Methods for Locating Distinct Features in Fingerprint Images

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Abstract
With the advance of the modern information society, the importance of reliable identity authentication has increased dramatically. Using biometrics as a means for verifying the identity of a person increases both the security and the convenience of the systems. By using yourself to verify your identity such risks as lost keys and misplaced passwords are removed and by virtue of this, convenience is also increased. The most mature and well-developed biometric technique is fingerprint recognition. Fingerprints are unique for each individual and they do not change over time, which is very desirable in this application. There are multitudes of approaches to fingerprint recognition, most of which work by identifying so called minutiae and match fingerprints based on these.

In this diploma work, two alternative methods for locating distinct features in fingerprint images have been evaluated. The Template Correlation Method is based on the correlation between the image and templates created to approximate the homogenous ridge/valley areas in the fingerprint. The high-dimension of the feature vectors from correlation is reduced through principal component analysis. By visualising the dimension reduced data by ordinary plotting and observing the result classification is performed by locating anomalies in feature space, where distinct features are located away from the non-distinct.

The Circular Sampling Method works by sampling in concentric circles around selected points in the image and evaluating the frequency content of the resulting functions. Each images used here contains 30400 pixels which leads to sampling in many points that are of no interest. By selecting the sampling points this number can be reduced. Two approaches to sampling points selection has been evaluated. The first restricts sampling to occur only along valley bottoms of the image, whereas the second uses orientation histograms to select regions where there is no single dominant direction as sampling positions. For each sampling position an intensity function is achieved by circular sampling and a frequency spectrum of this function is achieved through the Fast Fourier Transform. Applying criteria to the relationships of the frequency components classifies each sampling location as either distinct or non-distinct.

Using a cyclic approach to evaluate the methods and their potential makes selection at various stages possible. Only the Circular Sampling Method survived the first cycle, and therefore all tests from that point on are performed on this method alone. Two main errors arise from the tests, where the most prominent being the number of spurious points located by the method. The second, which is equally serious but not as common, is when the method misclassifies visually distinct features as non-distinct. Regardless of the problems, these tests indicate that the method holds potential but that it needs to be subject to further testing and optimisation. These tests should focus on the three main properties of the method: noise sensitivity, radial dependency and translation sensitivity.

Keywords
fingerprint recognition, feature extraction, biometrics, pattern recognition, template correlation, circular sampling
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Preface

There are a few persons I would like to thank.

This diploma work has been carried out in co-operation with Fingerprint Cards AB and so I would like to thank my supervisor Pär Sivertsson for the support, the opportunity to attend the algorithm meetings and for the work itself.

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1 Introduction

Fingerprints are the ridge and valley pattern on the fingertips. They are unique for each individual and they do not change over time, except in size when a person grows. A fingerprint image is an image of this pattern captured by a sensor. A distinct feature in a fingerprint image is one that contains characteristic information, and is distinguishable from the rest of the image in some sense. A stable feature in a fingerprint image is one that is present in all instances of the image, even when the image is captured some time apart. Distinct features give characteristic information at one time instant, but may not be present the next, so in order for the feature to be useful it is necessary to combine the two requirements. Features that are both stable and distinct can be stored at one moment in time and still be valid for comparison at another. The term stable used above pertains to the short-term stability of a feature, which differentiates it from noise. There is another aspect of stability concerning the long-term stability over months or years. When the term distinct is used in this report it combines the notions of distinctness and short-term stability, which is important to bear in mind. The purpose of this report is to present the work with the evaluation of methods used for locating distinct features in fingerprint images. It will give the reader an insight into areas such as fingerprinting, biometrics and pattern recognition as well as providing detailed information about the development and evaluation of two methods.

As the title states, this work is an evaluation of methods for locating distinct features in fingerprint images. It is not a complete system for fingerprint recognition, nor is it the development of one single method. The tests are designed so that they give a good understanding of the methods and a good appreciation of their potential, but they are not tests of the fingerprint recognition ability of the methods. The diploma work has been carried out in co-operation with the Gothenburg based company Fingerprint Cards AB, and it is with their platform in mind that the methods have been evaluated. The FPC2000 ASIC processor is the core of a complete embedded system, containing sensor and algorithm as well. The fingerprint images used in this work have been captured using the capacitive FPC1010 sensor, delivering images of 363 dpi geometric and 8 bit photometric resolution. The active sensing area of the sensor is 10.64x14.00 mm giving 152x200 pixel images. More details on the company and their technology can be found in [12].

This report begins with the theoretical background to the areas of biometrics and pattern recognition in Chapters 2 and 3, respectively. These two chapters are very general in their content and they are here to provide the appropriate understanding of the problem. Following this theoretical overview of the topic is the description of the two evaluated methods in Chapter 4. Here is presented not only the methods, but also the cyclic approach in which they have been evaluated. Chapter 5 – Method Analysis and Evaluation contains the description and results of the experimental analysis. Each section describes one test, and each method is evaluated separately. Conclusions and suggestion of improvements are given in Chapter 6 – Conclusions and future work, which is the last in the report. Following the report are appendices A to E, each of which refers to testing one test. Chapters 5.5 – Distinctness Measurement and 6.2, 3 – Further testing are confidential on the request of Fingerprint Cards AB.
2 An Overview of Biometrics

The word biometrics refers to measuring a biological characteristic, which may seem like a far-fetched activity. Yet when considering a more specific definition, given in [1], it poses several interesting questions. The definition states that ‘Biometrics is a technology that (uniquely) identifies a person based on his physiological or behavioural characteristics’. In other words, using the measurements of a biological characteristic to determine the identity of a person. Can this be useful, and if it is, how do we measure something biological? This chapter presents an overview of identity authentication, biometrics and fingerprinting which is based on [1] unless otherwise stated.

2.1 Identity Authentication

When it comes to systems that automatically help establish the identity of a person, there is a need for distinction between two types: Verification and Identification. In the case of verification the person tells the system who he is through the use of, for instance, a code or a magnetic card. The task of the system is then to answer the question ‘Is he who he claims to be?’. In the identification case it is a matter of identifying the person without him telling the system who he is, thus answering the question ‘Who is he?’. The main difference between these two types of systems is the time and effort demanded to identify a person. In verification it is only necessary to perform one comparison, while in identification the number of comparisons is related to the number of identities stored in the database.

Consider the ways in which a person can identify himself. These can be divided into three categories, of which the first is using something that you know, a code for instance. The second is the use of something that you have, for instance a key or an identification card. The third and last is the use of something that you are, some biological characteristic that you possess, such as your fingerprint. Now, codes can be forgotten, written down or told to unauthorised personnel. Keys can be misplaced, stolen or copied. Fingerprints, on the other hand, cannot be forgotten, misplaced or copied without tremendous effort and knowledge. It therefore the most secure and convenient of the three. Even considering the fact that it is impossible to obtain an absolute yes or no answer to the question of identity in biometrics, it is still more secure than more traditional identity authentication methods.

Biometric identity authentication systems have the potential to be adopted in a very broad range of civilian applications. The list is only limited by the imagination, but includes:

- Cellular phones and Handheld Computers, as a replacement for PIN codes
- Physical Access Control, as a replacement for keys or magnetic cards
- Information System Security, as a replacement for passwords
- Cash Machines (ATM:s), as a replacement for the card and code approach of today.
Some applications may be more suited for the use of biometrics than others, but regardless of the suitability of the application one must ask in which way this can be performed, and what biometric characteristic that should be measured.

### 2.2 Biometric technologies

Although biometrics is in no way limited to fingerprinting, this is probably the most popular and extensively researched of the current biometric techniques. Regardless of the technique used there is a number of requirements that need to be satisfied for the examined characteristic:

1. *Universality*, everyone should possess the characteristic.
2. *Uniqueness*, the characteristic should be unique to each individual.
3. *Permanence*, the characteristic should not change over time.
4. *Collectability*, the characteristic should be measurable.

There are numerous characteristics that satisfy these criteria, of which fingerprints is but one. Other characteristics include, but are not limited to, face, iris, retina, voice, and hand geometry. In a complex biometric system it is possible to measure several of these to enhance system performance, which will of course increase the cost of the system as well as the necessary user-input.

In the biometric system there is generally a database of enrolled templates, one or several for each user depending on system design. The process of enrolment is important since it is here that the first selection is made based on template quality. If the quality is much too low, the user should be asked to re-enrol. Each time a person attempts to authenticate his identity, a sample of the biometric characteristic is created and input to the system, which is compared to the enrolled templates in the database. A decision is made regarding the validity of the sample and the identity of the person providing it. There are four outcomes from this decision process: A genuine individual is accepted, a genuine individual is rejected, an impostor is rejected and an impostor is accepted. The first and the third results are correct, while the other two are incorrect. Regarding this, one must ask the question of how to measure system performance. According to [2], there are a few basic measurements that should be taken into account when considering the performance of a general biometric system:

1. *Penetration coefficient*, reflecting the expected portion of the enrolled templates to be compared to a single input.
2. *Bin-error rate*, or probability that a search is unsuccessful because the sample and the template was erroneously placed in different bins.
3. *Single-comparison false-match rate* (or False Accept Rate) reflecting the probability that an impostor sample is incorrectly matched to a template.
4. *Single-comparison false-non-match rate* (or False Reject Rate) reflecting the probability of a genuine sample being incorrectly rejected.
5. *Comparison rate* of the hardware, which reflects the number of sample-template comparisons per second.

For an identification system on a given platform each of these are important. In a verification system, when one sample is compared to a single template, the first two are of no real importance, however. The last measurement is hardware dependent, and must be evaluated using the platform on which the system is implemented in practice. The *False Accept Rate (FAR)* and *False Reject Rate*
are independent of the platform used (given that the data precision of the platform is high enough, which most often is the case), thus giving measurements of verification performance, which is of great importance. Exact mathematical definitions of these measurements can be found in [2].

2.3 Fingerprinting

Humans have used fingerprints as a means for identification for a very long time, but the modern fingerprint techniques where introduced in the late sixteenth century. Almost a century later, in 1684, N. Grew published what is believed to be the first scientific paper on fingerprinting. It reports his study on ridge, furrow and pore-structure in fingerprints. Another important landmark in the history of fingerprints came in the late nineteenth century, when E. Henry introduced the Henry system, a very detailed system for indexing fingerprints to match the human perception. Following this, fingerprinting became formally accepted as a means of identification by law-enforcement agencies, and was a standard method used in forensics. In the early 1960’s the Federal Bureau of Investigations, together with the United Kingdom Police Department, started to invest a large amount of effort into developing Automatic Fingerprint Identification Systems (AFIS). Since then, a number of large databases of fingerprints have been collected by law enforcement agencies. Today the need for fast and secure identity authentication has grown far beyond the mere military and law enforcement applications, into civilian areas such as bank security, physical access control and data security.

To accustom the reader with the common terms and notions used in fingerprinting, a short practical introduction to the subject is given here. Consider the fingerprint image in figure 1. At the top of the image are areas where the finger was not in contact with the sensor at the time of capture, which contain no significant information about the fingerprint. These so-called non-contact areas are most prominent in the upper right and left corners. To avoid this problem is to make sure that the finger is in contact with the entire sensor at the moment of capture, i.e. ensuring template quality at enrolment.

Figure 1. Fingerprint image with the core point marked by a white circular region.
As stated in [9], fingerprints are the ridge and furrow pattern on the tip of the finger. In Figure 1 the furrows, commonly known as valleys, are white and the ridges are black. The small white spots upon the ridges are the result from pores, i.e., parts of the ridges that are not in contact with the sensor. In determining the uniqueness of a fingerprint one can consider the overall pattern as well as the local ridge anomalies, also called minutiae. Several of the approaches in fingerprint identification are based on the location of a core point in the image (marked by O in Figure 1). Examples of such approaches are given in [4] and [9]. There are difficulties in locating the core of fingerprint, however. For one, there may not exist a core point, or the finger may be translated in such a way that the core of the fingerprint is placed outside of the sensor.

In a verification system using fingerprints there is a need for only one sample-to-template comparison to verify the identity of the user. The process of comparing one fingerprint to others to be able to uniquely determine the correspondence between them is known as fingerprint matching. There is a myriad of different approaches to fingerprint matching, ranging from filter based ([4], [9]) to wavelets based ([10]). It is not possible to cover them all here, but there is one group of methods that has had such an impact on the field of fingerprint recognition that it demands to be handled nonetheless. These are called minutiae-based methods ([11]). The word minutia means small, or trivial, detail and the methods are based on locating a number of such details in the fingerprint image. There is a very large number of different minutiae-types that has been identified, but the methods most often limit themselves to ridge endings and ridge bifurcations (Figure 2). In short, the methods are based on the location of ridge endings and ridge bifurcations in a binary image, and a subsequent matching of the point pattern defined by the extracted minutiae points.

![Figure 2. The image on the left shows a ridge-bifurcation and the image on the right shows a ridge ending](image)

For the identification system there are considerations to make in addition to those of fingerprint matching. When matching occurs between one sample and one, or a few, templates the search space is very small. But when a sample is compared to every template in an entire database, this space is much too large to browse through quickly, and it needs to be reduced. Reduction of search space can be done by fingerprint classification. An overview of fingerprint classification techniques is given in [3]. The classifier is divided into two parts, the classifier and the feature extractor. The feature extractor generates a criterion matrix upon which the classifier acts by classifying the feature set into one of the predetermined fingerprint classes. These classes are arch, tented arch, whorl, left loop and right loop. Examples of images of all these classes are given in [1]. Fingerprint classification does not identify fingerprints uniquely, but reduces the number of comparisons made. Once this has been done, fingerprint matching is performed on the smaller search space.
3 Pattern Recognition

If biometrics was the new way of authenticating an identity, then Pattern Recognition is the new way of seeing, hearing, touching and tasting. In this sense, working with pattern recognition is a daunting and disconsolate task. The human pattern recognition system is superior to all machine-based systems. No matter if the patterns come in the form of sounds, images or pressure no computer can even come close to the performance of the human senses. Coupled with the fact that the human senses can recognise all these types of patterns you have to ask yourself: Why do so many researchers pursue this field? Is pattern recognition even worth the computing time it takes? The answer, of course, depends on whom you ask, but there are certain areas in which pattern recognition is an invaluable tool. Consider, as an example, the Physical Access Control application mentioned above. If a pattern recognition system is located at each entrance, verifying the identity of the user we would eliminate the risk of fake or stolen keys, but we would also eliminate the need for a security guard to some extent. It is of course naive to think that the pattern recognition system would replace the security guard altogether, but it would certainly alleviate his work burden or at least refocus it to other tasks. But how is this possible? What type of system is needed in order to perform this task? The outline of a pattern recognition system together with examples from the minutiae method presented in [1] is presented in Italics below.

3.1 Features, Feature Vectors and Feature Space

Before the design of a pattern recognition system is considered, it is necessary to introduce and explain the terms features, feature vectors and feature space. For a pattern recognition system to be able to determine the class of the pattern it analyses, it needs measures. These measures are called features, and they are generally grouped together to form feature vectors. A feature vector with L features has the form

\[ X = [x_1, x_2, \ldots, x_L] \]

Examples of features are sample mean and sample variance of the signal, giving a 2-dimensional feature vector, with \( X = [x_1, x_2] = [\mu, \sigma] \).

The number of features used gives the dimension of feature space. Two features give a two-dimensional (planar) feature space, while eight features give an eight-dimensional space in which to set the decision boundary. In the two-dimensional case it is easy to visualise feature space, and the decision boundary (figure 3). This boundary says that if the analysed pattern is on one side the pattern it should be classified as A and if it is on the other side it should be classified as B. It does not, however, mean that the decision is correct. It is just a decision saying that this pattern is more likely to belong to this class than any other. If this turns out to be incorrect, a misclassification has occurred.
To give a simple example from a minutiae-based fingerprint recognition method, we consider the task of determining if the image point \((x,y)\) is a minutia or not. Feature generation in this case is only a matter of calculating the area around the image point, thus we have one feature per pixel, giving a one-dimensional feature space with feature vector:

\[
X = [\text{area around point } (x,y)]
\]

The exact manner in which this feature is generated is considered below.

![Figure 3. Points in the two-dimensional feature space along with the decision boundary and the class belongings.](image)

### 3.2 Pattern Recognition Systems

No pattern recognition system will have exactly the same design as the other, but there are still some main parts that are general to most, if not all, systems. This particular description of the Pattern Recognition System is based on a combination of descriptions taken from [7] and [8]. Figure 4 shows an overview of the design stages in the development of a pattern recognition system.

![Figure 4. Overview of the design stages for a Pattern Recognition System. The Arrows correspond to the flow of information.](image)

#### 3.2.1 Sensing/Data Collection

The input to the pattern recognition system comes in the form of patterns. These are captured using some sort of sensor such as a camera or a microphone. It is necessary to collect a large set of example patterns to be able to assure good performance of the system. When considering the fingerprint recognition application there are three major groups of sensors, namely optical, capacitive and pressure sensors. While the optical sensors are based on the principal of total internal reflection [1], the capacitive sensors are based on the difference in
capacitance between the ridges and the valleys in the fingerprint [12]. Pressure sensors work by measuring the difference in pressure between areas of the sensor.

3.2.2 Feature Generation

Feature generation can be divided into two major categories: Application Independent and Application Dependent. The first approach uses no, or very few, facts about the application at hand, whereas the second uses as much a priori knowledge as possible to be able to improve classifier performance. Since most systems are designed for one, or a group of, specific applications most systems are application dependent. Such systems are, however, based on the methods from the application independent techniques, with limitations and adaptations to the current application. Regardless of the approach taken, feature extraction is a procedure that computes new variables that in one way or the other originate from the analysed pattern. In [7] is stated that “The goal is to generate features that exhibit high information packing properties, from the class separability point of view”.

One major class of feature generation techniques is the linear transforms. These transforms the input signal, and if the transform is properly chosen, the features thus created can exhibit the desired properties (i.e. information packing), which will lead to a reduction of the feature space dimensionality. Considering an image it is obvious that the pixels have a large degree of correlation, which results in information redundancy. By transforming the image using the Discrete Fourier Transform, it turns out that most of the energy lies in the low-frequency components. This enables information packing by removing the high-frequency components because of their low energy content. The Discrete Fourier Transform is only an example of a linear transform that has information packing properties. Others include the Karhunen-Loève Transform, the Discrete Time Wavelet Transform and the Discrete Cosine Transform. The feature generation properties of these transformed are covered in detail in [7]. All linear transforms are application independent, although all transforms will not give equally good results for all applications.

When considering application dependent feature generation approaches, the most interesting application to look at, in this case, is image analysis. The data in image analysis is two-dimensional, consisting of an MxN pixels image. Using all MxN pixel intensities I(x,y) will result in a very large number of features even for a small image. It is therefore necessary to generate features that are fewer in number than the raw data, yet exhibit discriminative properties. Examples are edge length, region area, grey level variance and geometric moments. A full discussion of such properties is beyond the scope of this paper but can be found in [6] and [7].

As stated above, there is but a single feature when determining if an image point is a minutia or not. This may be misleading in the way that the problem seems easy to solve. It isn’t. There are lots of problems in detecting minutiae, of which low-quality fingerprint images is among the hardest to solve. Let alone the problems, the feature generation is trivial, and only a matter of calculating the area around an image point (x,y) in an ideal thinned ridge map. This ridge map, also known as a skeleton image, is the binary image in which the width of the ridges is one pixel (figure 5).
3.2.3 Feature Selection

This part of the system is sometimes incorporated into the feature generation, but is of enough importance to be handled separately. To be able to answer the question “What is the best number of features to use?” it is necessary to determine which of the features are most important to the classification problem at hand. This results in the selection of the L “best” features from the feature generation part of the system. As with feature generation it is very often necessary to use knowledge about the problem at hand to be able to perform it adequately. Selection, which should be based on combinations rather than individual features should ensure large inter-class distance and low intra-class distance, meaning that the features should be close together within one class and far apart between classes. Although the selection must be based on the current application there are a few basic operations that can be performed regardless of the application. Examples are Outlier removal that removes data highly separated from the mean, Data Normalisation that normalises data into a given interval (e.g. [0,1]) and handling missing data. Details are covered in [7].

![Figure 5. A ridge map of a fingerprint image.](image)

In this example no feature selection in the basic sense of the word is performed, simply because no reduction of feature space dimensionality is possible. But considering the massive pre-processing work needed to ensure that the minutiae detection algorithm performs well, one can see this as feature selection in a sense. If this pre-processing, which contains skeletonising the image, bridging gaps in- and removing spikes from the ridges, was not performed, the use of the area feature would be almost totally useless.

3.2.4 Classifier Design

Having selected the appropriate features, how is the classifier designed to accommodate them? In other words, which optimality criterion is used to draw the decision boundaries in feature space? In most cases the decision boundary is not linear and it is necessary to determine what type of non-linearity it is necessary to adopt to locate the right decision surfaces.
From the feature generation and selection part of the system comes the single feature. This is fed to the classifier, the task of which is to classify the image point as minutia or non-minutia. Given the fact that the ridge map was ideal and thinned, it is straightforward to realise that the (eight connected) image point is a ridge ending if the sum of the pixel values of the eight neighbours around the point equals 1. A ridge bifurcation if the same sum is greater than 2, and a non-minutia otherwise. Since the ridge map is binary the sums will be integers. Thus the classifier sets two decision boundaries in feature space, the first between one and two and the second between two and three. This is shown in figure 6.

![](image1.png)

*Figure 6. One-dimensional feature space along with decision boundaries.*

### 3.2.5 System Evaluation

How can we assess the performance of the system? What is the error rate of the classifier? Have we generated and selected the best features? How can the system be altered, so that the error rate of the classifier is minimised? All these questions need to be answered before altering the system and starting the evaluation all over again, to enhance system performance to an optimum.

Simple Bayesian classification considers two classes, $W_1$ and $W_2$, and each of the objects can belong to any of them, but which is unknown. Minimising the error rate of such a classifier is a matter of minimising the probability of ascribing an object to class $W_1$ given that it belongs to $W_2$ and vice versa. In figure 7, a one-dimensional classifier is shown and here, the first case corresponds to the area below the area below the grey curve and to the left of the decision boundary and the other way around.

![](image2.png)

*Figure 7. Showing the probability functions of a two-class system, along with the decision boundary. On the x-axis is the value of the feature $x$, and on the y-axis is the probability of each class for each value of $x).*

In figure 7 the decision boundary is located with symmetry between the probability function giving an equal probability of misclassification for each class. In reality, however, there is often a cost associated with each
misclassification. If it is more serious to misclassify an object from class \( W_1 \) as belonging to \( W_2 \) than the other way around, the decision boundary will move to the right, thus reducing the probability of such errors. In such a system it is a matter of placing the decision boundary in such a way that the cost is minimised instead of the probability of error.

When considering the biometric application there are two types of errors as explained in section 2.2. It is, of course, more serious to have a high FAR than FRR because this grants fraudulent users unwanted access, whereas a higher FRR is just inconvenient for the users. Thus, the cost for FAR is much higher than for FRR.
4 Method Descriptions

There is no single way in which to locate the distinct features of a fingerprint image. In some methods distinct features are minutiae, while in others they are certain responses from filtering. Regardless of the approach, it is not an easy problem to solve. In this chapter, two methods designed to perform this task are described in detail. The Template Correlation Method (TCM) based on correlation with filters from a bank and the Circular Sampling Method (CSM) based on circular sampling and frequency component analysis. These are mainly feature generation methods, but they contain a classifier element in the sense that their purpose is to separate between distinct and non-distinct features.

A cyclic approach has been used (figure 8) when developing the methods. This cycle, called the Method Development Cycle or MDC, contain the steps description, implementation, test and evaluation. However, the descriptions given here are independent of this approach in such a way that all alternative solutions within the frame of the methods are covered. It is important to note that the MDC has no manual but is rather the author’s device for handling the development of the method in a structured manner.

Using a cyclic approach is not only beneficial when developing these types of methods; it is necessary. No matter of how well defined the method is in theory, practical problems will arise. The descriptions given here are the first cycle descriptions. Once these have been implemented and tested, without any of the suggested refinements, the evaluation determines in which way to head. What are the most prominent problems and which of these are possible to solve? Yet another important aspect of the cycles is the estimation of the methods potential. There can be many theoretical benefits from the method, but these may not hold in practice, or maybe it is simply a matter of the basic hypothesis not being adequate for the problem at hand. If this is the case there is no use in performing extensive testing upon the method when it can be eliminated at an early stage. More about the MDC can be found in Chapter 5 - Method Analysis and Evaluation chapter.

![Diagram](Figure 8. A schematic image of the Method Development Cycle)

4.1 Template Correlation Method

The basic idea behind this method is to locate distinct features through correlation with templates. These templates are generated by functions that in some way estimate the homogenous ridge/valley pattern of the fingerprint images. Correlation results in one feature vector for each pixel, and the task of selecting the distinct features is a matter of observing anomalies in feature-space, i.e. points that are located away from the others. This method is based on
the hypothesis that such anomalies in feature space correspond to distinct areas in the fingerprint. In other words, the method is based on the comparison of the actual fingerprint to a perfectly homogenous one defined by the templates, and the positions in which these two differ give the distinct points. The notion of perfectly homogenous in this context means a fingerprint without any singularities or distinct features. Examples of distinct regions are ridge endings and ridge bifurcations, see figure 2.

The method can be divided into five major parts
1. Locate the frequency band of interest (offline).
2. Generate the appropriate templates using selected filter function (offline)
3. Template Correlation
4. Principal Component Analysis (PCA)
5. Clustering

From the first step, which is carried out only once for the entire database, a frequency band is fed unto the next step. By sampling this band and defining functions of these frequencies, a bank of templates is created. The templates from this bank are correlated with the image and the principal components of the result are extracted via the PCA. Subsequent clustering enables classification of the points into distinct or non-distinct categories.

4.1.1 Locate the Frequency Band of Interest

This part of the method is based on the assumption that all fingerprint images have the same approximate frequency contents, but it is of course possible to compute the frequency content of each finger separately. This assumption is reasonable regarding the fact that all fingerprint images are captured using the same imaging device ([12]), always delivering images of the same size and resolution, and that all fingerprints are captured from adult subjects, thus giving approximately the same ridge/valley distance in the images. Its purpose is to locate within which frequency band most of the energy of the fingerprints in the FPC1010 database is contained. From this result it is then possible to generate the templates.

Working under the similar frequency content assumption it is possible to create a mean effect-spectrum of the images as

\[ F_{\text{mean}}(u, v) = \frac{1}{K} \sum_{i=1}^{K} | F_i(u, v)|^2 \]

where \( F_i \) is the two-dimensional Fourier transform of image \( i \) defined as

\[ F_i(u, v) = \frac{1}{MN} \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} f(m, n) e^{-2\pi i (\frac{mu}{M} + \frac{nv}{N})} \]

In figure 9 is shown an example of a typical two-dimensional frequency spectrum of a fingerprint image from the FPC1010 database. The image intensities correspond to the energy content of the frequencies. Centred in the image is a rather obvious intensity peak that, when using this definition of the Discrete Fourier Transform, corresponds to the mean grey-level in the image. As the distance from the position of this point increases so does the frequency. By calculating the Euclidean distance from the position of the mean grey-level
point in pixels, one achieves the number of periods per image extension. The angle between the line connecting a point in the frequency plane with the mean grey-level and the x-axis corresponds to the direction in the image that has given rise to this particular point. Following this it is not hard to realise that there are a number of frequencies that hold the greater part of the energy in the fingerprint. This can be seen as a ‘circle’ of higher image intensities in the spectrum. By locating this frequency band in the mean effect-spectrum, which corresponds to the ridge/valley frequencies in the image, one has located between which frequencies most of the energy is contained in the fingerprint images. A more extensive discussion on the two-dimensional Fourier Transform and its application to image processing is given in [5].

When locating the frequency band there are a few things that have to be considered. First, the removal of the mean grey-level which is the single frequency having the highest energy content. Second the removal of the image-edge artefacts. In figure 9 it is clearly seen one horizontal and one vertical line of high-intensity pixels. These are the result from the edges in the images. Both of these problems can be solved easily by setting the pixels along the centre horizontal and vertical lines to zero. The result of this can be seen in figure 10.

With the content of the spectrum ‘cleaned’ to contain only the frequencies of interest it is rather straightforward to locate the interesting frequency band. It is only a matter of calculating the Euclidean distance for all points in the spectrum and creating an energy content function of this distance. Thus, the values on the x-axis are the distance from the mean grey-level position, and the values on the y-axis is the accumulated energy content of all points located at the same distance.

The Euclidean distance for point $(u,v)$ is calculated as:

$$d_{E} = \sqrt{du^2 + dv^2}$$
where

\[
du = |u - uc| \\
dv = |v - vc|
\]

And \((u_c, v_c)\) is the position of the mean grey-level.

The energy content function is calculated as

\[
E(d_g) = \sum_{V(u,v)} F_{mean}(u, v)
\]

where \(d_E = d_{Ec}\) (i.e. a constant Euclidean distance)

A plot of the energy content function is shown in figure 10. The global maximum of the function gives the value of the most commonly occurring frequency in the fingerprint images. From here it is only a matter of choosing the fraction of the total energy that should be contained within the frequency band. This choice results in the upper and lower limits \([W_{min}, W_{max}]\), which defines the frequency band. The frequency centred in this band is the centre frequency \(W_c\) which corresponds to the most commonly occurring frequency of the fingerprint images in the database.

![Figure 10. Shows the distribution of the energy in the accumulated spectra as a function of distance from the DC-level. No normalisation has been performed. With \(W_c = 41.5\), \(W_{min} = 26\) and \(W_{max} = 57\) the frequency band contains approximately 70% of the total energy in the spectrum.](image)

4.1.2 Generate the Appropriate Templates Using Selected Filter Functions

Once the frequency band has been identified it is possible to generate the templates. As stated above, these templates should in some manner represent a completely perfect version of the fingerprint image, in the sense that it contains no anomalies. One basic assumption regarding the functions is that they are periodic, and therefore the choice is not arbitrary. As with the location of the frequency band, this step is performed only once and the result is used as a base for the correlation.
The templates are defined as

\[ h_{i,j} = f_i \left( W_j \right) \]

where \( W_j \) are samples within the frequency band \([W_{\text{min}}, W_{\text{max}}], j = 1...M\)

\( f_i \) is the \( i \)th filter function, \( i = 1...L \)

Giving \( M \times L \) templates if only one orientation, \( \theta \), is considered. This is not realistic, since there are no fingerprint images containing only one orientation. Therefore each of the templates, \( h_{i,j} \), is defined for \( K \) orientations, giving a total of \( N = M \times K \times L \) templates. \( M \) is the number of samples within the frequency band, \( K \) is the number of orientations and \( L \) is the number of filter functions. For instance if \( h_{ij} = \cos(W_j) \) and \( h_{ij} = \sin(W_j) \), \( L = 2 \) and if eight orientations and eight frequencies are used the number of templates \( N = 8 \times 8 \times 2 = 128 \).

The result of the generation is stored in a three dimensional array with the orientations along the x-axis, the frequencies along the y-axis and filter functions along the z-axis. Thanks to their simplicity it is certainly possible to generate the templates, one by one, as an on-line process. Saving memory at the expense of a slight increase in execution time. A schematic image of the filterbank can be seen in figure 11.

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\[ \text{Figure 11. Schematic image of the filterbank, showing the way in which the templates are stored} \]

4.1.3 Template Correlation

Correlating the fingerprint images with the templates generated in the previous step constitute the feature generation of this method. Discrete two-dimensional correlation, also called convolution, of an image \( f(x,y) \) and another two-dimensional signal \( g(x) \) is defined as:
\[ f_s(x, y) = f \otimes g_s = \sum_{j=1}^{P} \sum_{k=1}^{Q} f(x, y) g_s(x - j\Delta x, y - k\Delta y) \]

where \( \Delta x \) and \( \Delta y \) are the sampling periods in the x and y directions, while \( P \) and \( Q \) are the image dimensions, in pixels, in the x and the y directions.

In the positions where the result from correlation is high there is a good match, or similarity, between the image and the other signal, in this case the template. Since the templates represent the homogenous areas of the fingerprint, there should be a lower match for the regions that do not exhibit homogenous properties, i.e. distinct areas.

Correlation is performed between all the templates in the bank and the fingerprint, resulting in one feature vector for each pixel in the fingerprint image. The dimension of feature space thus equals the number of templates, \( N \), if no post-processing is considered. As stated in the above example, this can be as high as 128. If simple post-processing is performed, by accumulating the results in either frequency or orientation, the dimension is reduced by a factor \( L \) or \( M \). There is an obvious advantage in reducing feature space dimensionality, but which way is preferable? Accumulating over frequency implicitly states that the distinct areas are distinct regardless of the template function frequency, and accumulating over orientation states that the distinct areas are distinct regardless of the orientation of the template. While the first assumption may be true, the second definitely is. Distinct regions of the image should be independent of the image rotation. But of which have been tested but the details of the first approach are given below.

For each orientation the image \( f(x, y) \) is correlated with each filter function \( h_i \)

\[ S_{ij}(x, y) = f \otimes h_{ij} \]

where \( S_{ij}(x, y) \) is the correlation result for frequency \( j \) and filter function \( i \). These results are squared and summed, giving

\[ S = \sum S_{ij}(x, y)^2 \]

Which is a frequency-accumulated correlation result for each of the \( K \) directions. Thus, for each pixel is generated a \( K \)-dimensional feature vector. The result from correlation with eight vertical filters, along with the fingerprint image, is shown in figure 12. The image intensities correspond to the correlation result. It is clearly seen that areas in fingerprint that have a vertically oriented ridge/valley pattern yield the highest correlation results, which is to expect since they should match the selected templates the best. More details on correlation and matching are given in [5] and [18].

4.1.4 Principal Component Analysis

Regardless of the manner in which the correlation result is handled in the former step, the dimension of feature space will be high. As an example can be said, that when the result is accumulated over frequencies and eight directions are used when generating the templates, feature space will be eight-
dimensional. This is not possible to visualise with ordinary methods and furthermore, the decision boundaries in eight dimensions tend to be very complex. To reduce the dimensionality of feature space, it is possible to perform what is known as Principal Component Analysis, or PCA. This is basically a projection of the high-dimensional data unto a lower-dimensional space defined by the axes corresponding to the directions in which the original data exhibit maximum variation. Details of the PCA are given in [14]. In this application the goal of the PCA is to reduce dimensionality to two so that the results can be easily represented on the screen to enable evaluation.

4.1.5 Clustering

This is the classifier part of the system and should be able to group together distinct points and non-distinct points into different clusters. It would be possible, in theory, to implement a clustering algorithm on the data directly from the template correlation, but this would be very complex because of its high dimensionality. Once the PCA has been performed on the data, the task of clustering becomes much easier, provided that the data is grouped together properly in feature space.

4.2 Circular Sampling Method

This method is based on the assumption that when viewing the image intensities of a region in a fingerprint image along circles with properly selected radii, there will be a difference in frequency content between the distinct and the non-distinct regions. Although circular sampling has not been used in this exact manner, one example in which it is used as a texture analysis tool for Brodatz textures is presented in [17].

The basic hypothesis for this method states that the third frequency component, $C_3$, is of greater magnitude than the second, $C_2$, when a distinct region is considered. This criterion, called the $C_2C_3$ criterion, is supposed to hold for distinct regions alone. Consider figures 12 to 14. In figure 13 two regions
selected based on their apparent distinct and non-distinct properties have been circularly sampled. Intensity functions from this are shown in figure 14, and here it is clear that there is a difference in frequency content where the left plot holds three periods when the right holds only two. A more exact way of analysing frequency content is given by the Fourier Transform, and the result of this applied to the intensity functions are given in figure 15. Here it is clear that the third component is of greater magnitude than the second in the left figure and the opposite holds for the right figure. This supports the basic hypothesis although it is in no way conclusive.

Even though the $C_3C_2$ criterion is the basic hypothesis, the method is more general than this and can be used to evaluate the frequency content in any other manner as well. In this method, feature generation occurs in the frequency domain, and results in what is called a frequency signature for each sampling position. The manner in which this is performed eliminates all rotational effects when determining if a region is distinct or non-distinct, which is a very desirable attribute for any feature generation method. In figure 13 are shown regions along with sampling positions and one circle along which sampling is performed. It shows certain properties of the basic hypothesis, such as where sampling should occur and which approximate radius is suitable. For the basic hypothesis it is appropriate to select the sampling positions along valley bottoms in the way it is exemplified in figure 13.

The method can be divided into four main steps
1. Selection of sampling locations
2. Circular sampling
3. Discrete Fourier Transform
4. Frequency Component Analysis

The selected sampling positions are fed to the circular sampling step, in which sampling occurs along a number of radii, giving an intensity function along each of the circles. This function is transformed using the Discrete Fourier Transform, and the frequency signature is extracted from the spectrum. Analysing the frequency signature with regard to the $C_3C_2$ criterion determines the class of the region.

![Image](image.png)

*Figure 13. In the image on the left a valley bifurcation is shown along with an appropriate circle along which sampling can occur, while in the figure on the right a homogenous valley is shown. The white dot, almost invisible in the right image, is the sampling location or centre of the circle.*

4.2.1 Selection of sampling locations

Selection of sampling locations can be performed in several ways, of which the most straightforward is to sample in every image pixel. Given that the image dimension is $M \times N$ pixels, this will result in $M \times N$ sampling locations, which is
often a very large number (in the case of the FPC1010 database the number of sampling locations would be 30400 for each image). To reduce this number, other more refined selection methods can be used. Following the basic hypothesis sampling locations should be located along valley bottoms. This can be achieved by sampling along a skeleton image of the fingerprint (figure 3). Examples of properly chosen sampling positions according to this method are shown in figure 13.

Yet another approach, which strays somewhat from the basic hypothesis, is to select sampling locations as the regions of the image that does not contain one single dominant orientation. This eliminates areas of homogenous ridge/valley patterns from sampling, since these do not fulfil this criterion. Reducing the number of sampling locations will reduce execution time significantly, but there are risks in doing so. The most prominent is that the selection fails in some respect and eliminates distinct regions from the sampling locations, which will result in deterioration of method performance. Advantages and disadvantages of all these approaches as well as test results from them will be presented in Chapter 5 - Method Analysis and Evaluation.

4.2.2 Circular Sampling

Once the sampling locations have been selected the region around these points is sampled circularly along a number of circles. This sampling, which may be considered sampling in a polar co-ordinate space ([13]), results in one intensity function, \( g[k] \), for each radius. While in the end application of the method there should be only one radius, the need for a higher number will be necessary in method evaluation.

In practice the regions that are centred on the sampling location are scaled by a factor \( S \), using the appropriate interpolation technique, and the \( K \) radii are defined in this co-ordinate system. Re-sampling is performed to minimise artefacts such as jagged intensity functions that is the result of a too low resolution. The sampling locations \((x_i, y_i)\) along the circles defined by these radii are defined as

\[
\begin{align*}
x &= O_j + r_i \cos(\phi_k) \\
y &= O_j + r_i \sin(\phi_k)
\end{align*}
\]

where \( O_j \) is the centre point of region \( j \), \( r_i \) is the \( i \)th radius, \( i = 1...K \), and \( \phi_k \) is the angle from the horizontal axis in a clockwise direction, \( k = 1...N_p \).

Since the circle begins and ends in adjacent image points, the function resulting from this sampling is periodic with \( N_p \) samples. The number \( N_p \) should be large enough to ensure that the information contained in the sampling result enables adequate frequency analysis. The intensity function \( g[k] \) is the sampling of the image function \( I(x, y) \) in positions \((x_i, y_i)\).

\[
g[k] = I(x_i, y_i) = I(O_j + r_i \cos(\phi_k), O_j + r_i \sin(\phi_k))
\]
Intensity functions from circular sampling of the regions in figure 13 are given in figure 14. Each of these corresponds to one sampling position and one circle for each position.

![Intensity functions from circular sampling](image)

*Figure 14. The image on the left is the intensity function achieved through circular sampling of the valley-bifurcation from figure 13 and the figure on the right corresponds to the homogenous valley in the same figure. On the x-axis is the angle and on the y-axis is the pixel intensities along the circle.*

It is not hard to realise that this method relies heavily on the proper selection of radius, and although the proper radius will differ depending on the area of the image in which sampling occurs, there are a few basic considerations. First, the circle defined by the radius should encompass only one single ridge or valley, since one distinct region pertain to one ridge or valley. Second, the radius should be large enough for the circle to encompass all different types of distinct regions. Whether it is possible for single radius to fulfil these considerations, or if radius adaptation to the local neighbourhood is necessary, will be considered in Chapter 5 - Method Analysis and Evaluation.

### 4.2.3 Discrete Fourier Transform

Features are generated from the data collected in the previous step by creating one frequency spectra for each intensity function through the one-dimensional Discrete Fourier Transform

\[
X_k = \sum_{n=0}^{N-1} x[n] e^{-\frac{2\pi i k}{N}}
\]

where \(N\) is the number of samples in the discrete signal \(x[n]\) and \(k\) denotes the discrete points in the frequency domain. The Discrete Fourier Transform of \(g[k]\) is thus given

\[
G_k = \mathcal{F}[g[k]]
\]

where \(\mathcal{F}\) denotes the Discrete Fourier Transform operation and \(k\) is the number of the frequency in the spectra, \(k = 0, \ldots, N_\phi - 1\). The frequencies, \(\omega_k\), corresponding to the \(k\)-values are given by

\[
\omega_k = \frac{2\pi k}{N_\phi}
\]

which is a result of the Discrete Fourier Transform property always being periodic with \(2\pi (\{6\})\).
So, for each sampling location and radius, one feature vector of dimension $N_\phi$ is generated. The first ten coefficients of the feature vectors, or frequency spectra, of the intensity functions from figure 14 are given in figure 15. On the y-axis the logarithm of the absolute value is given since it gives a clearer result in visualisation.

![Figure 15. Showing the logarithm of the absolute value of the first ten coefficients of the one-dimensional Fourier transform of the intensity functions in figure 14, left and right. On the x-axis is the number of frequency components and on the y-axis is the magnitude of the corresponding components.](image)

### 4.2.4 Frequency Component Analysis

Feature generation by Discrete Fourier Transform gives a feature vector of the same dimension as the length of the signal it transforms. Needless to say, this number may be very high in this application, and feature selection will be necessary. From the $C_3C_2$ criterion it is obvious that at least these two frequency components should be selected, but selecting them alone will limit the information content significantly. Starting from the mean grey-level of the frequency spectra it is assumed that neither this or the first component holds any information about the distinctness of the area. On the other end are the higher-frequency components that correspond to fast fluctuations in the image. Most of these are not interesting, since they are the result of noise, but there are those that still may hold relevant information. In light of this, the feature selection also considers the fourth and fifth overtone of the spectra. Thus the feature vectors have the form

$$\mathbf{X} = [C_2 \ C_3 \ C_4 \ C_5]$$

The basic hypothesis states that the $C_3C_2$ criterion should hold for all distinct regions in the image, but what other criteria may be considered, using the information present in the frequency signatures? Such criteria include, but are of course not limited to, thresholding the value of $C_3$ against a fraction of its maximum value, and inferring other relationships such as $C_4 > C_3$ and $C_5 > C_3$. All this is a matter of classifier design, i.e. determining the decision boundaries in feature space. Since all criteria are simple comparisons all the boundaries will, in this case, be linear in four dimensions. Each criterion is also independent of the others and can therefore be considered by itself. The two-dimensional feature space when only features $C_2$ and $C_3$ have been extracted, along with the decision boundary given by the $C_3C_2$ criterion are shown in figure 16. Further discussion of these additional criteria is held in the Method Analysis and Evaluation section.
Figure 16. Showing the magnitude of the logarithm of the second frequency component on the x-axis and the third frequency component on the y-axis. The diagonal line is the decision boundary resulting from the $C_2^3C_2$ criterion. The points placed below and to the right of the decision boundary are classified as non-distinct and vice versa.
5 Method Analysis and Evaluation

Both the Template Correlation Method and Circular Sampling Method are based on basic hypotheses about certain characteristics of the distinct regions in the image. By using the cyclic approach of the MDC, these hypotheses are put to test regarding the potential of the methods as well as their performance. Using the method descriptions as a base, the methods where implemented in MATLAB and tested on the FPC1010 database collected by Fingerprint Cards AB, containing 880 fingerprints from 110 different fingers. The fingerprints in the database have been collected by capturing the index finger, middle finger, and ring finger of each hand and person. All three fingers are captured at the same time in the order left, left, and left repeatedly, until eight images of each finger have been captured. Alternating the fingers in this manner eliminates the risk of the subject fixing the hand for all eight captures and just moving the finger, which will result in an unnaturally small translation between the images. Once all eight images of each finger have been captured for one hand, the same procedure is repeated for the other.

No optimisation has been performed with regard to execution time. If there are obvious ways in which the complexity of the method can be reduced these are noted, but not elaborated upon. The format of the test description will be based on the design of the Method Development Cycle.

A note on pre-processing:
The images in the raw data part of FPC1010 have not been pre-processed whatsoever. Before performing any test described in this chapter all images are subject to local mean shifting and linear stretching with the purpose of normalising the images.

5.1 The Method Development Cycle

While using an iterative approach when developing these methods has been absolutely necessary, putting a name to and defining the steps of, the model is nothing more than a matter of structuring. A clear structure not only enables a way of thinking in development, it also simplifies the explanation to those not so involved. This is the only reason for its occurrence here. By arranging each test for each method in the same way as the MDC, it is easy to locate and compare the results. The main steps of the MDC and the general contents of these are the same for all tests, although the details will differ. The main steps of the MDC, explained below, are also depicted in figure 8.

5.1.1 Description

This describes what aspects of the method that have been evaluated. If there are differences from the method descriptions given above, these are explained.

5.1.2 Implementation and Test

There are three main steps in the implementation and testing part of the MDC and each of these pertain to one part of the implementation. Although this is the
closest to programming language details we get, there will be no code presented. The first step is region extraction, in which the regions to be analysed are extracted. Secondly the feature generation and selection is performed. This is the part of the test where the method is applied to the regions, generating the appropriate features. Details of this step will of course depend in which method is tested. Following the feature generation is the visualisation, in which the results from the feature generation are visualised to enable evaluation. If feature space is of low dimension (two or three), plotting the results may be feasible but if it is not, dimension reduction is necessary.

5.1.3 Evaluation

Once the features have been generated, selected and visualised they will be evaluated. This is done by inspection in most of the cases, since there is no other way of assuring performance. In this step, the potential of the method’s ability to locate distinct features in fingerprint images is determined. This potential is a matter of observing differences in feature space between distinct and non-distinct regions. If the method holds no potential it will not be subject to further testing.

5.2 Testing Regions Located by Inspection

Cycle one of the MDC is based on the simple assumption that there should be observable differences in the features generated from distinct and non-distinct regions of the image. By manually inspecting the responses of the methods to these regions it is possible to determine whether the basic criteria holds or not. Although the criteria in inspection differ for each method, the tests are similar. Selection of regions to evaluate is based on the apparent distinct/non-distinct properties of the area around the centre point. Examples of areas that exhibit distinct properties under inspection are ridge endings and ridge bifurcations (see figure 2), whereas areas that are considered non-distinct have a homogenous ridge/valley pattern.

5.2.1 Template Correlation Method

By analysing the response of the method to manually selected regions it is possible to determine if the method holds a potential of being able to distinguish between distinct and non-distinct regions. The basic hypothesis states that the distinct regions should give rise to anomalies in feature space. Since the regions are selected manually based on appearance, the conditions for testing can be considered ideal and if the method does not perform well under such conditions it is unlikely that it will under any other conditions are non-ideal.

For this method, features are generated through the correlation with templates and the result is one feature vector for each pixel in the region. Feature selection is performed as accumulation over either frequency or orientation reducing the dimension of feature space significantly. Both these approaches are evaluated in this test, determining which yields the best result. This test is performed on a small fraction of the database, since the potential can be appreciated from a small set of regions if these are selected carefully.

There are two separate parts of this test, in which differences occur in feature selection. The first part (Appendix A – TCMI) considers the method when
accumulation is performed over orientation while the second part (*Appendix B – TCM2*) considers the method when accumulation occurs over frequency. In both of these tests the number of orientations as well as the number of frequencies are eight, giving an eight-dimensional feature space.

As the offline part of the method, the location of the frequency band and the generation of templates are performed only once and as such, none of them depend on how the test is formulated. When generating the mean spectra over all 880 fingerprints in the *FPC1010* database, the images are padded with the average value of the analysed fingerprint image that is, to a size of 256x256 pixels. This is done because the *Fast Fourier Transform (FFT)* algorithm performs much faster when dealing with signal lengths that are a power of two. As already explained in the *Method Description* chapter, the mean spectra $F_{mean}(u,v)$ is used to calculate the energy content function $E(d_j)$. This function is shown in figure 10 and it can be seen that the most commonly occurring frequency, $W_c$, in the fingerprint images is about 40 periods per image extension. To be more specific, the value of $W_c$ is 41.5. By arbitrarily selecting the fraction of the total energy to be contained within the frequency band as 0.7, the interval’s upper and lower limits, $W_{min}$ and $W_{max}$, are obtained at 26 and 57 respectively.

Given the frequency band and the number of sampling positions therein, the templates for each orientation are defined as

$$h_{2j} = \cos(W_j)$$

$$h_{2j+1} = \sin(W_j)$$

where $j = 1, 2, ..., 8$, giving a total of 8x8x2=128 templates. The filterbank for $h_{2j}$ is shown in figure 17.

![Figure 17. Filterbank for filter function $h_{2j} = \cos(W_j)$](image)

Each template is correlated with the selected regions in an order depending on the feature selection. If the feature selection considers accumulation over frequency then all templates for one direction are correlated with the selected region before moving on to the next orientation. When accumulating over orientation all templates for one frequency are correlated with the image before frequency is changed.

To avoid the error that is introduced when MATLAB zero-pads the regions in template correlation, only the central parts of the regions are considered. In this
test regions are of size 16x16 pixels and the templates are of size 11x11 pixels, giving a central part, unaffected by the zero padding, of 6x6 pixels. There are thus 36, eight-dimensional, feature vectors for each region. Figure 18a and b shows the 16x16 pixel regions centred on the selected points, where a corresponds to a distinct region and b to a non-distinct. Figure 18c is the centre of the region in a, unaffected by the zero-padding and the same relationship holds for b and d. In figure 18c there is a 3x3 region of green-marked pixels centred on the singularity. The purpose of these markings is to determine how the centre of the distinct regions responds to the method. It is these pixels that correspond to the “blobs” in figure 19, and their position in feature space is important in estimating method potential, since at least the centre of the singularity should give rise to an obvious anomaly in feature space.

Regardless of which feature selection approach is used the result from correlation is eight-dimensional and dimension reduction is necessary. This is achieved through Principal Component Analysis, projecting the eight-dimensional data unto two dimensions. Given in figure 19 is one example of a comparison of the response of the method to one distinct and one non-distinct region. Several other examples along with test specifications are given in Appendix A and B. Figure 19, as well as the appendices, contain colour images and should be viewed as such.

In figure 19 the x- and y-axes correspond to the first and second axis onto which the original data is projected. The values themselves are unimportant; it is the
comparisons that are of interest. Each x in the figure corresponds to one pixel in
figure 18c, whereas the o:s correspond to figure 18d. Only one example is
given here but it illustrates the response of the method well. This specific
example has used accumulation over orientation as feature selection, but the
results are not very different when accumulation is performed over frequency.
In figure 18c and d the central parts of the analysed regions are shown, and in c
the green-marked pixels are chosen so that they are centred on the singularity.
These pixels correspond to the blob-marked PCA-values in figure 19. If the
method responds well, these blob-markers should be located well away from all
the o:s in the figure, which is not the case.

From figure 19 it is clearly seen that no groupings are present in feature space.
Not even the pixels centred on the singularity itself are located away from the
others. This gives the indication that it is not possible to perform clustering as
classification with good results. Furthermore, there are no simple decision
boundaries that can be drawn between the two classes. Now, the regions where
selected because of their perfectly distinct and non-distinct characteristics, and
if the method is not able to distinguish between them at this stage it probably
never will be. When considering the results given in Appendix A and B, there
are ambiguities in how the method responds to comparisons with similar
characteristics. In one case the method responds rather well, whereas in the next
it responds very poorly. Nonetheless, not even when the method performs well
it is able to classify the regions distinctly. There are still parts of the distinct
regions that respond equally to the method as does the non-distinct regions,
which is undesirable to say the least. Since this test was designed to determine
the potential of the method, and the method has not responded well, the method
is deemed as having low potential in classifying regions and no further testing
will be conducted. Further discussion on the potential of the method and
suggestions for alterations are given in section 6.1.

5.2.2 Circular Sampling Method

The first step in determining if this method has potential is to apply the basic
steps of the method on selected regions of the image. Manual selection of the
sampling points ensures that the selection is performed with precision only
depending on the person extracting the regions. This is very important, since it
determines how the method performs under ideal circumstances. Will the basic
hypothesis, stating that \( C_2 > C_1 \) for distinct regions, hold under these
conditions? If it does not, it will not do so when the selection of sampling
locations is performed in an automated manner. From the basic hypothesis it is
clear that the sampling locations should be chosen along valleys, or more
specifically valley bottoms. Therefore, in the test presented here, the sampling
locations have been selected according to this.

Circular sampling of the selected region along a number of circles will generate
one frequency signature for each radius. Each of these frequency signatures is in
itself a feature vector. However, in this first test only one radius is used, giving
a single feature vector for each region. The dimension of the feature vector
depends solely on the number of frequency components that are extracted,
which in turn depends on in how many points sampling occurs along each
circle. If sampling occurs in \( M \) positions along each circle, the dimension of the
feature vector is \( M \). From these \( M \) features there is a need for selecting the
“best”. But which are these? No feature selection will be performed in this test,
but the principle of it is to determine which of the frequency components that
has the highest information content. Only a small part of the database has been used in this test, since it is possible to determine if there are observable differences between distinct and non-distinct regions even then, given that the regions are carefully selected to represent the two types.

In the above description of the Template Correlation Method, we established the most commonly occurring frequency, $W_c$, as 41.5 periods per image extension. If we denote the length, in pixels, of one image side as $w$, the most commonly occurring period length can be calculated as

$$p_c = \frac{w}{W_c} = \frac{256}{41.5} = 6.2 \text{ pixels / period}$$

which gives an appreciation of the average ridge-peak to ridge-peak (or valley-bottom to valley-bottom) distance. This number is very important in the initial selection of the sampling radius. Since the test is based on the manual location of distinct and non-distinct regions, selected by identifying irregularities in individual valleys, the radius of choice should only generate information about one valley. In section 5.2.1 is also given the upper and lower limits of the frequency band as 26 and 57 fluctuations per image extension. These give a longest period of 9.8 pixels and a shortest period of 4.3 pixels. Given that the sampling locations are situated along valley-bottoms the most important consideration is that the radius should not stretch over more than one valley. Based on the shortest period within the frequency band the radius is selected as 4 pixels, and along the circle thus defined sampling occurs 128 times. The latter parameter has been selected in an ad hoc manner and is not a direct result of the sampling radius. Further discussion on the selection of radius will be held in section 5.3.

Although no feature selection has been performed, the visualisation only considers the ten first frequency components. This is more than enough, since the basic hypothesis is only concerned with the second and third. There are countless examples of regions, both distinct and non-distinct, in the database and it is not possible to present them all here. However, consider figures 12 to 14 in section 4.2, which show typical examples of feature extraction results. Several other regions along with test specifications are given in Appendix C – CSM1. An important consideration is the fact the in the definition of the frequency signature in section 4.2.4 the feature vectors contains $C_2$ to $C_4$.

In figure 15 the values on the x-axis correspond to the number of the frequency components, i.e. the 0th index corresponds to the mean-grey-level, the 1st index to the first harmonic and so on. The values on the y-axis are the logarithms of the magnitudes of these frequency components, calculated as

$$y(x) = \log(|x| + 1)$$

Selecting the logarithm is only a matter of elucidating the visualisation. From the left image in figure 15 it is clearly seen that the third frequency component is of greater magnitude than the second, thus fulfilling the $C_2C_3$-criterion, while in the right image the second component is of greater magnitude. In Appendix C the results from noise regions are shown as well, giving an indication of the noise sensitivity of the method. As expected from noise, the response is random, giving a distinct answer in one case and a non-distinct in the next.
These carefully chosen examples of regions thus promote the basic hypothesis stating that there are differences in the second and third frequency components between distinct and non-distinct regions. While this test shows that the method responds well to optimally selected regions, with regard to both position and visual characteristics, it is not conclusive. Further testing, as to the response of the method to non-optimally selected sampling locations and other conditions, are necessary to estimate the full potential of the method.

5.3 Evaluating frequency signatures over entire fingerprint images

All testing from this point on is performed using the Circular Sampling Method. At this point it is also important to distinguish between two terms: distinct point and located point. The term distinct point refers points in the images that exhibit visually distinct properties, while located point refers to points the method considers distinct, i.e. have located.

MD Cycle One indicated that, in visually distinct regions, the third frequency component of the one-dimensional Discrete Fourier Transform is of greater magnitude than the second component. The goal of the first part of this MD Cycle is to determine whether this is true over entire fingerprint images, and what other regions fall into the distinct category when the basic $C_2C_2$ criterion is used for classification. By applying the circular sampling method on all image points in the valid region of the fingerprint image, and inspecting the second and third components of the frequency spectra, this goal is achieved. The second part of the test differs from the first only in which criteria are used for classification, introducing the thresholding criteria in practice. Both parts of the test are performed on the first 7 images of the FPC1010 database.

Since this method is based on circular sampling it is not hard to realise that the result of the method depends heavily on the selection of radius. By sampling along a number of radii for each sampling location the radius dependency is evaluated. In this test the radius ranges from two to twelve pixels in steps of two pixels, giving a total of six radii.

![Figure 20. Fingerprint image along with its valid region.](image-url)
The sampling locations are all image points within the valid region, defined as

\[
X \in [r_{\text{max}} + 1, \ w_{\text{image}} - r_{\text{max}} - 1]
\]
\[
Y \in [r_{\text{max}} + 1, \ h_{\text{image}} - r_{\text{max}} - 1]
\]

where X is the column index and Y is the row index of the image matrix, \( r_{\text{max}} \) is the biggest of the K radii along which the image intensities are sampled, \( w_{\text{image}} \) and \( h_{\text{image}} \) is the image width and height, respectively (figure 20). This is simply the centre region of the image where the edges of the images are removed to ensure that sampling is not performed outside the image domain.

For each point within the valid region one frequency spectrum is generated for each radius. Using six radii generates six frequency spectra for each region, and from all of these the frequency signature is extracted.

Visualisation of the test results is not as straightforward as in the previous cycle of the MDC. For each fingerprint image there are 20691 sampling locations and for each of these there are six frequency signatures, which would result in 20691x6 plots per image. This is not convenient. Instead of using plots, the results from the classification is displayed as RGB images. In the first channel, R, the analysed image is stored giving a base for all evaluation, and in the second channel, G, the distinct points are stored. The last channel, B, is empty, and can be used for purposes such as displaying the valid region or other data. For each fingerprint image in the FPC1010 database six resulting images are achieved, one for each radius. Since RGB is used for visualisation the results are not obvious on greyscale displays and it is therefore advantageous to view the results in Appendices D and E in colour. One single figure is shown here (figure 21) whereas the rest is placed in the above mentioned appendices.

![Figure 21. From top left to bottom right the radius used for sampling increases from 2 to 12 pixels in steps of 2, giving a total of six radii. This figure corresponds to the first in Appendix D-CSM2.](image)
Part one of the test corresponds to Appendix D – CSM2, and tests the basic $C_3C_2$ hypothesis over the valid region of the fingerprint images to determine the response of the method to different areas of the fingerprint images. The test shows that the distinct points are present among the located points, but that there are lots of spurious non-distinct points as well. Some of the spurious points are the result from noise and this is hard to predict, but most are the result from sampling along improperly selected radii. Yet another problem is the fact that in the non-contact areas of the fingerprint images the result is only noise, and the behaviour of the frequency components is random. This gives rise to located points in these areas. A discussion of the response to each radius is held below.

For $R = 2$ pixels the results are merely the edges of the valley-edges which is the result when the radius does not reach across one single valley. There are few spurious points on the ridges in the image, but the advantage of this is reduced due to the fact that a large fraction of the points missing from valley-pixels are distinct. $R = 2$ is of course way too small since the circle it defines is not able to contain the singularities which the method aims to locate. $R = 4$ pixels gives an almost perfect outline of the valley-edges. There are more spurious points than $R = 2$, but there are also fewer distinct points missing. Close inspection reveals that almost all located points are located on ridges, except those that are visually distinct which are located on the valleys. This is not true in all image points but it gives the indication that sampling with $R = 4$ may perform better if sampling occurs only along valleys, which is the way the basic hypothesis is formulated.

When $R = 6$ pixels it is evident that something occurs. In $R = 2$ and $R = 4$ pixels the results where rather homogenous over the entire fingerprint, but with $R = 6$ there are significant differences depending on the valley-to-valley distance. In the areas where this distance is short the method responds well, whereas it responds worse to regions in which the distance is greater. Where the valley-to-valley distance is approximately six pixels there are fewer spurious points and the located points are clustered around the visually distinct points, while in the other regions almost every point is located. As a counterpart to the six pixels radius, $R = 8$ responds well to regions where the valley-to-valley distance is approximately eight pixels and worse when it is nearer to six pixels. The result from this radius is almost the complement of the result from $R = 6$ in the sense that it behave well in the regions where $R = 6$ behaves badly and vice versa. The relationship between $R = 10$ and $R = 12$ pixels is similar to the one between $R = 6$ and $R = 8$. Considering the ridge/valley distance in the images the last two radii are too large to be practical, and in addition to that they reduce the area of the valid region since sampling is not possible nearer the edge than the higher radius.

In order to remove the large number of spurious points present in the result from each radius, the thresholding criteria is applied. This states that for the points to be considered distinct the value of $C_3$ has to be greater than a fraction of the maximum value of $C_3$ in the entire image. Formally this criteria is defined as

$$C_3 > T \max \{C_3\}$$

where $T$ is the fraction and the $\max$ operator calculates that maximum of the argument over an entire image. In this particular test $T = 0.9$. To clarify, this criterion states that for the points to be considered distinct the value of its third frequency component has to be greater than 90% of the maximum third
component over the entire image. Selection of $T$ in this criterion is based on observing the results from a small number of tests with different values, it is thus not optimised in any manner.

Apart from this criterion there are no differences in the implementation from the test described above. This criterion is added to remove the result from noise but it will not have a very big impact on those points that are located due to improper radius selection. An example of a result from this test is given in figure 22, whereas the rest of the results are given in Appendix E.

The additional criterion yielded the expected result. It removes the weak located points that are the responses to non-contact areas and noise, but little or nothing else. For $R = 4$ the result has not improved significantly. There are fewer spurious points, but as a side effect there are quite a few distinct points that have been removed from the response. In this test the complementary characteristics of $R = 6$ and $R = 8$ pixels is even more evident than in the former, as is it for $R = 10$ and 12.

![Figure 22](image)

*Figure 22. From top left to bottom right the radius used for sampling increases from 2 to 12 pixels in steps of 2, giving a total of six radii. This figure corresponds to the first in Appendix E-CSM2, which differs from appendix D only in the addition of the thresholding criterion.*

Conclusions from this test are twofold. First, the response of the method over entire fingerprint images is highly radius dependent, and will yield different results in different regions depending on the ridge/valley distance. There are basically two problems regarding the radii selection. The first is the too-small-radius problem (figure 23a) and the second is the too-big-radius problem (figure 23b).
Careful observation of the results has indicated that the radius should be adapted to the local neighbourhood in such a way that the radius is approximately the same as the valley-to-valley distance in the region.

Second, the number of spurious points is too high. It is of utter importance to reduce this number greatly. Adapting the radius to the local neighbourhood can solve a part of this problem, but not all. An efficient way of reducing the number of located points is the selection of sampling points in some manner. Doing so not only reduces the number of located points but it also reduces the execution time since fewer samplings are performed. Although other approaches, such as adding further criteria may improve results, this is the natural and probably most powerful continuation in the removal of spurious points.

While this may be to soon to conclude at this point, the selection of radius points toward selecting a radius of four or six pixels. Depending on the manner in which sampling points selection is performed, the radius should be either of these, at least as a first approximation of a proper radius.

### 5.4 Selection of sampling locations

The primary path to the reduction of spurious points indicated in the previous cycle of the MDC was the selection of sampling points. Results from the selection will be twofold since it also reduces execution time. Striving for both these goals but most importantly the former, this test will evaluate two ways in which selection of sampling points can be performed. By sampling along a Skeleton Image the basic hypothesis is followed. This is the first approach. The second does not follow the basic hypothesis with regard to selection, but rather the assumption that no distinct regions are located in regions where there is one single dominant direction. The key to the second approach is Orientation Histograms. Thus, there are two parts of this MD Cycle, one corresponding to each approach. Both tests are performed on the entire FPC1010 database, but the observations are based on a subset of the database. Evaluation of each approach will be presented as well as a conclusion regarding the selection of sampling points in general and suggestions of how to improve this important step of the Circular Sampling Method.

The analysis is twofold, the first part analyses the number of sampling locations and located points by the different approaches, while the second is an observation of images showing the results. Analysing the number of located...
points may seem futile, but it is of importance. If the located points are considered containing all distinct points in an image regardless of the number of located points then the lower the number, the better the response of the method. This is, of course, only true to a certain extent since there may be too few located points. Assuming this is not quite realistic, since there will always be distinct points missing from those located, but it is a base for the analysis of the number of located points. Coupling this analysis with an observation part will improve the certainty of the results, and hopefully support the above assumption.

5.4.1 Skeleton Image

By applying morphological skeletonisation to the binarised fingerprint image, all lines are reduced to one pixel in width, but no objects are broken apart. What remain are the sampling locations. Sampling along this skeleton image eliminates all spurious points stemming from sampling in ridges of the fingerprint. It also removes all points that are located along valley-edges, since these will not be present after skeletonisation. More details on mathematical morphology are found in [5]. In figure 5, section 3.2.2, is shown an example of a skeleton image. When using this way selecting points, sampling should occur in all image points with an intensity of one.

Sampling occurs with a radius of four pixels using the \( C_2C_2 \) and the thresholding criterion with \( T = 0.9 \). Selecting the radius to four pixels is based on the observations of the previous test that most distinct regions along valley bottoms where located using this value. Although the latter has shown a tendency to remove some of the distinct points its advantages in removing responses from noisy regions is more significant. This is especially important in the non-contact regions of the image. An important note is that skeletonisation is only performed in the valid region of the image.

Visualisation of this test is divided into two parts. One for visualising the numerical data, i.e. the number of distinct points as well as the number of sampling locations, and one for visualising the images used for observational analysis. The latter is performed in exactly the same manner as in the previous test with the difference that the results are not given here nor in an appendix, only the conclusions. The numerical data is given in figure 24 as a histogram of

![Histogram of sampling locations](image)

*Figure 24. Shows the histogram of the number of sampling locations when sampling along the skeleton image. On the x-axis is the number of sampling locations and on the y-axis is the number of fingerprint images in which this number of sampling locations have been selected.*
the number of sampling locations whereas figure 25 shows the histogram of the number of located points. Each of these images shows the results from tests performed on the entire FPC1010 database.

The number of sampling locations reaches from 3566 to 6204, with a mean value of 4720. Comparing these numbers to the total number of pixels in the valid region, which is 27264, shows that the reduction of sampling locations is significant. While it may seem odd that there are so big differences in the numbers, it is actually quite natural since the shorter the valley-to-valley distance in the image, the more sampling locations. But the higher numbers do not only stem from short inter-valley distance, but also from noise in the image, and scars and marks on the finger. Since the binarisation is performed with one single global threshold, all pixel intensities superseding the mean of the entire image will be present before morphological operations are applied and thus give rise to sampling locations.

The number of sampling locations may not be so interesting to consider on their own, but once they are put in relation to the number of located points their significance increases dramatically. The number of located points reach from 79 to 686, with a mean value of 282. The method classifies from 1.76 to 12.1 percent of the sampling locations as distinct with a mean value of 5.85 percent. An interesting comparison that is possible to determine the quality of the selection, would be to sample in all image pixels and determine how big fraction of these points that are classified as distinct.

Coupling the numerical analysis from above with the observation of images showing the results, it is clear that even though the number of spurious points is reduced significantly using this method, it is still too high. Most of the spurious points stem from either noise or the improper selection of radius as described above. The most prominent being the too-big-radius problem, which is evident in regions where the valley-to-valley distances are short. Yet another observation is that the method responds well to images of good quality and bad to images of poor quality, which is to expect. This indicates that the method is noise sensitive and that this sensitivity has to be decreased. Some of the images that have a comparably low number of located points contain large non-contact areas, which will result in very few located points, if any.

![Histogram of the number of located points when sampling along the skeleton image.](image)

Figure 25. Histogram of the number of located points when sampling along the skeleton image.
Considering the assumption stated above that all distinct points are contained within the located points, together with the observation, one can conclude that we are facing a problem of removing spurious located points rather than locating more distinct points. A note on the assumption is that although most distinct points are contained within the located points there are some missing, telling us that the criteria may not be optimally selected.

From the result, two ways of reducing the number of sampling locations are evident.
1. Eliminate homogenous problem regions from sampling
2. Adapt the radius to the local neighbourhood

The first approach results in further reduction of sampling locations and located points by removing regions of homogenous ridge/valley pattern that result in located points due to improper radius. Such regions should not be selected for sampling since they contain no distinctness information. Using the second approach alters the result from sampling in such a way that there are fewer located points, but does nothing to reduce the number of sampling locations. Adapting the radius to the local neighbourhood should remove the response from improperly selected radii.

5.4.2 Orientation Histograms

While sampling along a skeleton image removes the majority of the spurious points, it may be a too restrictive way of selecting sampling points selection since it limits the sampling to occur only along valley bottoms. This approach is based on the assumption that no distinct regions are located in areas of the image where there is only one single dominant orientation. Regions in which there is one single dominant direction correspond to homogenous ridge/valley patterns, whereas regions in which there is no single dominant orientation corresponds to interesting regions, for instance valley-bifurcations. To be able to determine the orientation characteristics of image regions, we introduce the notion of orientation histograms. Orientation histograms have been applied to Hand Gesture Recognition [15], [16], and although in both those cases it was used as a feature generation technique there are similarities.

First, the vertical and horizontal gradients over the entire fingerprint image $I(x,y)$ are estimated using 5x5 Sobel filters, giving a gradient image $\nabla I(x,y)$ for each of these. Using 5x5 filters gives a more detailed and noise-resistant response than the ordinary 3x3 filters most commonly used. These are defined as

$$S_x = \begin{bmatrix} -1 & -2 & 0 & 2 & 1 \\ -4 & -8 & 0 & 8 & 4 \\ -6 & -12 & 0 & 12 & 6 \\ -4 & -8 & 0 & 8 & 4 \\ -1 & -2 & 0 & 2 & 1 \end{bmatrix} \quad S_y = \begin{bmatrix} 1 & 4 & 6 & 4 & 1 \\ -2 & 8 & 12 & 8 & 2 \\ 0 & 0 & 0 & 0 & 0 \\ -2 & -8 & -12 & -8 & -2 \\ -1 & -4 & -6 & -4 & -1 \end{bmatrix}$$

where $S_x$ is used to estimate the horizontal gradient, $\nabla X_{ij}$, and $S_y$ the vertical gradient, $\nabla Y_{ij}$.
The gradient image is divided into blocks of 12x12 pixels and the orientation in pixel \((i,j)\) in the block is calculated as

\[
\varphi_{ij} = \tan^{-1}\left(\frac{\nabla Y_{i,j}}{\nabla X_{i,j}}\right)
\]

where \(\nabla Y_{i,j}\) and \(\nabla X_{i,j}\) are the vertical and horizontal gradient estimates in pixel \((i,j)\) respectively. Selecting the region size as 12x12 pixels is a matter of observing the size of singularities and choosing the parameter in such a way that most singularities are contained within one single region.

Each of these angles are categorised into category \(C_i, i = 0, 1, ..., 15\) each corresponding to a \(\pi/16\) interval in the upper half plane.

If these angle categories where used directly to calculated the orientation histograms, there would be a problem with low magnitude gradients in both X and Y directions. Such regions are the response from noise, and are thus removed. Once the pixels with small gradient magnitudes have been removed, the orientation histogram for each block is calculated by counting the number of occurrences for each category.

To determine if a region should be used as sampling locations, it is necessary to somehow determine if there exists one dominant direction or not. The most straightforward way of doing this is simply to compare the most commonly occurring category to the second most dominant, and threshold the quotient between them. This is an oversimplification and will not work well, since there are regions that contain many occurrences two adjacent orientations. Such regions will, using the simple approach, be used as sampling locations but most often they are the results from homogenous ridge/valley patterns that are not perfect and thus contain more than one orientation. A more general approach is used here. Base functions, or base histograms, are generated from a set of training histograms and each sample histogram is expressed as a linear combination of these.

The training set is manually collected as orientation histograms of a selection of visually distinct regions from images in the database. These histograms are normalised so that the most commonly occurring orientation is shifted to the first position in the histogram, using wrap-around for those indices that are negative after shifting. Figure 26 shows one orientation histogram and the normalised version of the same.

![Figure 26 - One orientation histogram of a single block and the normalised version of the same. The normalised histogram is plotted with a dashed line.](image)
From the training set, in this test containing 504 normalised orientation histograms of manually selected regions, a number of base functions is generated through Principal Component Analysis. These base functions are

\[
\Phi_i = [\varphi_1, \varphi_2, \ldots \varphi_{16}]
\]

where \(i = 1, 2, \ldots 16\) and each of the elements of the base functions correspond to one orientation category. \(\Phi_1\) corresponds to the axis of maximum variation \(\Phi_2\) to the axis of maximum variation given that it is uncorrelated to \(\Phi_1\). The base functions \(\Phi_1\) and \(\Phi_2\) are shown in figure 27.

![Figure 27. \(\Phi_1\) and \(\Phi_2\). The dashed line corresponds to the second base function. Each orientation histogram is expressed as a linear combination of these and the other \(\bar{N}-2\) base functions.](image)

Each sample histogram, \(O\), is estimated as linear combinations of these base functions as

\[
\tilde{O} = \sum_{j=1}^{\bar{N}} a_j \Phi_j
\]

where \(\bar{N} \leq 16\) and \(a_j\) are the coefficients of \(\tilde{O}\) in the base \(\Phi_j\) calculated as

\[
a_j = <H, \Phi_j>
\]

where \(<a, b>\) denotes the scalar product of vectors \(a\) and \(b\). \(H\) is the normalised orientation histogram for the current region.

Since \(\tilde{O}\) is the reconstruction of \(O\) using \(\bar{N}\) base function there will be a difference between them and, thus, and error in reconstruction. This error can be calculated as the Mean-Square Error, or MSE, between \(O\) and \(\tilde{O}\)

\[
MSE = \frac{1}{N} \sum_{k=1}^{\bar{N}} |O[k] - \tilde{O}[k]|^2
\]

where \(k = 1, 2, \ldots 16\) refers to the indices of vectors \(O\) and \(\tilde{O}\).

The MSE will decrease as \(\bar{N}\) increases and since the base functions where created from a set of distinct regions, it is easy to realise that if the sample orientation histogram \(H\) is created from a distinct region the MSE will decrease more rapidly than if \(H\) is created from a non-distinct region. Since this is the
case $\bar{N}$ will be lower for a distinct region than for a non-distinct given a certain MSE. In other words fewer base functions are needed to reconstruct a distinct region. By thresholding the number of base functions needed for reconstruction using an upper threshold it is possible to determine which regions should be used as sampling locations. In this test the thresholds have been set in an ad hoc manner, and are very relaxed, i.e. they tend to consider more points valid for sampling than is actually the case.

Circular sampling is now performed with a radius of six pixels in the selected sampling positions. Observations from the previous test show as in the previous part of this MD Cycle the images used for observation of the results are not presented in the report. Histograms of the number of sampling locations and located points are given in figure 28 and 28, respectively. It is important not to confuse these histograms with the orientation histograms!

![Histogram showing the number of sampling positions when using orientation histograms as the selection method.](image)

When this sampling-point selection is used the number of sampling locations range from 8208 to 18288, with a mean value of 13778. All the number of sampling locations are even multiples of 144 (12 x 12) as a result of the selected block size. If this approach was perfect with regard to selecting only the regions in which there are distinct points, a higher number of sampling locations is better than a lower number since a higher number of distinct points give better matching-results. There are two considerations that lead to the conclusion that it is not, however. The first is the intrinsic problem that arises when analysing non-overlapping blocks in an image and the second is the fact that there are non-distinct regions in which there is no single dominant direction. The former problem is evident whenever a distinct points is placed in the vicinity of a block border in such a way that one part of the singularity is placed in one block and the rest in another. Each of the parts may in themselves be inadequate to make the blocks distinct and will therefore not be considered for sampling. The second problem gives rise to sampling locations that are of no real interest. It may be difficult to determine that this is the case, however, since there are regions that are not visually distinct that are distinct in the pattern recognition sense, i.e. always classifies as distinct. Even though this problem may seem to be just an increase of execution time, it also deteriorates method performance by adding spurious located points in non-distinct regions.

The resulting number of located points ranges from 480 to 5678 with a mean value of 2411. Since sampling here is not limited to the valley bottoms, there are spurious points spread throughout the ridges as well as the valleys. From the
previous MD Cycle it was evident that when sampling along a radius which was
equal to, or approximately equal to, the local valley-to-valley distance the
method responded well, whereas it did not in other regions. This is also evident
in this test since sampling only occurs using one single radius for all the
selected regions. The main part of spurious points is located in areas where the
radius and valley-to-valley distance differ. Not only does the number of located
points differ significantly from the previous approach in sampling-point
selection, the formation is not the same either. This approach yields coherent
areas of distinct points, which the previous did not. When comparing the
number of located points to the number of sampling positions, the method
classifies from 2.95 to 50.96 percent of the sampling points as distinct. With a
mean of 18.2 percent classified as distinct it is evident that this approach
coupled with the current criteria and parameters, does not perform well in
classification, simply because it is way too generous in ascribing distinct
characteristics to sampling points. Although the number of spurious points is
this high there are visually distinct points missing from the results, which is due
to the block problem discussed above.

When observing the images of the test results it is clear that the images with the
lowest numbers of located points are of very low quality. At the other extreme
are the images containing a high number of located points. These images are of
good quality and with large average valley-to-valley distances, giving lots of
spurious points due to improper radius selection. The rest of the images fall
somewhere in between these categories. There seem to be no direct connection
between the number of sampling locations and the number of located points. In
the images that hold the fewest located points the number of sampling locations
is still in the neighbourhood of the average.

With a mean distinct classification of 18.2 percent this approach is not suitable
for selection of sampling points using the parameters and criteria of this test.
The problem here can be divided into two sub-problems, the first being the
removal of spurious points and the second being the addition of missing distinct
points due to the block partitioning of the image. Adapting the radius to the
local neighbourhood can solve the first problem. This approach would alter the
result from sampling and the current criteria may be kept. It would also improve
method performance significantly by removing the spurious points due to
improper radii, which is clearly the majority of the spurious points.

The second problem has two solutions as well, i.e. block-shifting and using all
pixels as region centres. By shifting the blocks in the appropriate manner, e.g.
one half-block up and to the left and one half-block down and to the right, each image pixel is considered twice in two different blocks. If a singularity is placed near the edge in one block, it is highly unlikely that it will be in the shifted version of the same block. Combining the result from the overlapping blocks and calculating the orientation histogram from the combined gradient data would remove most of the problems with near-edge singularities. Using all pixels as region centres increases the number of histograms by 144 (12x12) and is not feasible for a real-time application. It does, however, estimate the full potential of this sampling points selection approach and is therefore important.

A last note on the orientation histogram approach regards the training set of normalised orientation histograms. While the current base function is created from 504 histograms, expanding this set may improve performance.

5.5 Distinctness Measurement [confidential]
6 Conclusions and Future Work

Two methods for locating distinct features in fingerprint images have been evaluated. Both are alternative methods and although the ideas are not entirely new they have not been used in exactly the same manner as described here. Template correlation is not a new notion but it has been used in lots of different applications ([5], [18]), whereas circular sampling as texture analysis has been used for Brodatz textures ([17]), but not for locating distinct features in fingerprint images. None of the methods have been fully developed or optimised and there are many improvements that can be made to their performance. Following the individual improvement suggestions from each of the MD Cycles this chapter concludes the report by summarising and elaborating on these. Even though the Template Correlation Method was abandoned rather early in testing it is important not to leave it behind without considering ways in which to improve it. Therefore there is one section for this method and another for the circular sampling method. First a number of general remarks concerning both methods are given.

In the Method Evaluation and Analysis chapter, there is a short note on pre-processing. Currently, local mean shifting and linear stretching is performed to normalise the images, but for the end application there is a need for determining what pre-processing should be applied to the images. All such operations are time demanding and the ideal case is where no pre-processing is needed for the methods to perform well. The subject is not delved further into, but it is important.

As have been noted in all individual tests, all parts of the method and every parameter in these parts should be subject to parameter optimisation. The manner in which all parameters have been set in the work presented here has been based on the observation of a few results, which is probably inadequate in many cases. More details on neural networks can be found in [8].

Since, in the tests, no consideration has been given the execution time optimisation it is necessary to consider this aspect as well. Before this is done, however, it is important to know that the method can perform well when it is not subject to the additional constraints placed by such optimisations.

6.1 Template Correlation Method

Already in the first cycle of the MDC the Template Correlation Method was deemed to have low potential in distinguishing between distinct and non-distinct regions. The basic hypothesis stated that there should be anomalies in feature space where distinct regions are located in the fingerprint image, but from the set of selected regions this was not the case and the method was abandoned. This does not mean that nothing useful was learned, however.

Starting from the mean-spectra it is noted that this way of analysing the frequency content of images in a database is only valid if they contain approximately the same frequencies. When they do, however, it gives a good understanding of the frequency contents of images in the database. Using the
energy content function as a base for generating the templates may also be useful in similar applications. Here is seen the first hands-on improvement that can be performed, which is the generation of templates using other filter functions. One class of filters that have similar characteristics to the sine and cosine filters are the Gabor filters ([4]). They are periodic but the convolution results are weighted higher nearer the centre of the filter. Since a discrete number of frequencies are determined as samples in the frequency band, there is also a matter of choosing the number of and the density with which to sample. Straying from this line of thought and considering adapting the frequencies of the functions to the local neighbourhood it is possible to use only one frequency depending on the characteristics of the region. Coupling this approach with the estimation of local orientation in the image it is possible to use one single filter function for each image region. These solutions introduce other difficulties, which may be hard to solve, including the intrinsic in-exactness of orientation and radius estimation. Parameters that should be subject to optimisation include the number of orientations, the number of frequencies and the size of the templates.

Some valuable analysis tools have been used in this method but the basic hypothesis did not stand the test. This renders the method useless in its present form. By reformulating the basic hypothesis it may be possible to use the same, or similar, tools but interpreting the results in a different manner.

6.2 Circular Sampling Method

From the first MD Cycle it was seen that this methods holds a high potential of being able to distinguish the distinct regions from the non-distinct. By manual selection of regions it was seen that the basic hypothesis held stating that the $C_3C_2$ criterion should be fulfilled for distinct regions. When moving from this test to the next it was evident that there were too many spurious points located by the method when sampling over the entire fingerprint image. It was also evident that the method was highly radius dependent. In this test it was also seen that the non-contact regions of the image gave rise to spurious points and therefore the thresholding criterion was introduced. The most effective and straightforward way of reducing the number of spurious points is by selecting sampling locations. MD Cycle three evaluates two ways of doing so. The first, in concord with the basic hypothesis, uses a skeleton image as sampling locations and while this reduces the number of sampling locations as well as located points very much it may also be a too harsh way of selection. From this stems the next way to select sampling locations, orientation histograms. By analysing orientation content within each 12x12 pixel region in the image and using the regions that does not have one single dominant direction as sampling locations, the method strays from the basic hypothesis somewhat is more refined than the skeleton image. Last, these two methods were combined into a test that measures the distinctness of the located points by autocorrelation thresholding and segment counting. The combination of the approaches and the results thereof are covered in Chapter 5.5, which is confidential and therefore not present in this report. This section is divided into three subsections, in which the first section contains a description of methods three main properties, the second evaluates each part of the method individually and the third give suggestions for further testing of the method.
6.2.1 Method Properties

During these tests a number of properties of the method was found. These are described here together with ways to handle them. The first property is the noise sensitivity of the method that is evident in all tests. In regions, or images, where the noise level is high there is no way to predict the frequency content of the intensity function gained through circular sampling. The points are randomly classified as distinct or non-distinct which is very undesirable. Some of these points, more specifically those located in the non-contact areas of the images, where removed through the use of the thresholding criteria. This does not solve all problems from noise and there is a need for reducing the noise sensitivity of the method further. Low-pass filtering, or smoothing, is the classic way of removing noise from images and even though this may work well, it removes information that may be useful for classification. More advanced filtering is of course possible and will probably work much better than global smoothing. Less information will be removed and classification is not influenced by the same amount of noise. More details on filtering can be found in ([5]). An alternative to filtering is to use several radii in circular sampling and average the results from these before calculating the Fourier transform. This will reduce noise-sensitivity without removing any information from the image itself. This should work well in regions containing some noise but it not very well in regions containing much or only noise, since then the averaging will be performed over responses from noise and the result will itself be the response from noise. Such regions are hopefully removed by the thresholding criterion and this may not be a problem.

Secondly is the fact that the method is highly radius dependent, which causes problems in regions where the radius is either too large or too small. By adapting the radius to the local valley-to-valley distance in the local neighbourhoods of the image one can circumscribe this problem. Radius adaptation is a difficult problem in itself and may yet introduce more problems than it solves. Nonetheless, there is no single radius that can capture the useful information over entire images and the need for a fast and robust radius adaptation method is evident.

Property number three is the translation sensitivity of the method. The way the method is devised makes it indifferent to rotational effects, but the problem in translation is still present. In MD Cycle one it was noted that the selection of sampling points was very important for the classification to perform well. This selection may also differ depending on the characteristics of the region that is analysed. There is no certainty that sampling in one position in singularity will yield the same result when sampling occurs in the same relative position in another. This problem is related to the radius dependency problem and the fact that the singularities in the images are not always of the same size. If a region is considered distinct in one position it is not certain that this is so when sampling occurs in the adjacent pixels. This property should be examined further by analysing the response of the method to different relative positions in synthetic images. Understanding of the translation sensitivity is very important to improve the method.
6.2.2 Evaluation of method steps

The above-described properties of the method are important to handle in themselves, but there are several other considerations that can be taken into account in improving the method. Each step of the method uses different approaches to solve its part of the problem. These may not be optimal and there are alternative ways of solving the problems. Each part of the method is evaluated here and alternative approaches are presented along with the evaluation.

Before sampling occurs the image is analysed to determine in which positions to sample. This has been done in two ways: skeleton image and orientation histograms. The current implementation of the skeleton image approach creates the skeleton by morphology without any post-processing whatsoever. Morphology is a rather time-consuming approach and it is not suitable in a real-time application of the method, but it is also the most straightforward way of creating a skeleton image. An alternative approach is ridge detection filtering ([1]), which convolves the image with two filters that are capable of adaptively accentuating the local-maximum grey-levels in a direction normal to the maximum gradients. If the result from both values are greater than a threshold the pixels is considered a ridge-pixel. From both approaches the resulting skeleton image is of low quality, containing holes and speckles which deteriorates method performance significantly. To alleviate this problem extensive post-processing is necessary. Using the skeleton image as the way of selecting sampling locations moves the method closer to classic minutiae-detection methods, with the significant difference in classification. If this is appropriate or not is a matter for discussion, but what is clear is that there are minutiae-based methods that perform very well. Moving the circular sampling method closer to those makes it an alternative approach to solve minutiae detection and lets face it, there are better ways of doing this.

Although the use of orientation histograms as a means for selecting sampling points results in far more spurious points than does the skeleton image, there are advantages. The most prominent being that the method distances itself from minutiae-based methods and works to locate more general distinct features. Certain problems where seen in the application of this approach. Some, but not all, resulting from the block division of the image. This problem can be solved in one of two ways, of which the first is more suited for a real-time application and the second is more of a way for understanding and evaluating the approach. The problem with block-division arises when a singularity, or area with no single dominant direction, is placed on the border of a block and therefore is not located. By shifting the blocks one half block-length down and to the right and up and to the left all pixels in the image are considered twice and no singularities are located on the borders. Although this approach solves some of the problems it does not give a full appreciation of the potential of the orientation histograms. By using each image pixel as the centres of blocks and creating an orientation histogram for every block each pixels neighbourhood is analysed with regard to orientation. This is the way the method should work and although it is not possible in real-time, it does give an appreciation of how good the method can become, which is very important.

Block-division is not the only problem when using orientation histograms. There where distinct points missing mid-block as well and although these where rather few, it gives rise to questions. One of the things to consider is, of course, the value of parameters. Two very important thresholds, i.e. the MSE threshold
and the base-function threshold where selected in an ad hoc manner and although the values of these where relaxed, the balance between them may result in the unwanted removal of certain regions. Yet another consideration is the training set. Increasing the number of training histograms will probably improve the method, but even further refinements may be needed. Consider a valley ending and valley bifurcation with regard to their orientation content. They are not very similar and yet they are considered one and the same here. Dividing these two types into one training set each and all other singularities into another, sampling points selection may improve significantly by creating one set of base functions from each of these. In the last test the selection of sampling points was a combination of the skeleton image and the orientation histograms. This was used because of the fact that both methods was already implemented and well tested, but there may be better ways in which to select sampling points from the blocks selected using orientation histograms. One way is to simple sample in the N positions that correspond to the N highest pixel intensities in the block, another is to sample in points where the orientation changes most rapidly within the block.

Once the sampling points have been selected circular sampling sets in. In the current application sampling occurs along a single circle and this alone is used as a base for classification. In the section regarding noise sensitivity above a suggestion was made regarding sampling along several radii and averaging radially. For each radius used, more information about the local neighbourhood is attained. This is important. Sampling along a number of radii to gather information and analysing each of these may be a way of improving method performance. It is of course not entirely problem free, since every circle used increases the execution time. In contrast to this is the radius adaptation approach outlined above. Which approach is to prefer is a matter for investigation, and it depends by large on if the information from each radius can be handled in a good way.

In connection with using several radii is the creation of one frequency signature for each of these. By expanding the frequency signatures to, say, frequency components two to eight and collecting a large set of training samples from distinct regions it is possible to create a set of base functions in the same manner as with the orientation histograms. Using the same thresholding approach as well, the classification part of the method changes. Hopefully it will be to the better. The two main goals of the classifier are to remove spurious points further and to guarantee that no distinct points are removed due to classification.

One thing that was evident in all the tests performed on entire fingerprint images was that sometimes one singularity gives rise to several located points. This is due to the translation sensitivity of the method. If these points actually correspond to the same distinct region, they should be grouped together in some manner because every distinct region should correspond to one located point. This can be done using some form of clustering method. Resulting from this is the removal of spurious points stemming from several located points in the same neighbourhood of the image. Since several of the tests where based partially on the numerical analysis, this would alter the results from these in a positive way.
6.2.3 Further testing [confidential]
7 References


Appendix A – TCM1

Test specification

Method
Template Correlation Method

Test purpose
Determine the potential of the method

Test name
TCM1

Parameter Specification
Number of orientations : 8
Number of frequencies : 8
Size of Regions : 16x16 pixels
Size of filter template : 11x11 pixels
Number or regions : 2

Additional Details
Accumulation is performed over orientation, yielding one response for each frequency.
The combination of region size and template size gives a valid response region from correlation that is 6x6 pixels.

Structure for figures
  a. 16x16 region one
  b. 16x16 region two
  c. 6x6 region one
  d. 6x6 region two
  e. Scatter of PCA result

Notes on figures
  c. The marked pixels in the region are selected manually based on their position within the singularity. These pixels are green in the image.

  e. The blob-marked positions in the figure correspond to the PCA-values of the marked pixels in figure c. The ‘x’ markers in the figure correspond to the PCA-values from region a. and the ‘o’ markers correspond to region b.
2. 

a. 

b. 

c. 

d. 

e. 

-1500 -6500 -5500 -4500 -3500 -2500 -2000 

-1000 

-500 

0 

500 

1000 

1500 

-6000 -6000 -5000 -4000 -3000 -2000
3.

a. 

b. 

c. 

d. 

e. 

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Appendix B – TCM2

Test specification

Method
Template Correlation Method

Test purpose
Determine the potential of the method

Test name
TCM2

Parameter Specification
Number of orientations : 8
Number of frequencies : 8
Size of Region : 16x16 pixels
Size of filter template : 11x11 pixels
Number or regions : 2

Additional Details
Accumulation is performed over frequency, yielding one response for each orientation. The combination of region size and template size gives a valid response region from correlation that is 6x6 pixels.

Structure for figures
a. 16x16 region one
b. 16x16 region two
c. 6x6 region one
d. 6x6 region two
e. Scatter of PCA result

Notes on figures
- The marked pixels in the region are selected manually based on their position within the singularity. These pixels are green in the image.
- The blob-marked positions in the figure correspond to the PCA-values of the marked pixels in figure c. The ‘x’ markers in the figure correspond to the PCA-values from region a. and the ‘o’ markers correspond to region b.
1.

a. b. c. d.

e.
3.

a.

b.

c.

d.

e.
4.

a. 

b. 

c. 

d. 

e. 

![Image]
5.

a. b. c. d. e.
6.

a. b. c. d. e.
Appendix C – CSM1

Test specification

Method
Circular Sampling Method

Test purpose
Determine the potential of the method

Test name
CSM1

Parameter Specification
Size of Region(s) : 16x16 pixels
Number of Sampling Locations : 1
Number of Radiuses : 1
First Radius : 4 pixels
Radius Increment : -
Factor of scale : 4
Number of samples : 128

Additional Details
Scaling is performed using bicubic interpolation.

Structure for figures
a. Region 16x16 pixels
b. Intensity function
c. Frequency spectra

Notes on figures
a. The circle in the figure corresponds to the circle along which image intensity is sampled. The regions shown are scaled by ‘factor of scale’.
2.

a. 

b. 

c.
4.

a.

b.

c.
6.
7.

a.

b.

c.
8.

a.

b.

c.
Appendix D – CSM2

*Test specification*

**Method**
Circular Sampling Method

**Test purpose**
Evaluate the response of the method to entire fingerprint images

**Test name**
CSM2

**Parameter Specification**
- Size of Region(s) : 121x171 pixels
- Number of Sampling Locations : 20691
- Number of radiuses : 6
- First Radius : 2 pixels
- Radius Increment : 2 pixels
- Factor of scale : 3
- Number of samples : 128

**Additional Details**
Scaling is performed using bilinear interpolation.

**Structure for figures**
The figures are ordered by increasing radius from radius = 2 pixels in the top-left corner, radius = 6 pixels in the top-right corner and radius = 12 pixels in the lower-right corner of the figure.
Appendix E – CSM3

Test specification

Method
Circular Sampling Method

Test purpose
Evaluate the response of the method to entire fingerprint images

Test name
CSM2

Parameter Specification

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<th>Parameter</th>
<th>Specification</th>
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</thead>
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</tr>
<tr>
<td>Number of Sampling Locations</td>
<td>20691</td>
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<tr>
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<tr>
<td>Number of samples</td>
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</tr>
</tbody>
</table>

Additional Details
Scaling is performed using bilinear interpolation.
This test introduces the thresholding criteria.

Structure for figures
The figures are ordered by increasing radius from radius = 2 pixels in the top-left corner, radius = 6 pixels in the top-right corner and radius = 12 pixels in the lower-right corner of the figure.