45, 54, 69, 73, 74, 75, 91, 95, 130
<b>new</b>	1, 2, 3, 4, 5, 10, 11, 16, 23, 27, 28, 33, 34, 37, 38, 46, 51, 52, 54, 55, 62, 65, 70, 79, 80, 89, 97, 104, 110, 112, 118, 138, 141, 142, 161, 162, 165, 168, 175, 178, 181, 185, 187
<b>crossed</b>	9, 12, 25, 26, 36, 39, 40, 45, 48, 49, 50, 53, 54,56, 64, 67, 69, 73, 74, 75, 77, 78, 91, 95, 99, 130, 143, 144, 163, 164, 167, 180, 183

Table 103: User exhibiting a lamb/wolf-like behavior in the NEURO data sets including all sensors but using just impostor scores without time span information.

Data Set	User ID
<b>matcher</b>	<b>FC</b>
	<b>mean method</b>
<b>old</b>	10, 41, 75, 133, 135, 148, 153, 160, 166, 182, 186
<b>new</b>	2, 3, 6, 7, 8, 10, 13, 18, 19, 20, 26, 29, 30, 34, 36, 38, 43, 46, 53, 54, 58, 62, 63, 65, 66, 67, 73, 78, 85, 86, 99, 118, 126, 137, 138, 139, 140, 151, 152, 156, 157, 182, 190, 192
<b>crossed</b>	1, 8, 10, 41, 56, 64, 65, 68, 75, 80, 92, 97, 103, 104, 130, 131, 133, 135, 139, 140, 145, 148, 149, 151, 153, 160, 166, 182, 190
	<b>variance method</b>
<b>old</b>	12, 15, 53, 77, 81, 90, 100, 102, 121, 127, 128
<b>new</b>	2, 4, 5, 7, 10, 11, 24, 35, 38, 42, 44, 46, 47, 51, 52, 57, 58, 59, 66, 67, 68, 69, 70, 96, 97, 100, 103, 104, 105, 107, 112, 116, 118, 120, 126, 127, 133, 134, 142, 153, 155, 163, 173, 174, 178, 180, 182, 187, 190
<b>crossed</b>	2, 5, 12, 15, 19, 41, 53, 77, 81, 85, 90, 100, 102, 118, 121, 122, 127, 128, 144, 155, 163, 181, 182
	<b>mean2 method</b>
<b>old</b>	19, 56, 92, 104, 148, 160, 166, 182, 184, 186
<b>new</b>	7, 10, 13, 14, 16, 26, 34, 36, 38, 46, 53, 54, 58, 62, 72, 77, 78, 85, 86, 101, 103, 109, 114, 117, 118, 129, 137, 138, 139, 140, 142, 150, 151, 166, 168, 182
<b>crossed</b>	15, 16, 34, 36, 56, 64, 79, 80, 88, 90, 92, 99, 102, 103, 104, 116, 120, 121, 127, 130, 131, 139, 140, 148, 149, 151, 160, 166, 172, 182, 184
	<b>maximum sore method</b>
<b>old</b>	25, 33, 50, 54, 92, 93, 148, 160, 166, 182
<b>new</b>	7, 10, 11, 13, 16, 26, 36, 38, 45, 46, 51, 52, 53, 54, 55, 58, 62, 66, 77, 79, 80, 82, 84, 85, 86, 97, 101, 103, 106, 110, 114, 137, 138, 139, 140, 142, 150, 157, 158, 159, 160, 161, 166, 182, 185, 189
<b>crossed</b>	15, 25, 33, 50, 54, 90, 92, 93, 102, 109, 121, 127, 148, 160, 166, 182, 186

Table 104: User exhibiting a lamb/wolf-like behavior in the FC data sets including all sensors but using just impostor scores without time span information.

<b>Data Set</b>	<b>User ID</b>
<b>matcher</b>	<b>POC</b>
	<b>mean method</b>
<b>old</b>	25, 27, 50, 64, 71, 105, 108, 115, 122, 123, 153
<b>new</b>	6, 10, 12, 13, 14, 21, 22, 23, 38, 40, 51, 52, 60, 64, 74, 78, 79, 105, 107, 121, 139, 143, 145, 151, 156, 169, 171, 183, 184, 188, 189, 190, 191, 192, 193, 194, 195, 196
<b>crossed</b>	8, 12, 16, 21, 22, 25, 27, 40, 49, 50, 62, 64, 76, 80, 105, 108, 112, 123, 130, 149, 153, 169, 181, 189, 190, 191, 193, 195
	<b>variance method</b>
<b>old</b>	40, 63, 66, 72, 75, 93, 95, 110, 125, 132, 136
<b>new</b>	1, 5, 6, 7, 10, 11, 15, 23, 24, 25, 30, 32, 33, 37, 38, 39, 46, 48, 51, 52, 54, 55, 63, 66, 67, 74, 75, 80, 81, 94, 95, 100, 106, 111, 112, 119, 128, 137, 150, 158, 160, 168, 169, 173, 178, 185, 186, 192, 196
<b>crossed</b>	1, 5, 6, 9, 12, 21, 22, 26, 49, 50, 51, 52, 53, 56, 65, 66, 72, 75, 76, 84, 87, 93, 95, 97, 105, 110, 115, 124, 125, 132, 136, 160, 169, 188, 193
	<b>mean2 method</b>
<b>old</b>	16, 25, 27, 50, 62, 64, 89, 115, 118, 130
<b>new</b>	1, 6, 10, 11, 12, 13, 14, 21, 22, 23, 24, 27, 35, 38, 40, 51, 52, 54, 59, 60, 62, 64, 74, 78, 79, 80, 82, 98, 102, 119, 137, 139, 140, 150, 151, 160, 166, 168, 186, 188, 192
<b>crossed</b>	1, 6, 8, 10, 12, 16, 21, 22, 25, 27, 38, 40, 49, 50, 58, 62, 64, 72, 76, 80, 84, 118, 130, 137, 138, 139, 149, 158, 186
	<b>maximum sore method</b>
<b>old</b>	27, 40, 62, 73, 74, 93, 95, 115, 132, 136
<b>new</b>	5, 6, 10, 11, 12, 13, 15, 16, 21, 23, 24, 27, 37, 38, 40, 41, 51, 52, 53, 54, 55, 57, 60, 62, 64, 67, 74, 79, 80, 98, 100, 111, 128, 137, 158, 159, 163, 168, 178, 188
<b>crossed</b>	27, 40, 62, 73, 74, 93, 95, 115, 132, 136

Table 105: User exhibiting a lamb/wolf-like behavior in the POC data sets including all sensors but using just impostor scores without time span information.

matcher	number of lamb/wolf-like users								
	O	N	C	NwO	NwO/N	CwO	CwO/C	OC	OC/C
	<b>mean method</b>								
<b>NBIS</b>	11	46	35	43	93.47%	25	71.42%	19	54.28%
<b>NEURO</b>	11	28	27	21	75%	17	62.96%	17	62.96%
<b>FC</b>	11	44	29	42	95.45%	19	65.51%	13	44.82%
<b>POC</b>	11	38	28	36	94.73%	20	71.42%	10	35.71%
	<b>variance method</b>								
<b>NBIS</b>	11	52	44	48	92.30%	36	81.81%	31	70.45%
<b>NEURO</b>	11	27	25	20	74.07%	15	60%	15	60%
<b>FC</b>	11	49	23	47	95.91%	12	52.17%	6	26.08%
<b>POC</b>	11	50	35	46	92%	26	74.28%	18	51.42%
	<b>mean2 method</b>								
<b>NBIS</b>	10	44	31	42	95.45%	22	70.96%	17	54.83%
<b>NEURO</b>	10	43	33	42	97.67%	23	69.69%	23	69.69%
<b>FC</b>	10	35	27	33	94.28%	19	70.37%	12	44.44%
<b>POC</b>	10	36	25	33	91.66%	17	68%	8	32%
	<b>maximum score method</b>								
<b>NBIS</b>	10	41	10	38	92.68%	0	-	0	-
<b>NEURO</b>	10	43	32	42	97.67%	22	68.75%	22	68.75%
<b>FC</b>	10	42	12	38	90.47%	2	16.66%	2	16.66%
<b>POC</b>	10	40	10	36	90%	0	-	0	-

Table 106: Number of users exhibiting a lamb/wolf-like behavior in the data sets including all sensors, but using only time span excluding impostor scores.

Similar to the goats analysis the total number of lambs/wolves was analyzed as well, which is displayed in Table 106. In this table the same naming was used as in Table 100. The influence of the lambs/wolves, detected in 2009, in the 'new' and 'crossed' case is not very high. Basically in the 2013 data it is even lower compared to the goats' case. For the crossed data bases the opposite is detectable. For this purpose a

higher impact of the lamb/wolf-like volunteers, which have been marked in 2009, in the crossed data sets as for the goats analysis can be stated. Furthermore a more or less stable amount of users, which have been signed in 2013, are responsible for the lamb/wolf observations in the crossed data using NBIS and NEURO. A different situation is present for the two non-minutiae based fingerprint recognition systems. For those it seems that the lambs/wolves of 2013 are causing more of 50% of the retrieved users. Based on those results it is possible to state not the assumed stability in case of this first impostor score dependent volunteer analysis. This is the opposite of what was expected. It seems that regardless which animal type is considered an identical tendency can be described. In fact there is a big difference between the goats and lambs/wolves case. This fluctuation is based on the non-minutiae fingerprint recognition systems. Their results are much lower compared to the goats analysis. So it seems that in case of lambs and wolves the minutiae based approaches are better suited to retrieve and display the situation. It was also possible to get the information that the minimum/maximum method is delivering a different result for NBIS and POC compared to the other two recognition systems. For all data sets the same volunteers in the old and crossed data bases could be signed. Additionally no correspondence to the new data set was given. It will be interesting to see if the same results can be described for the second lambs/wolves analysis once more.

For the further analysis, the lamb/wolf-like users are separated according to matcher, analysis method and data sets. So in Tables 107, 108, 109, 110 and 111 the outcomes of the comparison between the 2009 and 2013 data, the 2009 and crossed data sets and the 2013 and crossed data sets are displayed. It is interesting to observe different types of tendencies. The overall tendency is almost similar to the goats case, but looking at the NEURO results an interesting difference can be detected.

In the Tables 107, 110 and 111 some problems are displayed, which occur using the NEURO impostor scores. There are six users, represented by ID 191, 192, 193, 194, 195, 196, who are always signed for the mean and variance analysis method. Considering the circumstances this means that those are signed as lamb or wolf in 2009, 2013 and the crossed data set. But they are never marked in any other menagerie analysis method or in none of the other matching results. They are labeled as goat in two single cases but are not interesting otherwise. There is a pattern that the signed users have in common. This pattern is an important step of the mean and variance

	<b>menagerie analyzing method</b>			
<b>data set</b>	<b>mean method</b>	<b>variance method</b>	<b>mean2 method</b>	<b>maximum method</b>
	<b>NBIS</b>			
<b>A vs B1</b>	98	158	166	166
<b>A vs B2</b>	64, 98	39, 98		
<b>A vs B3</b>			162	162
<b>A vs B4</b>	98, 100			
<b>A vs B5</b>	98	54		54
	<b>NEURO</b>			
<b>A vs B1</b>	191 till 196	191 till 196		
<b>A vs B2</b>	191 till 196	191 till 196		
<b>A vs B3</b>	191 till 196	191 till 196		
<b>A vs B4</b>	191 till 196	191 till 196		
<b>A vs B5</b>	54, 191 till 196	54, 191 till 196	54	54
	<b>FC</b>			
<b>A vs B1</b>	10	127	166	166
<b>A vs B2</b>		100		
<b>A vs B3</b>				54, 160, 182
<b>A vs B4</b>	182			182
<b>A vs B5</b>	10		182	54
	<b>POC</b>			
<b>A vs B1</b>	105		27	40, 74
<b>A vs B2</b>		63, 66, 75	62	62, 74
<b>A vs B3</b>			27	27
<b>A vs B4</b>		95	62	
<b>A vs B5</b>	64		64	27, 74

Table 107: Displaying the 'stable lambs/wolves' which can be detected comparing data set finger1267 and the data sets from 2013 using just impostor scores without time span information.

	<b>menagerie analyzing method</b>			
<b>data set</b>	<b>mean method</b>	<b>variance method</b>	<b>mean2 method</b>	<b>maximum method</b>
	<b>NBIS</b>			
<b>A vs C1</b>	47, 86, 100, 165		25, 130, 165, 182	8, 54, 109, 126, 160, 162, 165, 166, 182, 188
<b>A vs C2</b>	64, 86, 92, 100, 165, 166	165	8, 25, 130, 165, 166	8, 54, 109, 126, 160, 162, 165, 166, 182, 188
<b>A vs C3</b>	86, 92, 100, 166	26, 88, 143	8, 25, 131, 162, 165, 166	8, 54, 109, 126, 160, 162, 165, 166, 182, 188
<b>A vs C4</b>	86, 98, 100, 165, 166	39, 54, 129, 158	130, 131, 134, 162, 165, 166, 182	8, 54, 109, 126, 160, 162, 165, 166, 182, 188
<b>A vs C5</b>	8, 64, 86, 98, 100, 182	39, 143, 165	8, 130, 134, 165, 166, 182	11, 36, 55, 56, 75, 86, 87, 112
	<b>NEURO</b>			
<b>A vs C1</b>	73, 74, 95, 191, 192, 193, 194, 195, 196	73, 74, 95, 191, 192, 193, 194, 195, 196	45, 54, 69, 73, 74, 75, 95, 130	45, 54, 69, 73, 74, 75, 95, 130
<b>A vs C2</b>	54, 73, 74, 191, 192, 193, 194, 195, 196	54, 73, 74, 191, 192, 193, 194, 195, 196	54, 69, 73, 74, 75, 95, 130	54, 69, 73, 74, 75, 95, 130
<b>A vs C3</b>	191, 192, 193, 194, 195, 196	191, 192, 193, 194, 195, 196	40	40
<b>A vs C4</b>	191, 192, 193, 194, 195, 196	73, 74, 191, 192, 193, 194,	73, 74, 91	73, 74, 91, 95, 130
<b>A vs C5</b>	191, 192, 193, 194, 195, 196	73, 191, 192, 193, 194,	73, 74, 95, 130	54, 69, 73, 74, 95, 130

Table 108: Displaying the 'stable lambs/wolves' which can be detected comparing data set finger1267 and the crossed data sets for the minutiae matching results using just impostor scores without time span information.

	menagerie analyzing method			
data set	mean method	variance method	mean2 method	maximum method
	<b>FC</b>			
<b>A vs C1</b>	10, 41, 75, 133, 135, 148, 153, 160, 182	12, 15, 53, 77, 81, 102,	56, 92, 104, 148, 160, 166, 182, 184	25, 33, 50, 92, 93, 148, 166, 182
<b>A vs C2</b>	41, 153, 166	12, 15, 53, 77, 81, 90, 100, 102, 121, 127, 128	160, 166	25, 33, 50, 54, 92, 93, 148, 160, 166, 182
<b>A vs C3</b>	41, 75, 133, 153, 160, 166	12, 15, 53, 77, 81, 90, 100, 102, 121, 127, 128	56, 160, 166	25, 33, 50, 54, 92, 93, 148, 160, 166, 182
<b>A vs C4</b>	41, 75, 133, 153	15, 90, 102	56, 104, 166	25, 33, 50, 54, 92, 93, 148, 160, 166, 182
<b>A vs C5</b>	41, 75, 133, 153, 166	12, 15, 53, 77, 81, 90, 100, 102, 121, 127, 128	56, 92, 166	25, 33, 50, 54, 92, 93, 148, 160, 166, 182
	<b>POC</b>			
<b>A vs C1</b>	25, 27, 105, 108, 123, 153	72, 93, 132, 136	16, 25, 27, 50	27, 40, 62, 73, 74, 93, 95, 115, 132, 136
<b>A vs C2</b>	27, 64, 105, 123	66, 75, 93, 95, 132, 136	27, 50, 64	27, 40, 62, 73, 74, 93, 95, 115, 132, 136
<b>A vs C3</b>	25, 27, 105, 123, 153	75, 93, 95, 132, 136	16, 25, 27, 50, 64, 118, 130	27, 40, 62, 73, 74, 93, 95, 115, 132, 136
<b>A vs C4</b>	25, 27, 64, 105, 123, 153	72, 75, 93, 95, 110,	16, 25, 27, 50,64 125, 136	27, 40, 62, 73, 74, 93, 95, 115, 132, 136
<b>A vs C5</b>	105, 123, 153	72, 136	16, 25, 27, 52,64	27, 40, 62, 73, 74, 93, 95, 115, 132, 136

Table 109: Displaying the 'stable lambs/wolves' which can be detected comparing data set finger1267 and the crossed data sets for the non-minutiae matching results using just impostor scores without time span information.



	<b>menagerie analyzing method</b>			
<b>data set</b>	<b>mean method</b>	<b>variance method</b>	<b>mean2 method</b>	<b>maximum method</b>
	<b>NBIS</b>			
<b>B1 vs C1</b>		185		166
<b>B2 vs C2</b>	64			
<b>B3 vs C3</b>			162	162
<b>B4 vs C4</b>	98, 100			
<b>B5 vs C5</b>	98			54
	<b>NEURO</b>			
<b>B1 vs C1</b>	191, 192, 193, 194, 195, 196	191, 192, 193, 194, 195, 196		
<b>B2 vs C2</b>	191, 192, 193, 194, 195, 196	191, 192, 193, 194, 195, 196		
<b>B3 vs C3</b>	191, 192, 193, 194, 195, 196	191, 192, 193, 194, 195, 196		
<b>B4 vs C4</b>	191, 192, 193, 194, 195, 196	191, 192, 193, 194, 195, 196		
<b>B5 vs C5</b>	191, 192, 193, 194, 195, 196	191, 192, 193, 194, 195, 196		
	<b>FC</b>			
<b>B1 vs C1</b>	10		166	166
<b>B2 vs C2</b>	65	100	103	
<b>B3 vs C3</b>	65		34	54, 160, 182
<b>B4 vs C4</b>		155		182
<b>B5 vs C5</b>	190			54
	<b>POC</b>			
<b>B1 vs C1</b>	40, 105		27, 38, 40	40, 74
<b>B2 vs C2</b>	22, 193, 195	66, 75	22	62, 74
<b>B3 vs C3</b>			27	27
<b>B4 vs C4</b>	169	95	137, 139	
<b>B5 vs C5</b>	12, 189, 190, 191	1	10, 12, 64	27, 74

Table 110: Displaying the 'stable lambs/wolves' which can be detected comparing data sets from 2013 and the crossed data sets using just impostor scores without time span information.

menagerie analyzing method				
data set	mean method	variance method	mean2 method	maximum method
<b>NBIS</b>				
A vs B1 vs C1				166
A vs B2 vs C2	64			
A vs B3 vs C3			162	162
A vs B4 vs C4	98, 100			
A vs B5 vs C5	98			54
<b>NEURO</b>				
A vs B1 vs C1	191 to 196	191 to 196		
A vs B2 vs C2	191 to 196	191 to 196		
A vs B3 vs C3	191 to 196	191 to 196		
A vs B4 vs C4	191 to 196	191 to 196		
A vs B5 vs C5	191 to 196	191 to 196		54
<b>FC</b>				
A vs B1 vs C1	10		166	166
A vs B2 vs C2		100		
A vs B3 vs C3				54, 160, 182
A vs B4 vs C4				182
A vs B5 vs C5				54
<b>POC</b>				
A vs B1 vs C1	105		27	40, 74
A vs B2 vs C2		66, 75		62, 74
A vs B3 vs C3			27	27
A vs B4 vs C4		95		
A vs B5 vs C5			64	27, 74

Table 111: Displaying the 'stable lambs/wolves' which can be detected in 2009, 2013 and in the crossed data sets using just impostor scores without time span information.

method. Both are marking those volunteers which are below the 2.5 percentile and those that are above the 97.5 percentile. This strategy is the reason why the six users are only detected by these two methods. Especially the mean2 method is not able to detect them because only the users are labeled which mean score value is below the 5 percentile.

Apart from this abnormality it is hard to retrieve a certain tendency when a user is lamb/wolf-like. Similar to the goats' case no volunteer can be signed as the 'regular' lamb or wolf. It is even hard to mark those, which represent a 'stable' behavior. Of course it is possible to find them - introduced in Table 111, but they do not share a regularity.

**Lambs/Wolves analysis for time span in- and excluding impostor scores:**

In particular there will not be another strategy for the second lambs/wolves analysis. The same concept was used to perform a similar analysis compared to the goats and first lambs/wolves investigations. So no distinction between lambs and wolves is present as well.

	number of no lambs/wolves-like users			
	NBIS	NEURO	FC	POC
<b>mean method</b>	119	145	123	131
<b>variance method</b>	109	148	114	118
<b>mean2 method</b>	121	121	133	139
<b>maximum sore method</b>	126	122	136	137

Table 112: Number of users exhibiting no lambs/wolves-like behavior in the data sets including all sensors including all impostor scores.

In the first result table, Table 112, the number of those volunteer which were never assigned to behave like the characteristic described in Section 6.3. Basically an analogical overall tendency like in the first lambs/wolves analysis can be measured. The lowest amount of users labeled as lamb or wolf is detectable using the NEURO matching results and the variance method once more. Those 109 users represent 55.61%

of all volunteers which are included in the given data bases. Opposed to this lower boundary, the highest number of users which were never signed as lamb or wolf is 148. According to these information, the margin between those who are never labeled as lamb or wolf in any data set, analysis and matcher method is 19.90%. Compared to the goat margin it is much lower again and slightly lower compared to the first

<b>Data Set</b>	<b>User ID</b>
<b>matcher</b>	<b>NBIS</b>
	<b>mean method</b>
<b>crossed</b>	8, 9, 12, 23, 25, 31, 37, 39, 47, 49, 50, 52, 56, 57, 64, 75, 77, 78, 80, 86, 87, 88, 92, 98, 100, 109, 134, 139, 144, 145, 148, 164, 165, 166, 168, 177, 178, 182, 183, 185, 196
	<b>variance method</b>
<b>crossed</b>	6, 8, 9, 12, 15, 25, 26, 27, 31, 37, 40, 44, 45, 47, 49, 50, 53, 54, 55, 56, 59, 60, 61, 63, 64, 70, 75, 77, 78, 117, 123, 128, 129, 134, 143, 145, 163, 165, 168, 170, 175, 182, 184, 185, 192
	<b>mean2 method</b>
<b>crossed</b>	8, 9, 12, 18, 25, 40, 49, 50, 53, 76, 77, 78, 80, 81, 101, 109, 110, 114, 124, 129, 131, 134, 144, 148, 161, 162, 164, 165, 166, 168, 177, 178, 182, 185, 186, 187, 196
	<b>maximum sore method</b>
<b>crossed</b>	8, 9, 12, 13, 15, 25, 26, 40, 49, 50, 53, 56, 69, 76, 77, 78, 80, 89, 110, 113, 129, 134, 143, 144, 160, 163, 164, 165, 168, 182, 185, 186, 188, 196

Table 113: User exhibiting a lamb/wolf-like behavior in the NBIS data sets including all sensors and impostor scores.

lambs/wolves analysis using only time span independent impostor scores. Also the high fluctuation in the goat case is also not detectable once more. Of course there is a small difference of 2.55% between both lambs/wolves margins. So it could be that

<b>Data Set</b>	<b>User ID</b>
<b>matcher</b>	<b>NEURO</b>
	<b>mean method</b>
<b>crossed</b>	9, 12, 25, 26, 36, 48, 49, 50, 53, 56, 64, 73, 74, 77, 78, 95, 140, 143, 167, 180, 183, 190, 191, 192, 193, 194, 195, 196
	<b>variance method</b>
<b>crossed</b>	9, 12, 25, 26, 48, 49, 50, 53, 56, 64, 73, 74, 77, 78, 95, 143, 167, 180, 183, 190, 191, 192, 193, 194, 195, 196
	<b>mean2 method</b>
<b>crossed</b>	9, 10, 11, 12, 25, 26, 36, 37, 40, 48, 49, 50, 53, 54, 56, 58, 64, 69, 73, 74, 77, 78, 91, 95, 99, 130, 140, 143, 144, 163, 164, 167, 180, 181, 183, 187
	<b>maximum sore method</b>
<b>crossed</b>	9, 10, 12, 25, 26, 37, 38, 48, 49, 50, 53, 54, 56, 58, 64, 67, 69, 73, 74, 77, 78, 91, 95, 99, 130, 143, 144, 163, 164, 167, 180, 183

Table 114: User exhibiting a lamb/wolf-like behavior in the NEURO data sets including all sensors and impostor scores.

the combination of time span in- and excluding impostor scores is providing a more stable performance with regard to those two interesting matching behaviors.

In Tables 113, 114, 115 and 116 the corresponding lamb/wolf-like users for using all impostor scores were displayed. Because there is no chance in 2009 and 2013 impostor scores - the additional impostor scores are causing an effect on the crossed data sets, only those outcomes will not be displayed once more. They can be found in the Tables 102, 103, 104 and 105 in the first lambs/wolves analysis.

In the following it is possible to find differences and similarities between those volunteers and the users which have been detected in the lambs/wolves analysis of Section 6.4. Nevertheless there won't be a detailed discussion about the stable behavior of

<b>Data Set</b>	<b>User ID</b>
<b>matcher</b>	<b>FC</b>
	<b>mean method</b>
<b>crossed</b>	3, 9, 10, 12, 14, 19, 35, 44, 65, 66, 72, 100, 105, 107, 111, 113, 116, 121, 123, 129, 131, 137, 143, 151, 172, 181, 192, 196
	<b>variance method</b>
<b>crossed</b>	5, 12, 14, 21, 33, 34, 35, 37, 66, 71, 72, 74, 79, 80, 92, 100, 106, 110, 111, 114, 123, 135, 142, 143, 147, 149, 151, 159, 163, 168, 171, 178
	<b>mean2 method</b>
<b>crossed</b>	12, 13, 14, 17, 19, 35, 44, 47, 65, 66, 75, 80, 92, 100, 116, 126, 135, 143, 153, 156, 158, 171, 172, 196
	<b>maximum sore method</b>
<b>crossed</b>	12, 14, 18, 32, 35, 44, 65, 66, 71, 84, 92, 100, 143, 171, 172

Table 115: User exhibiting a lamb/wolf-like behavior in the FC data sets including all sensors and impostor scores.

lamb/wolf-like users like introduced in Table 107, 108, 109 and 110 because no clear tendency could be retrieved. The only exception will be the presentation of those volunteers, which are labeled in 2009, 2013 and in the crossed data sets. They can be looked up in Table 117. It is interesting to observe the same abnormality for mean and var method using the NEURO scores. Apart from this aspect it is also possible to gather the information that there must be some time span based influence on the lamb/wolf characteristic of the given data sets. Comparing the results presented in Table 111 and 117 there is a high number of similarity observable, but also differences. So the additional usage of the time span including impostor scores has some effect on the overall result of the second lamb/wolf analysis. This observation can be verified looking at Table 118. As described in the first lamb/wolf analysis there have been some interesting effects. The most important one can be confirmed in the second analysis as well. There is no stability in terms of the user dependent impostor score analysis. Basically the same amount of fluctuation as for the goats' case is present.

<b>Data Set</b>	<b>User ID</b>
<b>matcher</b>	<b>POC</b>
	<b>mean method</b>
<b>crossed</b>	1, 3, 12, 16, 25, 31, 41, 47, 48, 50, 62, 64, 71, 75, 76, 87, 104, 115, 128, 137, 148, 149, 153, 158, 176, 189, 190, 193
	<b>variance method</b>
<b>crossed</b>	1, 2,5, 8, 9, 10, 12, 14, 21, 22, 26, 30, 40, 49, 50, 53, 65, 70, 72, 75, 76, 80, 87, 93, 95, 105, 110, 120, 123, 136, 142, 146, 176, 178, 196
	<b>mean2 method</b>
<b>crossed</b>	10, 12, 16, 25, 27, 49, 50, 62, 64, 76, 104, 115, 118, 126, 127, 128, 130, 136, 137, 138, 139, 8, 149, 158, 176, 180, 182
	<b>maximum sore method</b>
<b>crossed</b>	7, 8, 9, 10, 12, 14, 21, 27, 40, 49, 50, 53, 65, 70, 76, 93, 95, 98, 104, 132, 136, 137, 176, 186

Table 116: User exhibiting a lamb/wolf-like behavior in the POC data sets including all sensors and impostor scores.

But it can not be stated if fingerprint ageing, quality or volunteer dependent influences are responsible for this observation. Nevertheless it is likely - between 43.91% and 16.67% - to detect a user marked as lamb or wolf in a crossed data base once more if the same one was signed in one of the single cases before. Of course there are some variances based on the used fingerprint recognition system, the analysis method and used data sets. But the majority of the reoccurrence likelihood is around 30%. Besides, the abnormality in case of the minimum/maximum method for NBIS and POC was not observable once again. All in all it seems that the influence of the probably ageing related impostor matches is certainly detectable in the lambs/wolves analysis.

menagerie analyzing method				
data set	mean method	variance method	mean2 method	minimum method
<b>NBIS</b>				
A vs B1 vs C1				
A vs B2 vs C2	64			
A vs B3 vs C3				
A vs B4 vs C4	98, 100			
A vs B5 vs C5	98			
<b>NEURO</b>				
A vs B1 vs C1	191 to 196	191 to 196		
A vs B2 vs C2	191 to 196	191 to 196		
A vs B3 vs C3	191 to 196	191 to 196		
A vs B4 vs C4	191 to 196	191 to 196		
A vs B5 vs C5	191 to 196	191 to 196		54
<b>FC</b>				
A vs B1 vs C1				
A vs B2 vs C2		100		
A vs B3 vs C3				
A vs B4 vs C4				
A vs B5 vs C5				
<b>POC</b>				
A vs B1 vs C1			27	40
A vs B2 vs C2		75		
A vs B3 vs C3			27	27
A vs B4 vs C4		95	62	
A vs B5 vs C5			64	

Table 117: Displaying the 'stable lambs/wolves' which can be detected in 2009, 2013 and in the crossed data sets using all impostor scores.



According to the results displayed in Table 106 a weakness for the lamb/wolf behavior in the crossed data sets was observable. The lamb/wolf users of 2013 were influencing the detection of new lambs/wolves in the crossed data sets for FC and POC. In the most cases much more than 50% of the signed lambs and wolves have been marked in 2013 before. On the opposite for NBIS and NEURO the impact could be located between roughly 30% and 46%. For the present second lamb/wolf analysis a different situation can be described: The time span including impostor scores' addition improves this impact. That means that the total number of lamb/wolf-like volunteers, which are labeled in 2013 and who are marked in the crossed sets as well is not that high as discussed for the first lamb/wolf analysis. To be more precise, in most of the cases between 20% and 30% of all 2013 lamb/wolf-like users can be labeled in the crossed data sets again. The only exception can be found for the mean2 method using POC scores. But even in this case the total amount is lower than 50%. For this purpose it can be stated that more fluctuation within the location of the lambs and wolves is present. That means, it is not so likely to label a volunteer in the 2013 and in the crossed sets. So using the present impostor data without time span information causes a higher number of fluctuation in terms of reoccurrence of the signed users. Furthermore it was not possible to detect the abnormality based on NBIS and POC using the maximum method. So there are other users signed in 2009 and in the crossed sets. Especially the total number of them is not similar like it could be described for the first lamb/wolf analysis.

After the menagerie analysis result description it is necessary to compare the goat and lamb/wolf cases a last time. As displayed in the goats analysis it was possible to observe 5 different classes of user behavior. So the same classes can be detected in lamb/wolf analysis as well. There are volunteers, who are only signed in 2009, or 2013 or in the crossed data set for example. Additionally having a look at the differences and similarities of those two animal cases, another structure can be presented. This ordering is taking into account that there are volunteers which are labeled not only once. It is possible to detect four types of user tendency:

- **Type 1:** There are some users who are labeled just as 'goat'. As example for this case user 1 can be quoted using NBIS implementation and mean method.

matcher	number of lamb/wolf-like users									
	O	N	C	NwO	NwO/N	CwO	CwO/C	OC	OC/C	
	<b>mean method</b>									
<b>NBIS</b>	11	46	41	43	93.47%	31	75.60%	23	56.09%	
<b>NEURO</b>	11	28	28	21	75%	19	67.85%	19	67.85%	
<b>FC</b>	11	44	28	42	95.45%	27	96.42%	20	71.42%	
<b>POC</b>	11	38	28	36	94.73%	22	78.57%	18	64.28%	
	<b>variance method</b>									
<b>NBIS</b>	11	52	45	48	92.30%	40	88.88%	28	62.22%	
<b>NEURO</b>	11	27	26	20	74.07%	17	65.38%	17	65.38%	
<b>FC</b>	11	49	32	47	95.91%	30	93.75%	24	75%	
<b>POC</b>	11	50	35	46	92%	28	80%	21	60%	
	<b>mean2 method</b>									
<b>NBIS</b>	10	44	37	42	95.45%	29	78.37%	23	62.16%	
<b>NEURO</b>	10	43	36	42	97.67%	28	77.77%	23	63.88%	
<b>FC</b>	10	35	24	33	94.28%	22	91.66%	20	83.33%	
<b>POC</b>	10	36	27	33	91.66%	18	66.66%	14	51.85%	
	<b>maximum score method</b>									
<b>NBIS</b>	10	41	34	38	92.68%	28	82.35%	22	64.70%	
<b>NEURO</b>	10	43	32	42	97.67%	25	78.12%	22	68.75%	
<b>FC</b>	10	42	15	38	90.47%	14	93.33%	12	80%	
<b>POC</b>	10	40	25	36	90%	19	76%	13	68.42%	

Table 118: Number of users exhibiting a lamb/wolf-like behavior in the data sets including all sensors, and using all impostor scores.

- **Type 2:** The second type of volunteer group is that one denoting the just 'lamb/wolf' case. Again a certain user of the NBIS and mean method analysis can be found, it is user 8.

- **Type 3:** If a volunteer is detected as goat and as lamb/wolf than it will belong to this type. User 68 is one of those special 'animal'-users. The volunteer was labeled using FC and the variance method.
- **Type 4:** Combining the information about non goat-like and non lamb/wolf users leads to this last type. Within this list the lowest number of volunteers are included. In the NBIS and mean method results for example user 128 can be detected.

The total number of those volunteers belonging to one of the four types is displayed in the following Tables 119 and 120. In Table 119 the score analysis without ageing influence is displayed. The knowledge which was gathered from the second lambs/wolves analysis was taken into account and Table 120 describes this situation.

As it is possible to see there are no specific tendencies or abnormalities observable. It seems that there is not a big difference comparing the matching results/menagerie analysis methods and data sets. Of course there are fluctuations detectable, but all of them are caused either by the fingerprint recognition system, the menagerie analysis method or the data sets themselves. For example the outlier problem, present for the min/max method, is the most prominent variation in Tables 119 and 120. In particular the differences between the both impostor score analysis investigations are displayed once more. But in general no certain tendency can be described.

## 6.5 Mean scores and System errors

Before performing a characterizing analysis concerning goats, lambs and wolves it is necessary to discuss the before mentioned problems described in Section 6.3. According to [40] there are several problems.

Looking at the results of the goats and lambs/wolves analysis revealed an obvious situation. The big difference between low matching scores and high ones cause some troubles. Especially looking at the results provided by NBIS, NEURO and POC the sensitivity to outliers could be detected easily. So the gap within the highest and lowest matching scores introducing a number of so called outliers represents the main problem using the minimum/maximum analysis method. Therefore at a specific level within the goats analysis this method was not used any longer. Opposed to this, the same method was useful during the lamb/wolf analysis. So in the used data sets,

menagerie method	all goats	all lambs/ wolves	only goats	only lambs/ wolves	goats and lambs/wolves	never goat or lamb/wolf
<b>NBIS</b>						
<b>mean</b>	58	73	28	41	32	65
<b>variance</b>	70	90	37	55	35	36
<b>mean2</b>	51	69	22	40	29	76
<b>min/max</b>	110	48	77	28	20	38
<b>NEURO</b>						
<b>mean</b>	63	49	46	33	16	84
<b>variance</b>	77	46	59	29	17	73
<b>mean2</b>	67	75	36	44	31	54
<b>min/max</b>	169	74	108	13	61	-
<b>FC</b>						
<b>mean</b>	73	66	40	37	29	57
<b>variance</b>	71	64	43	43	21	61
<b>mean2</b>	65	55	49	33	22	76
<b>min/max</b>	59	50	43	37	13	87
<b>POC</b>						
<b>mean</b>	74	57	40	27	30	65
<b>variance</b>	78	75	53	52	23	43
<b>mean2</b>	51	51	24	23	28	94
<b>min/max</b>	105	46	85	30	16	45

Table 119: Displaying the total number of users labeled as goat, or lamb/wolf or as both 'animal types' using only time span excluding impostor scores.

the high distinctiveness related to the genuine matching scores was a good attribute looking at the performance analysis, but not in case of the menagerie comparison. The second major problem is caused by the mean method. For sure the influence of the outlier scores is not a problem in this case. So representing the user behavior within the given recognition system with the central moments of the genuine/impostor user score distributions is a good idea on the one hand. But on the other hand the same

menagerie method	all goats	all lambs/ wolves	only goats	only lambs/ wolves	goats and lambs/wolves	never goat or lamb/wolf
<b>NBIS</b>						
<b>mean</b>	58	77	28	47	30	61
<b>variance</b>	70	87	37	54	33	39
<b>mean2</b>	51	75	22	46	29	70
<b>min/max</b>	110	70	77	37	33	16
<b>NEURO</b>						
<b>mean</b>	63	51	46	34	17	82
<b>variance</b>	77	48	59	30	18	71
<b>mean2</b>	67	75	36	44	31	54
<b>min/max</b>	169	74	108	13	61	-
<b>FC</b>						
<b>mean</b>	73	73	40	40	33	50
<b>variance</b>	71	82	43	54	28	43
<b>mean2</b>	65	63	49	47	16	68
<b>min/max</b>	59	60	43	44	16	77
<b>POC</b>						
<b>mean</b>	74	65	40	31	34	57
<b>variance</b>	78	78	53	53	25	40
<b>mean2</b>	51	57	24	30	27	88
<b>min/max</b>	105	59	85	39	20	32

Table 120: Displaying the total number of users labeled as goat, or lamb/wolf or as both 'animal types' using all matching scores.

approach is vulnerable too. It is possible that no direct relationship between a user's mean score value and his/her participation in system errors is given. The detected user behavior to be a so called goat or lamb/wolf probably does not exist. It would be introduced using the mean method. Therefore it is necessary to have a closer look at this situation. It would be a significant problem if system errors would be introduced by almost all outliers. In this case the user's mean average genuine and impostor

scores cannot be used as key number to detect false rejected/accepted user.

data set	mean genuine score vs false rejected	mean impostor score vs false accepted	var genuine score vs false rejected	var impostor score vs false accepted
<b>NBIS</b>				
<b>A</b>	0.7662	-0.4962	-0.3919	-0.3769
<b>B1</b>	0.7467	-0.4678	-0.3576	-0.3543
<b>B2</b>	0.7501	-0.4591	-0.3186	-0.3643
<b>B3</b>	0.8315	-0.4664	-0.3573	0.0309
<b>B4</b>	0.7084	-0.4720	-0.3839	0.0658
<b>B5</b>	0.7303	-0.4507	-0.3752	0.1162
<b>C1</b>	0.8740	-0.5118	-0.4823	-0.3964
<b>C2</b>	0.8969	-0.5100	-0.4609	-0.4144
<b>C3</b>	0.8964	-0.5128	-0.4904	-0.1840
<b>C4</b>	0.8664	-0.5127	-0.5087	-0.0398
<b>C5</b>	0.8750	-0.5060	-0.4771	0.0436
<b>NEURO</b>				
<b>A</b>	-0.5439	-0.4357	-0.5034	0.2536
<b>B1</b>	-0.5128	-0.4418	-0.5341	-0.0420
<b>B2</b>	0.7501	-0.5315	-0.4276	0.2423
<b>B3</b>	0.8315	-0.4908	-0.3639	0.3120
<b>B4</b>	0.7084	-0.5347	-0.4092	0.1761
<b>B5</b>	0.7303	-0.4921	-0.3649	0.2240
<b>C1</b>	-0.4748	-0.5263	-0.6534	0.1576
<b>C2</b>	-0.4721	-0.5216	-0.6367	0.2947
<b>C3</b>	-0.4636	-0.4881	-0.6327	0.3147
<b>C4</b>	-0.4775	-0.5088	-0.6125	0.1794
<b>C5</b>	-0.4711	-0.4912	-0.6308	0.2236

Table 121: NBIS and NEURO correlation based analysis' results excluding time span impostor scores.

As said before, the outlier problem of the minimum/maximum approach is obvious and will not be discussed in more detail. On the contrary, the potential mean method problem will be evaluated more precise. Therefore the relation between the mean user's scores and the system errors has to be taken into account. This analysis depending on the score distribution must be performed for the genuine and the impostor

matching scores as well. Besides, to be on the safe side, because mean method and variance method are related, the correlation based comparison was also performed for the variance method.

<b>data set</b>	<b>mean genuine score vs false rejected</b>	<b>mean impostor score vs false accepted</b>	<b>var genuine score vs false rejected</b>	<b>var impostor score vs false accepted</b>
<b>FC</b>				
<b>A</b>	-0.5439	0.5197	0.9168	-0.0005
<b>B1</b>	0.4861	-0.4418	0.9659	0.0168
<b>B2</b>	0.4845	-0.0644	0.9974	-0.0145
<b>B3</b>	0.5078	-0.0472	0.9928	0.0285
<b>B4</b>	0.4898	-0.0583	0.9950	-0.0099
<b>B5</b>	0.5066	-0.0317	0.9892	0.0010
<b>C1</b>	0.5174	-0.0243	0.8686	-0.1882
<b>C2</b>	0.5787	-0.0124	0.9913	-0.1836
<b>C3</b>	0.5773	-0.0088	0.9945	-0.1832
<b>C4</b>	0.5731	0.0442	0.9917	-0.2991
<b>C5</b>	0.5802	0.0007	0.9918	-0.1841
<b>POC</b>				
<b>A</b>	0.9950	-0.5174	0.9995	-0.5335
<b>B1</b>	0.9996	-0.5024	0.9996	-0.5293
<b>B2</b>	0.9996	-0.5098	0.9996	-0.5370
<b>B3</b>	0.9996	-0.5039	0.9996	-0.5360
<b>B4</b>	0.9996	-0.5030	0.9996	-0.5278
<b>B5</b>	0.9996	-0.5082	0.9996	-0.5215
<b>C1</b>	0.9910	-0.5565	0.9910	-0.5701
<b>C2</b>	0.9930	-0.5586	0.9930	-0.5736
<b>C3</b>	0.9933	-0.5574	0.9933	-0.5737
<b>C4</b>	0.9936	-0.5566	0.9936	-0.5687
<b>C5</b>	0.9928	-0.5586	0.9928	-0.5666

Table 122: FC and POC correlation based analysis' results excluding time span impostor scores.

So the first part of this analysis must be on the one hand to calculate the user's mean and variance average genuine/impostor scores. On the other hand the system errors, the number of falsely rejected or accepted users, have to be determined. This determi-

nation needs a certain threshold to distinguish between a system failure and a correct system decision. As introduced by [40] it is necessary to use a global threshold based on the data set and the used matching method. Therefore the *EER* threshold was chosen. Subsequently for each user the same calculation was performed. The number of genuine matches according to the user that are below this threshold are selected. They are representing the false rejected matches. Using the same method according to the user's impostor scores the false accepted matches are selected.

data set	mean genuine score vs false rejected	mean impostor score vs false accepted	var genuine score vs false rejected	var impostor score vs false accepted
<b>NBIS</b>				
<b>A</b>	0.7662	-0.4962	-0.3919	-0.3769
<b>B1</b>	0.7467	-0.4678	-0.3576	-0.3543
<b>B2</b>	0.7501	-0.4591	-0.3186	-0.3643
<b>B3</b>	0.8315	-0.4664	-0.3573	0.0309
<b>B4</b>	0.7084	-0.4720	-0.3839	0.0658
<b>B5</b>	0.7303	-0.4507	-0.3752	0.1162
<b>C1</b>	0.8740	-0.6311	-0.4823	-0.5720
<b>C2</b>	0.8964	-0.6307	-0.4609	-0.5659
<b>C3</b>	0.8984	-0.6317	-0.4904	-0.3330
<b>C4</b>	0.8665	-0.6336	-0.5087	-0.1370
<b>C5</b>	0.8750	-0.6282	-0.4771	-0.0281
<b>NEURO</b>				
<b>A</b>	-0.5439	-0.4357	-0.5034	0.2536
<b>B1</b>	-0.5128	-0.4418	-0.5341	-0.0420
<b>B2</b>	0.7501	-0.5315	-0.4276	0.2423
<b>B3</b>	0.8315	-0.4908	-0.3639	0.3120
<b>B4</b>	0.7084	-0.5347	-0.4092	0.1761
<b>B5</b>	0.7303	-0.4921	-0.3649	0.2240
<b>C1</b>	-0.4748	-0.6827	-0.6534	0.0914
<b>C2</b>	-0.4721	-0.6762	-0.6367	0.3133
<b>C3</b>	-0.4636	-0.6263	-0.6327	0.2649
<b>C4</b>	-0.4775	-0.6606	-0.6125	0.1386
<b>C5</b>	-0.4711	-0.6424	-0.6308	0.1721

Table 123: NBIS and NEURO correlation based analysis' results using all scores.



data set	mean genuine score vs false rejected	mean impostor score vs false accepted	var genuine score vs false rejected	var impostor score vs false accepted
<b>FC</b>				
<b>A</b>	-0.5439	0.5197	0.9168	-0.0005
<b>B1</b>	0.4861	-0.4418	0.9659	0.0168
<b>B2</b>	0.4845	-0.0644	0.9974	-0.0145
<b>B3</b>	0.5078	-0.0472	0.9928	0.0285
<b>B4</b>	0.4898	-0.0583	0.9950	-0.0099
<b>B5</b>	0.5066	-0.0317	0.9892	0.0010
<b>C1</b>	0.5174	-0.5606	0.8686	-0.6938
<b>C2</b>	0.5787	-0.5608	0.9913	-0.6792
<b>C3</b>	0.5773	-0.5572	0.9945	-0.6858
<b>C4</b>	0.5731	-0.5590	0.9917	-0.6860
<b>C5</b>	0.5802	-0.5524	0.9918	-0.6825
<b>POC</b>				
<b>A</b>	0.9950	-0.5174	0.9995	-0.5335
<b>B1</b>	0.9996	-0.5024	0.9996	-0.5293
<b>B2</b>	0.9996	-0.5098	0.9996	-0.5370
<b>B3</b>	0.9996	-0.5039	0.9996	-0.5360
<b>B4</b>	0.9996	-0.5030	0.9996	-0.5278
<b>B5</b>	0.9996	-0.5082	0.9996	-0.5215
<b>C1</b>	0.9910	-0.7143	0.9910	-0.7141
<b>C2</b>	0.9930	-0.7142	0.9930	-0.7129
<b>C3</b>	0.9933	-0.7129	0.9933	-0.7107
<b>C4</b>	0.9936	-0.7123	0.9936	-0.7093
<b>C5</b>	0.9928	-0.7112	0.9928	-0.7084

Table 124: FC and POC correlation based analysis' results using all scores.

After this first step, preparing the needed information of the recognition system the Pearson product-moment correlation coefficient was calculated for each data set. The correlation value is used to display the linear relationship between two or more data sets or random variables. In this case the linear relationship between the user's mean/variance genuine/impostor scores and the detected system errors was calculated. Since four matching implementations and eleven different data sets have been used in this master thesis, the analysis had to be executed for all possible combinations between recognition systems and data sets. The statistically significant results at the 0.01 level can be found in Tables 121, 122, 123 and 124 for the mean and the

variance method. As can be seen in those tables, the linear relationship between the user's average mean and variance scores and the system errors is detectable in all data sets and matcher types, despite there is not always an identical tendency observable. So only for the POC results the correlation between mean/var genuine scores and false rejected matches is positive across all data bases and negative for the mean/var impostor scores compared to the false accepted matches. In all other cases this tendency is changing depending on the data set and the recognition method. But not only this fluctuation can be looked up. The strength of the correlation is also not consistent. In some cases a very high positive correlation can be detected and sometimes a very low negative one as well. Nevertheless the linear correlation can be detected for each data set and matcher type and this information guarantees that the analysis concerning the mean and variance zoo method is consistent according to the actual system errors.

## **6.6 Menagerie Analysis and Ageing Effects detected in Section 5**

The investigations that have been performed in Section 5 yield to an interesting outcome. The shift in the genuine score distributions to the left, the decrease of the higher genuine scores and the increase of the lower ones indicated a first effect that could be initiated by ageing.

In this part of the current thesis the aim will be to combine the information of Section 5 and the menagerie analysis introduced in Section 6. Since the shift in the genuine score distribution could be verified the main task is to have a look what does this mean for 'Doddington's Zoo'. On the other hand the almost stable impostor score distribution will be taken into account if this stability could be used as reference in case of looking at menagerie ageing effects.

At first the focus will lie on the genuine score distribution and the genuine score related goats analysis. The results of the first experimental setup are quite clear. Because the decrease in the genuine scores is unmistakable the impression is that there must be an effect detectable in the goats analysis as well. As introduced in Section 6.1 the goat's characteristic is related to low genuine scores. That would lead to the suggestion that due to the fact the number of low genuine scores is raised in the crossed data sets compared to the single data sets, also the number of detected goats must increase too. But, as readable in Table 100 a different observation can be detected. To be more precise, the total number of goats in the crossed data sets is higher as in

the older data set from 2009 and lower as in the younger data sets from 2013. Having a even closer look at the results, the number of users labeled as goats is always identical for each set. This outcome seems to be a contradiction to the direct relationship between low genuine scores and the definition of goats. To solve the contradiction it is necessary to think once again what is done while performing the menagerie analysis.

Basically the idea of the menagerie analysis is, to have a look how many users are included and than have a look at the matching scores. Those users who have the lowest percentage of matching scores are labeled as goat or lamb or wolf. This methodology is performed for each data set independently. So there is no information about what scores are available in which data base. So the lowest percentage of matching scores will be the same for each set, but the lowest scores may differ a lot. Look at the following example. Consider two different data bases. In the first one the matching scores are located between 0.5 and 1 and in the other case between 0 and 0.6. It is obvious that the matching scores in the first data set are higher than in the other example set on average. So the user depending matching scores in the first set will also be higher on average. Therefore it is clear that roughly summarized the lowest user depending scores will be also higher. But for each set the same percentage will be used to label the 'animals'. So the marking is not connected directly to the size of the scores. Of course the scores are used to build up the selection basis to separate the users, but they are not involved during the labeling process. Therefore the results from Section 6.4 cannot be used to indicate the outcomes of the experiments described in Section 5 and vice versa concerning the genuine scores. The shift in the genuine score distributions and the decrease of the total number of goats in the crossed data sets are both independent from each other. Both are ageing effects, but effects depending on different experimental setups.

But nevertheless there are some goats depending aspects detectable that can be summarized to be ageing effects in case of menagerie analysis concerning the goat definition. First depending on the data sets it is possible to label certain users more often than others independently from the used matching method. For example user 6 and 25 are detected more often as for example user 194. It seems that there are some volunteers which are prone to get low genuine matching scores. Especially because if this user is labeled once in the old data set it is very likely to detect the same volunteer in the newer data sets and the crossed data sets as well. Opposed to this the chance

to label a user in the crossed data sets if the volunteer was not labeled before is very rare. The second interesting observation is that there are some volunteers who are labeled in the old data set, but never again or in one of the new data sets and never again. For example user 14 and 44 in the NEURO results for variance analysis method or user 107 using FC and the mean method. So roughly spoken it is possible to summarize the 'goatish' behavior and create three classes:

- **Goat-free Class:** Not detected as goat in the old data set indicates a very high possibility to be never labeled as goat.
- **Goat-stable Class:** Labeled once in the old data set indicates a very high possibility to be labeled as goat again in a crossed data base.
- **Goat-once Class:** Those users who are labeled just once, which can be explained for example by ageing.

Nevertheless it also must be summarized that the assumption of detecting a very high amount of fluctuation within the goat-like volunteers could not be confirmed. According to the high amount of variance comparing the single and crossed data sets' genuine scores it was expected that in case of the corresponding goats' case very high fluctuation can be observed as well. Which would be indicating that a probably present fingerprint ageing is causing variances in terms of the goats characteristic. Users who are marked as goats in a specific year would not retain this characteristic across several years. But according to the results of the performed experiments this hypothesis must be rejected. There are certain volunteers who extend their goat-like behavior over several years. This effect can be caused by ageing. But as described in the enumeration above not only those 'stable-goats' seem to be influenced by a probably detectable ageing. It is also possible that fingerprint ageing is responsible for the fact that some volunteers are losing their goat characteristic. Of course those who are labeled only once can also be signed by accident because of some failure during the matching procedure or by some problems during the imprint acquisition. This quality based aspect will be discussed in the following Chapter 7.

The second interesting outcome from Section 6 was the almost stability of the impostor score distributions and on the other hand the decrease of the total number of lambs/wolves in the crossed data sets compared to the new data sets as described in the corresponding analysis' results. This decrease, which can be detected comparing the entire amount of lambs/wolves in Tables 106 and 118, indicates that the variabil-

ity of lamb/wolf-like users in the new data sets together is much higher compared to the crossed data sets. So despite the fact that the impostor score distributions seem to be more or less stable across the data sets there is an impact on the volunteer behavior. Especially comparing those lambs/wolves which are detected for FC and POC the first time in 2013 and once more in the crossed sets. It seems that using all impostor scores a more stable behavior is present. In particular the impact of the time span including impostor scores is most observable in this situation. The outcomes are more similar to NBIS and NEURO after all impostor scores were taken into account. For this purpose ageing could have an impact on the described aspect, but so far it could also be that the quality of the imprints is responsible as well because they could also influence the recognition performance of the used fingerprint recognition systems. Additionally it was very interesting to observe that there was more fluctuation as assumed in the lamb/wolf case. Due to the stability of the impostor scores a quite high amount of stability was expected for this characteristic as well. The number of stable lambs/wolves as detected in the experiments is a little bit lower as assumed. Of course the results display the a high chance of extending the users' lamb/wolf characteristic, but it is interesting to observe that there is a lot of correspondence to the goats case. It seems that the likelihood of an animal-like behavior extension is more or less same for both investigated animal cases.

Furthermore it is possible to say that there are basically the same classes observable as described above using the goat information. But it can be stated that there are much more users which can be grouped in a so called 'Lamb/Wolf-once Class'. Due to the fact that the lamb and wolf case is taken into account together it is not possible to say if the lamb-like characteristics are providing the high number of fluctuation or the wolf-like. So from this point of view it is also not possible to state if due to the variability - caused by ageing - a system weakness is detectable. This would need some further investigations, which would exceed this thesis.

Apart from this fact it will be interesting to see how important the impact of the quality aspect of the imprints is influencing the performed experiments so far. The quality analysis can be looked up in the following Section 7.

## 7 Fingerprint Ageing and Quality

In this final section of the master thesis a discussion about the quality information of the imprints will be taken into account because the performance of a fingerprint recognition system is affected by the quality of the imprints in the data base. So probably it is possible to explain the detected effects concerning the performance and menagerie analysis which have been discussed in Chapters 5 and 6. One question will be if the quality is influencing the possibility to assign a specific animal type to a certain user than it is not possible to speak of an ageing effect. But on the other side if quality has no impact on the menagerie recognition than the present chances detected in the analysis before are affected by ageing. Besides, it is also important to discuss if the outcomes of Chapter 5 can be explained by this analysis or not. So it will be interesting to see if the results are representing the results from [41] or not. Apart from the before mentioned [41] there are some very interesting effects that need to be discussed first, before starting to talk of certain quality measurements. One aspect is the sensor specific point of view. Results about cross-sensor matching have been presented in [7]. Using a multi-sensor data base, where for the same volunteers fingerprint images have been acquired with different sensors types. So the setup is similar to the data sets that are used in this master thesis. Of course the number of sensors included in the particular data set is higher in the data bases introduced for this thesis. In [7] it was possible to detect an increase of the user quality values for two single sensor types. At the same time the threshold value for the *EER* was raised as well. In the other case there was no increase or decrease detectable. Fusing the different sensors a high reduction of the *EER* could be observed. So it seems that fusing two sensor types can improve the performance independent of the imprint quality. The used matching algorithm was the *NBIS* implementation. Because in the multi-sensor data base no time span is included, it is hard to compare the results with the outcomes of the quality analysis of this thesis, but it is interesting to keep the information in mind if abnormalities occur.

Another interesting circumstance is discussed in [21]. As displayed in Section 4.4 there have been different acquisition conditions for the used data sets. One of the most eye-catching problems during the acquisition process is the fingerprint force. That means the different strength of pressure the finger is pressed on the sensor plate. This circumstance was considered into more detail in [21]. Selecting different

so called force levels it was possible to detect an impact of different pressure and the correlation to the imprint quality and minutiae detecting ability. They also used the *NBIS* fingerprint recognition system as well.

So it seems that the quality of imprints is influenced by a variety of conditions. Therefore to realize the quality analysis of Doddington's zoo results and the data base in general, different quality measurements will be taken into account. The results of the methods should be compared to verify that there is no quality method dependent deviation. Besides, because there are different strategies that can be used to retrieve quality information of an imprint it was necessary to select some specific methodologies. Basically it is possible to divide those theoretical concepts into 2 classes. First there is the class containing the ideas that are focusing on local features to describe the quality of an imprint. On the other side there is the second class containing global feature based measurements. In [6] there has been a study to compare the quality approaches and additionally a third class was also considered. This introduced third class is including all strategies that are addressing the quality problem to be a classification issue.

Due to the fact that the NIST Fingerprint Image Quality 2.0 (NFIQ 2.0) was not released the time the quality experiments have been performed, following methods have been taken into account:

- NIST Fingerprint Image Quality (NFIQ)
- Image Quality of Fingerprint (IQF)
- Gabor Filter Image Quality of Fingerprint (GFIQF)

According to the named quality measurements it is possible to characterize those methods. Especially the strategy to retrieve the needed information to compare the qualities of the imprints is important. The *NFIQ* implementation, introduced in 2004 is using minutiae feature information to gather the quality values. The more detailed discussion of this method will be in Subsection 7.1 and is based on [36].

The second method, the *IQF* implementation, is based on using the Fast Fourier Transform to select certain parameters of the power spectrum. In Subsection 7.2, after describing the *NFIQ*, this methodology will be analyzed. The main information therefore can be looked up in [26].

The last measurement is based on Gabor Filter application. The concept for the

methodology was presented in [34] and will be discussed in Subsection 7.3.

## 7.1 NIST Fingerprint Image Quality (NFIQ)

This first method was developed and implemented at the National Institute of Standards and Technology it is part of the before used NBIS software package. This standard fingerprint quality measurement was introduced in 2004 by several researchers, Elham Tabassi among others [36]. The main idea was to improve the performance of a fingerprint recognition system. So for example imprints with poor quality can be processed using different algorithms or thresholds or the imprint is acquired and the quality value is too low another imprint could be enrolled more easily. But to be able to perform those tasks a specific quality measurement was mandatory. There are two main steps that must be executed to gather the NFIQ value of an imprint.

- **Feature extraction:** In the first step the *mindtct* implementation is used to extract the needed features. Basically the same *mindtct* algorithm is used as in the NBIS software package. But there is a slight adaptation concerning the number of extracted minutiae information. Compared with original feature extraction method the dimension of the feature vector is restricted to 11 for each imprint. In the classical implementation this restriction is not included and the length of the feature vector can vary. The selected minutiae are the 11 most important and distinctive ones.
- **Classification:** After the feature extraction the feature vectors are forwarded to a neural network to classify the input information into five different classes. Each class is representing a separate quality value. Those values are varying between 1, the best quality measurement and 5, the poorest imprint quality that can be selected with the NFIQ software.

In [36] different characteristics for low quality values have been observed. The most important are distortion caused by the fingerprints itself, like scars or distortion that occurred during the acquisition or compression process.

Based on this quality measurement method the first calculation performed on the data sets was to gather an average quality value for all data sets. As visible in Table 125 it is not possible to detect any specific data set dependent abnormality. Nevertheless



there are some remarkable fluctuations present. Each time when imprints, acquired by the T2 sensor, are included in the data sets the quality is better compared to all other data bases. For example the average quality of B1 is the best among all data sets. The average quality of the other crossed data bases remains to be better then the corresponding single sets, but worse compared to data set A. In general it is possible to conclude that the quality performance of B2, B3, B4 and B5 is slightly worse as for C2, C3, C4 and C5.

<b>Data set</b>	<b>av. NFIQ value</b>
<b>A</b>	2.71
<b>B1</b>	2.44
<b>B2</b>	3.13
<b>B3</b>	3.19
<b>B4</b>	3.01
<b>B5</b>	2.90
<b>C1</b>	2.57
<b>C2</b>	2.92
<b>C3</b>	2.95
<b>C4</b>	2.86
<b>C5</b>	2.80

Table 125: Average NFIQ values per data set.

To get comparable measures with other data bases four additional data sets have been considered. They are called 'DB1<sub>A</sub>', 'DB2<sub>A</sub>', 'DB3<sub>A</sub>' and 'DB4<sub>A</sub>'. Further details and specifications about those data bases can be looked up at the FVC-2004 [1]. Their average quality results are displayed in Table 126. It is clearly observable that the average NFIQ of the master thesis' data sets is always worse compared to any value of the four reference data bases.

To retrieve a more detailed information based on the imprints the following approach has been performed additionally. In Table 125 it is not possible to gather any quality information of a single user or a certain imprint. For this purpose the correlation

between the single quality impact of the imprints will be discussed in a more detailed way. The results of these experiments can be looked up in Section 7.4.

Data set	av. NFIQ value
DB1 <sub>A</sub>	1.34
DB2 <sub>A</sub>	2.31
DB3 <sub>A</sub>	1.66
DB4 <sub>A</sub>	1.81

Table 126: Average NFIQ values of the FVC-2004 data sets.

## 7.2 Image Quality of Fingerprint (IQF)

The Image Quality of Fingerprint (IQF) software<sup>4</sup> is an application to measure visual quality of fingerprint images. The IQF implementation is based on the IQM implementation of MITRE, a non-profit research corporation. IQM is the abbreviation for Image Quality Measure what was developed as a quality measure for arbitrary images. The basic method behind both quality measures is the use of information that can be gathered in the Fourier domain. Therefore the most important calculation steps of the IQF measure, that are based on [26], are the following:

- **Windowing and Fast Fourier Transformation:** An input image is divided into overlapping windows first. For each of those sub-images the two dimensional Fast Fourier Transformation (FFT) is computed. To improve the accuracy of the implementation the sub-image power spectra are normalized taking the total power spectrum of the entire imprint into account and the area of the sub-images as well.
- **Filtering:** The calculated normalized power spectra are filtered in the second step. According to [26] a human visual system filter (HVS) is used because the quality measure should represent the human quality impression of an imprint. For that it is necessary to take care of spatial and temporal patterns the human visual system

<sup>4</sup> <http://www2.mitre.org/tech/mtf/>

is sensitive to which is provided using a HVS. So basically a HVS is a filter which has more or less similar characteristics to a low pass or band pass filter because in the human visual system the limited number of rods exceed the number of cones. So the high frequency information can not be used that good compared to lower frequencies. Based on this information during the filtering step the high frequency information of the normalized power spectra is cut off. The remaining entries of the normalized filtered power spectra sub-images are summed up. So for each sub-image one single value, the sub-image quality value, is derived. After those single quality values for each sub-image have been found they are compared to each other. The highest quality entry is selected. All other values are not needed anymore because the real IQF quality values is just based on that sub-image which contains the highest number of low frequency information.

- **Quality Calculation:** The final calculation step is performed on the detected sub-image which was introduced in the filtering step. The output values will be based not only on using the low frequency information, but also on more contrast information. So the quality value of the selected sub-image is normalized using the zero frequency power of the same sub-image. According to [26] this zero frequency normalization (dc normalization) could lead to overestimation of the output value if the entire fingerprint image is quite dark and to underestimation in case the imprint is a light one. To compensate this effect a weighting of the dc normalized quality value will be performed. That means that the actual value will be multiplied by the squared average gray level of the sub-image. After this multiplication the final output quality value is derived in the most cases. If the entire imprint is a very high contrast one or a very light image some additional adjustments must be performed. Otherwise for the high contrast case a overestimation of the IQF value would happen and a underestimation for the light image case. The adjustment is an additional multiplication with 0.17 for the high contrast specification and 2.5 for the other one. The idea behind is to mitigate the dc normalization step.

As described in [26] the output values are ranged between 0 and 100. The higher the quality value of an imprint gets, the better the quality of the fingerprint image is using this method. It will be interesting to compare the results with the other quality measurement methodologies because this method was designed to give quality feedback based on the human quality impression.

Based on the calculated IQF values, similar to the NFIQ calculation, the average IQF values for the single data sets has been derived. As visible in Table 127 there is no abnormality detectable. Those results display a slightly different tendency as detectable for the average NFIQ results that have been introduced in Table 125.

<b>Data set</b>	<b>av. IQF value</b>
<b>A</b>	12.26
<b>B1</b>	9.79
<b>B2</b>	12.39
<b>B3</b>	12.14
<b>B4</b>	12.10
<b>B5</b>	12.29
<b>C1</b>	11.02
<b>C2</b>	12.32
<b>C3</b>	12.20
<b>C4</b>	12.18
<b>C5</b>	12.27

Table 127: Average IQF values per data set.

<b>Data set</b>	<b>av. IQF value</b>
<b>DB1<sub>A</sub></b>	9.31
<b>DB2<sub>A</sub></b>	6.71
<b>DB3<sub>A</sub></b>	8.52
<b>DB4<sub>A</sub></b>	3.88

Table 128: Average IQF values for the FVC-2004 data sets.

Similar to the NFIQ case the average IQF values for the introduced four reference data sets have been calculated as well. The corresponding results, which are displayed in Table 128, reveal that the IQF of the used data bases A to C5 is better compared

to those reference data sets.

Independently from the similarity of the average IQF and the NFIQ results it is also clearly observable that there is a difference regarding the quality measure goodness. As introduced the output of the NFIQ measurement is a number between 1 and 5. Where 5 is the worst result an imprint can receive. The values of the IQF measure on the other hand is displayed using a number between 0 and 100 for each imprint. In this case the higher the value is the better the quality of the fingerprint image. Comparing the results thinking about this background information it is clear that the average IQF results are indicating that the imprints have a much worse quality than the NFIQ values provide. It seems that the impact of designing a quality measure based on the human quality impression is high on the used data sets. Additionally the IQF results display a quite bad quality of all data sets, so the tendency is the same one as compared to NFIQ.

Due to this circumstance it will be interesting to see how the IQF results for the average false accepted and rejected quality analysis, as introduced in the NFIQ section of this master' thesis, look like. They are displayed and discussed in Section 7.4.

### 7.3 Gabor Filter Image Quality of Fingerprint (GFIQF)

The Gabor Filter Image Quality of Fingerprint (GFIQF) is the third quality measurement method that has been taken into account for this master thesis. As opposed to the other two software applications for this method no free available implementations could be found. Therefore it was implemented based on [34]. As the name implies, the basic idea behind this method is the use of Gabor Filters. According to [34] the main steps can be summarized as follows:

- **Imprint division into non overlapping blocks:** Each input image is divided in a set of blocks. Each block has the same size of  $n \times n$  and they are not overlapping each other. For the experimental setup the block size of 16x16 pixel was used. The dimensions have not been chosen arbitrary, they are based on the one hand on the similarity to the setting introduced in [34]. On the other hand they are based on the dimensions of the fingerprint images. Due to the dimensions of 328x356 and 256x360 as discussed in Section 4.1 and Section 4.2 it was not possible to divide the imprints uniformly. There would have been a few blocks only consisting of a small number of pixels. Therefore the border pixels have been cut off to fulfill the

task of creating regular blocks of each imprint. The cut off is not a big problem because no quality dependent information is located there.

- **Gabor Filtering and feature calculation:** On each of the before introduced blocks a set of 8 Gabor Filters is applied to. There are a few important information necessary for this calculation step. As displayed in [34] the main parameters are the total number of orientations and the orientations itself and the frequency of the sinusoidal plane wave of the Gabor filters. The orientations  $\theta$  that have been chosen are  $\frac{\pi}{8}$ ,  $\frac{\pi}{4}$ ,  $\frac{3*\pi}{8}$ ,  $\frac{\pi}{2}$ ,  $\frac{5*\pi}{8}$ ,  $\frac{3*\pi}{4}$ ,  $\frac{7*\pi}{8}$  and  $\pi$ . The idea was to capture as much orientation information as possible and therefore those have been selected. The frequency of the sinusoidal plane  $f$  wave was set to  $\frac{1}{4}$ . Just like the before mentioned parameters, the characteristics for the standard deviations along the x- and y-axes have been determined empirically. The standard deviation along the x-axes  $\sigma_x$  was set to 4 and along the y-axes  $\sigma_y$  was set to 2. The result of the filtering process are 8 Gabor feature sets.
- **Gabor standard deviation calculation:** Based on the Gabor features the so called Gabor standard deviation is calculated as third part of this quality implementation. This standard deviation is measuring the amount of variation within the Gabor features. So the calculated features are following a distribution based on the 8 Gabor filtered block information and for each block one standard deviation value is derived. It is mandatory for the final calculation step.
- **Quality Index (QI):** The standard deviation values are used for two different approaches. The first one is to separate between foreground and background information. Due to the circumstance, that in a fingerprint image at the location where the imprint can be located a high number of edges is detectable, the Gabor features are useful to distinguish between imprint and background. If the standard deviation is less than a particular threshold  $T1$  than the block is marked as background.  
The second approach is the actual imprint quality measurement. For this purpose only the foreground blocks are taken into account. If the standard deviation of a foreground block is less than a threshold  $T2$  than this block is labeled as a poor foreground block. Those poor foreground block are used to calculate the Quality

Index (QI) of the imprint:

$$QI = 1 - \frac{\text{number of poor quality foreground blocks}}{\text{total number of foreground blocks}} \quad (1)$$

Looking at the formula above how the QI is calculated it is clear that a high number of poor quality foreground block is indicating a bad result. So if the QI is low this means that the quality of the fingerprint image is not good. Basically a QI value near 1 describes a image which has a good GFIQF value. The worst possible value is 0. Using the described method, the same approach as performed for the NFIQ and IQF quality measures has been done. Therefore the average GFIQF of the used data sets can be looked up in Table 129.

<b>Data set</b>	<b>av. GFIQF value</b>
<b>A</b>	0.1631
<b>B1</b>	0.8311
<b>B2</b>	0.1290
<b>B3</b>	0.1921
<b>B4</b>	0.0976
<b>B5</b>	0.0686
<b>C1</b>	0.4971
<b>C2</b>	0.1460
<b>C3</b>	0.1776
<b>C4</b>	0.1303
<b>C5</b>	0.1158

Table 129: Average GFIQF values per data sets.

Using the four reference data bases of FVC-2004 [1] the GFIQF values are presented in Table 130. There is a little bit more fluctuation between the data sets observable than for NFIQ and IQF. The quality values of B1 is always higher as for one of data base DB1<sub>A</sub> to DB4<sub>A</sub>. The GFIQF of C1 is quite similar to DB1<sub>A</sub>, DB2<sub>A</sub> and DB4<sub>A</sub>, but much higher compared to data set DB3<sub>A</sub>. The remaining data sets A, B2 to B5 and C2 to C5 are exhibiting a better GFIQF value then the one of data base DB3<sub>A</sub>,

but a lower quality value as those from the other reference data sets. In general it can be stated that the GFIQF for the reference data bases is better compared to the data bases used in the present master thesis.

<b>Data set</b>	<b>av. GFIQF value</b>
<b>DB1<sub>A</sub></b>	0.5030
<b>DB2<sub>A</sub></b>	0.6923
<b>DB3<sub>A</sub></b>	0.0402
<b>DB4<sub>A</sub></b>	0.5423

Table 130: Average GFIQF values for the FVC-2004 data set.

All in all the results of data base A to C5 confirm the outcomes which have been observed in the other average quality results NFIQ and IQF. It is important to mention that the low values for the GFIQF values indicate that a lot of poor foreground blocks can be detected. So finally it seems that the average NFIQ values are displaying an average quality of the data sets and the other two methods a bad quality. The only exception for this situation can be detected in data set B1. The GFIQF values indicate that the overall average quality in this data set is much better compared to the other sets. This extraordinary effect is only observable for the GFIQF method. So it seems that a sensor related effect can be detected because also for data set C1 the quality value is higher compared to the data sets using a different sensor type. In case of using IQF, the data set is even receiving a little bit worse average quality value than the others.

As mentioned in Section 7.1 and Section 7.2 the results of the overall average quality calculation are used to be get a more precise information about the quality behavior of the imprints. Those outcomes of the average false accepted and rejected quality analysis will be discussed in the following Section 7.4.

#### **7.4 Average False Accepted and Rejected Quality Analysis**

The selected strategy is based on the average quality of certain false rejected and false accepted input images. That means, that for specific decision thresholds the associated false accepted and false rejected imprints are detected. After this detection



step the quality values of those questionable inputs are computed using the described quality measurements NFIQ, IQF and GFIQF.

It is clear that the crucial task during the average false accepted and rejected quality calculation will be the selection of the decision thresholds. Because of the circumstance that four different fingerprint recognition system implementations are used in the experimental setups in this master thesis, four sets of threshold values must be selected. Each set, consisting of six values, was chosen experimentally, to get a broad variety of detectable false accepts and rejects. The values were set to a fixed number, to be able to compare the results. For this purpose five so called 'regular' values were defined and the final one was set to the fingerprint recognition system corresponding EER-threshold. At first the idea was to define the threshold setting such that the number of false accepts and false rejects is identical for each fingerprint recognition system, but this was not possible because of a high amount of variances between the used recognition systems. Based on this circumstance the setting was then defined to fulfill another issue. It should be ensured that the EER-threshold is around the middle value of the five so called 'regular' thresholds. This means that after getting the EER-thresholds the remaining decision thresholds were set around these values. In case of the NEURO fingerprint recognition system this task could not be solved in the wanted manner. Because of the good results of the NEURO fingerprint recognition system, there was no chance to select the 'regular' thresholds in a way that the EER-threshold is located between the second and third or third and fourth one. The chosen setting, that the EER-threshold is between the first and second threshold values, was the best what could be achieved. In the following enumeration the thresholds will be presented:

– **NBIS:**

- threshold values: 1.0, 5.0, 10.0, 20.0, 30.0 and the *EER* threshold
- The *EER* threshold of the NBIS matching results can be located between 9.0 and 11.0.

– **NEURO:**

- threshold values: 5.0, 20.0, 50.0, 70.0, 100.0 and the *EER* threshold
- The *EER* threshold of the NEURO matching results can be located around 15.0.

- **FC:**
  - threshold values: 90.0, 95.0, 100.0, 110.0, 115.0 and the *EER* threshold
  - The *EER* threshold of the FC matching results can be located around 105.0.
- **POC:**
  - threshold values: 0.01, 0.1, 0.2, 0.25, 0.3 and the *EER* threshold
  - The *EER* threshold of the POC matching results can be located around 0.15.

Based on the described experimental methodology it was possible to gather the results for each fingerprint recognition system. The outcomes based on the NBIS implementation can be looked up in Table 131. The results for the NEURO software are displayed in Table 132, for the FC fingerprint recognition system in Table 133 and for the POC fingerprint recognition system in Table 134. It is important to mention that despite the WA, OA and HH analysis which was performed in Chapter 5 no special separation of the calculated matches have been taken into account. So all derived genuine and impostor scores for each data set are used altogether for the following analysis.

Looking at the results displayed in Table 131, 132, 133 and 134, there are some interesting effects detectable. The following discussion will be based on the single quality measurements. But before the quality analysis will be described, it is necessary to rollback the information what the quality values mean.

As introduced in Sections 7.1, 7.2 and 7.3 there are three different ranges, one for each of the methods. The NFIQ outcomes can vary between 1 and 5, where 1 is the best and 5 the worst possible quality. For the second method, IQF, there is a much broader range from 0 to 100. In this case the opposite as for NFIQ is valid - the higher the resulting number the better the quality of the imprint is. Finally the GFIQF is using numbers from 0 to 1. The quality of the fingerprint image is best if the GFIQF output is 1 and worst if 0. So in general a high quality values means a better result for the IQF and GFIQF method and a more worse for NFIQ. As opposed to this a low number indicates good quality for NFIQ and a more or less bad one for the other two methods.

Regarding the possible quality outcomes the results of IQF and GFIQF will be taken into account at first. There is no doubt that for the IQF results the average false accepts and rejects quality values are more or less the same compared to the overall

NBIS false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						$\emptyset$ quality
	1.0	5.0	10.0	20.0	30.0	EER-thres.	1.0	5.0	10.0	20.0	30.0	EER-thres.	
<b>NFIQ</b>													
<b>A</b>	2.71	2.71	2.68	2.59	2.27	2.67	5	3.73	3.56	3.42	3.29	3.57	2.71
<b>B1</b>	2.44	2.44	2.41	2.34	1.81	2.39	2.62	3.07	3.31	3.21	3.01	3.31	2.44
<b>B2</b>	3.12	3.12	3.05	2.61	2.62	3	5	4.64	4.42	4.20	4.02	4.38	3.13
<b>B3</b>	3.19	3.19	3.16	2.75	3	3.17	5	4.55	4.15	3.92	3.77	4	3.19
<b>B4</b>	3	3	2.97	2.72	3	2.95	5	3.90	4.02	3.86	3.77	4.11	3.01
<b>B5</b>	2.89	2.89	2.88	2.74	2.6	2.88	2.5	3.16	3.52	3.59	3.52	3.62	2.90
<b>C1</b>	2.57	2.57	2.56	2.47	2.14	2.56	3.19	3.26	3.06	2.95	2.85	3.04	2.57
<b>C2</b>	2.91	2.91	2.86	2.66	2.34	2.88	3.16	3.25	3.09	3.02	3	3.09	2.92
<b>C3</b>	2.95	2.95	2.92	2.63	2.27	2.93	3.16	3.15	3.13	3.02	2.98	3.13	2.95
<b>C4</b>	2.86	2.85	2.84	2.67	2.08	2.84	3.36	3.42	3.21	3.09	3.02	3.21	2.86
<b>C5</b>	2.80	2.80	2.79	2.63	2.58	2.79	3.88	3.21	3.13	2.98	2.97	3.13	2.80
<b>IQF</b>													
<b>A</b>	12.26	12.26	12.25	12.51	13.18	12.27	14	12.52	11.94	11.91	11.95	11.95	12.26
<b>B1</b>	9.79	9.79	9.79	9.85	9.87	9.79	10.12	9.85	9.71	9.71	9.72	9.73	9.79
<b>B2</b>	12.38	12.38	12.44	12.42	12.75	12.44	13	12.78	12.31	12.11	12.12	12.17	12.39
<b>B3</b>	12.14	12.14	12.15	12.27	12.05	12.15	14	12.11	11.78	12.03	12.07	11.86	12.14
<b>B4</b>	12.11	12.11	12.10	12.40	12.40	12.10	14	12.80	12.13	12.02	12.01	12.07	12.10
<b>B5</b>	12.29	12.29	12.32	12.50	11.40	12.32	11.50	11.60	11.90	12.03	12.08	12.03	12.29
<b>C1</b>	11.03	11.03	11.08	11.47	11.79	11.08	11.35	11.65	11.65	11.64	11.52	11.63	11.02
<b>C2</b>	12.32	12.32	12.31	12.45	12.62	12.32	12	12.16	12.23	12.19	12.21	12.23	12.32
<b>C3</b>	12.20	12.20	12.19	12.34	12.22	12.19	12.66	12.03	12.19	12.28	12.26	12.19	12.20
<b>C4</b>	12.18	12.18	12.19	12.36	13.12	12.18	12.45	12.04	11.99	12.08	12.16	11.99	12.18
<b>C5</b>	12.27	12.27	12.28	12.44	12.32	12.27	11.44	11.87	12.05	12.15	12.20	12.05	12.27
<b>GFIQF</b>													
<b>A</b>	0.16	0.16	0.16	0.18	0.41	0.16	0.11	0.11	0.12	0.12	0.15	0.11	0.1631
<b>B1</b>	0.83	0.83	0.82	0.84	0.94	0.82	0.87	0.78	0.71	0.72	0.75	0.71	0.8311
<b>B2</b>	0.12	0.12	0.13	0.12	0.05	0.13	0.06	0.16	0.14	0.12	0.11	0.13	0.1290
<b>B3</b>	0.19	0.19	0.19	0.23	0.15	0.19	0.05	0.09	0.20	0.20	0.20	0.20	0.1921
<b>B4</b>	0.09	0.09	0.09	0.07	0.15	0.09	0.17	0.16	0.17	0.12	0.12	0.14	0.0976
<b>B5</b>	0.06	0.06	0.06	0.06	0.02	0.06	0.03	0.07	0.07	0.06	0.06	0.07	0.0686
<b>C1</b>	0.49	0.49	0.48	0.42	0.50	0.48	0.33	0.27	0.26	0.29	0.33	0.27	0.4971
<b>C2</b>	0.14	0.14	0.15	0.17	0.21	0.15	0.08	0.14	0.14	0.14	0.14	0.14	0.1460
<b>C3</b>	0.17	0.17	0.17	0.19	0.24	0.17	0.13	0.17	0.17	0.17	0.17	0.17	0.1776
<b>C4</b>	0.13	0.13	0.13	0.14	0.23	0.13	0.10	0.15	0.15	0.15	0.15	0.15	0.1303
<b>C5</b>	0.11	0.11	0.11	0.14	0.25	0.11	0.09	0.13	0.12	0.13	0.14	0.12	0.1158

Table 131: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the NBIS matching scores.

NEURO false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						∅ quality
	5.0	20.0	50.0	70.0	100.0	EER-thres.	5.0	20.0	50.0	70.0	100.0	EER-thres.	
<b>NFIQ</b>													
<b>A</b>	3.12	3.12	3.2	5	5	3.12	3.83	3.83	3.83	3.84	3.84	3.83	2.71
<b>B1</b>	1.66	1.66	1.5	2	3.75	1.66	3.77	3.77	3.76	3.79	3.84	3.77	2.44
<b>B2</b>	3.11	3.11	3.25	4.41	4.48	3.11	4.4	4.4	4.41	3.28	3.17	4.4	3.13
<b>B3</b>	3.08	3.08	3.08	3.33	3.33	3.08	4.27	4.27	4.28	4.29	4.30	4.27	3.19
<b>B4</b>	2.9	2.9	3	2.5	2	2.9	2.9	4.31	4.32	4.25	4.27	4.31	3.01
<b>B5</b>	3.42	3.42	3	2.5	2.5	3.42	4.14	4.14	4.14	4.22	4.06	4.14	2.90
<b>C1</b>	2.82	2.82	2.81	4	5	2.82	3.13	3.13	3.11	3.08	3.04	3.13	2.57
<b>C2</b>	3.08	3.08	2.93	5	5	3.08	3.14	3.14	3.13	3.12	3.13	3.14	2.92
<b>C3</b>	2.83	2.83	2.79	2.92	2.76	2.83	3.25	3.25	3.25	3.17	3.12	3.25	2.95
<b>C4</b>	2.91	2.91	3	3.5	3	2.91	3.43	3.43	3.43	3.33	3.25	3.43	2.86
<b>C5</b>	2.78	2.78	2.91	3	3	2.78	3.27	3.27	3.27	3.28	3.17	3.27	2.80
<b>IQF</b>													
<b>A</b>	12.37	12.37	11.8	9	9	12.37	12.26	12.26	12.26	12.21	12	12.26	12.26
<b>B1</b>	10.33	10.33	10.5	11	9.5	10.33	9.5	9.5	9.49	9.49	10.07	9.5	9.79
<b>B2</b>	11.77	11.77	11.5	12.69	12.51	11.77	12.75	12.75	11.73	12.04	12.12	12.75	12.39
<b>B3</b>	12.91	12.91	12.91	12.16	12.16	12.91	11.78	11.78	12.78	11.86	11.90	11.78	12.14
<b>B4</b>	12.2	12.2	11.87	13	13	12.2	12.31	12.31	12.32	12.25	12.16	12.31	12.10
<b>B5</b>	12.42	12.42	12	11.5	11.5	12.42	12.33	12.33	12.34	12.32	12.40	12.33	12.29
<b>C1</b>	12.17	12.17	11.81	11	9	12.17	11.57	11.57	11.56	11.59	11.68	11.57	11.02
<b>C2</b>	12.44	12.44	12.44	11	9	12.44	12.20	12.20	12.22	12.26	12.18	12.20	12.32
<b>C3</b>	12.36	12.36	12.27	11.78	11.84	12.36	12.14	12.14	12.15	12.20	12.19	12.14	12.20
<b>C4</b>	12.39	12.39	12.06	12.5	12.33	12.39	12.05	12.05	12.03	12.05	12.06	12.05	12.18
<b>C5</b>	12.31	12.31	12.16	11.4	11.4	12.31	12.05	12.05	12.05	12.04	12.12	12.05	12.27
<b>GFIQF</b>													
<b>A</b>	0.18	0.18	0.25	0.03	0.03	0.18	0.10	0.10	0.10	0.10	0.10	0.10	0.1631
<b>B1</b>	0.77	0.77	0.66	1	0.66	0.77	0.63	0.63	0.64	0.65	0.65	0.63	0.8311
<b>B2</b>	0.11	0.11	0.11	0.14	0.13	0.11	0.15	0.15	0.15	0.13	0.13	0.15	0.1290
<b>B3</b>	0.19	0.19	0.19	0.12	0.12	0.19	0.22	0.22	0.22	0.23	0.22	0.22	0.1921
<b>B4</b>	0.04	0.04	0.05	0.04	0.05	0.04	0.18	0.18	0.18	0.15	0.15	0.18	0.0976
<b>B5</b>	0.04	0.04	0.05	0.03	0.03	0.04	0.07	0.07	0.07	0.07	0.06	0.07	0.0686
<b>C1</b>	0.29	0.29	0.33	0.35	0.03	0.29	0.29	0.29	0.29	0.27	0.26	0.29	0.4971
<b>C2</b>	0.15	0.15	0.16	0.03	0.03	0.15	0.14	0.14	0.14	0.14	0.13	0.14	0.1460
<b>C3</b>	0.18	0.18	0.19	0.10	0.10	0.18	0.17	0.17	0.17	0.18	0.17	0.17	0.1776
<b>C4</b>	0.15	0.15	0.17	0.08	0.10	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.1303
<b>C5</b>	0.16	0.16	0.22	0.24	0.24	0.16	0.14	0.14	0.13	0.13	0.13	0.14	0.1158

Table 132: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the NEURO matching scores.

FC false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						$\emptyset$ quality
	90.0	95.0	100.0	110.0	115.0	EER-thres.	90.0	95.0	100.0	110.0	115.0	EER-thres.	
<b>NFIQ</b>													
<b>A</b>	2.70	2.70	2.70	2.54	2	2.68	3	2.58	2.65	2.75	2.72	2.73	2.71
<b>B1</b>	2.43	2.43	2.43	2.36	2	2.42	2	2.16	2.31	2.39	2.43	2.34	2.44
<b>B2</b>	3.11	3.11	3.11	2.96	2	3.05	3	5	4.08	3.57	3.25	3.6	3.13
<b>B3</b>	3.21	3.21	3.20	2.99	3.23	3.12	4	3.6	4.05	3.36	3.25	3.45	3.19
<b>B4</b>	3.06	3.06	3.06	2.79	2	3.03	4	4.33	3.36	3.30	3.09	3.39	3.01
<b>B5</b>	2.86	2.86	2.87	2.65	2	2.80	1	3.71	3.23	3.05	2.95	3.12	2.90
<b>C1</b>	2.57	2.57	2.57	2.53	3	2.58	3.83	2.77	2.53	2.57	2.56	2.57	2.57
<b>C2</b>	2.91	2.91	2.91	2.84	2.5	2.91	2.3	3	3.03	2.99	2.95	3.05	2.92
<b>C3</b>	2.94	2.94	2.94	2.85	3	2.94	3.53	3.05	3.07	3.04	2.98	3.07	2.95
<b>C4</b>	2.85	2.85	2.85	2.73	2.66	2.84	2.77	3.32	2.96	2.92	2.88	2.90	2.86
<b>C5</b>	2.79	2.79	2.79	2.65	3	2.77	3	3.31	2.92	2.86	2.82	2.90	2.80
<b>IQF</b>													
<b>A</b>	12.25	12.25	12.25	12.52	13	12.3	8	12.45	12.28	12.31	12.28	12.37	12.26
<b>B1</b>	9.79	9.79	9.79	9.77	9	9.78	10	9.83	9.75	9.80	9.78	9.78	9.79
<b>B2</b>	12.27	12.27	12.27	12.10	8	12.19	11.44	10.5	12.58	12.30	12.36	12.28	12.39
<b>B3</b>	12.27	12.27	12.26	12.14	12.12	12.26	8	11.6	12	12.30	12.36	12.10	12.14
<b>B4</b>	12.12	12.12	12.12	12.05	13	12.05	8	13.16	12.2	12.08	12.07	12.16	12.10
<b>B5</b>	12.53	12.53	12.52	12.58	13	12.52	14	12.78	12.02	12.20	12.20	12.23	12.29
<b>C1</b>	11.03	11.02	11.03	11.23	12.33	11.04	8	10.53	10.56	10.78	10.88	10.69	11.02
<b>C2</b>	12.32	12.32	12.32	12.35	11.83	12.31	11.9	12.25	12.35	12.36	12.34	12.36	12.32
<b>C3</b>	12.20	12.20	12.20	12.27	12.33	12.21	11.53	12.17	12.01	12.21	12.18	12.22	12.20
<b>C4</b>	12.18	12.18	12.18	12.21	12.5	12.17	11.44	11.97	11.99	12.18	12.18	12.16	12.18
<b>C5</b>	12.27	12.27	12.27	12.28	12.4	12.26	11.44	12.23	12.22	12.29	12.29	12.29	12.27
<b>GFIQF</b>													
<b>A</b>	0.16	0.16	0.16	0.15	1	0.16	0.03	0.15	0.13	0.14	0.14	0.14	0.1631
<b>B1</b>	0.83	0.83	0.83	0.82	1	0.82	1	1	0.94	0.81	0.82	0.83	0.8311
<b>B2</b>	0.15	0.15	0.15	0.15	0.11	0.15	0.08	0.05	0.14	0.09	0.10	0.10	0.1290
<b>B3</b>	0.19	0.19	0.19	0.17	0.18	0.19	0.20	0.28	0.23	0.20	0.10	0.21	0.1921
<b>B4</b>	0.13	0.13	0.13	0.12	0.07	0.12	0.20	0.12	0.09	0.09	0.09	0.09	0.0976
<b>B5</b>	0.08	0.08	0.08	0.08	0.04	0.08	0.01	0.06	0.05	0.05	0.06	0.05	0.0686
<b>C1</b>	0.49	0.49	0.49	0.44	0.40	0.48	0.34	0.44	0.57	0.55	0.53	0.56	0.4971
<b>C2</b>	0.14	0.14	0.14	0.14	0.21	0.14	0.09	0.11	0.10	0.13	0.13	0.12	0.1460
<b>C3</b>	0.17	0.17	0.17	0.17	0.40	0.17	0.39	0.16	0.16	0.17	0.17	0.17	0.1776
<b>C4</b>	0.12	0.12	0.12	0.12	0.30	0.12	0.08	0.13	0.11	0.11	0.11	0.11	0.1303
<b>C5</b>	0.11	0.11	0.11	0.12	0.26	0.11	0.08	0.09	0.10	0.09	0.10	0.09	0.1158

Table 133: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the FC matching scores.

POC false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						∅ quality
	0.01	0.1	0.2	0.25	0.3	EER-threshold	0.01	0.1	0.2	0.25	0.3	EER-threshold	
<b>NFIQ</b>													
<b>A</b>	2.44	2.71	2.8	2.85	2.25	2.72	2.44	2.92	2.73	2.73	2.74	2.81	2.71
<b>B1</b>	2.44	2.44	2.13	2.16	2	2.41	1.66	3.12	2.53	2.53	2.50	2.85	2.44
<b>B2</b>	3.12	3.10	2.77	2.4	1	3.03	2.33	3.54	3.24	3.20	3.17	3.45	3.13
<b>B3</b>	3.19	3.16	2.77	3.1	3.25	3.09	2.33	4.01	3.42	3.30	3.17	3.51	3.19
<b>B4</b>	3.00	2.99	2.77	2.4	2	2.90	2.33	4.16	3.38	3.18	3.13	3.65	3.01
<b>B5</b>	2.89	2.87	2.29	2.04	2.25	2.75	2.33	4.05	3.09	2.97	2.91	3.42	2.90
<b>C1</b>	2.57	2.57	2.51	2.63	2.33	2.57	2.33	2.75	2.63	2.63	2.62	2.70	2.57
<b>C2</b>	2.92	2.92	2.82	2.66	2.2	2.93	-	2.84	2.79	2.83	2.86	2.83	2.92
<b>C3</b>	2.95	2.95	2.88	3.02	2.2	2.96	-	2.96	2.84	2.86	2.87	2.88	2.95
<b>C4</b>	2.86	2.86	2.77	2.69	2.62	2.86	-	2.99	2.80	2.88	2.80	2.87	2.86
<b>C5</b>	2.80	2.80	2.72	2.85	2.33	2.81	-	2.97	2.76	2.77	2.76	2.89	2.80
<b>IQF</b>													
<b>A</b>	9.79	12.25	12.31	12.64	12	12.25	9.79	12.08	12.28	12.28	12.28	12.24	12.26
<b>B1</b>	9.79	9.79	9.86	10.16	9.5	9.81	10.66	9.70	9.76	9.76	9.77	9.77	9.79
<b>B2</b>	12.38	12.38	12.53	11	13	12.40	10	12.54	12.41	12.27	12.34	12.47	12.39
<b>B3</b>	12.14	12.14	11.86	10.9	12.26	12.13	10	11.92	12.29	12.29	12.34	12.08	12.14
<b>B4</b>	12.11	12.11	11.77	11.5	13	12.10	10	12.32	12.03	12.01	12.06	12.01	12.10
<b>B5</b>	12.29	12.28	12.41	13.13	12.5	12.27	10	12.67	12.37	12.26	12.23	12.57	12.29
<b>C1</b>	11.02	11.02	11.11	11	11.5	11.01	10	12.01	11.63	11.49	11.40	12.02	11.02
<b>C2</b>	12.32	12.32	12.31	12.47	12	12.32	-	12.20	12.28	12.24	12.26	12.27	12.32
<b>C3</b>	12.20	12.20	12.15	12.36	11.8	12.20	-	12.24	12.29	12.28	12.26	12.24	12.20
<b>C4</b>	12.18	12.18	11.99	12.12	12.37	12.18	-	12.08	12.21	12.23	12.23	12.19	12.18
<b>C5</b>	12.27	12.27	12.30	12.5	12.66	12.27	-	12.14	12.24	12.27	12.27	12.14	12.27
<b>GFIQF</b>													
<b>A</b>	0.83	0.16	0.14	0.08	0.10	0.16	0.83	0.14	0.15	0.16	0.16	0.15	0.1631
<b>B1</b>	0.83	0.82	0.90	1	1	0.83	1	0.63	0.76	0.79	0.80	0.70	0.8311
<b>B2</b>	0.12	0.13	0.17	0.12	0.03	0.13	1	0.20	0.10	0.11	0.12	0.11	0.1290
<b>B3</b>	0.19	0.19	0.14	0.05	0.21	0.18	1	0.26	0.22	0.22	0.12	0.23	0.1921
<b>B4</b>	0.09	0.09	0.09	0.12	0.04	0.09	1	0.11	0.10	0.10	0.10	0.11	0.0976
<b>B5</b>	0.06	0.06	0.07	0.07	0.10	0.07	1	0.05	0.05	0.05	0.05	0.11	0.0686
<b>C1</b>	0.49	0.49	0.64	0.64	0.40	0.49	1	0.21	0.32	0.36	0.39	0.21	0.4971
<b>C2</b>	0.14	0.14	0.13	0.19	0.09	0.14	-	0.16	0.15	0.14	0.15	0.16	0.1460
<b>C3</b>	0.17	0.17	0.16	0.16	0.09	0.17	-	0.17	0.18	0.18	0.17	0.17	0.1776
<b>C4</b>	0.13	0.13	0.11	0.06	0.08	0.12	-	0.15	0.15	0.15	0.14	0.16	0.1303
<b>C5</b>	0.11	0.11	0.09	0.09	0.19	0.11	-	0.15	0.13	0.13	0.12	0.15	0.1158

Table 134: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the POC matching scores.

average outcomes in the most cases. This can be easily detected comparing the information displayed in the tables mentioned above and Table 127. When comparing the values for the false accepts and those for the false rejects it is also obvious that there is not a real difference between their average quality values and the different matching methods as well. All in all it can be summarized that there is not a real difference between the single matching methods at all. For each selected threshold value and fingerprint recognition system type more or less very similar outcomes could be detected in the IQF measurements. In fact the quality results are quite low in every case. Of course there are some variations included based on the actual data set or chosen threshold, but they are present for each fingerprint recognition system type. So for example the data set where imprints are included which have been acquired using the T2 sensor, tend to have a lower quality compared to the other data bases. Additionally it is important to mention that if there is a divergence between the threshold based quality values and the entire data base based average ones, the single quality numbers seem to be worse. The outcomes for the GFIQF display the same tendency as the IQF results. The only differences can be found looking at the T2 data sets. In contrast to the IQF case the outcomes for GFIQF are much higher. That means that the second quality measurement is detecting a much better quality than in the previous one. So taking the information of the first analysis of the data base quality based on the threshold separation into account there are two possible point of views which can be stated for the IQF and GFIQF experiments.

As said before, there is almost no quality difference detectable independently which data set is taken into account based on IQF and GFIQF. On the one hand this circumstance can be explained as a consequence that there is no ageing observable because probably some measurable differences if ageing would be present in the data. On the other hand these results can be interpreted as assessment that there is just no quality difference in terms of the discussed acquisition conditions. This point of view also indicates that possible ageing effects cannot be measured using IQF and GFIQF because the used method are designed to quantify the quality of fingerprint images. Nevertheless the assumption of present ageing effect is not deniable.

As discussed before, it seems, that there is no degradation between the data sets in terms of the imprint quality. So the quality aspect is not influencing the analysis performed in Chapter 5 and 6 using those two measurements. But there is no doubt that no quality difference is not indicating that there is no ageing within the finger-

print images. The detection of ageing effects in Chapter 5 and 6 seem to support this opinion. Especially the shift of the genuine score distributions, the decrease of the *EER* for the crossed data sets and the not measurable quality degradation at the same time can only be initiated by ageing.

So as a final statement using the IQF and GFIQF results the following can be summarized. Both quality measurements indicate that regardless of which fingerprint recognition system type, decision threshold and data set is taken into account, the quality shows no degradation that would be more important than the detected ageing effects. So the possible problem that the quality aspect is influencing the experiments and gaining more impact as ageing like discussed in [41] cannot be detected. Furthermore it seems that the ageing effects introduced in Section 5 and 6 are not influenced by quality decline. This leads to the assumption that ageing must be present in the used data, but it is not possible to observe ageing characteristics in particular because the used methods are not designed to find them - basically there are no measurements available to detect any kind of ageing at all. It also must be mentioned that if differences in fingerprint quality would be present this aspect would be not indicating that there there is no fingerprint ageing at all. In this case ageing just cannot be measured because the quality aspect is more on the spot.

The remaining NFIQ results were not displaying such a homogenous situation as for the IQF and GFIQF cases detectable. Looking at the NBIS outcomes it is clear that the quality values for the false accepted matches are similar and quite often slightly lower then the average values. That means that the quality is slightly better than the average. The opposite is observable for the false rejected. For those are the quality values higher compared to the average one which means they have in general a worse quality. The same situation for the false accepted and rejected matches can be detected for the other fingerprint recognition systems in most of the cases. The T2 sensor based fluctuation within the other quality results can not be confirmed. This leads to the assumption that the imprints acquired by this sensor have better quality in terms of NFIQ compared to the other sensor types.

All in all it can be stated that the average false accepted quality is more or less equal or to be precise slightly lower as the overall average quality on the one hand. On the other hand the average false rejected quality for nearly all data sets, selected thresholds and fingerprint recognition system types is significantly higher then the



overall average quality outcomes as displayed in the last column in Table 125. So the quality of those imprints which are detected as false rejected is lower compared to the other imprints. This information is very interesting. As introduced in Section 5 and 6 and discussed before in the IQF and GFIQF case are the detectable ageing effects corresponding to the genuine matching scores. It is clear that the false rejected imprints also correspond to the genuine matches as well. So it seems that using the NFIQ values it is possible to detect a quality degradation which indicates a non ageing related influence for this quality measuring method.

So as introduced in Section 5 the genuine score distribution shift to the left and the more or less stable behavior of the impostor score distributions seem to correspond with the NFIQ based quality information. The assumption that quality outperforms the impact of ageing effects as discussed in [41] could probably be confirmed. To have a more detailed look at the described aspects of the IQF, GFIQF and NFIQ results, especially at the NFIQ outcomes, there will be a closer discussion on the crossed data sets.

As introduced in Section 4 imprints from 2009 and 2013 are included in the crossed data sets. Performing the matching procedure not only imprints from 2009 are matched against those from 2013 also imprint matches from 2009 against 2009 and from 2013 against 2013 are calculated. That means that the results for the crossed data sets displayed in Table 131, 132, 133 and 134 will be splitted into three classes. This splitting is done for the false accepted and the false rejected as well. The idea behind is to get a more detailed point of view based on those three type of time span including and excluding matches. So for each crossed data set, fingerprint recognition system type and threshold following three sets will be separated:

- 2009 *vs* 2009: Those false accepted and rejected matches corresponding to imprints from 2009 matched against 2009 imprints in the crossed sets are included.
- 2009 *vs* 2013: The false accepted and rejected matches corresponding to imprints from 2009 matched against 2013 imprints in the crossed sets are included.
- 2013 *vs* 2013: Finally the false accepted and rejected matches corresponding to imprints from 2013 matched against 2013imprints in the crossed sets are included.

After the splitting the average quality values as performed before are calculated and will be discussed in the following last Section 7.5 of this master thesis.

## 7.5 Refined Quality Analysis

As introduced above it is necessary to retrieve more detailed information concerning the behavior of the fingerprint images based on the quality aspect and the circumstance that for some matches the 4 year time span is included and for some not. Therefore the refinement of the results presented in Table 131, 132, 133 and 134 will probably give an better description of quality and ageing effects which may be included in the given data sets. For example it could be that the outcomes for the general quality analysis as introduced and discussed before is caused because one of those three types of matches is outperforming the other ones in terms of quality or ageing. Additionally it will be interesting to calculate the standard deviations for each data set using the single quality values for each threshold as observations of an random variable. The average quality values of the entire data sets will be the given mean values of this random variable. The reason for the use of the standard deviation in the present investigations is to get some more precise information about the stability of the single quality values which are calculated for the different thresholds. This research will be performed for the before discussed results of the entire data sets and for time span separated quality values as well. The calculation of the statistical measure for both consideration ensures the opportunity to compare the outcomes. For that reason it is possible look up the results for the NBIS fingerprint recognition system in Table 135 and 136. At the first sight it seems to be clear that the refinement using the splitting into the three types of matches is delivering more or less the same tendency for the NFIQ results as displayed in Table 131 and Table 135. But in fact there must be more precise discussion of those results.

For the general quality analysis of the NFIQ results which is readable in the previous Section 7.4 the hypothesis that quality is not outperforming the ageing aspect had to be rejected. For the present analysis another assumption can be stated: The reason for the false rejected NFIQ decrease is not quality degradation, but fingerprint ageing.

NBIS false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						$\emptyset$ quality
	1.0	5.0	10.0	20.0	30.0	EER-thres.	1.0	5.0	10.0	20.0	30.0	EER-thres.	
<b>NFIQ - 2009 vs. 2009</b>													
<b>C1</b>	2.71	2.71	2.74	2.72	2.71	2.74	5	3.30	3.61	3.42	3.29	3.62	2.57
<b>C2</b>	2.71	2.71	2.74	2.72	2.71	2.69	5	3.30	3.56	3.42	3.29	3.35	2.92
<b>C3</b>	2.71	2.71	2.74	2.72	2.71	2.69	5	3.30	3.56	3.42	3.29	3.35	2.95
<b>C4</b>	2.71	2.71	2.74	2.72	2.71	2.69	5	3.30	3.56	3.42	3.29	3.35	2.86
<b>C5</b>	2.71	2.71	2.74	2.72	2.71	2.69	5	3.30	3.56	3.42	3.29	3.35	2.80
<b>NFIQ - 2009 vs. 2013</b>													
<b>C1</b>	2.70	2.70	2.70	2.66	2.66	2.74	3.28	2.89	3.09	2.96	2.86	3.03	2.57
<b>C2</b>	2.70	2.70	2.70	2.67	2.66	2.70	3.32	2.83	2.90	2.82	2.80	3.06	2.92
<b>C3</b>	2.70	2.70	2.69	2.66	2.64	2.70	3.34	2.78	3.01	2.85	2.78	3.09	2.95
<b>C4</b>	2.70	2.70	2.69	2.66	2.64	2.71	3.34	2.90	3.11	2.97	2.88	3.21	2.86
<b>C5</b>	2.70	2.70	2.71	2.68	2.67	2.70	3.36	2.90	3.11	2.92	2.87	3.19	2.80
<b>NFIQ - 2013 vs. 2013</b>													
<b>C1</b>	2.45	2.45	2.42	2.47	2.47	2.42	2.88	2.99	2.85	2.88	2.97	2.85	2.57
<b>C2</b>	3.13	3.13	3.05	3.05	3.06	3.09	3.06	3.43	3.14	3.28	3.41	3.46	2.92
<b>C3</b>	3.19	3.19	3.16	3.11	3.10	3.17	3.09	3.36	3.15	3.35	3.35	3.36	2.95
<b>C4</b>	3.01	3.01	2.98	2.99	2.99	3	3.21	3.40	3.24	3.38	3.40	3.45	2.86
<b>C5</b>	2.90	2.89	2.89	2.88	2.87	2.91	3.19	3.30	3.21	3.34	3.30	3.31	2.80
<b>IQF - 2009 vs. 2009</b>													
<b>C1</b>	12.26	12.26	12.25	12.23	12.22	12.25	14	11.96	11.94	11.91	11.95	11.95	11.02
<b>C2</b>	12.26	12.26	12.25	12.23	12.22	12.25	14	11.96	11.94	11.91	11.95	11.88	12.32
<b>C3</b>	12.26	12.26	12.25	12.23	12.22	12.25	14	11.96	11.94	11.91	11.95	11.95	12.20
<b>C4</b>	12.26	12.26	12.25	12.23	12.22	12.25	14	11.96	11.94	11.91	11.95	11.88	12.18
<b>C5</b>	12.26	12.26	12.25	12.23	12.22	12.25	14	11.96	11.94	11.91	11.95	11.88	12.27
<b>IQF - 2009 vs. 2013</b>													
<b>C1</b>	12.26	12.26	12.26	12.26	12.25	12.26	11.92	12.04	12.10	12.12	12.16	12.07	11.02
<b>C2</b>	12.26	12.26	12.26	12.26	12.25	12.25	11.85	12.15	12.27	12.16	12.22	12.12	12.32
<b>C3</b>	12.26	12.26	12.26	12.26	12.25	12.25	11.95	12.17	12.12	12.22	12.25	12.15	12.20
<b>C4</b>	12.26	12.26	12.27	12.26	12.26	12.25	11.89	12.09	12	12.07	12.19	11.92	12.18
<b>C5</b>	12.26	12.26	12.26	12.24	12.22	12.26	11.83	12.11	11.99	12.16	12.23	11.95	12.27
<b>IQF - 2013 vs. 2013</b>													
<b>C1</b>	9.79	9.79	9.77	9.71	9.71	9.77	12.01	11.11	11.72	11.53	11.14	11.73	11.02
<b>C2</b>	12.36	12.36	12.32	12.29	12.28	12.32	12.12	12.01	12.07	12.07	12.01	12.05	12.32
<b>C3</b>	12.14	12.14	12.10	12.08	12.05	12.10	12.17	12.16	12.22	12.22	12.17	12.22	12.20
<b>C4</b>	12.11	12.11	12.10	12.14	12.14	12.09	11.92	11.88	11.84	11.85	12.19	11.85	12.18
<b>C5</b>	12.29	12.28	12.26	12.27	12.26	12.32	11.93	11.93	11.87	11.83	11.96	11.96	12.27

Table 135: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the NBIS matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

NBIS false accepts and false rejects depending on different thresholds															
	average quality values														
data sets	false accepts threshold values					false rejects threshold values								∅	quality
	1.0	5.0	10.0	20.0	30.0	EER-thres.	1.0	5.0	10.0	20.0	30.0	EER-thres.			
<b>GFIQF - 2009 vs. 2009</b>															
<b>C1</b>	0.16	0.16	0.16	0.17	0.18	0.16	0.11	0.14	0.12	0.12	0.15	0.12		0.4971	
<b>C2</b>	0.16	0.16	0.16	0.17	0.18	0.15	0.11	0.14	0.12	0.12	0.15	0.15		0.1460	
<b>C3</b>	0.16	0.16	0.16	0.17	0.18	0.16	0.11	0.14	0.12	0.12	0.15	0.12		0.1776	
<b>C4</b>	0.16	0.16	0.16	0.17	0.18	0.15	0.11	0.14	0.12	0.12	0.15	0.15		0.1303	
<b>C5</b>	0.16	0.16	0.16	0.17	0.18	0.15	0.11	0.14	0.12	0.12	0.15	0.15		0.1158	
<b>GFIQF - 2009 vs. 2013</b>															
<b>C1</b>	0.16	0.16	0.16	0.17	0.17	0.16	0.14	0.16	0.15	0.16	0.15	0.15		0.4971	
<b>C2</b>	0.16	0.16	0.16	0.17	0.17	0.16	0.14	0.16	0.15	0.15	0.15	0.16		0.1460	
<b>C3</b>	0.16	0.16	0.16	0.18	0.18	0.16	0.14	0.17	0.15	0.16	0.16	0.16		0.1776	
<b>C4</b>	0.16	0.16	0.16	0.17	0.17	0.16	0.15	0.17	0.16	0.16	0.16	0.16		0.1303	
<b>C5</b>	0.16	0.16	0.16	0.17	0.17	0.16	0.14	0.16	0.14	0.15	0.16	0.15		0.1158	
<b>GFIQF - 2013 vs. 2013</b>															
<b>C1</b>	0.83	0.83	0.83	0.83	0.83	0.83	0.17	0.41	0.25	0.31	0.41	0.25		0.4971	
<b>C2</b>	0.12	0.13	0.12	0.12	0.12	0.13	0.16	0.16	0.16	0.16	0.15	0.15		0.1460	
<b>C3</b>	0.19	0.19	0.18	0.17	0.17	0.18	0.17	0.19	0.17	0.18	0.19	0.17		0.1776	
<b>C4</b>	0.09	0.09	0.09	0.09	0.09	0.09	0.16	0.15	0.16	0.15	0.15	0.15		0.1303	
<b>C5</b>	0.06	0.07	0.06	0.06	0.07	0.07	0.15	0.13	0.15	0.14	0.12	0.13		0.1158	

Table 136: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the NBIS matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

Looking at the outcomes displayed in Table 135 it is obvious that not all average quality values for the different thresholds reflect a quality degradation. The false accepts values of the 2009 vs 2009 and 2009 vs 2013 cases are very similar to the average quality. A similar situation appears for two data sets of the remaining 2013 vs 2013 case. For data set C2, C3 and C4 the outcomes are slightly higher. This lower quality is also detectable in Table 138 where the standard deviation can be looked up. The difference for the described false accepted situation is clearly visible even when the fluctuation of the values is very small. Nevertheless the same variance for those three data sets is present in Table 137 as well. So based on this observation of the false accepted matches, which deliver quite stable quality values, it is unambiguous that the

<b>NBIS standard deviations (std) of the NFIQ quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.20	1.31
<b>B1</b>	0.28	0.76
<b>B2</b>	0.32	1.48
<b>B3</b>	0.21	1.23
<b>B4</b>	0.13	0.93
<b>B5</b>	0.15	0.63
<b>C1</b>	0.19	0.56
<b>C2</b>	0.28	0.22
<b>C3</b>	0.33	0.17
<b>C4</b>	0.35	0.42
<b>C5</b>	0.12	0.57

Table 137: Displaying the standard deviations of the NFIQ quality analysis based on the NBIS results.

<b>NBIS standard deviations (std) of the NFIQ quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	0.17	0.13	0.13
<b>C2</b>	0.22	0.24	0.19
<b>C3</b>	0.25	0.28	0.23
<b>C4</b>	0.15	0.18	0.15
<b>C5</b>	0.09	0.11	0.1
	<b>false rejected stds</b>		
<b>C1</b>	1.4	0.51	0.37
<b>C2</b>	1.04	0.20	0.44
<b>C3</b>	1.02	0.22	0.38
<b>C4</b>	1.09	0.29	0.54
<b>C5</b>	1.15	0.34	0.53

Table 138: Displaying the standard deviations of the NFIQ quality analysis based on the NBIS results taking the time span information into account.

results of C2, C3 and C4 for the 2013 vs 2013 case are influencing the whole situation for the entire NFIQ analysis of the NBIS fingerprint recognition system. Without the refinement it would not be possible to distinguish if the time span including matches are responsible for the higher quality values or not.

The same analysis as for the false accepts was performed for the crucial false rejected matches once more. Looking at the single values in Table 135 and at the standard deviations in Table 137 and 138 it was possible to retrieve a very interesting information. Based on the results of the those tables two observation can be summarized. The first observation is based on the 2009 vs 2009 case. The matches, which are included in this class are mainly responsible for the poor average quality values which have been detected in Table 131. In Table 138 the standard deviation is confirming this situation. The second very important information is that the assumption that quality is effecting the decrease of the *EER* and the genuine score shift, which are detectable in the crossed data sets, can be disproved. The quality values for the time span including 2009 vs 2013 case are not much higher as for the corresponding false accepted ones and the overall average of the entire data sets. Once more the consolidation of Table 138 confirms this aspect. Of course the standard deviation is a little bit higher compared to the false accepted case, but not that high - for almost all data sets lower than 0.5. So it seems that for NBIS based on the NFIQ analysis it valid to state that ageing is responsible for the detected effects in Chapter 5 and 6.

After discussing the NFIQ outcomes a detailed description of the derived IQF and GFIQF results is necessary. Especially interesting will be if there are also some differences detectable which improve the information obtained by the general quality analysis. Looking at the IQF results for the 2009 vs 2009 case it is observable that it seems that the differences between the quality values and the average quality values displayed in the last column are quite small. The only deviation is located in the quality values of the lowest threshold. Those entries are much higher compared to the others and they also remain stable across all data sets. This observation is shared with the corresponding NFIQ measurements. Apart from this fluctuation, basically a very small variation between the average and the other calculated threshold based quality values appears for 2009 vs 2013 and 2013 vs 2013 outcomes as well. In fact in the 2013 vs 2013 case there is some fluctuation in data set C1 which indicates that the false accepted matches tend to have a slightly worse quality. But even this deviation

<b>NBIS standard deviations (std) of the IQF quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.4	0.83
<b>B1</b>	0.04	0.16
<b>B2</b>	0.16	0.38
<b>B3</b>	0.07	0.85
<b>B4</b>	0.19	0.31
<b>B5</b>	0.4	0.53
<b>C1</b>	0.4	0.61
<b>C2</b>	0.14	0.18
<b>C3</b>	0.06	0.22
<b>C4</b>	0.43	0.18
<b>C5</b>	0.08	0.43

Table 139: Displaying the standard deviations of the IQF quality analysis based on the NBIS results.

<b>NBIS standard deviations (std) of the IQF quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	1.34	1.36	1.37
<b>C2</b>	0.08	0.06	0.03
<b>C3</b>	0.05	0.05	0.11
<b>C4</b>	0.07	0.09	0.08
<b>C5</b>	0.02	0.02	0.02
	<b>false rejected stds</b>		
<b>C1</b>	1.62	1.15	1.67
<b>C2</b>	0.84	0.25	0.28
<b>C3</b>	0.84	0.16	0.15
<b>C4</b>	0.85	0.19	0.33
<b>C5</b>	0.84	0.28	0.38

Table 140: Displaying the standard deviations of the IQF quality analysis based on the NBIS results taking the time span information into account.

can not disprove the results from the general quality analysis like displayed in Table 131 for the IQF measure. The corresponding quality values are more or less stable across all data sets and performed matches. The standard deviations for the general analysis, displayed in Table 139, and for the splitted analysis, displayed in Table 140, are conforming to the situation as well. In fact it is also possible to detect in Table 140 that for the false rejects the 2009 vs 2009 case there must be some higher deviation within as discussed before. The cross-sensor based effect for the data set including the imprints using the T2 sensor is also clearly visible for the standard deviations of the false accepted and rejected analysis. Concluding it can be said that for the NBIS fingerprint recognition system using IQF no quality based impact can be observed. Therefore, as for the NFIQ analysis, the detected probably ageing effects must be caused by fingerprint ageing.

Finally there will be a short discussion of the GFIQF quality refinement analysis. The reason for this is basically the fact that looking at Table 136, 139 and 140 reveals more or less the same situation which was described for the IQF analysis. There is hardly no real difference detectable. The cross-sensor effect of data set C1 can be introduced as most interesting aspect in this case. So the GFIQF results are conforming the no quality based impact on the fingerprints and the clear existence of ageing.

In the following the results for the other fingerprint recognition system based on the quality refinement analysis will be presented. According to this at first the outcomes for the second fingerprint recognition system using the minutiae concept were described. The results displayed in Table 143, 144, 147 and 148 were confirming all of the aspects detected for the NBIS fingerprint recognition system. In fact there were different values and in case of the standard deviations a little bit more

fluctuations detectable.

Those variations are in most of the cases lower than 0.5. Of course looking at the NFIQ outcomes the standard deviations are higher than 1.0 which indicates a quite high number of divergences but there is no doubt that the same tendency is present. Especially because those higher fluctuations are only present in the 2009 vs 2009 case and for data set C1. So the time span and ageing including case is not influenced for the remaining data sets using different sensor types. The cross-sensor related aspect of sensor T2 in data set C1 observed for IQF and GFIQF in the previous fingerprint



<b>NBIS standard deviations (std) of the GFIQF quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.11	0.04
<b>B1</b>	0.05	0.09
<b>B2</b>	0.03	0.03
<b>B3</b>	0.02	0.07
<b>B4</b>	0.02	0.06
<b>B5</b>	0.01	0.01
<b>C1</b>	0.03	0.22
<b>C2</b>	0.03	0.02
<b>C3</b>	0.03	0.02
<b>C4</b>	0.04	0.02
<b>C5</b>	0.06	0.02

Table 141: Displaying the standard deviations of the GFIQF quality analysis based on the NBIS results.

<b>NBIS standard deviations (std) of the GFIQF quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	0.35	0.36	0.36
<b>C2</b>	0.02	0.02	0.01
<b>C3</b>	0.01	0.01	0.01
<b>C4</b>	0.04	0.03	0.03
<b>C5</b>	0.05	0.05	0.04
	<b>false rejected stds</b>		
<b>C1</b>	0.4	0.37	0.23
<b>C2</b>	0.02	0.01	0.01
<b>C3</b>	0.04	0.01	0.01
<b>C4</b>	0.01	0.03	0.03
<b>C5</b>	0.02	0.04	0.03

Table 142: Displaying the standard deviations of the GFIQF quality analysis based on the NBIS results taking the time span information into account.

NEURO false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						$\emptyset$ quality
	5.0	20.0	50.0	70.0	100.0	EER-thres.	5.0	20.0	50.0	70.0	100.0	EER-thres.	
<b>NFIQ - 2009 vs. 2009</b>													
<b>C1</b>	3.12	3.12	3.12	3.5	3.5	3.12	3.81	3.81	3.81	3.81	3.84	3.83	2.57
<b>C2</b>	3.12	3.12	3.12	3.5	3.5	3.12	3.81	3.81	3.81	3.81	3.84	3.83	2.92
<b>C3</b>	3.12	3.12	3.12	3.5	3.5	3.12	3.81	3.81	3.81	3.81	3.84	3.83	2.95
<b>C4</b>	3.12	3.12	3.12	3.5	3.5	3.12	3.81	3.81	3.81	3.81	3.84	3.83	2.86
<b>C5</b>	3.12	3.12	3.12	3.5	3.5	3.12	3.81	3.81	3.81	3.81	3.84	3.83	2.80
<b>NFIQ - 2009 vs. 2013</b>													
<b>C1</b>	2.87	2.87	3.25	3.62	2.87	2.87	3.26	3.26	3.23	3.14	2.99	3.08	2.57
<b>C2</b>	2.94	2.94	2.89	3	2.94	2.94	3.14	3.14	3.12	3.04	2.91	2.94	2.92
<b>C3</b>	2.64	2.64	2.88	3.05	2.82	2.64	3.17	3.17	3.19	3.04	2.90	3.03	2.95
<b>C4</b>	2.62	2.62	2.75	3.12	2.62	2.62	3.31	3.31	3.31	3.24	3.10	3.27	2.86
<b>C5</b>	2.87	2.87	3.37	3.5	3	2.87	3.25	3.25	3.24	3.17	3.01	3.13	2.80
<b>NFIQ - 2013 vs. 2013</b>													
<b>C1</b>	2.87	2.87	2.87	2.87	2.87	2.87	3.14	3.14	3.14	3.14	3.17	3.11	2.57
<b>C2</b>	3.21	3.21	3.31	3.31	3.21	3.21	3.26	3.26	3.26	3.23	3.27	3.12	2.92
<b>C3</b>	3.41	3.41	3.35	3.52	3.58	3.41	3.33	3.33	3.33	3.33	3.34	3.19	2.95
<b>C4</b>	2.7	2.7	3.1	3	2.6	2.7	3.4	3.4	3.4	3.38	3.38	3.31	2.86
<b>C5</b>	2.25	2.25	2.12	2.12	2.12	2.25	3.38	3.38	3.38	3.40	3.43	3.29	2.80
<b>IQF - 2009 vs. 2009</b>													
<b>C1</b>	12.37	12.37	11.87	11.37	11.75	12.37	12.16	12.16	12.16	12.13	12	12.26	11.02
<b>C2</b>	12.37	12.37	11.87	11.37	11.75	12.37	12.16	12.16	12.16	12.13	12	12.26	12.32
<b>C3</b>	12.37	12.37	11.87	11.37	11.75	12.37	12.16	12.16	12.16	12.13	12	12.26	12.20
<b>C4</b>	12.37	12.37	11.87	11.37	11.75	12.37	12.16	12.16	12.16	12.13	12	12.26	12.18
<b>C5</b>	12.37	12.37	11.87	11.37	11.75	12.37	12.16	12.16	12.16	12.13	12	12.26	12.27
<b>IQF - 2009 vs. 2013</b>													
<b>C1</b>	12.87	12.87	13	12.87	12.87	12.87	11.94	11.94	11.93	12.03	12.11	12.26	11.02
<b>C2</b>	12.68	12.68	12.94	12.89	12.68	12.68	12.08	12.08	12.09	12.20	12.23	12.13	12.32
<b>C3</b>	12.58	12.58	12.29	11.82	12.11	12.58	11.96	11.96	11.96	12.07	12.14	12.05	12.20
<b>C4</b>	12.87	12.87	12.75	13	12.87	12.87	11.97	12.97	12	12	12	11.97	12.18
<b>C5</b>	12.37	12.37	12.25	12.25	12.37	12.37	11.87	11.87	11.88	11.95	12.12	11.97	12.27
<b>IQF - 2013 vs. 2013</b>													
<b>C1</b>	12.37	12.37	12.25	12.25	12.37	12.37	11.5	11.5	11.5	11.5	11.49	11.62	11.02
<b>C2</b>	12.73	12.73	12.73	12.73	12.73	12.73	12.15	12.15	12.15	12.15	12.04	12.20	12.32
<b>C3</b>	11.88	11.88	12.11	12.05	11.88	11.88	12.06	12.06	12.06	12.08	12.06	12	12.20
<b>C4</b>	12.1	12.1	12.2	12.5	12.2	12.1	11.95	11.95	11.94	11.93	11.91	11.96	12.18
<b>C5</b>	12.37	12.37	13.12	13.25	12.62	12.37	11.84	11.84	11.83	11.84	11.83	11.89	12.27

Table 143: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the NEURO matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

NEURO false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						∅ quality
	5.0	20.0	50.0	70.0	100.0	EER-thres.	5.0	20.0	50.0	70.0	100.0	EER-thres.	
<b>GFIQF - 2009 vs. 2009</b>													
<b>C1</b>	0.18	0.18	0.17	0.05	0.18	0.18	0.09	0.09	0.09	0.1	0.1	0.1	0.4971
<b>C2</b>	0.18	0.18	0.17	0.05	0.18	0.18	0.09	0.09	0.09	0.1	0.1	0.1	0.1460
<b>C3</b>	0.18	0.18	0.17	0.05	0.18	0.18	0.09	0.09	0.09	0.1	0.1	0.1	0.1776
<b>C4</b>	0.18	0.18	0.17	0.05	0.18	0.18	0.09	0.09	0.09	0.1	0.1	0.1	0.1303
<b>C5</b>	0.18	0.18	0.17	0.05	0.18	0.18	0.09	0.09	0.09	0.1	0.1	0.1	0.1158
<b>GFIQF - 2009 vs. 2013</b>													
<b>C1</b>	0.07	0.07	0.08	0.06	0.07	0.07	0.16	0.16	0.16	0.15	0.15	0.16	0.4971
<b>C2</b>	0.15	0.15	0.14	0.13	0.15	0.15	0.14	0.14	0.14	0.14	0.14	0.14	0.1460
<b>C3</b>	0.17	0.17	0.15	0.16	0.17	0.17	0.16	0.16	0.16	0.16	0.16	0.16	0.1776
<b>C4</b>	0.12	0.12	0.06	0.06	0.12	0.12	0.15	0.15	0.15	0.15	0.15	0.15	0.1303
<b>C5</b>	0.07	0.07	0.07	0.05	0.05	0.07	0.15	0.15	0.15	0.15	0.15	0.15	0.1158
<b>GFIQF - 2013 vs. 2013</b>													
<b>C1</b>	0.41	0.41	0.41	0.41	0.41	0.41	0.3	0.3	0.3	0.31	0.31	0.28	0.4971
<b>C2</b>	0.08	0.08	0.09	0.09	0.08	0.08	0.15	0.15	0.15	0.15	0.15	0.15	0.1460
<b>C3</b>	0.14	0.14	0.14	0.08	0.10	0.14	0.2	0.2	0.2	0.2	0.19	0.19	0.1776
<b>C4</b>	0.13	0.13	0.22	0.23	0.13	0.13	0.16	0.16	0.16	0.16	0.16	0.16	0.1303
<b>C5</b>	0.16	0.16	0.29	0.41	0.29	0.16	0.13	0.13	0.14	0.14	0.14	0.14	0.1158

Table 144: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the NEURO matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

recognition system analysis can be found once more as introduced. This time not only for those two

quality methods rather for the NFIQ 2009 vs 2009 case as well. Another interesting observation of the splitted quality analysis is the information that the results for the lowest threshold are not so different to the others. But it is clear that this effect in the NBIS case was based on the choice of the certain value.

The confirmation of ageing in the used fingerprint data sets with an time span of 4 years for both minutiae based fingerprint recognition system seems to be a very solid foundation to expect basically the same results for the upcoming refinement analysis

<b>NEURO standard deviations (std) of the NFIQ quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	1.49	1.23
<b>B1</b>	0.95	1.72
<b>B2</b>	0.83	1.41
<b>B3</b>	0.13	1.20
<b>B4</b>	0.51	1.41
<b>B5</b>	0.48	1.36
<b>C1</b>	1.28	0.58
<b>C2</b>	1.32	0.24
<b>C3</b>	0.14	0.29
<b>C4</b>	0.30	0.58
<b>C5</b>	0.13	0.50

Table 145: Displaying the standard deviations of the NFIQ quality analysis based on the NEURO results.

<b>NEURO standard deviations (std) of the NFIQ quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	0.76	0.62	0.33
<b>C2</b>	0.41	0.04	0.36
<b>C3</b>	0.38	0.24	0.55
<b>C4</b>	0.46	0.24	0.21
<b>C5</b>	0.52	0.41	0.67
	<b>false rejected stds</b>		
<b>C1</b>	1.37	0.66	0.63
<b>C2</b>	0.98	0.17	0.35
<b>C3</b>	0.95	0.19	0.40
<b>C4</b>	1.05	0.44	0.57
<b>C5</b>	1.11	0.43	0.64

Table 146: Displaying the standard deviations of the NFIQ quality analysis based on the NEURO results taking the time span information into account.

<b>NEURO standard deviations (std) of the IQF quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	2.07	0.11
<b>B1</b>	0.76	0.32
<b>B2</b>	0.63	0.35
<b>B3</b>	0.69	0.35
<b>B4</b>	0.58	0.2
<b>B5</b>	0.52	0.06
<b>C1</b>	1.32	0.63
<b>C2</b>	1.6	0.11
<b>C3</b>	0.27	0.04
<b>C4</b>	0.23	0.13
<b>C5</b>	0.55	0.22

Table 147: Displaying the standard deviations of the IQF quality analysis based on the NEURO results.

<b>NEURO standard deviations (std) of the IQF quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	1.17	2.05	1.44
<b>C2</b>	0.53	0.5	0.45
<b>C3</b>	0.46	0.34	0.29
<b>C4</b>	0.45	0.76	0.15
<b>C5</b>	0.5	0.09	0.6
	<b>false rejected stds</b>		
<b>C1</b>	1.23	1.07	0.55
<b>C2</b>	0.2	0.2	0.19
<b>C3</b>	0.1	0.19	0.15
<b>C4</b>	0.09	0.2	0.25
<b>C5</b>	0.15	0.36	0.46

Table 148: Displaying the standard deviations of the IQF quality analysis based on the NEURO results taking the time span information into account.

<b>NEURO standard deviations (std) of the GFIQF quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.09	0.06
<b>B1</b>	0.13	0.41
<b>B2</b>	0.01	0.02
<b>B3</b>	0.04	0.04
<b>B4</b>	0.05	0.08
<b>B5</b>	0.02	0.006
<b>C1</b>	0.27	0.22
<b>C2</b>	0.07	0.003
<b>C3</b>	0.04	0.003
<b>C4</b>	0.03	0.02
<b>C5</b>	0.1	0.02

Table 149: Displaying the standard deviations of the GFIQF quality analysis based on the NEURO results.

<b>NEURO standard deviations (std) of the GFIQF quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	0.37	0.46	0.08
<b>C2</b>	0.05	0.009	0.06
<b>C3</b>	0.05	0.01	0.05
<b>C4</b>	0.06	0.04	0.06
<b>C5</b>	0.07	0.05	0.17
	<b>false rejected stds</b>		
<b>C1</b>	0.43	0.36	0.21
<b>C2</b>	0.05	0.001	0.008
<b>C3</b>	0.08	0.01	0.02
<b>C4</b>	0.03	0.02	0.04
<b>C5</b>	0.01	0.04	0.02

Table 150: Displaying the standard deviations of the GFIQF quality analysis based on the NEURO results taking the time span information into account.

FC false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						$\emptyset$ quality
	90.0	95.0	100.0	110.0	115.0	EER-thres.	90.0	95.0	100.0	110.0	115.0	EER-thres.	
<b>NFIQ - 2009 vs. 2009</b>													
<b>C1</b>	2.7	2.7	2.7	2.82	2.82	2.7	2.72	2.71	2.63	2.76	2.72	2.76	2.57
<b>C2</b>	2.7	2.7	2.7	2.81	2.81	2.69	2.71	2.71	2.66	2.71	2.71	2.76	2.92
<b>C3</b>	2.7	2.7	2.7	2.81	2.81	2.69	2.71	2.71	2.66	2.77	2.71	2.76	2.95
<b>C4</b>	2.74	2.74	2.74	2.85	2.85	2.74	2.71	2.71	2.66	2.77	2.71	2.75	2.86
<b>C5</b>	2.7	2.7	2.7	2.82	2.82	2.7	2.71	2.71	2.66	2.77	2.71	2.74	2.80
<b>NFIQ - 2009 vs. 2013</b>													
<b>C1</b>	2.70	2.70	2.70	2.74	2.74	2.70	2.44	2.46	2.68	2.44	2.44	3.63	2.57
<b>C2</b>	2.70	2.70	2.70	2.74	2.74	2.69	3.12	3.15	2.92	3.13	3.13	3.19	2.92
<b>C3</b>	2.70	2.70	2.70	2.74	2.74	2.69	3.2	3.21	2.89	3.21	3.19	3.21	2.95
<b>C4</b>	2.70	2.70	2.70	2.74	2.74	2.70	3.01	3.06	2.92	3.02	3.01	3.01	2.86
<b>C5</b>	2.70	2.70	2.70	2.74	2.74	2.70	2.89	2.95	2.93	2.91	2.9	3	2.80
<b>NFIQ - 2013 vs. 2013</b>													
<b>C1</b>	2.44	2.44	2.44	2.46	2.46	2.46	2.48	2.48	2.45	2.45	2.48	2.45	2.57
<b>C2</b>	3.13	3.13	3.13	3.04	3.03	3.13	3.14	3.41	3.16	3.29	3.14	3.19	2.92
<b>C3</b>	3.19	3.19	3.18	3.08	3.08	3.18	2.78	3.22	2.85	3.03	3.22	2.84	2.95
<b>C4</b>	3	3	3	2.92	2.91	2.98	2.95	2.96	3.05	3.06	2.95	3.07	2.86
<b>C5</b>	2.89	2.89	2.89	2.74	2.73	2.86	2.87	2.89	2.93	3	2.87	2.94	2.80
<b>IQF - 2009 vs. 2009</b>													
<b>C1</b>	12.25	12.25	12.25	12.29	12.29	12.27	12.29	12.28	12.25	12.3	12.29	12.32	11.02
<b>C2</b>	12.25	12.25	12.25	12.30	12.30	12.30	12.28	12.26	11.98	12.31	12.29	12.28	12.32
<b>C3</b>	12.25	12.25	12.25	12.31	12.31	12.31	12.28	12.26	11.98	12.31	12.29	12.28	12.20
<b>C4</b>	12.21	12.21	12.21	12.27	12.27	12.25	12.28	12.26	11.98	12.31	12.29	12.28	12.18
<b>C5</b>	12.25	12.25	12.25	12.29	12.29	12.29	12.28	12.26	11.98	12.31	12.29	12.28	12.27
<b>IQF - 2009 vs. 2013</b>													
<b>C1</b>	12.26	12.26	12.26	12.26	12.26	12.25	9.79	9.76	11.54	9.78	9.79	10.4	11.02
<b>C2</b>	12.26	12.26	12.26	12.26	12.26	12.25	12.39	12.39	11.98	12.39	12.39	12.39	12.32
<b>C3</b>	12.26	12.26	12.26	12.26	12.26	12.25	12.13	12.11	12.1	12.13	12.14	12.15	12.20
<b>C4</b>	12.26	12.26	12.26	12.26	12.26	12.25	12.1	12.08	12.08	12.1	12.1	12.09	12.18
<b>C5</b>	12.26	12.26	12.26	12.26	12.26	12.29	12.29	12.25	12.18	12.28	12.29	12.29	12.27
<b>IQF - 2013 vs. 2013</b>													
<b>C1</b>	9.79	9.79	9.79	9.72	9.72	9.76	9.72	9.72	9.78	9.75	9.72	9.78	11.02
<b>C2</b>	12.37	12.37	12.37	12.31	12.31	12.34	12.38	12.38	12.38	12.31	12.38	12.35	12.32
<b>C3</b>	12.13	12.13	12.14	12.11	12.11	12.13	12.09	12.08	12.13	12.11	12.08	12.1	12.20
<b>C4</b>	12.08	12.08	12.09	12.04	12.05	12.07	12.09	12.09	12.09	12.07	12.09	12.13	12.18
<b>C5</b>	12.27	12.27	12.28	12.28	12.29	12.27	12.25	11.25	12.27	12.33	12.25	12.28	12.27

Table 151: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the FC matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

FC false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values					false rejects threshold values					$\emptyset$	quality	
	90.0	95.0	100.0	110.0	115.0	EER-thres.	90.0	95.0	100.0	110.0	115.0	EER-thres.	
<b>GFIQF - 2009 vs. 2009</b>													
<b>C1</b>	0.16	0.16	0.16	0.15	0.15	0.15	0.14	0.14	0.14	0.14	0.14	0.13	0.4971
<b>C2</b>	0.16	0.16	0.16	0.15	0.15	0.15	0.14	0.14	0.14	0.15	0.14	0.14	0.1460
<b>C3</b>	0.16	0.16	0.16	0.15	0.15	0.15	0.14	0.14	0.14	0.15	0.14	0.14	0.1776
<b>C4</b>	0.16	0.16	0.16	0.15	0.15	0.16	0.16	0.14	0.14	0.15	0.14	0.13	0.1303
<b>C5</b>	0.16	0.16	0.16	0.15	0.16	0.15	0.14	0.14	0.14	0.15	0.14	0.13	0.1158
<b>GFIQF - 2009 vs. 2013</b>													
<b>C1</b>	0.16	0.16	0.16	0.15	0.15	0.15	0.82	0.82	0.82	0.82	0.83	0.62	0.4971
<b>C2</b>	0.16	0.16	0.16	0.15	0.15	0.16	0.12	0.12	0.13	0.12	0.12	0.11	0.1460
<b>C3</b>	0.16	0.16	0.16	0.15	0.15	0.16	0.19	0.18	0.15	0.19	0.19	0.17	0.1776
<b>C4</b>	0.16	0.16	0.16	0.15	0.15	0.16	0.09	0.1	0.13	0.09	0.09	0.13	0.1303
<b>C5</b>	0.16	0.16	0.16	0.15	0.15	0.16	0.06	0.06	0.13	0.06	0.06	0.07	0.1158
<b>GFIQF - 2013 vs. 2013</b>													
<b>C1</b>	0.82	0.82	0.82	0.82	0.82	0.82	0.81	0.81	0.82	0.82	0.81	0.83	0.4971
<b>C2</b>	0.12	0.12	0.12	0.11	0.11	0.12	0.11	0.11	0.12	0.12	0.11	0.12	0.1460
<b>C3</b>	0.18	0.18	0.18	0.18	0.18	0.18	0.17	0.16	0.18	0.2	0.17	0.18	0.1776
<b>C4</b>	0.09	0.09	0.09	0.1	0.1	0.09	0.09	0.09	0.09	0.1	0.09	0.1	0.1303
<b>C5</b>	0.06	0.06	0.06	0.07	0.07	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.1158

Table 152: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the FC matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

of the non-minutiae fingerprint recognition system results.

The output of the quality refinement analysis using the FC fingerprint recognition system can be read in Table 151, 152, 155 and 156. It is even harder to detect any differences in the non minutiae fingerprint recognition system results as for the minutiae fingerprint recognition system quality analysis variations. That means that first of all the same overall tendency as for the previously discussed quality outcomes can be detected. There are just two types of varieties. For the 2009 vs 2009 case there is no real discrepancy observable as before and the quality values seem to be more similar as for the minutiae based fingerprint recognition system. This stronger similarity



<b>FC standard deviations (std) of the NFIQ quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.32	0.14
<b>B1</b>	0.19	0.24
<b>B2</b>	0.51	0.98
<b>B3</b>	0.09	0.57
<b>B4</b>	0.46	0.65
<b>B5</b>	0.42	0.94
<b>C1</b>	0.19	0.57
<b>C2</b>	0.19	0.29
<b>C3</b>	0.04	0.28
<b>C4</b>	0.10	0.21
<b>C5</b>	0.11	0.25

Table 153: Displaying the standard deviations of the NFIQ quality analysis based on the FC results.

<b>FC standard deviations (std) of the NFIQ quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	0.20	0.16	0.12
<b>C2</b>	0.20	0.22	0.20
<b>C3</b>	0.23	0.25	0.23
<b>C4</b>	0.10	0.15	0.13
<b>C5</b>	0.08	0.08	0.08
	<b>false rejected stds</b>		
<b>C1</b>	0.17	0.12	0.11
<b>C2</b>	0.21	0.23	0.29
<b>C3</b>	0.25	0.25	0.27
<b>C4</b>	0.15	0.16	0.17
<b>C5</b>	0.09	0.15	0.13

Table 154: Displaying the standard deviations of the NFIQ quality analysis based on the FC results taking the time span information into account.

<b>FC standard deviations (std) of the IQF quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.35	1.90
<b>B1</b>	0.35	0.09
<b>B2</b>	1.97	0.85
<b>B3</b>	0.11	1.86
<b>B4</b>	0.4	0.48
<b>B5</b>	0.4	0.80
<b>C1</b>	0.59	0.96
<b>C2</b>	0.21	0.19
<b>C3</b>	0.06	0.3
<b>C4</b>	0.14	0.35
<b>C5</b>	0.05	0.37

Table 155: Displaying the standard deviations of the IQF quality analysis based on the FC results.

<b>FC standard deviations (std) of the IQF quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	1.37	1.36	1.37
<b>C2</b>	0.04	0.06	0.04
<b>C3</b>	0.09	0.06	0.07
<b>C4</b>	0.07	0.09	0.11
<b>C5</b>	0.02	0.008	0.01
	<b>false rejected stds</b>		
<b>C1</b>	1.39	1.16	1.39
<b>C2</b>	0.15	0.08	0.06
<b>C3</b>	0.13	0.07	0.10
<b>C4</b>	0.14	0.09	0.09
<b>C5</b>	0.13	0.04	0.03

Table 156: Displaying the standard deviations of the IQF quality analysis based on the FC results taking the time span information into account.

<b>FC standard deviations (std) of the GFIQF quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.37	0.06
<b>B1</b>	0.07	0.11
<b>B2</b>	0.02	0.03
<b>B3</b>	0.007	0.04
<b>B4</b>	0.03	0.02
<b>B5</b>	0.02	0.02
<b>C1</b>	0.04	0.09
<b>C2</b>	0.03	0.03
<b>C3</b>	0.09	0.09
<b>C4</b>	0.07	0.02
<b>C5</b>	0.06	0.02

Table 157: Displaying the standard deviations of the GFIQF quality analysis based on the FC results.

<b>FC standard deviations (std) of the GFIQF quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	0.36	0.36	0.36
<b>C2</b>	0.01	0.01	0.02
<b>C3</b>	0.01	0.01	0.01
<b>C4</b>	0.03	0.03	0.03
<b>C5</b>	0.04	0.05	0.05
	<b>false rejected stds</b>		
<b>C1</b>	0.38	0.31	0.35
<b>C2</b>	0.004	0.02	0.03
<b>C3</b>	0.03	0.01	0.01
<b>C4</b>	0.01	0.03	0.03
<b>C5</b>	0.03	0.04	0.05

Table 158: Displaying the standard deviations of the GFIQF quality analysis based on the FC results taking the time span information into account.

POC false accepts and false rejects depending on different thresholds													
average quality values													
data sets	false accepts threshold values						false rejects threshold values						∅ quality
	0.01	0.1	0.2	0.25	0.3	EER-thres.	0.01	0.1	0.2	0.25	0.3	EER-thres.	
<b>NFIQ - 2009 vs. 2009</b>													
<b>C1</b>	2.71	2.71	2.68	2.71	2.68	2.72	2.84	2.73	2.74	2.78	2.70	3.05	2.57
<b>C2</b>	2.71	2.71	2.68	2.71	2.68	2.72	-	3.04	2.78	2.73	2.74	2.79	2.92
<b>C3</b>	2.71	2.71	2.69	2.71	2.69	2.73	-	3.05	2.78	2.73	2.74	2.85	2.95
<b>C4</b>	2.71	2.71	2.68	2.71	2.68	2.72	-	3.04	2.78	2.73	2.74	2.82	2.86
<b>C5</b>	2.71	2.71	2.68	2.71	2.68	2.72	-	3.03	2.78	2.73	2.74	2.81	2.80
<b>NFIQ - 2009 vs. 2013</b>													
<b>C1</b>	2.44	2.44	2.47	2.44	2.47	2.44	2.74	2.82	2.70	2.70	2.78	2.69	2.57
<b>C2</b>	3.13	3.13	3.13	3.13	3.13	3.13	-	2.96	2.72	2.70	2.70	2.80	2.92
<b>C3</b>	3.19	3.19	3.13	3.19	3.13	3.19	-	3.08	2.73	2.71	2.7	2.89	2.95
<b>C4</b>	3.01	3.01	2.97	3.02	2.97	3.01	-	3.13	2.77	2.71	2.71	2.89	2.86
<b>C5</b>	2.90	2.90	2.87	2.91	2.86	2.89	-	3.12	2.72	2.70	2.70	2.90	2.80
<b>NFIQ - 2013 vs. 2013</b>													
<b>C1</b>	2.44	2.44	2.43	2.44	2.43	2.44	2.70	2.68	2.69	2.75	2.78	2.68	2.57
<b>C2</b>	3.12	3.10	3.10	3.09	3.10	3.06	-	2.74	2.96	3.01	3.12	2.73	2.92
<b>C3</b>	3.18	3.17	3.16	3.17	3.16	3.14	-	2.76	3.05	3.05	3.16	2.75	2.95
<b>C4</b>	3	2.99	2.98	2.99	2.98	2.96	-	2.76	2.89	2.88	2.96	2.75	2.86
<b>C5</b>	2.89	2.87	2.84	2.87	2.84	2.83	-	2.75	2.91	2.93	2.99	2.75	2.80
<b>IQF - 2009 vs. 2009</b>													
<b>C1</b>	12.26	12.24	12.18	12.24	12.18	12.25	12.23	12.28	12.28	12.29	12.26	12.01	11.02
<b>C2</b>	12.26	12.24	12.18	12.24	12.18	12.26	-	12.06	12.29	12.28	12.28	12.26	12.32
<b>C3</b>	12.26	12.24	12.18	12.24	12.18	12.26	-	12.05	12.29	12.28	12.28	12.26	12.20
<b>C4</b>	12.26	12.24	12.18	12.24	12.18	12.25	-	12.06	12.29	12.28	12.28	12.25	12.18
<b>C5</b>	12.26	12.24	12.18	12.24	12.18	12.26	-	12.08	12.29	12.28	12.28	12.25	12.27
<b>IQF - 2009 vs. 2013</b>													
<b>C1</b>	9.79	9.79	9.74	9.78	9.74	9.79	12.28	12.22	12.26	12.26	12.26	12.25	11.02
<b>C2</b>	12.26	12.24	12.18	12.24	12.18	12.26	-	12.16	12.26	12.26	12.26	12.27	12.32
<b>C3</b>	12.14	12.14	12.11	12.12	12.11	12.14	-	12.18	12.25	12.25	12.25	12.26	12.20
<b>C4</b>	12.26	12.24	12.18	12.24	12.18	12.10	-	12	12.23	12.26	12.27	12.16	12.18
<b>C5</b>	12.29	12.29	12.30	12.27	12.31	12.29	-	12.02	12.23	12.25	12.26	12.16	12.27
<b>IQF - 2013 vs. 2013</b>													
<b>C1</b>	9.8	9.8	9.76	9.79	9.76	9.8	12.25	11.98	11	11.01	11.8	11.98	11.02
<b>C2</b>	12.38	12.38	12.39	12.38	12.39	12.36	-	12.23	12.19	12.15	12.14	12.23	12.32
<b>C3</b>	12.13	12.11	12.10	12.11	12.10	12.11	-	12.26	12.24	12.19	12.13	12.23	12.20
<b>C4</b>	12.10	12.09	12.10	12.08	12.10	12.06	-	12.25	12.13	12.14	12.13	12.25	12.18
<b>C5</b>	12.29	12.3	12.28	12.3	12.29	12.29	-	12.17	12.13	12.19	12.16	12.18	12.27

Table 159: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the POC matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

POC false accepts and false rejects depending on different thresholds														
average quality values														
data sets	false accepts threshold values						false rejects threshold values						∅	quality
	0.01	0.1	0.2	0.25	0.3	EER-thres.	0.01	0.1	0.2	0.25	0.3	EER-thres.		
<b>GFIQF - 2009 vs. 2009</b>														
<b>C1</b>	0.16	0.16	0.16	0.16	0.16	0.16	0.14	0.16	0.16	0.15	0.16	0.13	0.4971	
<b>C2</b>	0.16	0.16	0.16	0.16	0.16	0.15	-	0.15	0.15	0.16	0.16	0.14	0.1460	
<b>C3</b>	0.16	0.16	0.16	0.16	0.16	0.15	-	0.15	0.15	0.16	0.16	0.14	0.1776	
<b>C4</b>	0.16	0.16	0.16	0.16	0.16	0.15	-	0.15	0.15	0.16	0.16	0.14	0.1303	
<b>C5</b>	0.16	0.16	0.16	0.16	0.16	0.15	-	0.15	0.15	0.16	0.16	0.14	0.1158	
<b>GFIQF - 2009 vs. 2013</b>														
<b>C1</b>	0.83	0.83	0.85	0.83	0.85	0.83	0.16	0.16	0.15	0.16	0.16	0.16	0.4971	
<b>C2</b>	0.12	0.12	0.13	0.12	0.13	0.12	-	0.16	0.16	0.16	0.16	0.16	0.1460	
<b>C3</b>	0.19	0.19	0.18	0.18	0.18	0.19	-	0.16	0.16	0.16	0.16	0.17	0.1776	
<b>C4</b>	0.09	0.09	0.10	0.09	0.10	0.09	-	0.14	0.16	0.16	0.16	0.15	0.1303	
<b>C5</b>	0.06	0.06	0.07	0.06	0.07	0.06	-	0.16	0.16	0.16	0.16	0.16	0.1158	
<b>GFIQF - 2013 vs. 2013</b>														
<b>C1</b>	0.83	0.83	0.85	0.83	0.85	0.83	0.16	0.22	0.47	0.47	0.52	0.22	0.4971	
<b>C2</b>	0.12	0.13	0.13	0.13	0.13	0.12	-	0.16	0.15	0.15	0.15	0.16	0.1460	
<b>C3</b>	0.19	0.19	0.18	0.18	0.18	0.18	-	0.17	0.20	0.20	0.19	0.17	0.1776	
<b>C4</b>	0.09	0.10	0.10	0.10	0.10	0.09	-	0.16	0.17	0.16	0.15	0.16	0.1303	
<b>C5</b>	0.07	0.07	0.07	0.07	0.07	0.07	-	0.15	0.13	0.13	0.11	0.15	0.1158	

Table 160: Displaying the average quality analysis results concerning the false accepts and false rejects at specific thresholds for the POC matching scores using the crossed data sets and split the false accepts and false rejects information according to the years of the imprints.

could be described for the entire data sets the first time and the refinement analysis is conforming this tendency. Therefore the standard deviation values are much lower than 0.5. In fact they are never higher than 0.3. The only exception is the 2009 vs 2009 case.

Based on the FC results it is easy to analyze the outcomes of the POC refinement research. As readable in Table 159, 160, 163 and 164 just one disparity between the non minutiae based fingerprint recognition system is observable. This difference is that there are other output values of the calculations. The standard deviations are never higher than 0.3 and most of the time they are lower than for all the other fingerprint recognition systems. Of course the cross-sensor effect is the exception for

POC standard deviations (std) of the NFIQ quality analysis		
data sets	false accepts std	false rejects std
<b>A</b>	1.23	0.11
<b>B1</b>	0.27	0.5
<b>B2</b>	1.02	0.24
<b>B3</b>	0.19	0.41
<b>B4</b>	0.53	0.62
<b>B5</b>	0.55	0.57
<b>C1</b>	0.11	0.15
<b>C2</b>	0.34	0.08
<b>C3</b>	0.33	0.07
<b>C4</b>	0.13	0.07
<b>C5</b>	0.21	0.09

Table 161: Displaying the standard deviations of the NFIQ quality analysis based on the POC results.

POC standard deviations (std) of the NFIQ quality analysis for the splitted sets			
data sets	2009 vs 2009	2009 vs 2013	2013 vs 2013
	<b>false accepted stds</b>		
<b>C1</b>	0.15	0.12	0.14
<b>C2</b>	0.23	0.23	0.19
<b>C3</b>	0.26	0.25	0.24
<b>C4</b>	0.16	0.15	0.13
<b>C5</b>	0.10	0.10	0.07
	<b>false rejected stds</b>		
<b>C1</b>	0.12	0.18	0.16
<b>C2</b>	0.16	0.18	0.17
<b>C3</b>	0.18	0.21	0.18
<b>C4</b>	0.13	0.17	0.08
<b>C5</b>	0.12	0.18	0.13

Table 162: Displaying the standard deviations of the NFIQ quality analysis based on the POC results taking the time span information into account.

POC standard deviations (std) of the IQF quality analysis		
data sets	false accepts std	false rejects std
A	1.12	0.08
B1	0.21	0.39
B2	0.68	0.09
B3	0.57	0.14
B4	0.5	0.11
B5	0.39	0.21
C1	0.35	0.86
C2	0.16	0.06
C3	0.19	0.06
C4	0.09	0.05
C5	0.2	0.08

Table 163: Displaying the standard deviations of the IQF quality analysis based on the POC results.

POC standard deviations (std) of the IQF quality analysis for the splitted sets			
data sets	2009 vs 2009	2009 vs 2013	2013 vs 2013
<b>false accepted stds</b>			
C1	1.32	1.36	1.34
C2	0.1	0.06	0.07
C3	0.04	0.07	0.09
C4	0.06	0.1	0.09
C5	0.05	0.03	0.02
<b>false rejected stds</b>			
C1	1.32	1.35	0.82
C2	0.13	0.09	0.14
C3	0.1	0.06	0.05
C4	0.11	0.11	0.06
C5	0.09	0.13	0.11

Table 164: Displaying the standard deviations of the IQF quality analysis based on the POC results taking the time span information into account.

<b>POC standard deviations (std) of the GFIQF quality analysis</b>		
<b>data sets</b>	<b>false accepts std</b>	<b>false rejects std</b>
<b>A</b>	0.08	0.01
<b>B1</b>	0.11	0.13
<b>B2</b>	0.04	0.03
<b>B3</b>	0.06	0.04
<b>B4</b>	0.02	0.01
<b>B5</b>	0.01	0.01
<b>C1</b>	0.1	0.3
<b>C2</b>	0.03	0.01
<b>C3</b>	0.03	0.002
<b>C4</b>	0.03	0.02
<b>C5</b>	0.03	0.03

Table 165: Displaying the standard deviations of the GFIQF quality analysis based on the POC results.

<b>POC standard deviations (std) of the GFIQF quality analysis for the splitted sets</b>			
<b>data sets</b>	<b>2009 vs 2009</b>	<b>2009 vs 2013</b>	<b>2013 vs 2013</b>
	<b>false accepted stds</b>		
<b>C1</b>	0.36	0.37	0.36
<b>C2</b>	0.01	0.01	0.01
<b>C3</b>	0.01	0.01	0.01
<b>C4</b>	0.03	0.03	0.03
<b>C5</b>	0.05	0.05	0.04
	<b>false rejected stds</b>		
<b>C1</b>	0.37	0.36	0.22
<b>C2</b>	0.01	0.01	0.01
<b>C3</b>	0.02	0.01	0.02
<b>C4</b>	0.03	0.03	0.03
<b>C5</b>	0.05	0.05	0.03

Table 166: Displaying the standard deviations of the GFIQF quality analysis based on the POC results taking the time span information into account.



this statement like before.

As last part of the present Chapter 7 it is necessary to summarize the information which has been discussed. Especially the aspect of quality and ageing in terms of the detected effects of the previous chapters will be in the main focus.

In Section 7.1 the NFIQ quality measure was introduced. The results of the calculations using this method are located between 1 and 5. It is easy to understand the meaning of those values. 1 denotes the best possible quality and 5 the worst. The idea of using a low number for better quality is not repeated for the other two methods. For IQF and GFIQF a low output indicates worse and a high one good quality of the fingerprint image. In Section 7.2 the range of IQF is introduced to be between 0 and 100. But this range was never covered of one of the used data bases. All quality values of the present fingerprints are always lower than 20 which is a reference for a quite bad quality at all. This assumption was confirmed by the other two measurements. Particularly the range of GFIQF, which was described in Section 7.3 the first time, supported the outcomes of IQF mainly. The GFIQF values are located between 0 and 1 and for the most of the fingerprint images in the present data sets they never exceeded 0.2. This is interesting because both methods are using a total different concept. The NFIQ measure was the only one for which the whole range was covered by the imprints. Based on this information it is probably valid to state that the NFIQ measure is the most important one of those three quality measurements because the outcomes can describe the actual quality of the fingerprints in a more sophisticated way.

Another aspect that is very important to discuss is the circumstance if it is realistic that ageing is influencing the matching performance so much that false positive matches occur. Those type of matches would be included in the impostor matches. If the number of those falsely accepted matches would be influenced by ageing that much, this could lead to a lot of troubles in terms of security aspects. But what does this potential high degradation of the fingerprints mean? In fact there would be a part of the human population for whom the persistence aspect of their imprints would not be given. Their fingerprints could change that much that they would get a new biometric identification feature. That would imply that there are people having the potential to be a kind of 'human chameleons'. So far as it is known this would violate a lot of laws of nature - especially thinking about the generally accepted concept of

DNA as main genetic code book for development and reproduction of cells. Therefore the results displayed in Chapter 5 based on the stability of the impostor score distributions is a result which seems to be realistic to detect. Based on the stability of the impostor score distribution it is also not surprising that there is hardly no quality based impact detectable in the present Chapter 7 concerning the quality analysis of the used fingerprints.

A slightly different point of view is necessary for the genuine score distribution and the corresponding quality analysis. Because of the aspect mentioned above ageing can only cause some troubles in terms of convenience. In the quality analysis of this chapter it was possible to gather the information that the average quality of the entire data sets and the quality based on certain thresholds and matching classes (2009 vs 2009, 2009 vs 2013, 2013 vs 2013) is very similar. Various variations which have been discussed using the standard deviation are not influencing the aspect that quality degradation is not present in the false rejected matches. So the quality of the falsely rejected matches is also not better or worse than the average quality of the complete data bases. Because of the clearly observable decrease of the *EER* for the crossed data sets it is valid to say that this effect is caused by ageing. The assurance that ageing is the reason therefore is ensured by the stability of the quality values. If this stability would not be present a total different situation could be described. An increase or decrease concerning the quality of the false rejected matches could only be caused by quality itself. Otherwise ageing would violate the persistence characteristic of biometric features like discussed above.

So based on the quality investigations which have been presented in this chapter of the current master thesis the assumption that ageing is causing the detected effects of the previous chapters can be confirmed.

## 8 Conclusion

Three main goals have been stated in the introduction of this master thesis. In this final section of the thesis there will be a closing discussion to summarize the before presented results. On a CASIA fingerprint data base, including imprints, which have been acquired with a time interval of four years, the experiments, examining the major tasks, are performed.

As described in Chapter 3 four fingerprint recognition systems are employed on the data sets to derive the matching performance. For this purpose the results, described in Chapter 5, revealed that the characteristic values of each data base and system type can be used to observe some interesting effects. In fact there are irregularities concerning the matching score distributions detectable. The clearly present shift to the left in the genuine score distributions of the crossed data bases led to the hypothesis that ageing is influencing the number of falsely rejected matches. This shift is also indicating that the number of low genuine scores is increased. Furthermore it can be stated that the genuine and impostor score distributions for the crossed data set tend to be more similar as for the single data sets. The security based point of view of this statement can be discussed as well. The increase of false rejected matches is not a big problem in terms of security, but in convenience. In terms of security the results revealed that nearly no change in the impostor score distribution is detectable and also not in the number of false accepted users. Despite it is important to add the information that within the calculated matching scores of the crossed data sets it seems that it does not matter which type of impostor matches are taken into account. As discussed in WA, OA and HH analysis of Chapter 5 using different score subsets of the entire crossed matching scores there is hardly no difference between the 3 chosen experimental setups. Furthermore a randomly performed adaptation of the used scores' size during the experiments did not change the results either. Nevertheless after performing the first main task of the master thesis it was not possible to be sure that ageing is responsible for the observed effects. It was a regular assumption that fingerprint quality and ageing as well could cause the discussed aspects. For this purpose a more detailed study on this topic was performed in the last Chapter 7. Looking at the outcomes of the experiments displayed in Section 3 it is possible to receive a different point of view in terms of fingerprint ageing using the so called 'Doddington's Zoo' concept. Especially the goats characteristic is interesting because

they are related to low genuine scores and as discussed before an irregularity concerning the genuine scores is observable within the crossed data. As described in Chapter 6 some experiments have been performed to get a closer look at the menagerie investigation. The intuition would probably lead to the suggestion that an increase of low genuine scores must also give rise to the number of detectable goat-like user's. But against this proposition nearly no difference between the number of goat labeled user's in the used data can be proven. It seems that the number is more or less stable. Of course it is a little bit difficult to state data set specific results because of the structure of the used method to find certain users. For the mean, var, mean2 and min/max a fixed number of volunteers is labeled for each data base. So the only aspect which can be compared is based on all data set information. That means that all volunteers of 2013 and of the crossed sets have been taken into account. So it is possible to gather a total number of all users, which have been labeled in 2009, 2013 and the crossed data bases. These sets of volunteers are compared for each data set. In particular it can be stated that if a volunteer has been labeled in 2009 or 2013 the first time then the probability to sign the same user in the crossed sets can be located between at least 30% and 40%. An additional assumption that the decrease within the genuine scores and the stability of the impostor scores is influencing the overall observation could not be confirmed. Contrary to what was expected there was no high amount of fluctuation/stability in the extension of the users' goats/lambs and wolves characteristic detectable. For both goats and lambs/wolves a more or less identical likelihood of resigning a volunteer in the crossed data sets can be described. Of course there are differences which are caused by the variances in data bases, recognition system and menagerie analysis method. But a more detailed discussion was presented in Chapter 6.6.

The final main goal of this master thesis was to determine the impact of the fingerprint quality. It is clear that the quality of the imprints is a very crucial key aspect. There is no doubt, bad quality of imprints can lead to several troubles performing a fingerprint recognition. So it also is possible that quality which is bad enough and has a much higher impact as ageing effects. For this purpose a very detailed discussion has been performed about this topic. It was possible to get the information that not quality is responsible for the before discussed effects in terms of performance and menagerie analysis. Fingerprint ageing is detectable in the data sets and this biological aspect is also more influencing the described experiments than quality. Apart

form the results it is possible to state the following general assumption: If bad quality is detectable then it could be that the effects detected in the before mentioned experimental setups are caused by low quality and not because of ageing. But, if there is hardly no quality based bias then for example the trend of the genuine score distributions adaptation of the impostor ones for the crossed data sets would be caused by fingerprint ageing. After the quality based investigations it was clear that there are more or less no quality based aspects for the time span including matches detectable. So the observed effects of the other main parts of the present master thesis are caused by fingerprint ageing itself. Furthermore it is also important to mention that there are false rejected matches which correspond to imprints from 2009 and for whom an quality bias is verifiable. But those matches are not responsible for the time span based effects and due to this their quality degradation is not important for this study. Apart from this the false accepted matches seem to be not influenced by quality at all. This observation is a realistic one because otherwise there could be a problem in terms of fingerprint recognition security which would refer to a weakness in the concepts of biometric persistence and uniqueness.

All in all it is possible to reveal ageing effects in fingerprint recognition in the used experimental setups and data bases. It would be interesting to have a closer look at other data sets on the one hand and especially on data sets including a larger time span. A more detailed look at the genuine score distributions could be also very informative due to more concrete convenience aspects. In terms of the very important quality analysis the application of further quality measures, for example NFIQ 2.0, to separate the gray area between ageing effects and quality into more detail would be an interesting task. Even though it seems that the quality aspect in the used data set is not biasing the ageing related matches in a strong manner.

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