A Topology based Approach to Categorization of Fingerprint Images

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Abstract: This paper discusses the use of betti numbers to characterize fingerprint and iris images. The goal is to automatically separate fingerprint images from non-fingerprint images; where non-fingerprint images of special interest are biometric samples which are not fingerprints. In this regard, an image is viewed as a triangulated point cloud and the topology associated with this construct is summarized using its first betti number - a number that indicates the number of distinct cycles in the triangulation associated to the particular image. This number is then compared against the first betti numbers of "n" prototype images in order to perform classification ("fingerprint" vs "non-fingerprint"). The proposed method is compared against SIVV (a tool provided by NIST). Experimental results on fingerprint and iris databases demonstrate the potential of the scheme.

1 Introduction

Recent developments in engineering and other sciences have presented the need for new mathematical tools in order to tackle even the simplest manual tasks like categorization of biometric samples. The human brain can easily distuingish between an iris scan and a fingerprint image; yet doing so for millions of images will undoubtedly take too long to be practically possible. So a need for automatic processing of images by means of computers is present. This area of research requires skills from many different disciplines, including mathematics, computer science and biometrics; where computer science and biometrics are multi-disciplinary sciences.

Classical tools in mathematical analysis, like Fourier analysis, are often the primary tools in applying mathematics to a given problem. Unfortunately requirements of continuity and rigid geometric properties may not always be viable. Mathematicians have recently been more active in refining considerably more advanced tools from mathematics to suit applicational needs. The success of these efforts show promising results in areas like cryptography, statistical mechanics and robotics, to name a few.

The purpose of this article is to present some results indicating the use of modern mathematics to tackle a concrete problem, namely categorization of fingerprint images from a

database of mixed biometric samples. Instead of using representations like Fourier transforms, a fingerprint will be represented as a network in 3-dimensional Euclidean space. In topology, a network is called a cell complex which is a generalization of a triangulation. Once a cell complex is constructed, it no longer matters how long the edges are or if the cell complex is deformed into another geometric shape, provided edges cannot be crossed. This means that the analysis will be the same if a given cell complex is equivalent to a triangulation of a cube or if it is equivalent to a triangulation of a sphere. More so the choice of triangulation is not important, e.g. using 18 or 36 triangles to cover a torus would yield the same topology. Topology is sometimes referred to as rubber geometry because it studies properties which persist throughout continuous deformation of objects; such deformations are called homeomorphisms, which are continuous mappings of topological spaces with continuous inverses. Metrics are obviously sensitive to such deformations and therefore a metric is a geometric property. In topology it is not important how far two points are from each other, what matters is how they are connected. In relation to biometric samples, the main idea is to construct an information network, a cell complex, which accurately captures features unique to the particular type of biometric sample, e.g. iris or fingerprint.

1.1 Related work

In 2009 Libert et al. published a detailed validation metric for fingerprint images using Fourier analysis [LGO09]. The peak height of a specially derived power spectrum was found as the most significant classifier based on their analysis on multiple datasets. Moreover applying a windowing function, specifically the blackman window function, the accuracy of the Spectral Image Validation and Verification (SIVV) method was greatly improved, see [LGO09]. The authors illustrated results by thresholding on the peak height. In 2010 an analysis was conducted which is somewhat similar to the usage of the method proposed here, see [SLL10].

The method SIVV, in its current implementation in NIST Biometric Image Software [NIST-NBIS-2012], was used in this work as baseline algorithm to benchmark our own method.

2 Fundamentals of topology and homology

One of the most challenging aspects of the method proposed here is that the mathematical machinary for conducting such an analysis requires knowledge of algebraic topology, specifically homology theory. These topics in mathematics are considered modern topics which means they employ advanced algebraic methods developed as late as the second half of the twentieth century. It is therefore recommended that the interested reader seek information from one of the numerous textbooks on the subject. It is recommended that the reader start with the article [Ghr08].

The way the method presented here differentiates from the usual methods in applying mathematics is that instead of considering a function which maps some domain to some

range, say the discrete Fourier transform; a sequence of functions H_n are to be considered. These functions work on both spaces and maps since they induce a structure on the maps between two spaces. As an example consider the graph in figure 1. Denote the triangulation by X.

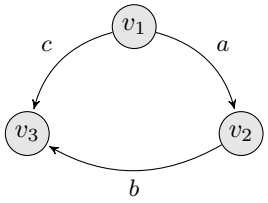


Figure 1: Example triangulation with three edges and three vertices.

Let $\mathrm{C}_1(\mathrm{X})$ be a vector space spanned by the edges $\{a, b, c\}$ and $\mathrm{C}_0(\mathrm{X})$ the vector space spanned by the vertices $\{v_1, v_2, v_3\}$. Assume that the coefficients in the two vector spaces are real numbers. Let the map

$$f : \mathrm{C}_1(\mathrm{X}) \to \mathrm{C}_0(\mathrm{X})$$

be one which sends edges of the graph to their vertices. In general homology theories there are analog maps for sending surfaces to edges etc. but in the current context, where we only study graphs, it will suffice to only consider the map f. The homology group $\mathrm{H}_1(\mathrm{X})$ consists of 1-dimensional loops in X. Homology ensures that loops in spaces commute, e.g. it does not matter if one traverses paths abc^{-1} or $b^{-1}a^{-1}c$, i.e.

$$abc^{-1} = b^{-1}a^{-1}c,$$

where the inverse notation means traversing a path in the opposite direction of the arrows in the graph. The elements in the kernel $\ker f$ of the map f are called cycles. The idea of homology is to count distinct cycles regardless of starting point or direction taken. In the above example both starting point and direction of the two traversals are different, yet the cycle is the same. For a finite graph like X the first homology group is given by

$$\mathrm{H}_1(\mathrm{X}) = \ker f = \{x \in \mathrm{C}_1(\mathrm{X}) \,|\, f(x) = 0\}.$$

A certain number is associated to each of the groups $\mathrm{H}_n(\mathrm{X})$. It is called the n'th betti number and it is given by the rank of the n'th homology group,

$$\beta_n = \operatorname{rank} \mathrm{H}_n(\mathrm{X}).$$

This number is equal to the number of distinct n-dimensional "holes" in the space. For the example above, the betti numbers are $\beta_0 = 1$, $\beta_1 = 1$ and $\beta_n = 0$ for $n \geq 2$.

In relation to biometric samples, the betti number of special interest is β_1. It is important to note that a homology theory ensures that topological distinct spaces produce algebraically distinct homology groups, in particular the set of all betti numbers are not the same for topological distinct spaces.

It should be clear that empirical data is not ideal, i.e. there will be some variation in the observations made. In relation to fingerprints and the methodology proposed here, this means that two biometric samples will most likely produce two distinct topological spaces, even though the samples are acquired from the same source. As will be observed in a later section, the variation in the population will typically be centered around a mean.

Since graphs are our primary focus of investigation (1-dimensional cell complexes) a much simpler way of calculating homology can be used as opposed to the cases where surfaces and the higher dimensional analogs are taken into account. First of all only one map is of particular interest, namely the one sending edges to its corresponding boundary vertices. This is exactly what we illustrated in the above example, yet the actual map is somewhat unclear at this point. It happens that we can construct this linear map in such a way that the transformation matrix become explicit. One definition of f could be to use the orientation of the edges, e.g. define the boundary of an edge by a linear combination of the vertices of the edge with the sign of the individual terms depending on orientation. Define the starting vertex to have a negative coefficient and the ending vertex to have a positive coefficient. Figure 2 illustrates the idea.

Figure 2: Definition of boundary map.

With this definition the edges in X are mapped to their boundary by

$$\begin{aligned} f(a) &= v_2 - v_1, \\ f(b) &= v_3 - v_2, \\ f(c) &= v_3 - v_1. \end{aligned}$$

The map f can then be described by a matrix $\mathbf{F}$ given by

$$\mathbf{F} = \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \\ -1 & 0 & 1 \end{bmatrix},$$

The kernel $\ker f$ of the map f is the null space of the matrix $\mathbf{F}$. It is a subspace of $\mathrm{C}_1(\mathrm{X})$ and the dimension of this subspace is the betti number β_1 of the graph in figure 1, i.e.

$$\beta_1 = \dim \ker f = 1.$$

We now state a simple relation without proof, which gives us a very easy way to compute the betti number β_1 of a finite graph, e.g. a 1-dimensional triangulation of a point cloud in 3-dimensional Euclidean space. For a graph it holds that

$$\begin{aligned} \beta_1 &= 1 + \dim \mathrm{C}_1(\mathrm{X}) - \dim \mathrm{C}_0(\mathrm{X}) \\ &= 1 + (\text{number of edges}) - (\text{number of vertices}). \end{aligned}$$

Finding the higher betti numbers in higher dimensional cell complexes requires more advanced constructions from homology theory.

2.1 Application to biometric samples

Consider each grayscale image as a point cloud in $\mathbb{R}^3$, one point per pixel, i.e. the first two coordinates is the position of the pixel and the third coordinate is the grayscale intensity. A special way of constructing a triangulation of a point cloud called a Witness complex will be used, see [dSC04]. In loose terms, it limits the number of vertices and edges in a triangulation by choosing the vertices according to distances to other vertices in a point cloud. It is a cell complex where a small number of points from the point cloud are choosen as vertices and edges are then constructed iteratively according to a set of criterias as described in [dSC04].

Once the triangulation is constructed, the betti numbers are calculated using homology and the metric will be constructed. For simplicity a weighted Euclidean metric is chosen. Initially only two types of images are used, e.g. fingerprint or non-fingerprint. The non-fingerprint database will be either face samples or iris scan samples.

Assume that a vector is given consisting of n numbers acquired from a sample of fingerprint images, each the 1st betti number of a fingerprint; one for each image in the sample. Denote this vector by v and let the variance of v be denoted by σ^2. Given an image, it is possible to calculate the corresponding 1st betti number β_1. Let x denote the vector where each element is equal to this betti number for a given image.

Then for a fixed training set v, a metric can be constructed by

$$D(\beta_1) = D(\beta_1; x, v) = \frac{1}{\sigma}\left(\sum_{i=1}^{n}(x_i - v_i)^2\right)^{1/2}. \tag{1}$$

For the topological method presented here, the metric in equation 1 is used. For every image and corresponding 1st betti number β_1, calculate two numbers: 1) the distance $D_f(\beta_1)$ to a sample set of fingerprints. 2) the distance $D_g(\beta_1)$ to the sample set of non-fingerprints.

Now in order to be able to control the error rates of the overall analysis, a few simple functions are introduced. The two functions are

$$F_1(s, \beta_1) = sD_g(\beta_1) \quad \text{and} \quad F_2(s, \beta_1) = (1-s)D_f(\beta_1)\,, \quad s \in [0; 1].$$

Given a value of s, let $F_1 \geq F_2$ determine a false match increase by 1. Otherwise a false non match increase of 1. The proportion of the number of false matches (resp. false non matches) with respect to the number of non-fingerprints (resp. fingerprints) is the corresponding error rate. The value of s can be determined experimentally and thus depends on the choice of training sets. The variable s is used to calculate the ROC curve in the section presenting the results.

This method shall be thought of as a way to coarsely characterize a biometric sample or rather a point cloud.

3 Results

The results presented here will highlight both strengths and weaknesses of the method derived from topology which will be denoted TOP and the already known method SIVV. Some of the most interesting results are found when considering mixed biometric databases, i.e. databases where both fingerprints, iris and other biometric samples are contained. In order to see how the constructed metrics work on such databases when categorizing joint data sets with various fingerprint databases a DET curve is determined and the equal error rate EER is calculated.

Portions of the research in this article use the database CASIA-FingerprintV5 and CASIA-IrisV4 collected by the Chinese Academy of Sciences' Institute of Automation (CASIA), see [oSIoAC]. A fingerprint database acquired by Association BioSecure is used and referred to here simply as Biosecure. Also used is the MCYT database involving fingerprints which was collected in a project conducted in 2003, see [OGFAS$^+$03].

All calculations are carried out on a computer running Linux (kernel 3.3.2-1) with a Quad-core (3.10 GHz each) Intel Xeon E3-1225 processor and 4 GB memory. The software used for computation are Javaplex version 4.0 and the SIVVUtility package which is part of NIST Biometric Image Software version 4.0.1. All algorithms were run in parallel on three of the cores due to the large number of images needed to be processed. User interfaces have been rewritten in order to control output formats for both software packages.

3.1 General observations

There are a number of general observations to be made. The classifier used in this section is the 1st betti number. Considering the betti number of fingerprint images yield a bell shaped curve when approximating to the histogram in the figure below. A similar yet skewed result is found for non-fingerprints. The databases used to produce figure 3 are the CASIA-Fingerprint and CASIA-Iris databases.

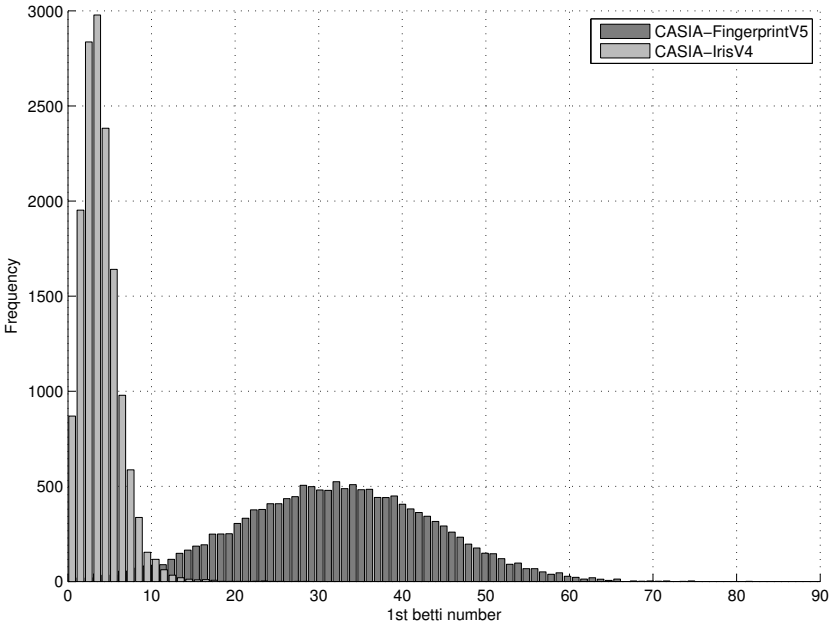
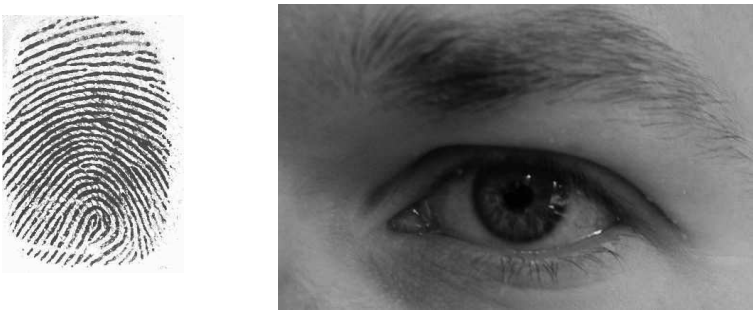


Figure 3: Histogram of the 1st betti numbers of CASIA fingerprint and iris images

These bell curve shapes, although one is skewed, may be a product of the method by which the betti numbers are calculated.

3.2 Mixed biometric (iris vs. fingerprint) database

In this section an analysis of the method is done using the iris database CASIA-IrisV4, see [oSIoAC]. The fingerprint databases are analyzed separately and the results are highlighted in a table in the end of this section. To illustrate the difference in the betti numbers a couple of examples are shown. The fingerprint is taken from the public database FVC2000Db2, see [MMC$^+$02], and the iris is the one from one of the authors. Note that this is meant merely as an example. The iris images used in the experiment are non-segmented ocular images.



(a) 1st betti number 57 (b) 1st betti number 2

Figure 4: Examples of 1st betti numbers of some images via witness complexes.

The examples in figure 4 indicate the difference of the betti numbers for the two types of biometric samples.

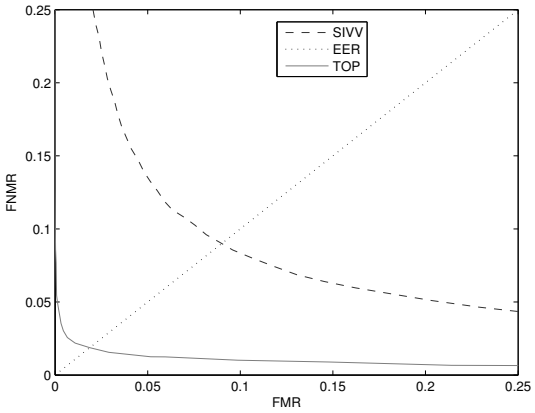


Figure 5: fingerprint vs. iris database: EER(TOP) = 2.7%, EER(SIVV)=9.0%.

Comparing with the SIVV method it becomes clear that the topological approach performs better for fingerprints vs. iris databases. The most interesting aspect of considering mixed biometric databases is that when Fourier analysis seem to produce misleading features; coarse topological features tend to correctly partition the database into biometric types.

The following table illustrates how the equal error rate varies between fingerprint databases for the two methods.

Database	SIVV	Topological method	Summary
MCYT dp	12.9%	0.2%	Largest observed difference between methods.
Biosecure	6.2%	1.9%	Smallest absolute difference.
CASIA	9.0%	2.7%	Medium difference between methods.

The results clearly suggests that using the TOP-method will produce much better results when categorizing fingerprints and iris scans. The most extreme case is the MCYT dp database. It is the database with best performance using the topological approach and the worst performance when using SIVV. An interesting observation has been made; the choice of fingerprint reference database, also called training set, does not produce a significant change in the results. So one may choose a subset from either MCYT dp, Biosecure or CASIA-fingerprintV5 as a sample reference to a fingerprint database. The following table illustrates the observed equal error rates when utilizing various training sets.

		Training set		
		MCYT dp	Biosecure	CASIA
Database	MCYT dp	0.2%	0.2%	0.2%
	Biosecure	1.9%	1.9%	1.9%
	CASIA	2.7%	2.7%	2.7%

At least from a statistical point of view it seems that the TOP-method is invariant of fingerprint reference database chosen. That is the equal error rate remains the same under different training sets. The table only illustrates this observation for the combinations of the three databases, MCYT dp, Biosecure and CASIA. One should be very careful before making any inference based on these preliminary observations. Note that the non-fingerprint image training set is not varied in this experiment.

3.3 Mixed biometric (face vs. fingerprint) database

A similar analysis as the one from the previous section will be carried out. The non-fingerprints in this section consists of facial images from the CASIA-FaceV5 database.

Database	SIVV	Topological method	Summary
MCYT dp	5.0%	1.0%	Largest observed difference between methods.
Biosecure	2.5%	3.0%	Smallest absolute difference.
CASIA	3.7%	4.1%	Medium difference between methods.

It is observed that SIVV performs slightly better for both CASIA fingerprints and Biosecure databases. A significant difference is observed when comparing with the MCYT database. In this particular case the method TOP performs better than SIVV. The results

shown here simply states that the TOP method does not yield better results than SIVV for all biometric samples when categorizing. In complete analogy with the study of iris vs. fingerprint, the equal error rates can be seen to be robust with respect to the choice of fingerprint training set.

		Training set		
		MCYT dp	Biosecure	CASIA
Database	MCYT dp	1.0%	1.0%	1.0%
	Biosecure	3.1%	3.0%	3.1%
	CASIA	4.2%	4.2%	4.1%

For the databases used in this study, it can be concluded that the variances imposed by changing the training set for the fingerprint database is not significant.

4 Discussion and conclusions

It has been shown that, given an image, homology of a specially constructed triangulation of the image, viewed as a point cloud will enable the separation of fingerprint images from other biometric samples, in particular when categorizing iris scans and fingerprints. For the iris scans the topological approach seems to perform better than the SIVV method. When categorizing fingerprints and face samples the method SIVV seem to perform better, if only slightly, for the databases Biosecure and CASIA-FingerprintV5. For the database MCYT the method TOP seem to perform significantly better. The result indicate that the acquisition of samples in the MCYT database or some form of processing of the images may cause this significant decrease in equal error rate. Moreover it is observed that the opposite holds for the SIVV method, where a significant increase in equal error rate is observed for the MCYT database compared against both iris and face databases. Our method seem to be invariant with respect to the choice of fingerprint training set.

The method of constructing the triangulation from a biometric sample, in this case a fingerprint image, can be improved. The general construction could be to consider particularly important landmarks in the fingerprint as vertices in the triangulation. Edges should then be assigned between two vertices in such a way that certain information about the sample specific to the landmarks yield a denser network, e.g. more information is retained in the triangulation, which in turn should indicate a higher quality. This latter part is an extensive work in progress, requiring many simulations to be run and much statistics to be collected. It is possible that the method TOP can be extended to categorize the types of fingerprints as well, e.g. identify whorl or arch structures.

Another possible extension of this study would be to study the same source under varying conditions, e.g. time, pressure variation and humidity conditions. This would give us an indication of the ability of the method to identify individual samples as being from captured from the same source. The relation to well-known image features and the importance of these are still unclear at this point, this being yet another interesting topic to study next.

References

[dSC04] Vin de Silva and Gunnar Carlsson. Topological estimation using witness complexes. In *SPBG04 Symposium on Point-Based Graphics*, pages 157–166, 2004.

[Ghr08] R. Ghrist. Three examples of applied and computational homology. *Nieuw Archief voor Wiskunde*, 5/9(2), 2008.

[LGO09] J. M. Libert, J. Grantham, and S. Orandi. A 1D Spectral Image Validation/Verification Metric for Fingerprints. *NISTIR 7599*, 2009.

[MMC+02] D. Maio, D. Maltoni, R. Cappelli, J.L. Wayman, A. K. Jain, and A. K. Jain. FVC2002: Second Fingerprint Verification Competition. pages 811–814, 2002.

[OGFAS+03] J. Ortega-Garcia, J. Fierrez-Aguilar, D. Simon, J. Gonzalez, M. Faundez-Zanuy, V. Espinosa, A. Satue, I. Hernaez, J.-J. Igarza, C. Vivaracho, D. Escudero, and Q.-I. Moro. MCYT baseline corpus: a bimodal biometric database. *IEE Proceedings - Vision, Image, and Signal Processing*, 150(6):395–401, 2003.

[oSIoAC] "Chinese Academy of Sciences' Institute of Automation (CASIA)". "CASIA-FingerprintV5, http://biometrics.idealtest.org/".

[SLL10] B. Scott Swann, John M. Libert, and Margaret A. Lepley. Tools for quality control of fingerprint databases. *Proc. SPIE*, 7667(766709), 2010.