An Artificial Immune System for Multimodality Image Alignment

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Abstract. Alignment of multimodality images is the process that attempts to find the geometric transformation overlapping at best the common part of two images. The process requires the definition of a similarity measure and a search strategy. In the literature, several studies have shown the ability and effectiveness of entropy-based similarity measures to compare multimodality images. However, the employed search strategies are based on some optimization schemes which require a good initial guess. A combinatorial optimization method is critically needed to develop an effective search strategy. Artificial Immune Systems (AIS_s) have been proposed as a powerful addition to the canon of meta-heuristics. In this paper, we describe a framework which combines the use of an entropy-based measure with an AIS-based search strategy. We show how AIS_s have been tailored to explore efficiently the space of transformations. Experimental results are very encouraging and show the feasibility and effectiveness of the proposed approach.

1 Introduction

For many computer vision applications such as pattern recognition, 3D reconstruction and image data fusion, image alignment is an essential platform. Basically, image alignment or registration is the process that aims to find the geometric transformation that allows the best superposition of the common part of two images. A great deal of effort has been devoted to develop image registration methods. Good and comprehensive surveys have been proposed in the literature [1-3]. These methods fall into two broad categories: feature-based methods and intensity-based methods. For the first ones, homologous features are extracted from the images to be aligned and put into one to one correspondence. The geometric transformation parameters are then estimated from the obtained correspondences [4]. For the second ones, no feature extraction task is needed. They require the definition of a similarity measure and a search strategy. The similarity measure, as suggested by its name, is used to have a quantitative evaluation of how much two images or their parts are similar. The search strategy acts to describe how the search space i.e. the space of allowable transformations, is explored to find the best alignment. When the two images to be aligned are provided by two different imagery systems they contain different but complementary information. As a consequence, their fusion is a useful tool to get an evolved description of the scene under consideration. As the images are highly dissimilar, it is very hard to detect homologous features in both of them. That is why it is very hard to apply a

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feature-based method to align them. Intensity-based methods are more suitable in this case. Entropy-based measures like mutual information [5-8] have been shown in several studies to be the most appropriate and effective similarity measures to compare multimodality images. However the employed search strategies rely on some optimization schemes like hill climbing and gradient descent to avoid being trapped by local minima. The exploration of the search space is labor intensive and can be viewed as a combinatorial optimization task. As a consequence, a combinatorial optimization method is critically needed when developing a search strategy for multimodality alignment. Recently, there has been a boost of interest in applying naturally inspired optimization methods.

During the last decade and independently to computer vision, a new emerging area called artificial life is born. Artificial life is devoted to new field that researchers exploit to solve real world problems, using ideas gleaned from natural mechanisms. An artificial life approach to the image processing offers a chance to discover techniques perhaps more novels, more efficient or just unusual [9]. Neural networks, genetic algorithms, ant colonies and recently immune systems are paradigms from this area. Artificial immune systems have aroused great interest among researchers. This is motivated by the fact that natural mechanisms such as: recognition, identification and post processing by which the human body attains it immunity, suggest new ideas for patter recognition, learning, communication, adaptation, self organization, and distributed control [10]. Artificial immune systems have significantly contributed in the artificial intelligence field. Their applications range from network security, data mining, robotics, image classification to optimization.

In this paper, we suggest the use of an artificial immune system for solving the multi modality images alignment problem. In [11] authors have described a solution based on a genetic algorithm. Promising results were obtained however some limitations have been encountered especially those related to the algorithm convergence, the diversification and the exploration of the search process. Furthermore, recent work described the artificial immune systems as an approach that can overcome these restrictions [12]. This explains our motivation in using this new paradigm. We propose an intensity-based approach for multi modality image registration based on the maximization of the mutual information, as a similarity measure and an artificial immune system, with a real valued representation, as a search strategy.

The remainder of the paper is organized as follows: In Section 2, we formulate the problem to be solved. In section 3, we present a brief introduction to the natural immune system and an overview of artificial immune systems and related work. Section 4, is devoted to the description of the proposed approach. Experimental results and a comparison with an approach based on genetic algorithm are presented in section 5. Finally, conclusion and further work are drawn.

2 Problem Formulation

The addressed problem can be formulated as follow. Let two images I_1 and I_2 acquired from two different imagery systems, where I_1 is the sensed image and I_2 is the reference one. We have to find a geometric transformation T that correctly aligns the two images. T is a non-linear transformation defined by a set of parameters (a_0, a_1, a_2, a_3, b_0, b_1, b_2, b_3) such as:

$$x' = a_0 + a_1 x + a_2 y + a_3 xy$$
$$y' = b_0 + b_1 x + b_2 y + b_3 xy$$

Where (x', y') are coordinates of a point in I_1, and (x, y) are the coordinates of its corresponding point in I_2. We seek for parameters values in R^8 space that provide a best superposition of the two images. For this purpose, we need a measure that quantitatively evaluates the relationship between the two images when they are superimposed, and a search strategy.

- **Similarity Measure:**

Most of the existing similarity measures are based on the hypothesis of similarity between intensity values up to an unknown geometrical transformation. This assumption is very restrictive and makes methods inefficient in practice especially in multimodality alignment. The reason is that the acquired images are similar in structures but present very different characteristics. So, instead of expressing the sensed image as a function of the reference image, the idea is to predict the sensed image from the reference image. In information theory, predictability is closely related to an old concept introduced by Shannon, known as *Entropy*.

Formally, entropy summarizes the randomness of a certain random variable. Given a certain random variable represented by a probability distribution X i.e. a set of couples (x_i, p_i) where x_i is a value and $p_i = p(X=x_i)$ is the probability of occurrence of value x_i. Entropy of X denoted by $H(X)$ is defined as an expectation:

$$H(X) = - E_x [log(X)] = -\Sigma p_i \log p_i$$

Entropy is defined in terms of the logarithm base 2. Intuitively, entropy measures the average information provided by a certain 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 dependent?. In total dependence case, a measurement of one distribution completely determines the other and hence removes any randomness about it, whereas knowledge of one does not help at all predict the other in total independence case. As a consequence, quantifying dependence is equivalent to quantifying randomness. So, entropy measure is a tool that allows evaluating the extent to which two distributions are dependent.

The joint distribution denoted by $P(X, Y)$ is a mathematical structure that relates the co-occurrence of events from distribution X and Y. It offers a complete description of a random behavior of X and Y. This can be evaluated by the joint entropy, given by:

$$H(X, Y) = -\Sigma\Sigma p(x,y) \log p(x,y)$$

The mutual information MI is a measure of the reduction on the entropy of Y given X. It is defined as the difference between the sum of marginal entropies and the joint entropy:

$$MI(X, Y) = H(X) + H(Y) - H(X, Y)$$

The mutual information is equal to zero when X and Y are independent and it is maximized when they are totally dependent.

- **The Search Strategy**

According to mutual information definition, maximizing this measure seems to be a promising alternative to find good alignment of multimodality images. Therefore, we have to define an efficient search strategy in order to find the transformation T* by exploring the search space $\Im$ such that:

$$T^* = \underset{T \in \Im}{\operatorname{argmax}} \left(MI\left(I_2, T\left(I_1\right)\right)\right)$$

The search space $\Im$ in the case of our study is the set of non-linear transformations. For this purpose, we suggest a population-based optimization approach that exploits the evolutionary characteristics of artificial immune systems.

3 From Natural Immune System to Artificial Immune System

3.1 Natural Immune System

The immune system is the name of a collection of molecules, cells, and organs whose complex interaction forms an efficient system that is usually able to identify and protect an individual from both exogenous agents, called antigens and its own altered internal cells, which lead to disease.

The basic building blocks of the immune system are white cells or lymphocytes. A lymphocyte has about 10^5 receptors. In particular, B cells, special lymphocytes, have the responsibility of secreting receptors called antibodies. A special part of the antibody, called paratope, is used to identify other molecule. In other side, antigens have also receptors called epitope. Binding between a paratope and an epitope is based on their complementary shapes that suppose the generation of an opposite structure that adjusts at best the antigenic receptor. The strength of this bind is termed affinity.

When a B cell recognizes an antigen i.e. its antibodies are strongly matched to the antigen, it clones itself producing identical copies. This B cells selection based on their antigenic affinity is called the clonal selection principle. The number of clones produced by a lymphocyte is proportional to its stimulation level. After the B cells proliferation, clones are not perfect. By allowing mutation the match could become better. So clones are subjected to somatic mutation called hypermutation, inversely proportional to their affinity. Therefore, the clones' affinity becomes better mature, leading to affinity maturation. Cells with low affinity or self-reactive receptors are subject to a process named negative selection, where they destroy their affinity by developing new receptors or by direct cells elimination. As a result of clonal expansion, an immune memory is built; some of the cloned cells differentiate into memory cells and the rest of clones become plasma cells. Thus, B cells remember the shape of the antigen during a probable intrusion. Theoretical insights of these concepts can be found in [13, 14].

3.2 Artificial Immune System

Artificial immune systems are adaptive systems inspired by the biologic immune system for solving different problems. Dasgupta [10] define them as a composition of intelligent methodologies, inspired by the natural immune system for the resolution of real world problems. In the AIS_s a problem with unknown solution is treated as an antigen while problem solutions are modeled by antibodies. There are many successful AIS implementations [15-18]. Typically, antibody-antigen interactions coupled with the somatic mutation are the basis of a lot of AIS applications. Various models and algorithms have been suggested : negative selection algorithm for networks security [17] and the anomalies detection [19] immune network dynamics and the negative selection for image inspection and segmentation [15,20], the clonal selection theory and its applications in the pattern recognition [20], the machine learning [20,21] and the optimization [21-25].

Particularly, optimization problems have been the subject of lot of investigations. Hajela and Yoo [18] have proposed an approach based AIS devoted to solving optimization problems that improves the classical genetic algorithm. They argued their approach by the fact that capabilities of an immune system for accomplishing recognition and adaptation schemes can be used for improving both optimization problems and convergence in classical genetic algorithms. That is ensured by mechanisms avoiding the premature convergence in GAs while maintaining diversity. Later on, other optimization approaches based on AIS_s have been developed.

Based on the clonal selection theory, the affinity maturation and the negative selection, the Clonalg algorithm (CLONal selection ALGorithm) has been developed and implemented by De Castro and Von Zuben [21,22], not only for accomplishing machine learning and pattern recognition tasks but also for solving optimization problems.

The proposed algorithm can be viewed as a multi-agent approach using competition and cooperation mechanisms. Individual antibodies are in competition in order to solve (optimize) the problem and the whole of the population cooperate given the final solution. The proposed algorithm has been successfully applied to a variety of problems like testing the learning capabilities and memory acquisition by a binary characters recognition system, multi modal optimization tasks and instance of the TSP for combinatorial optimization. In the next section, we describe how Clonalg algorithm has been tailored to our problem.

4 Description of the Proposed Framework

The proposed approach has been developed by taking inspiration from Clonalg. It assumes the existence of an antibodies folder that can be stimulated. Moreover no distinction between cells and theirs receptors is made.
The main immune aspects taken into account are:

- Maintenance of the memory cells;
- Selection and cloning of the most stimulated cells;
- Death of non-stimulated cells;
- Affinity maturation and re-selection of the higher affinity clones;
- Generation and maintenance of diversity;
- And hypermutation proportional to the cell affinity.

To adapt Clonalg our problem, we first need to define an appropriate representation scheme.

4.1 AIS Elements Representations

The representation scheme can be described by the following definitions of the key elements arising in AIS.

1. Antigen: It represents the problem to solve. In our context, it is the transformation T* which aligns at best the transformed sensed image and the reference one by maximizing their mutual information:

$$T^* = \underset{T \in \Im}{argmax}\,(MI\,(I_2, T\,(I_1)))$$

2. Antibody: As a non-linear transformation T is a potential solution to the problem, an antibody can be viewed as a possible parameter combination (a_0, a_1, a_2, a_3, b_0, b_1, b_2, b_3). A population of antibodies is therefore a set of non-linear transformations. A real valued representation of genes is used to encode the transformation parameters. For the need of the mutation of real values, we associate to each vector another vector (a_{0s}, a_{1s}, a_{2s}, a_{3s}, b_{0s}, b_{1s}, b_{2s}, b_{3s}) representing the values of the standard deviation for each parameter (see figure 1).

a_0	a_1	a_2	a_3	b_0	b_1	b_2	b_3
a_{0s}	a_{1s}	a_{2s}	a_{3s}	b_{0s}	b_{1s}	b_{2s}	b_{3s}

Fig. 1. Representation of a candidate solution: transformation.

3. Clone: solution's offspring. One clone has the same structure as a solution. It is also represented by a couple of real valued vectors.

4. Antigen-antibody affinity: According to the problem analysis, it seems obvious that the fitness function value of an antibody is closely related to mutual information value computed for the corresponding transformation. To compute mutual information value for a certain antibody (transformation) T relating the sensed image I_1 and the reference image I_2, we determine the joint distribution between I_2 and $T(I_1)$ by the computation of their joint histogram obtained by recording the occurrences of every pair of pixel values within I_2 and $T(I_1)$. From the joint histogram, we can deduce the marginal histograms X and Y corresponding to $T(I_1)$ and I_2 using formulas :

$$P(X)= \Sigma P(X,Y=y_i) \quad and \quad P(Y)= \Sigma P(Y, X=x_i)$$

From the joint and marginal histograms, we derive directly the entropies and the mutual information.

4.2 The Proposed Algorithm

The proposed algorithm proceeds as follows:

Step 1: Generation of a set (Ab) of candidate solutions, composed of the subset of memory cells (M) added to the remaining (Ab*r*) population (Ab = Ab*r* + M); It is the set of the potential transformations.

Step 2: Select the *n* best solutions of the population, based on the affinity measure MI.

Step 3: Clone (reproduce) these *n* best solutions of the population, giving rise to a temporary population of clones (*C*). The clone size is an increasing function of the mutual information;

$$N_c = \sum_{i=1}^{n} round\left(\frac{\beta * N}{i}\right)$$

Where N_c is the total amount of clones generated for the antigen, β is a multiplying factor and N is the total amount of antibodies. Each term of this sum corresponds to the size of each selected antibody.

Step 4: Submit the population of clones C to an hypermutation scheme, where the hypermutation is conversely proportional to the mutual information of the antibody. A maturated antibody population is generated *C**. We have chosen a Gaussian mutation with a real valued mutation.

Mutation: The mutation is an operator which changes the genetic information by modifying genes of the two vectors. For each gene of the first vector, a random number *r* in [0, 1] is generated. If *r* is smaller than a predefined mutation probability the value of the gene in the first vector is modified using its corresponding gene in the second vector which is taken as the standard deviation of a centered normal distribution, given by the formula:

$$a_i^* = a_i + K.X, \qquad X \sim \aleph\,(0, a_{is})$$

Where:
a_i* is the mutated value of the selected gene $a_{i.}$, *K* is a weight factor used to improve convergence and *X* is a random variable. An acceptable convergence occurs for *Kmax =60.*

The associated gene in the second vector is also modified according to a random variable normally distributed according to:

$$a_{is}^* = a_{is}.e^X, \qquad X \sim \aleph(0,0.5)$$

where:
a_{is}* is the mutated value of the correspondent gene a_{is} in the standard deviation vector.

The mutation rate, α, is such that:

$$\alpha = \ell^{-\rho f}$$

Where:

ρ is a factor controlling the decay and *F* is antigenic affinity (the mutual information value). ρ and *F* are normalized to the range [0..1].

Step 5: Re-select the improved individuals from *C** to compose the memory set. Some members of the Ab set can be replaced by other improved members of *C**;

Step 6: Finally, replace *d* low affinity antibodies of the population, maintaining its diversity.

The proposed algorithm is an iterative process. Starting with an initial population of potential solutions, the process is repeated numerous times until a maximum number of iterations is reached.

5 Experimental Results

To evaluate the performance of the proposed algorithm, different pairs of images have been used. In figure 2, we show two examples of medical image pairs. These images are acquired from Magnetic Resonance Imagery system and Computed Tomography system. Results are illustrated in table 1.

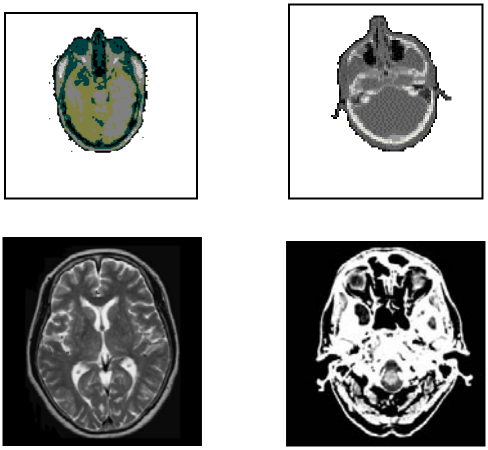

Fig. 2. Examples of image pairs.

Table 1. Results of the application of the proposed algorithm to both pairs of images.

Initial state.	***Final state***
Pair 1 : Marginal Entropy of (a) = 4.746. Marginal Entropy of (b) = 3.852. Joint Entropy of (a)and (b)= 7.494. MI (Mutual Information)= 1.104.	MI (Mutual Information) = 2.529. The best transformation parameters obtained are: $a_0 = 3.506$, $a_1 = 0.891$, $a_2 = 0.125$, $a_3 = 0.002$, $b_0 = 9.812$, $b_1 = -0.157$, $b_2 = 1.062$, $b_3 = 0.013$
Pair 2 : Marginal Entropy of (a) = 5.681. Marginal Entropy of (b)= 4.107. Joint entropy of (a) and (b)= 8.808. MI (Mutual Information) = 0.980.	MI (Mutual Information) = 1.735. The best transformation parameters obtained are: $a_0 =1.235$, $a_1 =0.992$, $a_2 =-0.125$, $a_3 =0.000$, $b_0 =1.214$, $b_1 =0.125$, $b_2 =0.982$, $b_3 =0.001$,

Convergence of the algorithm has been studied by monitoring the affinity function that is the mutual information during the search process. For this purpose, we have compared the results with those obtained from a genetic based algorithm [11].

For the case of genetic algorithm, the tunable parameter settings are as follows. The population size is set to 100 individuals. Mutation ant crossover rates are respectively set to Pm=0.01 and Pc=0.8. For the case the proposed algorithm, the population size is also set to 100 individuals. The parameters d and β are set respectively to 20% and 2. The number of antibodies to clone is set to 50. Both algorithms have been executed 20 times. Average values through iterations have been gathered and the obtained results are illustrated in figure 3.

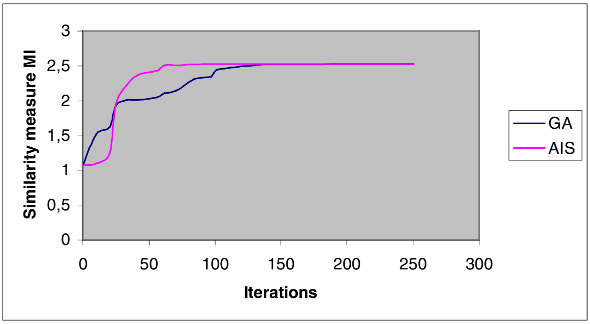

Fig. 3. Convergence of the proposed AIS algorithm and the classic GA-based algorithm.

The graph in figure 3 indicates that both strategies achieve the same quality solutions. Moreover, it is clear that the proposed algorithm reach different sets of local solutions which denotes a better-diversified search. This can be explained by the fact that the evolutionary searches of the two approaches proceed differently. Genetic algorithms tend to polarize the whole population of individuals towards the best solution whereas in the AIS-based algorithm, the mutation rate applied to an individual is a function of the individual affinity (MI value), contrary to a genetic algorithm that considers rates neglecting this affinity. In table 2, other statistics have been goatherd to get a closer insight into the performance of the algorithm.

Table 2. Results of the AIS based and classic GA based algorithms applied to pair1. Given are the best the best solution found (best MI), the average solution quality (Avg MI) and its percentage deviation from the optimum. Results are taken over 20 trials.

Algorithm	Best MI	Avg MI	Std
AIS	2,529	2,516	0.63 %
Classic GA	2.529	2.491	0.71 %

6 Conclusion

This paper described a search strategy that intends to achieve a good quality alignment for two multi modality images by maximizing their mutual information. The proposed strategy is a population-based approach for optimization based on an artificial immune system with a real valued representation.

The approach proposes an evolutionary search similar to a genetic-based approach but introduces new mechanisms like the somatic mutation and the clonal selection policy. Experiments on real images show not only the feasibility of the approach but also its ability to achieve good quality solutions. As ongoing work, it would be an interesting attempt to conduct an in-depth comparison with a more elaborate genetic algorithm using mutation rate control.

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