Organ Recognition using Gabor Filters

Shiva Zaboli†, Arash tabibiazar††, Paul Fieguth†
University of Waterloo
†Systems Design Engineering, ††Electrical and Computer Engineering
Waterloo, Canada, N2L 3G1
szaboli, atabibiazar, pfieguth@uwaterloo.ca

Abstract

The aim of this research is to investigate the possibility of using medical image information to extract unique features and classify different patients' organ tissues, such as the prostate, based on concepts related to what is already done in iris recognition. This paper therefore presents a new approach in medical imaging, an organ recognition system, tested on a standard database of grey scale prostate images in order to validate its performance.

In this research, features of the prostate image were encoded by convolving the normalized organ region with a 2D Gabor filter and then quantizing its phase in order to produce a bit-wise biometric template. Our experiments prove that prostate patterns have a low degree of freedom to be used in organ recognition systems and inter-class and intra-class distributions are highly correlated. However, there are still open issues that need to be addressed for future work on organ recognition, including precise segmentation and intensive computation cost.

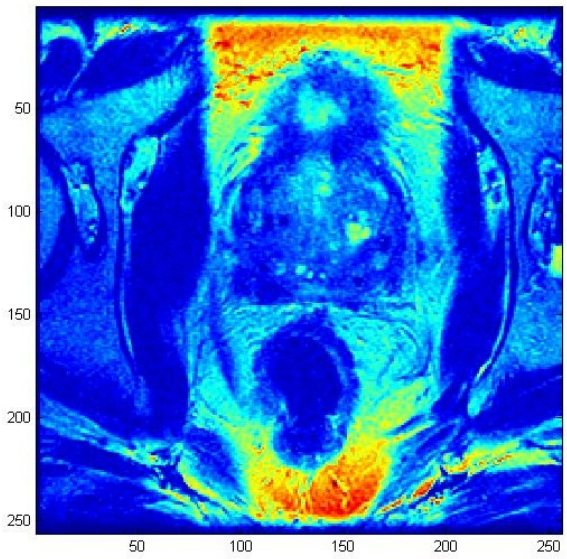

Figure 1. Sample prostate image from MICCAI09 database [MICCAI-2915]

1 Introduction

Biometrics is a branch of biology that studies biological phenomena - like various physiological, physical, or behavioral characteristics - and observations by means of statistical analysis. It usually refers to recognizing and identifying individuals using these biological metrics. This emerging science has recently become popular with the increasing need for higher authentication and identification systems and various applications. Among many biometric methods, iris recognition is very well known because of reliability and an easy acquisition of biometric data. It has a complex structure that is unique for each eye. The randomness of the human iris texture is stable over the life-span and the process of identification is easy and quick. We can use other biological metrics or organs for identification and especially for classification if uniqueness is not a concern. The main tasks of any organ recognition system are to provide a compact representation of the organ image (i.e., to encode the captured image) and to allow for a reliable pairwise comparison of the encoded images.

In general, any organ recognition system consists of three phases: (a) image acquisition and organ region localization; (b) feature extraction and encoding; and (c) feature comparison. Many researchers address the second phase (b) as the most challenging part of the system [11, 8]. The feature extraction usually can be performed in frequency and spatial domains. For frequency features, a transform (like Fourier or wavelet) must be performed on the image, while spatial features typically require image segmentation. Image retrieval algorithms are based on visual features and visual queries [7]. Query by image example, query by sketch

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and by region are some types of visual queries, and colour histograms, shape and texture descriptors are some types of visual features. However query formulation is difficult, so most algorithms focus on features. Exactly how these features are used will be application-dependent. If the aim is working on a biomedical computer-vision problem, the end goal may be the generation of a classification rule to assist with diagnosis. Feature-based algorithms try to match features and semantics to recognize the object. Most of the biometric recognition systems use feature extraction to determine a person's identity. They examine the unique physical or behavioral features to retrieve the specific person. These days, the variety of medical images, including diagnostic, treatment planning and so on is increasing and without medical image retrieval, it is hard to process everything very well. Currently, images are accessed by patient ID, but much information stored in images and connected text and only little of this knowledge is exploited.

In this paper, the possibility of extracting a biometric features from specific organ such as the prostate will be investigated to categorize patients based on these features. The goal of the proposed system is encoding the available features in medical image to classify different patients' organ tissues based on the same organ code. These organ codes can be used later to develop diagnosis system. The rest of this paper is organized as follows. First we review some basic concepts on retrieval systems in Section 2. In Section 3 the proposed method is explained and then evaluated in Section 4.

2 Retrieval system

One of the primary tools used by physicians is the comparison of previous and current medical images associated with pathologic conditions. As the amount of pictorial information stored in both local and public medical databases is growing, efficient image indexing and retrieval becomes a necessity. During the last decade, the advances in information technology allowed the development of content-based image retrieval (CBIR) systems, capable of retrieving images based on their similarity with one or more query images [9]. It is interesting that more than 50 CBIR systems are surveyed in [12]. Common ground for most image retrieval systems is that they are based on similarity measures estimated directly from low-level image features.

Each retrieval system has two parts: enrolment and verification. Each part consists of pre-processing and feature processing. In pre-processing, for example, an interesting area of the image is selected to pass through feature processing, where valuable features are extracted which are passed to a template to encode these features as a pattern. At the enrolment side the database is updated by this new pattern. When new data arrive to the system, the calculated pattern is compared with other patterns in the database to make a decision about identification.

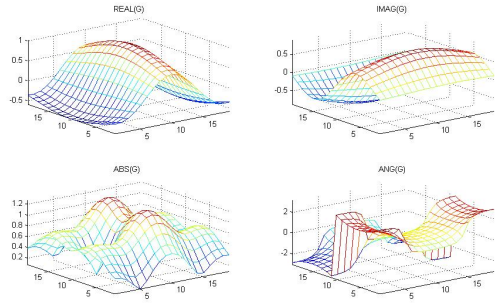


Figure 2. Gabor filter real and imaginary parts with absolute and phase information

Iris recognition is the best biometric example for image retrieval, where the iris has the great mathematical advantage that its pattern variability among different persons is enormous [4]. In addition, as an internal organ of the eye, it is stable over time. Given an image of the eye, the iris position is found and extracted,each isolated iris pattern is demodulated to extract its phase information using a quadrate 2-D Gabor wavelets [2, 5]. Altogether, 2048 such phase bits are computed for each iris. Finally a fractional Hamming Distance is computed as a measure of the dissimilarity between two phase code bit vectors (iris codes) of any two irises [4].

The aim of this research is the possibility of using the information in medical images to extract unique features and classify different patients' organ tissues based on the same organ code like what has been done in iris recognition.

3 Proposed method

Feature encoding has been implemented by convolving the normalized organ pattern with the 2D Gabor filter presented in (1). A 2D Gabor filter over an image domain (x,y) is represented as

$$G = e^{-\pi[\frac{(x-x_0)^2}{\alpha^2}+\frac{(y-y_0)^2}{\beta^2}]}e^{-2\pi i[u_0(x-x_0)+v_0(y-y_0)]} \quad (1)$$

where (x_0, y_0) specify position in the image, (α, β) specify the effective width and length, and (u_0, v_0) specify modulation, which has spatial frequency $\omega_0 = \sqrt{x_0^2 + y_0^2}$. Sometimes the polar coordination instead of Cartesian is used, therefore in polar form the filters are given as

$$H_{r\theta} = e^{-i\omega(\theta-\theta_0)}e^{-\frac{(r-r_0)^2}{\alpha^2}}e^{-i\frac{(\theta-\theta_0)^2}{\beta^2}} \quad (2)$$

where (α, β) are the same as in (1) and (r_0, θ_0) specify the centre frequency of the filter. The demodulation and phase

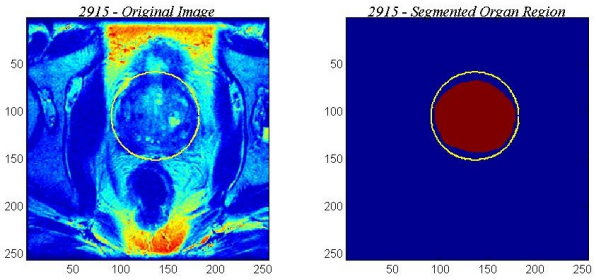


Figure 3. Prostate image with selected region on segmented area [MICCAI09-2915]

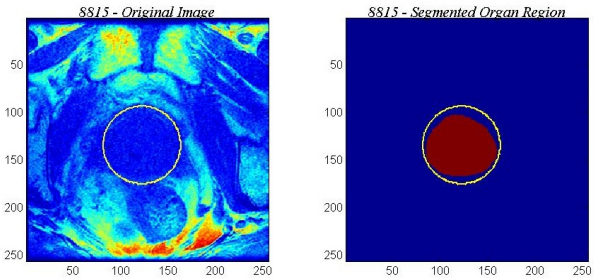


Figure 4. Prostate image with selected region on segmented area [MICCAI09-8815].

Quantization process can be represented as

$$h = \int_{\rho}\int_{\phi} I(\rho,\phi) e^{i\omega(\theta_0-\phi)} e^{-\frac{(r_0-\rho)^2}{\alpha^2}} e^{-\frac{(\theta_0-\phi)^2}{\beta^2}} \rho d\rho d\phi \tag{3}$$

where $h\{Re, Im\}$ is a vector of 2-bit elements whose real and imaginary components are dependent on the sign of the 2D integral, and $I(\rho,\phi)$ is the raw organ image in a dimensionless polar coordinate system [6].

The output of convolving is then phase quantized to four levels using the Daugman method [10]- which was used in the iris recognition system - with each filter producing two bits of data for each phasor in gray mode to prevent high mismatch if two intra-class patterns are slightly misaligned. The encoding process produces a bitwise template containing a number of bits of information (codes), and a corresponding noise mask which corresponds to corrupt areas within the pattern. Since the phase information is poor in regions where the amplitude is near zero, these regions are also marked in the noise mask. The total number of bits in the template will be the angular resolution times the radial resolution, multiplied by two. For matching, the Hamming distance (HD) is used as a metric for recognition (4), since bit-wise comparisons were necessary.

$$HD(X,Y) = \frac{1}{N}\sum_{i=1}^{N}(x_i \epsilon X \oplus y_i \epsilon Y) \tag{4}$$

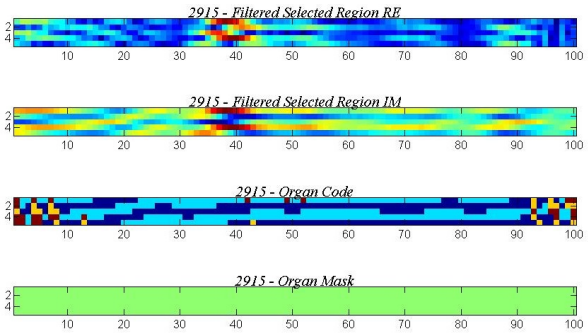
The HD algorithm uses noise masking, so only non-masked bits are being used in HD calculation between two organ templates. Although, in theory, two templates generated from the same organ must have a HD equal to zero, in practice it doesn't happen. In order to consider the rotational inconsistencies, when the HD of two templates is calculated, one template is shifted left and right bit-wise and a number of HD values are calculated from successive shifts. This bitwise shifting in the horizontal direction corresponds to rotation of the original organ region. Figures 3 and 4 show two samples of prostate images of two different patients. Figures 5a and 5b show the feature extraction for two prostate images. First, the template is extracted from the segmented organ area, convolved with a Gabor filter, quantized, and converted to an organ code.

4 Evaluation

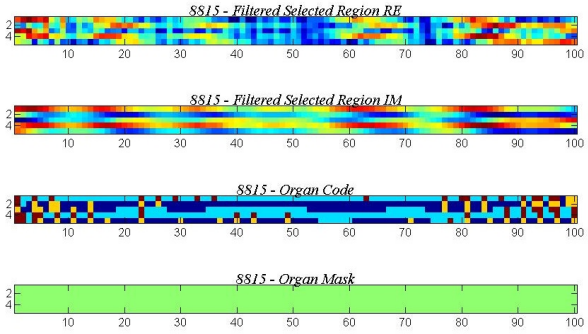
In this section, the performance of the organ recognition system as a whole is examined. Tests have been carried out to find minimum false match and false acceptance rates, and to confirm that organ recognition can or can't perform accurately as a biometric with accurate recognition, as well as to confirm the uniqueness of human prostate patterns by deducing the degrees of freedom present in the prostate template representation. There are a number of parameters - such as template resolutions, filter parameters and number of shifts required to consider rotational inconsistencies - in the recognition system, and optimum values for these parameters were required in order to provide the best recognition rate.

4.1 Data set

For evaluation, the MICCAI09 (Training Data Prostate Segmentation Challenge) image database is used that contains data sets of grey scale prostate images with 15 unique prostates (classes) and around 33 different images for every patient [1]. Each data set has anonymous prostate patient data corresponding to T1-weighted axial images, T2-weighted axial images and the T2-weighted segmented images. All images have been taken in a 1.5T MRI scanner. Figures 5a and 5b show the encoded outputs of samples from this data set that belong to the two different patients. In these figures the real and imaginary parts of the filtered image as well as template codes and corresponding masks have been shown. These images have different sizes and prostate shapes, so we need to extract features in an adaptive way to prevent resolution effects.



(a) MICCAI09-2915

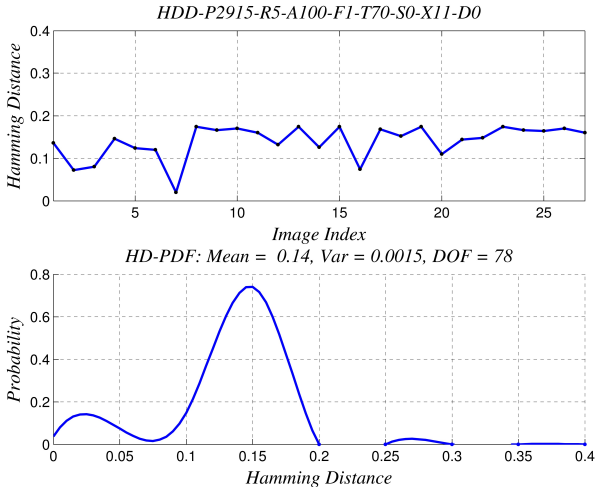


(b) MICCAI09-8815

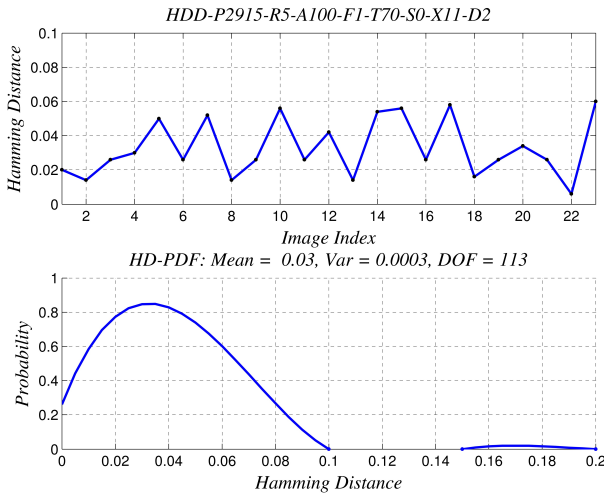
Figure 5. Organ code extraction: Gabor filter output real and imaginary parts for selected organ area and extracted organ code and corresponding mask for two images.

4.2 Uniqueness of prostate patterns

The first test was to investigate the uniqueness of prostate patterns, as recognition relies on the independence of prostate patterns from patient to patient. Uniqueness was determined by comparing templates generated from different patients, and examining the distribution of HD values, known as the inter-class distribution. According to statistical theory, the mean HD for comparisons between inter-class prostate templates must be 0.5, if samples are truly independent. As we mentioned, the templates are shifted left and right to account for inconsistencies in the prostate image, and the lowest HD is taken as the actual HD. Due to this, the mean HD for inter-class template comparisons will be slightly lower than 0.5. As the number of shifts increases, the mean HD for inter-class comparisons will decrease accordingly. Uniqueness can also be determined by measuring the number of degrees of freedom represented by the templates. This gives a measure of the complexity of organ patterns, and can be calculated by approximating the collection of inter-class HD values as a binomial distribution. The value of degrees of freedom (DOF) is usually



(a) no displacement



(b) with displacement in size of $2\times N(1,0)$ pixels

Figure 6. Inter-class Hamming distance distribution based on two prostate images of the same patient and its corresponding PDF.

computed by the following equation, where μ is the mean, and σ is the standard deviation of the distribution.

$$DOF = \frac{\mu(1-\mu)}{\sigma^2} \tag{5}$$

As Figure 6a shows, the inter-class HD distributions and its corresponding Probability Density Function (PDF) doesn't show statistical independency, since the mean of the distribution equals 0.14. Therefore it can be stated that in MICCAI09 data set, generated prostate templates are not highly unique. Also, the distribution shows the simplicity of the prostate structure with only 78 degrees of freedom.

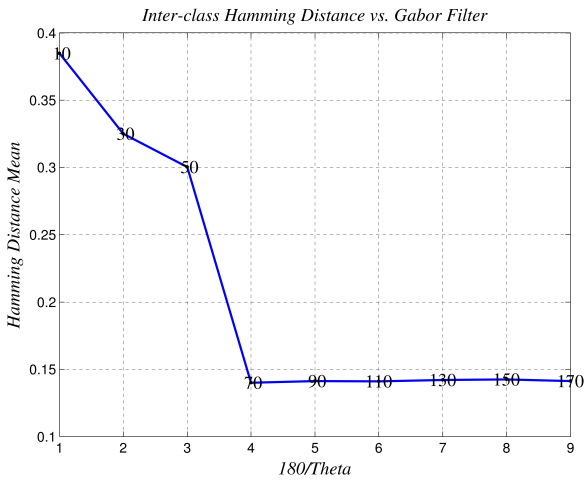


Figure 7. HD mean distribution vs. filter parameter (theta)

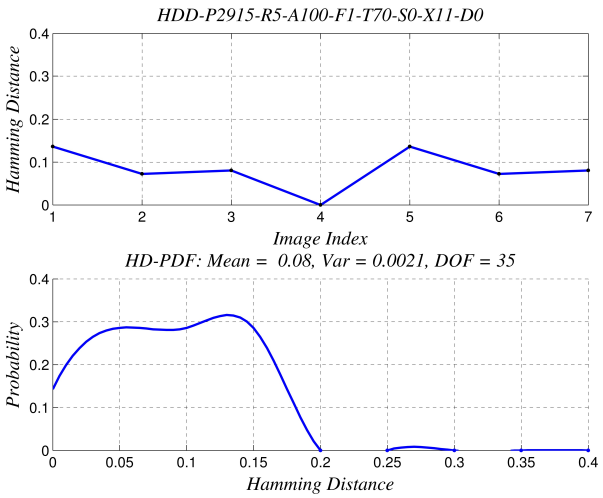


Figure 8. Intra-class distribution for $\theta = \pi/70$.

4.3 Displacement of organ image

The second test sought to find the effect of organ selected region displace on the Intra-class HD distribution. Figure 6b shows the HD distribution on the same image with displacements up to $2\times N(1,0)$ pixels. The results show that HD increases by increasing the displacement in the same patient image for prostate region, thus the generated organ code is location dependent.

4.4 Recognition

The key objective of any biometric system is its capability to achieve a distinct separation of intra-class and inter-class HD distributions. With a clear separation, a separating HD value can be defined for decision making in the comparison of two templates. If the HD between two templates is less than the separation point, the templates were generated from the same prostate and a match is found. Otherwise, they have been generated from different prostates. The distance between the minimum HD value for inter-class comparisons and the maximum HD value for intra-class comparisons could be used as a metric to measure separability; however, this is not a very accurate measure since outliers will corrupt the calculated value, and measuring is dependent on the number of prostates templates compared. A better metric is decidability [4], which takes into account the mean and standard deviation of the intra-class and inter-class distributions.

$$Decidability = \frac{|\mu_S - \mu_D|}{\sqrt{\frac{\sigma_S^2+\sigma_D^2}{2}}} \qquad (6)$$

Decidability is a distance measured in standard deviations and is a function of the magnitude of difference between the mean of the intra-class distribution μ_S, and the mean of the inter-class distribution μ_D, and also the standard deviation of the intra-class and inter-class distributions.

The higher the decidability, the greater the separation of intra-class and inter-class distributions, which allows for more accurate recognition. With a pre-determined separation, a decision can be made as to whether two templates were created from the same organ (a match), or whether they were created from different organs. However, the intra-class and inter-class distributions may have some overlap, which would result in a number of incorrect matches or false accepts, and a number of mismatches or false rejects. The False Reject Rate (FRR) measures the probability of an enrolled patient not being identified by the system. The False Accept Rate (FAR) measures the probability of an patient being wrongly identified as another patient [3]. The decidability metric will determine the optimum parameters. Once optimum parameters have been found, the performance of this optimal configuration will be measured by calculating the false accept and false reject rates.

4.5 Filter parameters

For the encoding process the outputs of each filter should be independent, so that there are no correlations in the encoded template, otherwise the filters would be redundant. For maximum independence, the bandwidths of each filter must not overlap in the frequency domain, and also the centre frequencies must be spread out. Figure 7 shows that the optimum θ value for encoding prostate image is $\pi/70$, where Figure 8 shows the corresponding HD distribution.

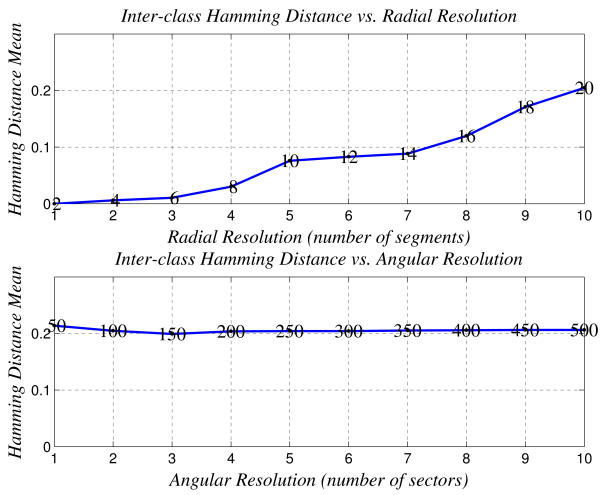


Figure 9. HD distribution vs. template radial and angular resolution.

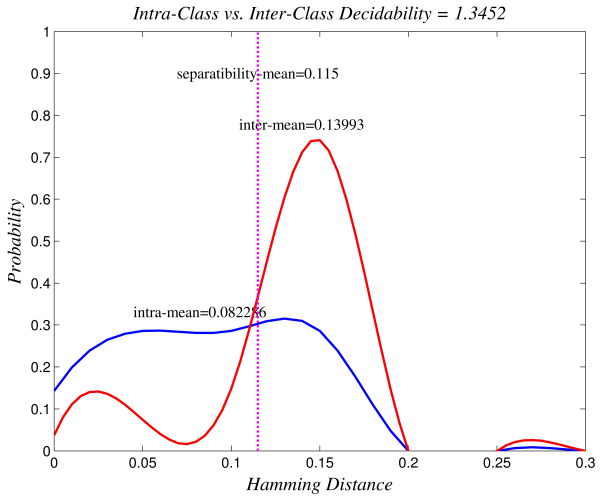


Figure 10. Decidability between inter-class and intra-class distributions for prostate samples taken from MICCAI09 database.

4.6 Template resolution

Template radial and angular resolution significantly influences the system performance, since this resolution determines the size of organ code. Figure 9 shows HD values generated from encoding templates with various radial and angular resolution dimensions. The optimum template size for our data set was found to be five pixels for radial resolution and one hundred pixels as angular resolution.

4.7 Number of shifts

The optimum number of template shifts to account for rotational inconsistencies can be determined by examining the mean and standard deviation of the intra-class distribution. Without template shifting the intra-class HD distribution will be more randomly distributed, since templates, which are not properly aligned, will produce HD values equivalent to comparing inter-class templates. As the number of shifts increases, the mean of the intra-class distribution will converge to a constant value. It is noted that two shifts are enough to be able to account for most of the rotational inconsistencies in our data set.

4.8 Evaluation summary

In summary, the optimum encoding of prostate features was with one 2D Gabor filter with $\theta = \pi/70$. An optimum template size with radial resolution of five pixels, and angular resolution of one hundred pixels was chosen for experiments. These parameters generate a biometric template that contains five hundred bits of information. In order to correct for rotational inconsistencies two shifts to the left and right were required for each template comparison. After determining these optimum parameters, Figure 10 shows a weak separation of intra-class and inter-class HD values. A HD value of 0.115 can be chosen as a separation point. The decidability value for our data set is 1.3452 which is very low for a standard recognition system.

5 Conclusion

This paper has looked into the problem of organ recognition using an approach developed for a quite different application (biometric identification). The goal of this research is to investigate the possibility of using the state-of-the-art in Iris research, used for identification and security, as a method to assess the variability of a particular organ. In particular, what degree of variability is exhibited by a single organ in one patient, as opposed to between patients, and furthermore as opposed to outliers (such as cancerous organs).

This research has presented an organ recognition system, tested using standard databases of grey-scale prostate images to validate its performance. In this research, features of the prostate were encoded by convolving the normalized organ region with a 2D Gabor filter, quantizing its phase to produce a bit-wise biometric template, and finally using a Hamming Distance as matching metric.

The analysis of the developed organ recognition system clearly reveals the importance of accurate segmentation, since areas that are wrongly identified as organ will corrupt the biometric templates, leading to poor recognition. Fur-

ther, the encoding process required only one 2D Gabor filter to provide recognition. Although the prostate can clearly not function as an accurate biomarker, as can the Iris, this could hardly be expected. However the results show a positive level of discriminability between prostate images from a single patient, as opposed to across patients, suggesting that biometric methods may offer approaches for organ segmentation and classification.

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