A Novel Quantum-Inspired Evolutionary Algorithm for Multi-Sensor Image Registration

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Abstract: *In this paper, we propose a new algorithm for image registration which is a key stage in almost every computer vision system. The algorithm is inspired from both evolutionary algorithms and quantum computing fields and uses the mutual information as a measure of similarity. The proposed approach is based on some concepts and principles of quantum computing such as quantum bit and states superposition. So, the definitions of the basic genetic operations have been adapted to use the new concepts. The evaluation of each solution is performed by the computation of mutual information between the reference image and the resulting image. The process aims to maximize this mutual information in order to get the best affine transformation parameters which allow the alignment of the two images belonging to either similar or different modalities.*

Keywords: *Image registration, evolutionary algorithms, mutual information, quantum computing, states' superposition.*

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1. Introduction

Image registration is a central task in most of vision systems. It is required in different applications such as objects recognition, 3D reconstructions and data fusion. Basically, image registration can be defined as the process which aims to find the best geometric transformation that allows the alignment of the common parts of two images. To solve this problem, which is a combinatorial optimization one, many approaches have been proposed. All of them intend to reduce the computing complexity and at the same time avoid local optimums. Among the proposed methods we can mention those based on artificial neural networks, simulated annealing, taboo search, genetic algorithms [4], ants colonies, and artificial immune systems.

Quantum computing is a new field in computer science which has induced intensive investigations and researches during the last decade. It takes its origins from the foundations of the quantum physics. The parallelism that the quantum computing provides reduces obviously the algorithmic complexity [1]. Such an ability of parallel processing can be used to solve combinatorial optimization problems which require the exploration of large solutions spaces. So, the quantum computing allows the design of more powerful algorithms that should change significantly our view about solving hard problems. However, the quantum machines that these algorithms require to be efficiently executed are not available yet. By the time when a powerful quantum machine would be constructed, some ideas such as simulating quantum algorithms on conventional computers or combining them to existing methods have been suggested to get benefit from this new science [2]. Within this perspective, we are interested in the combination of evolutionary algorithms and quantum computing for image registration with the use of the mutual information as a measure of similarity.

Consequently, the rest of the paper is organized as follows. Section 2 gives some concepts about genetic algorithms, mutual information and quantum computing. The proposed algorithm is described in section 3. Section 4 illustrates some experimental results and the main algorithm's properties are discussed in section 5. Finally, a conclusion and some perspectives are given in section 6.

2. Basic Concepts

2.1. Genetic Algorithms

Genetic algorithms derive from the evolution theory. They were introduced in 1975 by John Holland and his team as a highly parallel search algorithm. Later, they have been mainly used as optimization device.

According to the evolution theory, within a population only the individuals well adapted to their environment can survive and transmit some of their characters to their descendants. In genetic algorithms, this principle is traduced into the problem of finding the best individuals represented by chromosomes. So, each chromosome encodes a possible solution for the given problem and, starting from a population of chromosomes, the evolution process performs a parallel search through the solutions' space. The fitness is measured for each individual by a function related to the objective function of the problem to be solved.

Basically, a genetic algorithm consists of three major operations: Selection, crossover, and mutation. The selection evaluates each individual and keeps only the fittest ones in the population. In addition to those fittest individuals, some less fit ones could be selected according to a small probability. The others are removed from the current population. The crossover recombines two individuals to have new ones which might be better. The mutation operator induces changes in a small number of chromosomes units. Its purpose is to maintain the population diversified enough during the optimization process.

2.2. Entropy Based Measures and Mutual Information

The entropy is a statistical measure defined by Shannon in 1948. It summarizes the randomness of a given variable. The more random a variable is, the larger entropy it will have.

Given a random variable represented by a probability distribution X, i. e., a set of couples (x_i, p_i) where p_i is the probability to have the value x_i. The entropy of X is given by:

$$H(X) = -\sum p_i \log_2 p_i \quad (1)$$

Intuitively, entropy measures the average information provided by a given distribution.

When dealing with two random variables represented by two probability distributions X and Y, we are interested by answering the question: “How likely the two distributions are functionally dependant?” In total dependence case, a measurement of one distribution discards any randomness about the other. As a consequence, quantifying the independence is equivalent to quantifying the randomness. The joint entropy is given by:

$$H(X, Y) = -\sum \sum p(x, y) \log_2 p(x, y) \quad (2)$$

In the case of total independence between X and Y, the joint distribution is the product of the marginal distributions.

$$P(X, Y) = P(X) . P(Y) \quad (3)$$

In terms of entropy, this leads to:

$$H(X, Y) = (X) + H(Y) \quad (4)$$

The mutual information is a measure of the reduction on the entropy of Y given X and is then given by:

$$MI(X, Y) = H(X) + H(Y) - H(X, Y) \quad (5)$$

The mutual information is maximized when the two variables are totally dependant.

2.3. Quantum Computing

In early 80, Richard Feynman's observed that some quantum mechanical effects cannot be simulated efficiently on a computer. His observation led to speculation that computation in general could be done more efficiently if it used this quantum effects. This speculation proved justified in 1994 when Peter Shor described a polynomial time quantum algorithm for factoring numbers[6].

In quantum systems, the computational space increases exponentially with the size of the system which enables exponential parallelism. This parallelism could lead to exponentially faster quantum algorithms than possible classically [5].

The *quantum bit* (*qubit*) is the elementary information unit. Unlike the classical bit, the qubit does not represent only the value 0 or 1 but a superposition of the two. Its state can be given by:

$$\Psi = \alpha |0\rangle + \beta |1\rangle \quad (6)$$

Where $|0\rangle$ and $|1\rangle$ represent respectively the classical bit values 0 and 1; α and β are complex numbers such that:

$$|\alpha|^2 + |\beta|^2 = 1 \text{ n} \quad (7)$$

If a superposition is measured with respect to the basis $\{|0\rangle, |1\rangle\}$, the probability that the *measured* value is $|0\rangle$ is $|\alpha|^2$ and the probability that the measured value is $|1\rangle$ is $|\beta|^2$.

In classical computing, the possible states of a system of n bits form a vector space of n dimensions, i. e., we have 2^n possible states. However, in a quantum system of n qubits the resulting state space has 2^n dimensions. It is this exponential growth of the state space with the number of particles that suggests a possible exponential speed-up of computation on quantum computers over classical computers. Each quantum operation will deal with all the states present within the superposition in parallel. The basis of the state space of a quantum system of n qubits is:

$$\{|00...0\rangle, |00...1\rangle \ldots |11...1\rangle\}$$

The *measurement* of a single qubit projects the quantum state onto one of the basis states associated with the measuring device. The result of a measurement is probabilistic and the process of measurement changes the state to that measured. Multi-qubit measurement can be treated as a series of single-qubit measurements in the standard basis.

The dynamics of a quantum system are governed by *Schrödinger*'s equation. The *quantum gates* that perform transformations must preserve orthogonality. For a complex vector space, linear transformations that preserve orthogonality are unitary transformations, defined as follows. Any linear transformation on a complex vector space can be described by a matrix. A matrix M is unitary if $M.M' = I$. Any unitary transformation of a quantum state space is a legitimate quantum transformation and vice-versa. Rotations constitute one among the unitary transformations types.

One important consequence of the fact that quantum transformations are unitary is that they are reversible. Thus quantum gates, which can be represented by unitary matrices, must be reversible. It has been shown that all classical computations can be done reversibly.

3. The Proposed Algorithm

Having two images I_1 and I_2 obtained from either similar or different sensors, the proposed algorithm allows the estimating of the affine geometric transformation which overlays the two images. A similar work that concerns only rigid transformations class can be found in [7].

As in genetic algorithms, initial solutions are encoded in N chromosomes representing the initial population. The difference in our algorithm is that each chromosome is represented using quantum bits.

The geometric transformation that aligns the image I_2 on the image I_1 is affine. Affine transformations form the most commonly used type of spatial transformations for registration. A chromosome encodes the six parameters ($dx, dy, a_{11}, a_{12}, a_{21}, a_{22}$) of the affine transformation. Having such parameters, the position of each pixel in the resulting image (x', y') can be calculated from the original position in the second image (x_2, y_2) as follows:

$$\begin{pmatrix} x' \\ y' \end{pmatrix} = \begin{pmatrix} dx \\ dy \end{pmatrix} + \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} . \begin{pmatrix} x_2 \\ y_2 \end{pmatrix} \quad (8)$$

So, after applying the transformation on the second image, it must be aligned with the first one. This transformation does not have the properties associated with the orthogonal rotation matrix. Angles and lengths are no longer preserved, but parallel lines remain parallel. More general spatial distortions such as skew and changes in aspect ratio can be represented within this formulation.

Each parameter is encoded using a binary representation. A bit in a chromosome does not represent only the value 0 or 1 but a superposition of the two. In this way, all the possible solutions are represented in each chromosome and only one solution among them can be measured at each time according to the probabilities $|\alpha_i|^2$ and $|\beta_i|^2$. A chromosome is then represented by:

$$\left(\begin{array}{c|c|c|c} \alpha_1 & \alpha_2 & \ldots\ldots & \alpha_{48} \\ \beta_1 & \beta_2 & \ldots\ldots & \beta_{48} \end{array} \right)$$

Where each column represents a single qubit. In our algorithm α_i and β_i are real values only.

Initially we generate randomly 4 chromosomes. Each one is composed of $N = 48$ qubits, 8 qubits for each parameter, i. e., 2^8 possible value for each one. dx and dy are the 2D translation parameters and belong to the interval $[-127, +127]$. The other parameters belong to the interval $[-2, +2]$ (the interval is subdivided into $2^8 = 256$ real value).

During the whole process we keep in memory the global best solution.

The algorithm consists on applying cyclically 4 quantum genetic operations (Figure1):

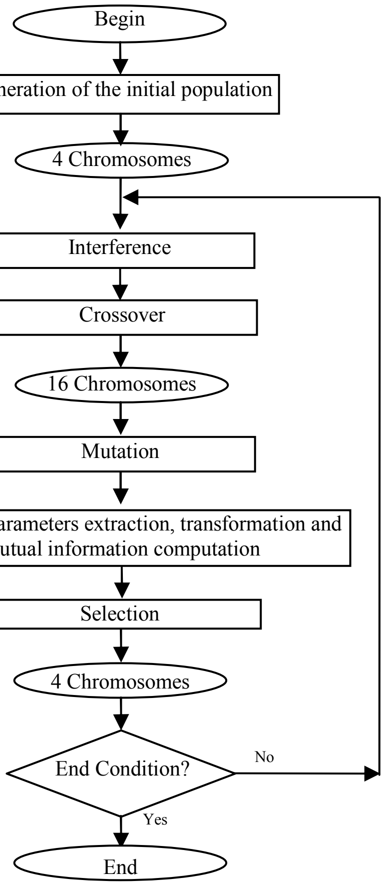

Figure 1. The proposed algorithm.

The first operation is a quantum interference which allows a shift of each qubit in the direction of the corresponding bit value in the current best solution. That is performed by applying a unitary quantum operator which achieves a rotation whose angle is function of α_i, β_i and the value of the corresponding bit in the best solution (Figure 2).

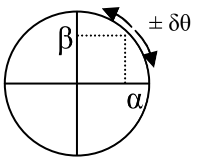

Figure 2. Quantum interference.

$\delta\theta$ has been chosen experimentally equal to $\pi/45$ (different values had been tested and this value was the one which gave the best solutions) and its direction is function of α, β and the bit's value in the best solution (Table 1).

Table 1. Lookup table of the rotation angle.

A	>0	>0	>0	>0	<0	<0	<0	<0
B	>0	>0	<0	<0	>0	>0	<0	<0
Reference bit value	1	0	1	0	1	0	1	0
Angle	+δθ	-δθ	-δθ	+δθ	-δθ	+δθ	+δθ	-δθ

The second operation is a crossover performed between each pair of chromosomes at a random position. Figure 3 shows an example of a crossover between two chromosomes.

$$\left(\begin{array}{cc|cccc} \mathbf{0.9501} & \mathbf{-0.8913} & \mathbf{0.8214} & \mathbf{0.9218} & \mathbf{-0.9355} & \mathbf{-0.0579} \\ \mathbf{0.3119} & \mathbf{0.4534} & \mathbf{-0.5703} & \mathbf{0.3876} & \mathbf{-0.3534} & \mathbf{0.9983} \end{array}\right)$$

$$\left(\begin{array}{cc|cccc} -0.2844 & -0.5828 & 0.4329 & -0.5298 & -0.7833 & 0.7942 \\ -0.9587 & 0.8126 & 0.9014 & -0.8481 & 0.6216 & -0.6076 \end{array}\right)$$

$$\Downarrow$$

$$\begin{pmatrix} \mathbf{0.9501} & \mathbf{-0.8913} & 0.4329 & -0.5298 & -0.7833 & 0.7942 \\ \mathbf{0.3119} & \mathbf{0.4534} & 0.9014 & -0.8481 & 0.6216 & -0.6076 \end{pmatrix}$$

$$\begin{pmatrix} -0.2844 & -0.5828 & \mathbf{0.8214} & \mathbf{0.9218} & \mathbf{-0.9355} & \mathbf{-0.0579} \\ -0.9587 & 0.8126 & \mathbf{-0.5703} & \mathbf{0.3876} & \mathbf{-0.3534} & \mathbf{0.9983} \end{pmatrix}$$

Figure 3. Quantum crossover.

At each iteration, we obtain from the 4 initial chromosomes 12 new ones. The population becomes composed of 16 chromosomes.

The third operation consists on a quantum mutation which will perform for some qubits, according to the mutation rate, a permutation between their values α_i and β_i. That will invert the probabilities of having the values 0 and 1 when applying a measurement (Figure 4).

$$\begin{pmatrix} 0.7446 & -0.6833 & 0.1338 & \overset{\downarrow}{\mathbf{0.3705}} & -0.0272 & 0.6831 \\ -0.6675 & 0.7301 & 0.9910 & \mathbf{-0.9288} & -0.9996 & 0.7303 \end{pmatrix}$$

$$\Downarrow$$

$$\begin{pmatrix} 0.7446 & -0.6833 & 0.1338 & \mathbf{-0.9288} & -0.0272 & 0.6831 \\ -0.6675 & 0.7301 & 0.9910 & \mathbf{0.3705} & -0.9996 & 0.7303 \end{pmatrix}$$

Figure 4. Quantum mutation.

A variable mutation rate has been chosen. Let *i* be the range of the chromosome (the 4 initial chromosomes are sorted according to their fitness after the previous iteration from the best to the worst one; the other 12 chromosomes are the result of the crossover between the 4 first ones). The mutation rate (MR) is set to the value:

$$MR = 0.003 * i^2$$

This means that only few qubits will be affected within the best chromosomes, whereas more qubits will be subject to mutation within the weak chromosomes.

Finally, we perform a selection of 4 chromosomes among the 16. For this, we apply first a measurement on each chromosome to have from it one solution among all those present in superposition. But unlike pure quantum systems, the measurement here does not destroy the states' superposition. Since our algorithm operates on a conventional computer and does not require the presence of a quantum machine, it is possible and in our interest to keep all the possible solutions in the superposition for the next iterations. For each measurement result, we extract the transformation parameters and use them to transform the second image (equation 8) and have a calculated image. To evaluate the quality (or the fitness) of an obtained solution, we compute the mutual information between the first image (reference image) and the calculated image. For calculating such mutual information we need first the calculation of the reference and result image histograms and also the joint histogram. Greater the mutual information is, better the solution will be considered [3]. Afterwards, we select the 3 chromosomes from which derive the 3 best results and we select also randomly one chromosome from the others (in order to maintain a good diversity). So we have all in all 4 chromosomes which form the new population. The global best solution is then updated if a better one is found and the whole process is repeated until having satisfaction of a stopping criterion (maximum number of iterations in our experiments).

4. Experimental Results

We have applied the proposed algorithm on many pairs of images obtained from different sources. The present section illustrates some obtained results when applying the registration algorithm.

Figure 5 shows at the left side two images belonging to the same modality (the second image is the result of the application of a geometric transformation on the first one) on which we have applied the proposed quantum genetic algorithm. The third image is calculated from the second one according the obtained transformation parameters values.

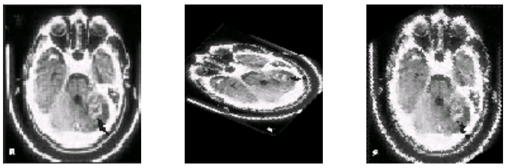

Figure 5. Test images and registration result.

Figure 6 illustrates the evolution of the best value of the mutual information through time. The obtained transformation parameters values are:

$$\begin{pmatrix} dx \\ dy \end{pmatrix} = \begin{pmatrix} +8 \\ -3 \end{pmatrix}$$

$$\begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} = \begin{pmatrix} +0.9531 & +0.8125 \\ -1.7344 & +0.5781 \end{pmatrix}$$

The final mutual information is 1.1743.

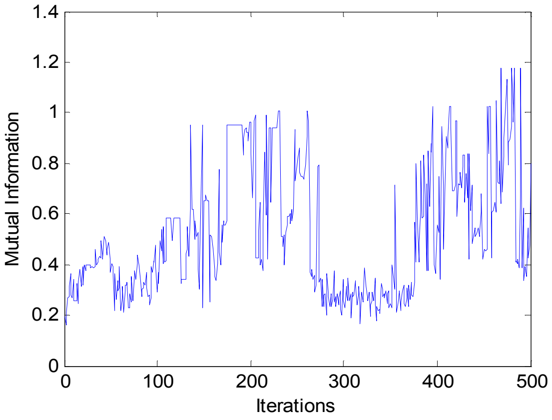

Figure 6. Best mutual information evolution.

The results below (Figure 7) concern two images obtained from different sensors. The first image is a Magnetic Resonance Image (MRI) and the second one is an X-ray Computed Tomography Image (CTI).

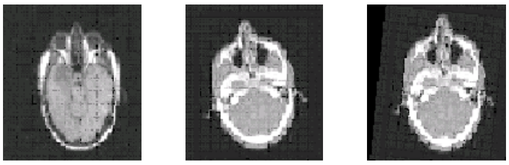

Figure 7. Test images and registration result.

Figure 8 illustrates the evolution of the best value of the mutual information through time. The obtained transformation parameters values are:

$$\begin{pmatrix} dx \\ dy \end{pmatrix} = \begin{pmatrix} -1 \\ +6 \end{pmatrix}$$

$$\begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} = \begin{pmatrix} +1.0469 & +0.1094 \\ -0.1094 & +0.9531 \end{pmatrix}$$

The final mutual information is 1.0015.

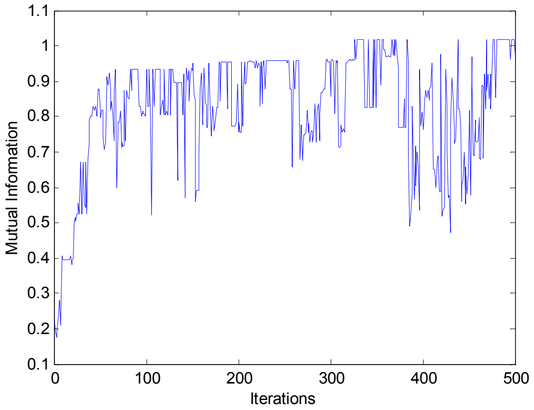

Figure 8. Best mutual information evolution.

The third sample given below (Figure 9) is about the registration of a MRI with a scintigraphical image.

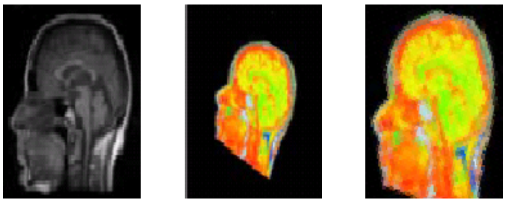

Figure 9. Test images and registration result.

Figure 10 illustrates the evolution of the best value of the mutual information through time. The obtained transformation parameters values are:

$$\begin{pmatrix} dx \\ dy \end{pmatrix} = \begin{pmatrix} +5 \\ -2 \end{pmatrix}$$

$$\begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} = \begin{pmatrix} +1.5000 & -0.5000 \\ +0.3281 & +1.5156 \end{pmatrix}$$

The final mutual information is 0.8634.

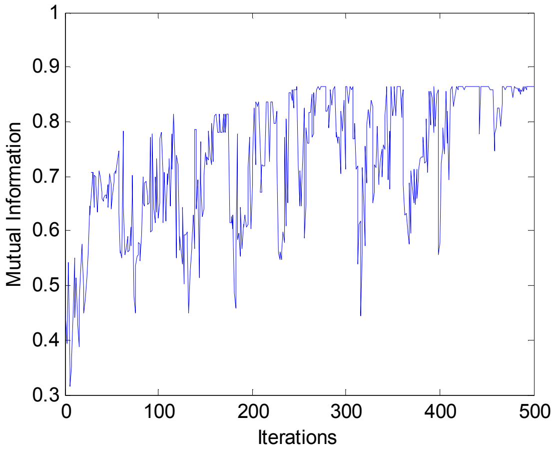

Figure 10. Best mutual information evolution.

5. Discussion

We should notice that very good solutions are obtained after less than 500 iterations.

Classical genetic algorithms used to perform the same task [4] require an obviously greater number of chromosomes (usually more than 50), and dozens of thousands of iterations are needed to have acceptable solutions.

There are two main reasons why our quantum-inspired algorithm is better than its classical counterparts. The first reason is that the quantum encoding of potential solutions reduces considerably the required number of chromosomes that guarantees good search diversity. So, each single chromosome represents at the same time all the possible solutions. The second reason is that the use of the quantum interference offers a powerful tool to reinforce the search stability. And then, it allows the speeding-up of the convergence.

Obtaining good results is conditioned by an adequate choice of the different algorithm parameters values. The first important parameter is the number of chromosomes. It is possible theoretically to use only one chromosome, but practically, this leads usually to the reinforcement of local optima. Thus, we need slightly more chromosomes to diversify enough the search. In spite of this, the needed number of chromosomes is very small compared to the classical genetic algorithms since 3 or 4 chromosomes are sufficient. The second parameter which plays an important role in the optimisation process is the interference angle. A small angle favours a slow convergence but may avoid local optimums whereas a large angle favours fast convergence but may reinforce false optimum. So, one should choose carefully the value of the interference angle to obtain an optimal solution in a reasonable number of iterations. The other parameter that should be chosen cautiously is the mutation rate. A small rate will limit the search diversity, whereas a big rate tends to make the search almost random.

6. Conclusion

Our algorithm, compared to genetic algorithms, provides the advantage of giving a greater diversity by using quantum coding of solutions, i. e., all the solutions exist within each chromosome and what change are the probabilities to have one of them as a result of a measurement. Therefore, the size of the population does not need to be great. So, we have chosen to have only 4 chromosomes at the origin of each generation. Another advantage is that the interference provides in some way a guide for the population individuals and reinforces therefore the algorithm convergence. The use of the mutual information has allowed the registration of images coming from different sensors. That will provide the possibility of data fusion.

The obtained results are usually good. In comparison to classical genetic algorithms, the proposed quantum genetic algorithm has the advantage of using a small population size and the number of necessary iterations to have acceptable solution is also obviously smaller.

As ongoing work, we have first to study more rigorously the role of each algorithm parameter and its influence on the algorithm behaviour in order to establish the optimal values of the population size, the mutation rate and the interference angle that guarantee an optimal alignment for every pair of images. We would also use similar algorithms to solve efficiently other optimization problems.

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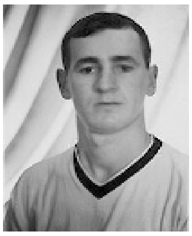

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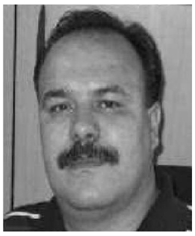

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