

JPEG Optimisation for Fingerprint Recognition: Generalisation Potential of an Evolutionary Approach

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Abstract: For fingerprint-based biometric systems, JPEG has traditionally been one of the primary storage formats. In this paper, we investigate methods of optimising JPEG compression for increased matching scores at constant compression rates. To achieve this, an evolutionary approach is employed to optimise the quantisation matrix used by JPEG. While finding matrices that are better suited for different sets of fingerprints, different fingerprint sensors, and different recognition algorithms as they have been optimised for remains elusive, we find improvements in matching performance for dataset fitting scenarios.

1 Introduction

Due to its inclusion in a former version of the ISO/IEC 19794 standard on Biometric Data Interchange Formats, biometric systems relying on fingerprint data have traditionally used JPEG [PM93] as their image storage format, besides other specialised formats such as WSQ [BBH93] or, more recently, JPEG2000, the current ISO/IEC 19794 recommendation. The optimisation of existing standardised compression algorithms to meet the specific properties of the biometric data to be compressed is a natural strategy. For example, JPEG quantisation matrix (QM) optimisation has been done to optimise results in face recognition [JKAA06] and iris recognition [KSU09]. JPEG2000 has been optimised w.r.t. possible wavelet packet decomposition structures for fingerprint recognition [MSU10] and iris recognition [HUKU13]. Even JPEG XR has been optimised for the iris recognition context [HSU12]. Optimisation of JPEG for fingerprint image compression is unexplored up to now.

Thus, in this paper, we will suggest to optimise the JPEG QM for optimal usage in fingerprint recognition by employing evolutionary optimisation. In particular, we will focus on the potential generalisation of evolved QMs to different datasets as well as different feature extraction and matching schemes. In the remainder of this section, we will motivate our approach. Section 2 explains the methodology used in this study while detailed results are presented in Section 3. Section 4 concludes the paper.

Because our goal is to optimise the QM, it makes sense to first look at the distribution of DCT coefficients. To this end, we took two generic images (photographs), and visualised



Figure 1: Average DCT coefficients of generic and fingerprint images (lighter areas indicate higher values)

the average of DCT coefficients over all image blocks, and did the same for two fingerprint images. DCT coefficients are laid out in a matrix: horizontal frequency increases as the x coordinate (left to right) increases, vertical frequency increases as the y coordinate (top to bottom) increases. Thus, the top left corner contains the lowest frequency and the lower right corner the highest frequency. As can be seen in Figure 1, more energy is contained in the lower frequency coefficients for fingerprints and increasingly high frequencies seem to be less relevant for fingerprint images than for generic images, at least for the four chosen example images.

The default QM in the luminance channel (as shown in Figure 3a) was obtained from a series of psychovisual experiments, and has “been known to offer satisfactory performance, on the average, over a wide variety of applications and viewing conditions” [Bov09]. As is stated in the JPEG specification itself: “These tables are provided as examples only and are not necessarily suitable for any particular application.”

Our hypothesis was that, since the default QM was designed for the general case, it should be possible to find better candidates for specific use cases. To test this hypothesis, we created a manually crafted QM, based on the default QM but with most higher frequency components set to 255 (the maximum value for baseline JPEG) due to the observations in Fig. 1. This QM (which we will call “manual QM” from now on) can be seen in Figure 3b.

In this paper, we employ genetic algorithms to optimise the QM for fingerprint images in general, fingerprint images from a specific scanning device, and a specific set of fingerprint images (dataset fitting). Lastly, we investigate whether the results obtained with a specific fingerprint recognition algorithm do generalise to different algorithms.

2 Methodology

2.1 Evolution

Our main approach for finding better adapted QMs was to use genetic algorithms. We used *Watchmaker* [Dye10], an open source framework for implementing genetic algorithms

Database	Description
FVC2002 DB3	capacitive sensor "100 SC" (Precise Biometrics)
FVC2004 DB1	optical sensor "V300" (CrossMatch)
FVC2004 DB2	optical sensor "U.are.U 4000" (Digital Persona)
FVC2004 DB3	thermal sweeping sensor "FingerChip FCD4B14CB" (Atmel)

Table 1: Fingerprint Databases

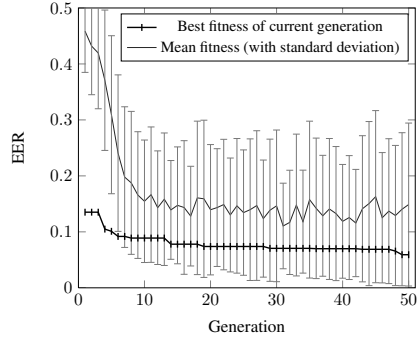


Figure 2: Example of fitness increase during an evolutionary run. (Data for this graph was collected by evolving a QM for 10 fingers (80 impressions) from FVC2002 DB3 over 50 generations.)

in Java. As source data, fingerprints from the databases of the Fingerprint Verification Competitions (FVC) of 2002 and 2004 were used, as shown in Table 1. Each database contains 8 impressions of 110 fingers.¹ We restricted our experiments to subsets of the first 100 fingers per database.

The basic idea of a genetic algorithm is as follows: There exists a population of individuals, and a fitness function that assigns each individual a specific fitness (a numeric value). The goal is to either maximise or minimise this fitness. An evolutionary run consists of multiple generations. In each generation, depending on the selection scheme, a subset of individuals are chosen to produce offspring (mostly via cross-over and mutation) for the next generation. The offspring constitute a new population and the algorithm starts over. This continues until some termination criteria is reached (e.g. a maximum number of generations, a target fitness threshold, fitness stagnation, ...).

Here, the individuals are QMs, represented by an array of $8 \times 8 = 64$ integer values (the quantisation coefficients). To get from a matrix to a one-dimensional array, the QM values are scanned in zigzag order [PM93]. As fitness function for a QM, the equal error rate (EER) is computed following the official FVC protocol [MMJP05]. Before that, the entire dataset subject to optimisation is compressed with JPEG as close as possible to the specified compression ratio (CR) using this QM.

Note that for evolutionary optimisation of the QMs, we use the freely available biometric software *NBIS* [NIS13] for template extraction (*MINDTCT* is used for minutiae extraction) and matching (using *BOZORTH3*).

For evolutionary cross-over, we use the existing class *IntArrayCrossover*, configured to use a single cross-over point. Given two parent individuals QM *a* and *b*, an index

¹In our copy of the data, images from FVC2004 DB3, fingerprint sets 5 and 54-60 were corrupt. Those sets have, for our experiments, been replaced with sets 102-109.

(point) $x \in \{0, \dots, 63\}$ is selected at random to generate the child c , where

$$c_i = \begin{cases} a_i & \text{if } i \leq x \\ b_i & \text{if } i > x \end{cases}, 0 \leq i < 64$$

For evolutionary mutation, we use an instance of the custom class `IntArrayMutation`, which (with a probability of $p = 0.02$ per array element) mutates an element x by a random value

$$m \in \mathbb{N}, -42 < m < 42$$

so that the final value is

$$y = \max(\min(x + m, 255), 0)$$

3 Experiments

3.1 Setup

Each evolution run in our experiments has the same basic steps and parameters: An instance of `QuantisationMatrixEvaluator` is created and parameterised with the employed fingerprint database, the number of individual fingers used from this database (10 to 100, in steps of 10), and the compression rate to aim for (which is set to 30 for our experiments, since this value represents a good compromise of file size reduction and still sensible matching results). A custom `IntArrayFactory` is created, which can create arrays of $8 \times 8 = 64$ randomly generated integer values of the form

$$x \in \mathbb{N}, 0 \leq x < 256$$

which are used as the initial population of QMs. A *Watchmaker* evolution engine instance is created and configured to use a roulette wheel selection algorithm, and a Mersenne Twister pseudorandom number generator. In addition to the initial random population, the engine is seeded with two predefined QMs: The default luminance QM from Figure 3a, and the manually crafted QM from Figure 3b. The evolution engine is started to run with a population of 100 individuals and an elite count² of 5 for 50 generations.

Figure 2 shows example results of an evolutionary run that took 12 hours and 3 minutes to complete on a Windows 7 (64 bit) computer with an Intel[®] Core[™] i5-2300 CPU and 8 GB of RAM.

3.2 Experimental Results

A visualization of two evolved QMs is shown in Figure 3, next to the default luminance (Figure 3a) and manual (Figure 3b) QMs.

²i.e. the number of individuals with highest fitness that are copied over to the next generation unchanged

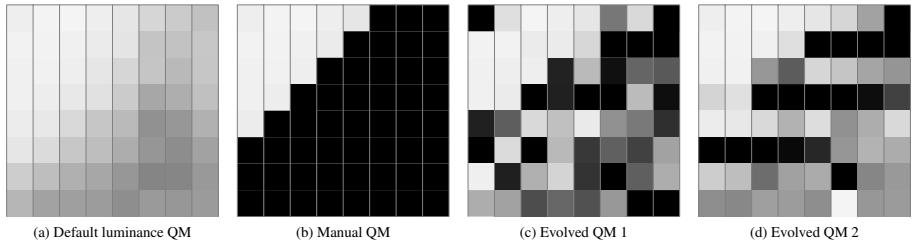


Figure 3: Visualization of select QMs (darker areas correspond to higher values)

The QM shown in Figure 3c was evolved using a set of 10 fingers (i.e. 80 impressions) from FVC2002 DB3 over 50 generations. Figure 3d shows a QM that was evolved on the same DB, but using a set of 100 fingers (i.e. 800 impressions). This suggests that it is possible, using an evolutionary search approach, to find non-obvious QM optimisations for a given set of images and a given application (i.e. biometric matching).

Figure 4 shows the results for dataset fitting (\triangle), i.e. a QM that is evolved for a certain set of fingers is evaluated over the same set of fingers of the identical database. The results are compared with default luminance (\times) and manual ($+$) QM performance.

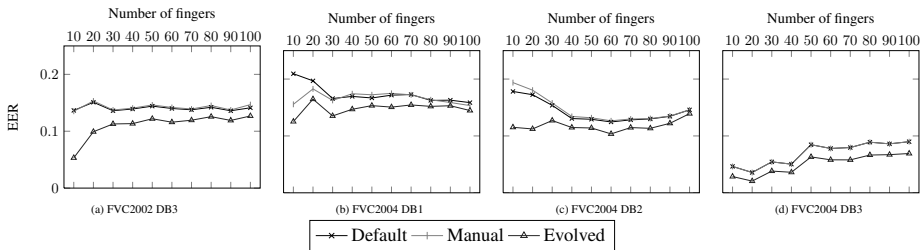


Figure 4: Dataset fitting EER for default, manual and evolved QMs using *NBIS*

We clearly notice that the EER is improved (i.e. decreased) for all four datasets in case of the evolved QM. Moreover, it turns out that, except for FVC2004 DB3, a low number of fingers involved in the optimisation process leads to higher gains in EER. This is to be expected since the adaptation process can really adapt to a low number of fingers almost individually.

To examine intra-database generalisation behaviour, we evolved QMs on a set of $n = 10k, k \in \{1, \dots, 9\}$ fingers, and evaluated the resulting QM on the remaining $100 - n$ fingers of the same database. The results are shown in Figure 5 (\circ), plotted against performance of the default luminance (\times) and manual ($+$) QMs.

Thus we can conclude that even for fingerprint images from the same sensor, matching performance gains from QM optimisation do not readily generalise across different sets of fingerprint impressions.

Figure 6 shows the EER for each of the four databases, when using QMs evolved for each

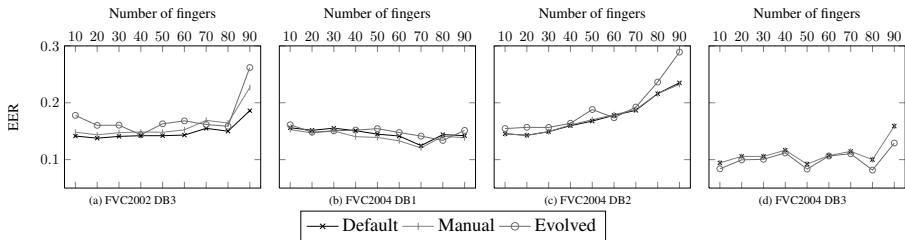


Figure 5: Intra-database EER for default, manual and evolved QMs. (Note that the number of fingers n indicates the number used for evolving the QM.)

database separately (on 100 fingers each, i.e. dataset fitting), compared with results for the default luminance and manual QMs (inter-database generalisation).

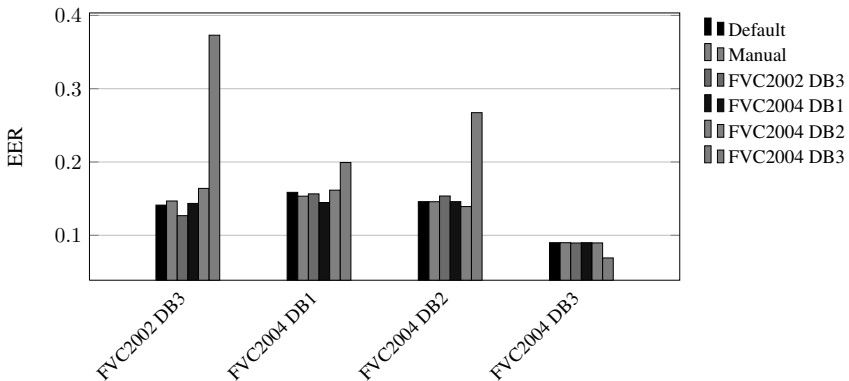


Figure 6: EER for default, manual and evolved QMs.

The EER when using a QM evolved for the same DB (on the same set of 100 fingers) clearly improves (decreases) as observed before. In contrast, when using “foreign” QMs (excluding the default and manual QMs), the average EER *increases* significantly. Using the manual QM leads to a slight average performance decrease. These results show that matching performance gains resulting from QM optimisation for a specific set of fingerprint images do not readily generalise to other sources of fingerprint image data.

Finally, we examine matching performance of different (non-*NBIS*) template extraction and matching engines when using QMs evolved using *NBIS* – cross-algorithm generalisation: *VeriFinger* and *Phase Only Correlation Matcher* (as re-implemented in [HUPU13]) are used.

Figures 7 and 8 show detailed results for cross-engine evaluation, with performance data for the default luminance (—x—), manual (—+—) and evolved (*VeriFinger* (—□—) and *Phase Only Correlation* (—◊—) QMs plotted against each other.

These results indicate that, while small performance increases appear for *Phase Only Cor-*

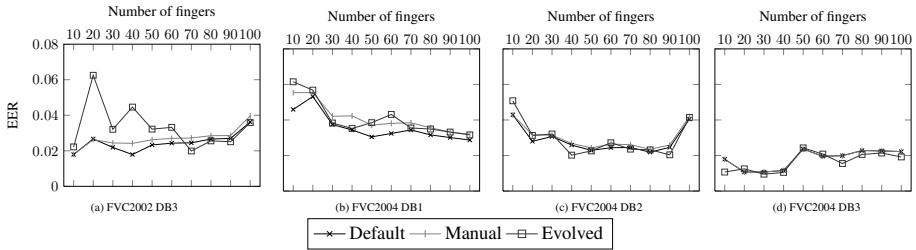


Figure 7: Dataset fitting EER for default, manual and evolved QMs using *VeriFinger*

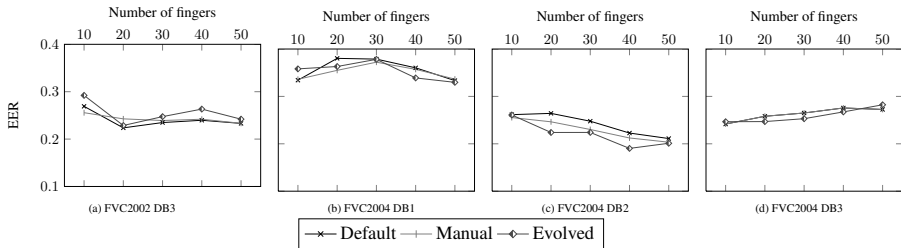


Figure 8: Dataset fitting EER for default, manual and evolved QMs using *Phase Only Correlation*

relation, significant performance gains (like those evidenced in the case of dataset fitting using *NBIS*) do not generalise to other template extraction and matching algorithms. In the case of *VeriFinger*, the manual as well as the evolved QMs lead to significantly worse performance.

4 Conclusion

Our experiments show that, while it is possible to tailor-fit JPEG for a specific set of fingerprint images by finding appropriate quantisation matrices via genetic algorithms, the resulting matching performance improvements do not, on average, generalise to other sets of fingerprint images, be it from the same database (and thus the same type of sensor) or from different ones. In addition, the evolved quantisation matrices do not, on average, lead to improved performance when employing template extraction and matching algorithms different than those used for evolution. The most promising result is an increase of on average more than 20% in matching performance for dataset fitting scenarios. Similar results and trends of poor generalisation behaviour have been reported for optimising JPEG2000 Part2 wavelet packet subband structures for iris recognition [HUKU13].

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