

Recent Research in Science and Technology 2011, 4(1): 33-39
 ISSN: 2076-5061
 Available Online: <http://recent-science.com/>



Automatic image registration using evolutionary algorithm

Sarfraz Ahmed Malik* Rakesh Singh Kunwar* and M. Ehtashamoul Haque*

*Department of Computer Science & IT, DBIT, Dehradun, India

Abstract

Image registration is a process to obtain the spatial transformation of an input image to a reference image by which similarity measure is optimized between the two images. Mutual information is a similarity measure based on information theory used in the process of image registration. Mutual information compares the statistical dependency between images. Registration based on mutual information is robust and could use for a large class of mono modality and multimodality images. In this work we use mutual information as the similarity measure. There is a requirement to finding the global maxima of similarity measure, for this we use two algorithm simple genetic algorithm and share genetic algorithm and compare the result of these algorithm. In these optimization technique require several decision to made during implementation, such as encoding, selection method and evolution operator. In this work we use two selection method roulette-wheel method and tournament selection method. Result indicates that these optimization techniques can be used for efficient image registration

Keywords: Image registration, genetic algorithm (simple and share), Roulette-wheel and tournament selection methods.

INTRODUCTION

Image registration is the process of overlaying one or more image to a reference image of the same scene taken at different time, from different view point and/or different sensor. Difference between images is introduced due to different imaging condition such that yields highest similarity between the input and the reference images. Image registration geometrically aligns two images the reference image and input image. Image registration is a crucial step in all image analysis tasks in which the final information is gained from the combination of various data sources like in image fusion, change detection, and multichannel image restoration. Typically, registration is required in remote sensing (multispectral classification, environmental monitoring, change detection, image mosaicing, weather forecasting, creating super-resolution images, integrating information into geographic information systems (GIS)), in medicine (combining computer tomography (CT) and NMR data to obtain more complete information about the patient, monitoring tumor growth, treatment verification, comparison of the patient's data with anatomical atlases), in cartography (map updating), and in computer vision (target localization, automatic quality control), to name a few.

In general, its applications can be divided into four main groups according to the manner of the image acquisition:

- Different viewpoints (multiview analysis)
- Different times (multitemporal analysis)
- Different sensors (multimodal analysis)

The registration process involves finding a single transformation imposed on the input image by which it can align with

the reference image. It can be viewed as different combination of choice for the following four components.

- (1) Feature space
- (2) Search space
- (3) Similarity measure
- (4) Search strategy

The Feature space extracts the information in the images that will be used for matching. The Search space is the class of transformation that is capable of aligning the images. The Similarity measure gives an indication of the similarity between two compared image regions. The Search strategy decides how to choose the next transformation from the search space, to be tested in the search to spatial transformation.

This work focuses on image registration of two medical images of having different modality i.e. image acquired with different sensor e.g. images, MRI images. We consider set of image pixel intensity as the feature space and affine transformation as the search space. A popular similarity measure is mutual information (in short MI) consider as the mutual information. MI is based on the information theory (figure 1). MI compares the statistical dependency between images. Registration based on the MI is robust and can be used for a large class of images acquired by the same sensor and different sensors. For the search strategy we use simple genetic algorithm and share genetic algorithm. Genetic algorithm (in short GA) is based on the concept of the natural process of specie evolution to realize simple and robust methods for optimization.

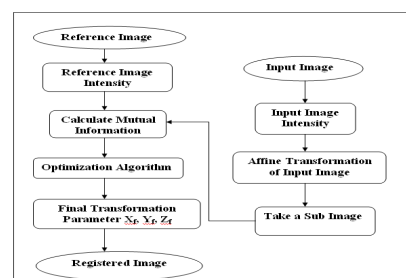


Fig 1. Image Registration using mutual information

Received: Nov 12, 2011; Revised: Dec 20, 2011; Accepted: Jan 15, 2012.

*Corresponding Author

Sarfraz Ahmed Malik
 Department of Computer Science & IT, DBIT, Dehradun, India

Email: malik.dsgi@gmail.com

This paper is organized as follows. In the next section, we discuss the background and related work. In Section 3, we discuss the details of genetic algorithms and method of selection Roulette and tournament. In section 4, we present our experimental results. Finally, we conclude in section 5.

REVIEW OF RWGISTRATION TECHNIQUES

Registration process mainly consists in determining the unknown transformation parameters required to map the input image to the reference image in order to compare and analyze both in a common reference frame. The task of determining the best spatial transformation for the registration of images can be characterized by four major components (Brown, 1992):

1. Feature space
2. Search space
3. Similarity measure
4. Search strategy

The feature space represents the information in the images that will be used for matching. According to the feature space employed, we can identify three classes of registration algorithms pixel-based registration [1], feature-based registration [2], and transform-based registration [3]. The search space is made of all possible transformations. The input image is transformed by means of the mapping functions. Image values in non-integer coordinates are computed by the appropriate interpolation technique. Some popular transformations are as follows:-

Transformation of the Cartesian coordinate system [4], affine transformation [5], projective transformation [6] and thin-plate splines (TPS) [7].

The similarity measure function, or cost function, gives an indication of the similarity between two compared image regions. The function may either be based on direct pixel intensity comparisons, or on other geometrical features within the regions. Some similarity measures are as follows:-

Sum of squared differences [8], sum of absolute differences [9], normalized cross correlation [10], variance [11], and mutual information method [12].

The search strategy governs how the search space is explored, and has a great impact on the efficiency of the image registration process. Here review a few common strategies:

MUTUAL INFORMATION

The research that eventually led to the introduction of mutual information as a registration measure dates back to the early 1990s. Woods *et al.* first introduced a registration measure for multimodality images based on the assumption that regions of similar tissue (and, hence, similar gray values) in one image would correspond to regions in the other image that also consist of similar gray values (though probably different values to those of the first image). Ideally, the ratio of the gray values for all corresponding points in a certain region in either image varies little. Consequently, the average variance of this ratio for all regions is minimized to achieve registration.

Two discrete random variables A and B with marginal probability distributions $p_A(a)$ and $p_B(b)$ and joint probability distribution $p_{AB}(a,b)$ are statistically independent if $p_{AB}(a,b) = p_A(a) \cdot p_B(b)$, while they are maximally dependent if they are related by a one-to-one mapping $T: p_A(a) = p_B(T(a)) = p_{AB}(a, T(a))$. The

mutual information $I(A,B)$ of A and B measures the degree of dependence of and as the distance between the joint distribution $p_{AB}(a,b)$ and the distribution associated to the case of complete independence $p_A(a) \cdot p_B(b)$, by means of the Kullback-Leibler measure i.e., Two discrete random variables A and B with marginal probability distributions $p_A(a)$ and $p_B(b)$ and joint probability distribution $p_{AB}(a,b)$ are statistically independent if $p_{AB}(a,b) = p_A(a) \cdot p_B(b)$, while they are maximally dependent if they are related by a one-to-one mapping $T: p_A(a) = p_B(T(a)) = p_{AB}(a, T(a))$. The mutual information $I(A,B)$ of A and B measures the degree of dependence of and as the distance between the joint distribution $p_{AB}(a,b)$ and the distribution associated to the case of complete independence $p_A(a) \cdot p_B(b)$, by means of the Kullback-Leibler measure i.e.,

$$I(A, B) = \sum_{a,b} p(a, b) \log \frac{p_{AB}(a, b)}{p_A(a) \cdot p_B(b)}$$

Mutual information is related to the information theoretic notion of entropy by the following equations

$$\begin{aligned} I(A, B) &= H(A) + H(B) - H(A, B) \\ &= H(A) - H(A/B) \\ &= H(B) - H(B/A) \end{aligned}$$

with $H(A)$ and $H(B)$ being the entropy of A and B respectively, $H(A, B)$ their joint entropy, and $H(A/B)$ and $H(B/A)$ the conditional entropy of A given B and of B given A , respectively.

GENETIC ALGORITHM

The problem solving methodology employed in a genetic algorithm closely resembles an evolutionary process, where successively more and more fit solutions are "evolved" through an iterative procedure.

The operations of the genetic algorithm are very simple. It maintains a population $x_1 \dots x_n = \{x_1, \dots, x_n\}$ of n individuals x_i (which may consist of a vector of parameters). These individuals are candidate solutions to some objective function $F(x_i)$ that is to be optimized to solve the given problem. The individuals are represented in the form of 'chromosomes,' which are strings defined over some alphabet that encode the properties of the individuals. More formally, using an alphabet $A = \{0, 1, \dots, k-1\}$, we define a chromosome $C = \{c_1 \dots c_l\}$ of length l as a member of the set $S = A^l$, i.e., chromosomes are strings of l symbols from A . Each position of the chromosome is called a *gene*, the value of a gene is called an *allele*, the chromosomal encoding of a solution is called the *genotype*, and the encoded properties themselves are called the *phenotype* of the individual. In the GA, typically a binary encoding is used, i.e., the alphabet is $A = \{0, 1\}$. The GA employs three operators, selection, crossover, and mutation.

Being metaheuristic GA require several decision to be made during implementation for encoding, selection, crossover and mutation.

The first decision to take when implementing a GA is how solution states should be encoded into chromosomes. Some

encoding techniques are

- (a) Binary Encoding
- (b) Octal Encoding
- (c) Hexadecimal Encoding
- (d) Gray Encoding
- (e) Floating Point Encoding

The best selection strategy for picking the parents to be the base for new offspring chromosomes is often problem specific. All strategies should however reflect the basic idea that a higher fitness means a higher likelihood of being selected.

Each individual in the selection pool receives a reproduction probability depending on the own objective value and the objective value of all other individuals in the selection pool. This fitness is used for the actual selection step afterwards.

The various methods for selecting chromosome for parent to crossover are as follows:-

i) Roulette wheel selection

The simplest selection scheme is roulette-wheel selection, also called stochastic sampling with replacement. This is a stochastic algorithm and involves the following technique:

The individuals are mapped to contiguous segments of a line, such that each individual's segment is equal in size to its fitness. A random number is generated and the individual whose segment spans the random number is selected. The process is repeated until the desired number of individuals is obtained (called mating population). This technique is analogous to a roulette wheel with each slice proportional in size to the fitness, see figure 3.

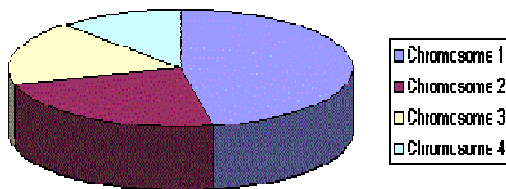


Fig 3. Roulette Wheel Chromosome with bigger fitness will be selected more times.

This can be simulated by following algorithm.

1. [Sum] Calculate sum of all chromosome fitnesses in population - sum S.
2. [Select] Generate random number from interval (0,S) - r.
3. [Loop] Go through the population and sum fitnesses from 0 - sum s. When the sum s is greater then r, stop and return the chromosome where you are.

ii) Tournament selection

In tournament selection a number *Tour* of individuals is chosen randomly from the population and the best individual from this group is selected as parent. This process is repeated as often as individuals must be chosen. These selected parents produce uniform at random offspring [18]. The parameter for tournament selection is the tournament size *Tour*. *Tour* takes values ranging from 2 to *Nind* (number of individuals in population).

Crossover

When parents have been selected according to the used selection strategy, crossovers are performed on the parents to breed new chromosomes. The aim of the crossover procedure is to combine traits from the selected chromosomes to form a new chromosome.

How crossover actually is done depends on the encoding used. Binary encoded chromosomes are usually crossed over by replacing a randomly chosen section of one chromosome with the corresponding content of the other (One Point Crossover). Alternatively, each bit position uses the bit at the corresponding position of a randomly chosen parent. Binary chromosomes can also be subject to some arithmetic operation to perform crossover.

The performance of GA greatly depends on the ability of the crossover operator to combine solutions into a solution more probable of being successful than a randomly selected solution. Unsuccessful crossover operators give recombination no better than randomly selected solutions. There are many types of crossover operations in genetic algorithm some of which are as follows: single point crossover, two point crossover, uniform crossover, arithmetic crossover, and real-number crossover.

Mutation

Mutation is performed to introduce slight variations to allow for the exploration of states not generated through crossover. Suitable mutation rates are problem dependent, but are usually low compare to the crossover rate. Mutation is critical to the performance of the genetic algorithm, as the crossover operator by itself requires large populations and is ineffective. Mutation is an important part of the genetic search as help helps to prevent the population from stagnating at any local optima. Mutation occurs during evolution according to a user-definable mutation probability. Mutation operators are as follows: flip bit mutation, boundary, non - uniform mutation, uniform mutation, and Gaussian mutation.

The idea behind the sharing method is to reduce the fitness of individuals that are very similar in their chromosome. In this way, individuals that uniquely exploit portions of the search space are privileged for reproduction, while discouraging redundant individuals in the same area. The method is based on the determination of the shared fitness of the individual *i* as

$$f'(i) = \frac{f(i)}{m_i}$$

where *f(i)* is the individual's raw fitness, and *m_i* is the niche count, that is defined as

$$m_i = \sum_{j=1}^n sh(d(i, j))$$

The sharing function *sh* depends on the distance (dissimilarity) *d(i, j)* between the individual *i* and the individual *j*. It is a monotonically decreasing function, so that the niche count is reduced if individuals are closer. In particular, it returns 1 if the elements are identical, and 0 if they exceed some threshold of dissimilarity. The function originally proposed by Goldberg (GOLD87) is defined as:

$$sh(d) = \begin{cases} 1 - \left(\frac{d}{\sigma_{share}}\right), & \text{if } d < \sigma_{share} \\ 0, & \text{otherwise} \end{cases}$$

where d is the distance, and the dissimilarity threshold [19].

EXPERIMENTS AND RESULTS

In this work we use following optimization algorithm as search strategy.

- (i) Simple Genetic algorithm
- (ii) Shared Genetic algorithm

The implementation issues for the genetic algorithm are as follows:

Chromosome encoding

The geometric parameter between the data sets of the two images are translation on the x-axis(s_x), translation on the y-axis(s_y) and the rotation(θ). We define three geometric parameter as a chromosome. Due to real-value nature of these parameter we choose the encoding technique of the chromosomes as floating-point encoding. It is fast relative to the binary coding and is also capable of representing large domains, where as in increase in domain size decrease the precision in fixed binary length representation.

Selection

In this work we implement two selection criteria.

(a) Roulette-wheel selection:- This is motivated by the fact that it is a commonly used selection scheme that is relatively easy to implement and understand. The strategy is also appealing due to its close resemblance with nature’s own selection strategy.

(b) Tournament selection:-The tournament selection strategy provides selective pressure by holding a tournament among the individuals. The higher the selective pressure the more, the better individual is favored.

Crossover

We use floating point encoding for the chromosomes, so the better choice for the crossover arithmetic crossover. We use arithmetic crossover in this work.

Mutation

We use uniform mutation as the mutation operator which is one of the mutation operator for the floating-point coded chromosome.

Stopping criteria

We use fixed number of generation as the stopping criteria. We tested the algorithm for different number of generation.

Accuracy of the image registration is calculated using the formula

$$err = \frac{\sum_{i=1}^l \sum_{j=1}^m (R(i,j) - S(i,j))}{lm}$$

where $R(i,j)$ is the reference image and $S(i,j)$ is the match sub image in the search space lm .

Matching is termed as mis registration if the err at the best match point exceeds the specific threshold.

We test the image registration of the 7 pair of medical images using the simple and share genetic algorithm with both roulette-wheel and tournament selection method and after all showing the accuracy in figure:

To illustrate the performance of our algorithm, we consider two type of medical images CT images and MRI images of the same patient. We take these images from the medical image database MEDIPIX. Table1, Table2, Table3, Table4, Table5, Table6 shows the result of the two (simple and share GA) algorithm for the three images such as amount of translation along the x-axis and y-axis and rotation angle required to achieve the registration. Maximum mutual information (MMI), the error and the time elapsed is also shown in each tables:

We experiment it with termination criteria of 50 generation with arithmetic crossover and mutation rate of .01.

Table 1. Result of Simple Genetic Algorithm using roulette-wheel selection (GAR)

index	Translation on the x-axis(X_t)	Translation On the y-axis (Y_t)	Rotation angle(Q_t)	Maximum MI	error	Time elapsed
Fig 4.1	51.0752	48.8278	-10.2901	1.1525	58.5806	476.729024
Fig4.2	16.7525	8.4617	-7.6914	0.8241	11.3149	117.645584
Fig 4.3	16.3042	8.2494	-8.7529	0.8420	3.0431	59.218707

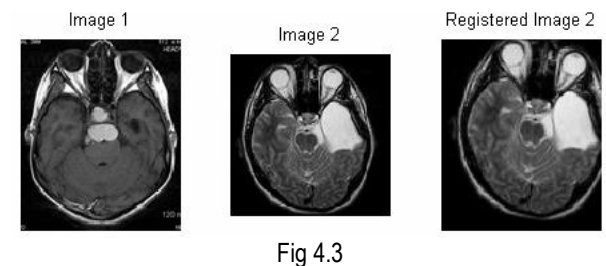
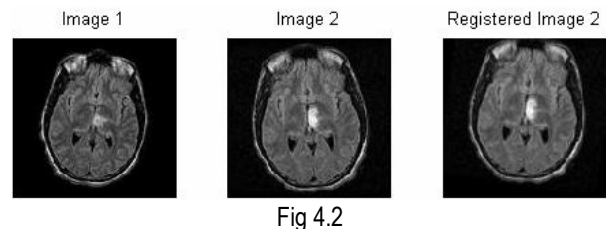
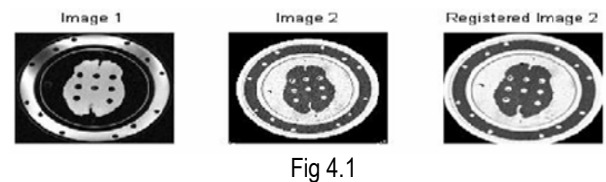


Fig 4. Result of Simple Genetic Algorithm using roulette-wheel selection (GAR)

Table 2. Result of shared Genetic Algorithm using roulette-wheel selection (SGAR)

index	Translation on the x-axis(X_f)	Translation On the y-axis(Y_f)	Rotation angle(Q_f)	Maximum MI	error	Time elapsed
Fig 5.1	50.5196	47.4520	-10.2255	1.1385	58.4737	453.742938
Fig 5.2	15.0336	7.6475	-11.7626	0.8225	11.3496	122.037564
Fig 5.3	12.7481	8.6518	-6.7858	0.8585	2.2227	55.953903

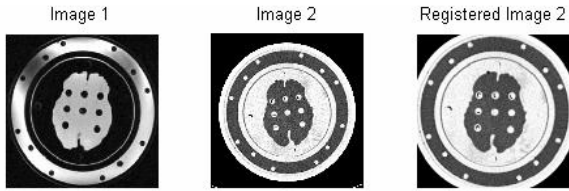


Fig 5.1

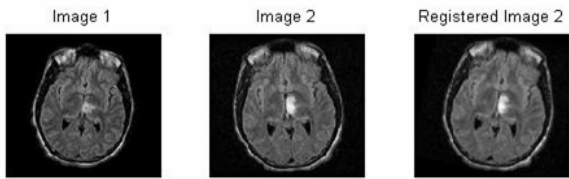


Fig 5.2

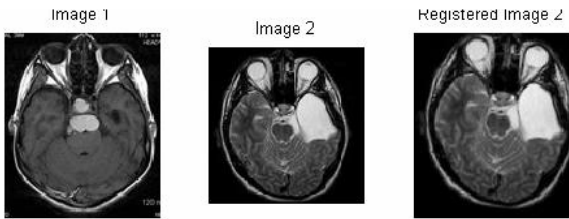


Fig 5.3

Fig 5. Result of Shared Genetic Algorithm using roulette-wheel selection (SGAR)

Table 3: Result of Simple Genetic Algorithm using tournament selection (GAT)

index	Translation on the x-axis(X_f)	Translation On the y-axis(Y_f)	Rotation angle(Q_f)	Maximum MI	error	Time elapsed
Fig 6.1	50.9748	49.1778	-10.3598	1.1552	58.5804	493.782633
Fig 6.2	9.2318	6.3446	-7.5331	0.8454	11.4737	57.948645
Fig 6.3	14.3027	7.3293	-11.9630	0.8262	4.4064	60.361226

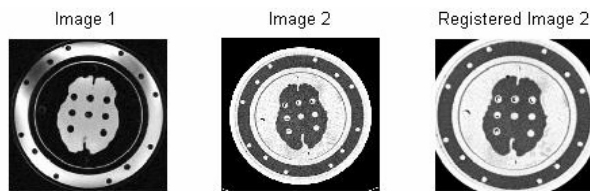


Fig 6.1

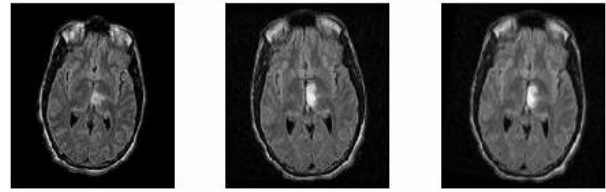


Fig 6.2

Figure 6. Result of Simple Genetic Algorithm using tournament selection (GAT)

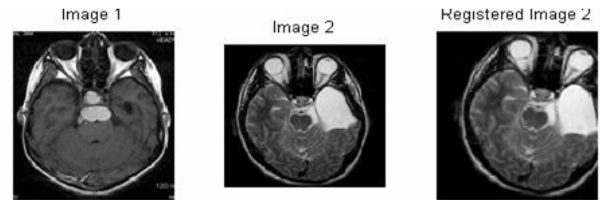


Table 4. Result of shared Genetic Algorithm using tournament selection (SGAT)

index	Translation on the x-axis(X_f)	Translation On the y-axis(Y_f)	Rotation angle(Q_f)	Maximum MI	error	Time elapsed
Fig 7.1	51.4870	46.5278	--9.3194	1.1581	58.5881	542.26250
Fig 7.2	14.6707	7.1739	-10.6536	0.8315	11.3659	58.188544
Fig 7.3	15.9948	8.1671	-9.2246	0.8414	3.0692	58.797584

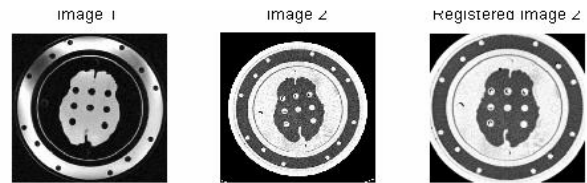


Fig 7.1



Fig 7.2

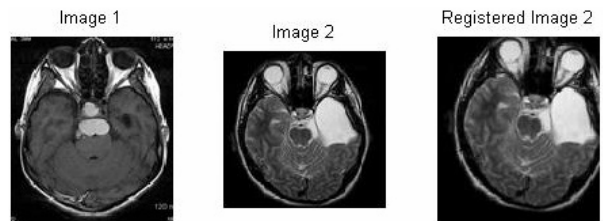
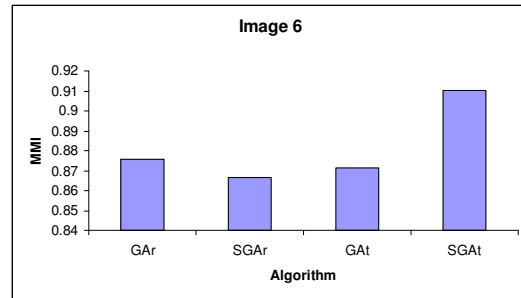
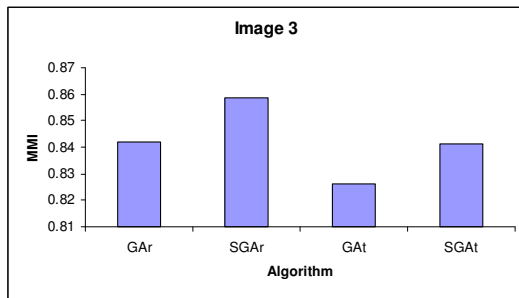
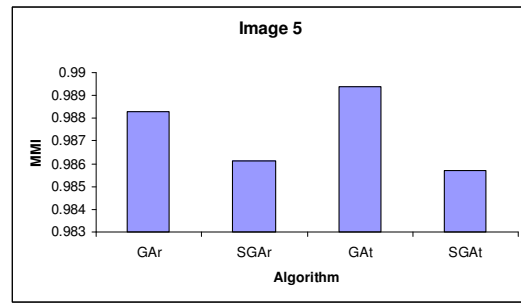
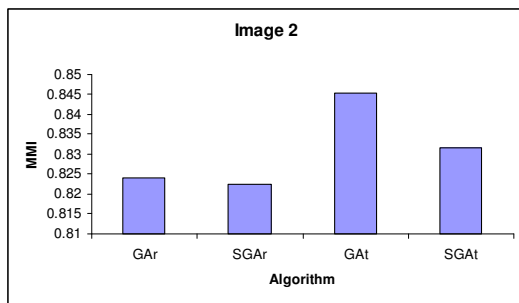
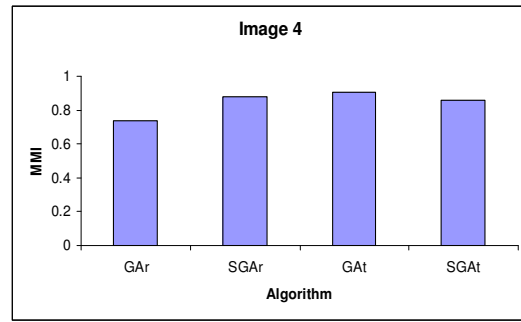
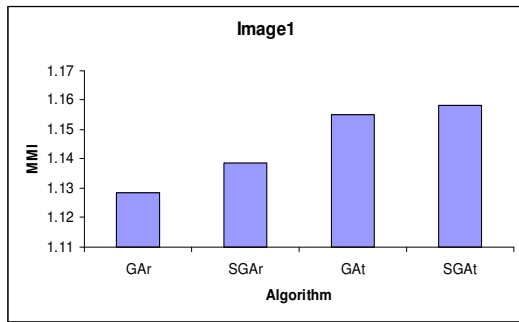


Fig 7.3

Figure 7. Result of shared Genetic Algorithm using tournament selection (SGAT)

Table 5: Performance in term of time, accuracy, MMI

Image	Size of Reference image	Size of input image	Algorithm	MMI	error	Time elapsed (sec)
Image1	230X230	512X512	GAr	1.1285	58.5168	462.520107
			SGAr	1.1385	58.4737	453.742938
			GAt	1.1552	58.5804	493.782633
			SGAt	1.1581	58.5881	542.262507
Image2	130X130	130X130	GAr	0.8241	11.3149	117.645584
			SGAr	0.8225	11.3496	122.037564
			GAt	0.8454	11.4737	57.948645
			SGAt	0.8315	11.3659	58.188544
Image3	110X130	130X129	GAr	0.8420	3.0431	59.218707
			SGAr	0.8585	2.2227	55.953903
			GAt	0.8262	4.4064	60.361226
			SGAt	0.8414	3.0692	58.797584
Image4	130X130	130X130	GAr	0.7393	39.6743	59.429631
			SGAr	0.8765	39.5868	68.551580
			GAt	0.9029	39.4859	61.288493
			SGAt	0.8590	39.7177	65.110044
Image5	114X130	130X128	GAr	0.9883	18.8118	56.001912
			SGAr	0.9861	19.3306	53.875786
			GAt	0.9894	18.7466	55.729798
			SGAt	0.9857	19.2972	54.863909
Image6	100X130	109X130	GAr	0.8757	2.1758	49.864333
			SGAr	0.8665	2.1630	50.687879
			GAt	0.8716	2.2650	50.600842
			SGAt	0.9105	1.7424	49.484485
Image7	120X130	130X129	GAr	0.7318	8.2672	65.710513
			SGAr	0.7399	7.9263	69.461862
			GAt	0.7406	7.4340	72.308400
			SGAt	0.7403	8.2097	61.784095



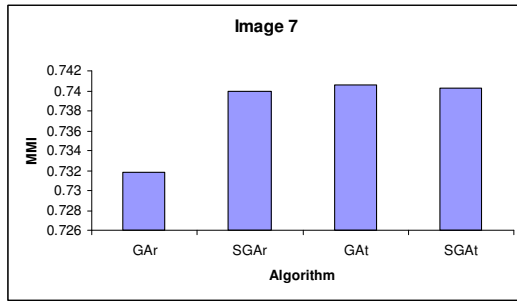


Fig 8. Performance in term of MMI of both algorithm with both selection method

CONCLUSION

In this work, we implement two genetic algorithms (simple genetic algorithm and shared genetic algorithm) with two selection criteria (Roulette-wheel and tournament selection method). We observe that both algorithms are feasible for image registration. For large size and complex images, share genetic algorithm with tournament selection as a selection criteria give overall better performance. But share genetic algorithm is highly sensitive to calibration parameter. Therefore some time it does not give better performance

REFERENCES

- [1] Barbara Zitova*, Jan Flusser, 2003. "Image registration methods: a survey", *Image and Vision Computing* 21:977–1000.
- [2] Mark P. Wachowiak, Renata Smolíková, Yufeng Zheng, Jacek M. Zurada, and Adel S. Elmaghraby, 2004. "An Approach to Multimodal Biomedical Image Registration Utilizing Particle Swarm Optimization", *IEEE transactions on evolutionary computation*, vol. 8, NO. 3.
- [3] Geoffrey Egnal, Kostas Daniilidis, "Image Registration Using Mutual Information" University of Pennsylvania Department of Computer and Information Science Technical, Report No. MS-CIS-00-05.
- [4] Frederic Maes, Dirk Vandermeulen, and Paul Suetens, 2003. "Medical Image Registration Using Mutual Information", *proceedings of the IEEE*, vol. 91, NO. 10.
- [5] Giuseppe Pascal, Luigi Troiano, 2007. "A Niche Based Genetic Algorithm For Image Registration", *Proceedings of the ICEIS 2007 - Ninth International conference on Enterprise Information Systems*, Volume AIDSS, Funchal, Madeira, Portugal, June 12-16.
- [6] Josien P. W. Pluim, J. B. Antoine Maintz, and Max A. Viergever, 2003. "Mutual-Information-Based Registration of Medical Images: A Survey", *IEEE transactions on medical imaging*, vol. 22, NO. 8.
- [7] Flávio Luiz Seixas, Luiz Satoru Ochi, Aura Conci, Débora C. M. Saade, 2008. "Image Registration Using Genetic Algorithms", *GECCO'08, July 12–16, Atlanta, Georgia, USA*. ACM 978-1-60558-130-9/08/07.
- [8] Jharna Majumdar and Y. Dilip, 2002. "Implementation of Image Registration Algorithms for Real-time Target Tracking Through Video Sequences", *Defence Science Journal*, Vol. 52, No. 3. pp. 227-242
- [9] Maslov, I. V. and Gertner, I. 2001. Gradient-based genetic algorithms in image registration. In *Proc. SPIE, Automatic Target Recognition XI: AeroSense 2001*, volume 4379, pages 15–34, Orlando, FL, USA.
- [10] Dasgupta, D. and McGregor, D. R. 1992. Digital image registration using structured genetic algorithms. In *Proceedings of SPIE the International Society for Optical Engineering*, Vol. 1766, pages 226–234.
- [11] Fitzpatrick, J. M., Grefenstette, J. J., and Van-Gucht, D. 1984. Image registration by genetic search. In *Proceedings of the IEEE SouthEast conference SOUTHEASTCON84*, pages 460–464.
- [12] L. G. Brown, 1992. "A survey of image registration techniques," *ACM Comput. Surv.*, vol. 24, no. 4, pp. 325–376.
- [13] M. Holden, D. L. G. Hill, E. R. E. Denton, J. M. Jarosz, T. C. S. Cox, T. Rohlfing, J. Goodey, and D. J. Hawkes, 2000. "Voxel similarity measures for 3-D serial MR brain image registration," *IEEE Trans. Med. Imag.*, vol. 19, pp. 94–102.
- [14] L.-Y. Hsu and M. H. Loew, 2001. "Fully automatic 3D feature-based registration of multimodality medical images," *Image Vis. Comput.*, vol. 19, no. 1–2, pp. 75–85.
- [15] L. Freire, A. Roche, and J.-F. Mangin, 2002. "What is the best similarity measure for motion correction in fMRI a time series?," *IEEE Trans. Med. Imag.*, vol. 21, pp. 470–484.
- [16] T. Gaens, F. Maes, D. Vandermeulen, and P. Suetens, "Non-rigid multimodal image registration using mutual information," in *Proc. Medical Image Computing and Computer-Assisted Intervention (MICCAI'98)*, vol. 1496, Lecture Notes in Computer Science, W. M. Wells, A. Colchester, and S. Delp, Eds., Cambridge, MA, Oct. 1998, pp. 1099–1106. [31] J. C. Gee and R. K. Bajcsy, "
- [17] Zhiyong Gao, Jiarui Lin, Bangquan Xu, 2004. "The affection of grey levels on mutual information based medical image registration," In: *Proc. of the 26th Annual International Conference of the IEEE EMBS*, pp. 1747-1750.
- [18] J. Pluim, J. Maintz, and M. Viergever, 2003. "Image registration by maximization of combined mutual information and gradient information," *IEEE Transactions on Medical Imaging*, vol. 19, no. 8, pp. 809-814.
- [19] R. Marti, R. Zwigelaar, C. Rubin, 2000. "A novel similarity measure to evaluate image correspondence," In *Proc. of 15th International Conference on Pattern Recognition*, pp. 167-170.
- [20] B. Likar, F. Pernu, 2001. "A hierarchical approach to elastic registration based on mutual information," *Image and Vision Computing*, vol. 19, no. 1-2, pp. 33-44.