Comparative Study on Image Registration Using Exhaustive Affine Transformation and Genetic Algorithms

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Abstract—The design of scaffolds with desirable internal and external structure represents a challenge for Tissue Engineering. A new method "Automated Scaffold Design" (ASD) is use for designing a 3D scaffold with a minimum mismatches for its geometrical parameters. The segmented portions of different slices are registered to construct the 3D volume for the data. Image Registration is the process of determining a transform that provides the most accurate match between two images, which will align between them. Using exhaustive search for affine transformation, parameters for the registration may take a longer time. This paper addresses the image registration problem by applying a global optimal method in order to get a registration approach with high accuracy based on the application of Genetic Algorithms (GA). GA has been known to be robust for search and optimization problems. Image registration can take this advantage of the robustness of GAs in finding the best transformation between two images. It can compute an optimal registration 10 times faster than a conventional registration method.

Index Terms— Affine Transformation, Genetic Algorithm, Image Registration, Scaffold Design.

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1 INTRODUCTION

APPROXIMATELY three decades ago a new alternative approach to tissue and organ reconstruction emerges; that is Tissue Engineering (TE). It is based on the understanding of tissue formation and regeneration, and aims to induce new functional tissues, rather than just to implant new spare parts [1], [2], [3], [4], [5]. One decisive factor to the success of TE strategies is the appropriate design of the scaffold; that effectively serves as man-made extracellular matrices. A scaffold should provide the optimal three-dimensional (3D) microenvironment for cells to attach and guide the overall shape needed to implement in [6], [7], [8].

A new approach, ASD aims to design 3D bone scaffolds, with a minimum mismatches for its geometrical parameters including a novel internal architecture design. To end up with an acceptable external geometrical scaffold representing the shape of the defect to implement it in the defected area, ASD passes throw three main stages (segmentation, registration, and rendering). It takes the entered input data (CT images) and segments the interest tissue boundaries from others on all the image slices. Then the segmented portions of different slices are registered to construct the 3D volume for the desirable scaffold.

This paper focuses on image registration stage performance, were image registration aligns the information in different images to visualize as a combined image [9]. Its goal is to establish the correspondence between two images and determine the optimum geometric transformation parameters that can best match the two images [10]. This geometrical alignment of images helps in determining the shape of the defected area in the bone. The four components of image registration, which contribute to the optimization, are feature space, search space, search strategy, and similarity metric. The feature space extracts the information in the images that will be used for matching. The search space is the class of transformations that is capable of aligning the images. The search strategy decides how to choose the next transformation from this space, to be tested in the search for the optimal transformation. The similarity metric determines the relative merit for each test. Search continues according to the search strategy until a transformation is found whose similarity measure is satisfactory with minimum error or minimum deviation [10], [11].

ASD uses the exhaustive affine transform to design the mapping functions for 2-D image registration. The affine transform has four parameters (scaling, translation (dx, dy), rotation), which gives a wide range and space to achieve the optimum alignment between two images. However the drawback or problem faces the exhaustive search is time consuming during the process. To overcome this problem the ASD tends to utilize GA.

GA iterative procedures maintain a population of candidate solutions encoded in the form of chromosome strings. The initial population can be generated randomly. These candidates will be selected using a selection criterion for the reproduction in the next generation based on their fitness values. GAs search is used to efficiently explore the huge solution space required by the image registration to sub pixel accuracy [12].

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The objective of this paper is to provide some comparative measures on the ASD registration efficiency using exhaustive search for affine transformation and GA in term of finding the best transformation parameters between two images and time needed to evaluate these parameters. The accuracy, speed and the robustness of the proposed methods are verified by a number of real experiments.

2 MATERIALS AND METHODS

The system methodology was performed with MATLAB (2010). The algorithm is tested with two-dimensional (2D) cross-section images (axial cuts) from CT acquired by a GE medical system CT scanner. After acquisition of CT image data is recorded in Digital Imaging and Communications in Medicine (DICOM) standard format, the most common in medical images management. In DICOM files, detailed information on scanning parameters is recorded too. The experimental study will be applied on three different patient cases with bone defect, each case contain 25 slices with image resolution of 512×512. The image should contain both legs of the patient and only one of them is defected as shown in Fig. 1.

2.1 ASD Registration Using exhaustive Affine Transformation

Registration is the procedure of mapping points from one image to corresponding points in another image in order to monitor subtle changes between the two images [13], [14]. The target of ASD registration is to align between the healthy bone and the defected one in order to determine the difference between them. This gives the ability to design a 3D scaffold model for the output difference, which represents the defected area. ASD divides registration phase in to three stages. First stage (transformation and translation) purpose is to align the healthy and defected bone on each other as shown Fig. 2. This process is done using affine transformation, which is sufficient to match two images of a scene taken from the same viewing angle but from different position [15]. The alignment set parameters is simply composed of rotation, translation and scaling, which can be expressed using the composite matrix in the following equation:

$$S = \begin{bmatrix} s & 0 & 0 \\ 0 & s & 0 \\ 0 & 0 & 1 \end{bmatrix} \tag{1}$$

$$T = \begin{bmatrix} 1 & 0 & t_x \\ 0 & 1 & t_y \\ 0 & 0 & 1 \end{bmatrix} \tag{2}$$

$$R = \begin{bmatrix} cos\theta & -sin\theta & 0 \\ sin\theta & cos\theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \tag{3}$$

$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = S\,T\,R \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} \tag{4}$$

$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} s\,cos\theta & -s\,sin\theta & t_x \\ s\,sin\theta & s\,cos\theta & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} \tag{5}$$

where θ is the angle of rotation, s scaling factor and (tx, ty) are translation vector. In the second stage (mean square error) at each transformation parameter set the Mean Square Error (MSE), [16] is calculated using the following equation:

$$\frac{1}{MN}\sum_{y=1}^{M}\sum_{x=1}^{N}(f(x,y)-f'(x,y))^2 \tag{6}$$

where f (x, y) is the first bone image, f '(x, y) is the other one and M, N are the dimensions of the images. The parameter set with the least MSE per sliced is selected as the candidate transformation parameters and used to transform one image to the other. If it happen and two parameter set with the same least MSE per sliced, then the parameter set, which is compatible with the pervious set is selected as the candidate. Third stage (determine the difference) is for determining the difference between two images per sliced after alignment using the following equation:

$$f(x,y) = \begin{cases} 1 & f(x,y) - f'(x,y) > 0 \\ 0 & otherwise \end{cases} \tag{7}$$

if the existing difference is greater than zero, it will be taken into the account, otherwise it won't be considered. By ending this sub-phase the difference output, which represents the defected area is identified as illustrated in Fig. 3c.

2.2 ASD Registration Using Genetic Algorithm

The ASD registration phase using GA has the same stages as the previous illustrated method. However, the only difference is in the first stage (transformation and translation) were the process used to align the two images is genetic algorithm. Unlike traditional linear search, the GAs adaptively explores the search solution space in a hyper – dimension fashion, [17], [12] so that they can improve computational efficiency.

GA are iterative procedures that maintain a population of candidate solutions encoded in the form of chromosome strings. A chromosome is a vector of length n of the form <x1, x2… xn>, where each xi is an allele or gene. The length of chromosomes vector is set to be 4 genes (θ, s, tx, ty).The initial population contains 20 individuals. Each candidate is evaluated and is assigned the fitness value that is generally a function of the decoded bits contained in each candidate's chromosome. These candidates will be selected using

selection criteria for the reproduction, based on their fitness values. Reproduction process uses three basic genetic operations called selection, crossover and mutation [18].

The selection rules select the individuals; called parents that contribute to the population at the next generation. The crossover rules combine two parents to form children for the next generation. The mutation rules apply random changes to individual parents to form children. The following outline summarizes how the genetic algorithm works [12]:

1. The algorithm begins by creating a random initial population.
2. The algorithm then creates a sequence of new populations, or generations. At each step, the algorithm uses the individuals in the current generation to create the next generation. To create the new generation, the algorithm performs the following steps:
   - Scores each member of the current population by computing its fitness value.
   - Scales the raw fitness scores to convert them into a more usable range of values.
   - Selects parents based on their fitness.
   - Produces children from the parents. Children are produced either by making random changes to a single parent mutation or by combining the vector entries of a pair of parents crossover.
   - Replaces the current population with the children to form the next generation.

The algorithm stops when one of the stopping criteria are met, see Table 1.

TABLE 1 THE GA PARAMETERS SET

GA Parameters Set	
Parameters	**Value**
Chromosomes vector	4
Initial population	20
Crossover probability	0.8
Mutation probability	0.2
Stopping criteria is taken as the maximum generation	120

Fig. 1. CT image (axial cut) contains both legs of the patient and only one of them is defected

Fig. 2. ASD perform an alignment between the healthy (the red one) and defected bone (the green one) based on affine transformation

3 RESULT

As mentioned earlier, the experimental study will be applied on three different cases of bone defect each contains 25 slices needed to align between healthy bone and defected one each separately. The same GA parameters setting as listed in Table 1 is applied in each case. However, the lower bounds (LB) and upper bounds (UB) of transformation parameters (θ, s, t_x, t_y) are different for each case. With the situation in mind that these bounds are the same bounds used for exhaustive affine transformation search as presented in TABLE 2.

After applying the ASD registration process using the exhaustive affine transformation search and GA individually on each case ultimately the results of best match using both methods per slice is estimated also the time needed to evaluate these results. By taking the average value of best match for 25 slices per case, we end up with

the average match for case using both methods shown in TABLE 3and Fig. 4

By comparing the accuracy we find that the ratio between affine transformation and GA is so close giving an acceptable result, however the difference between their time consummations is so far giving the advantage to the GA method especially when the bounds range increase.

Fig. 3. (a) The healthy bone bar slice; (b) The defected bone bar slice; (c) The output difference between a and b

TABLE 2. The Transformation Parameter Bounds

Cases	Transformation Parameters							
	t_x		t_y		θ		s	
	LB	UB	LB	UB	LB	UB	LB	UB
I	5	15	5	15	-5	5	0.95	1
II	5	20	5	20	-40	0	1	1
III	10	20	5	10	-7	5	1	1

TABLE 3 The Difference Between Exhaustive Search and GA

Cases	Comparative Study			
	Accuracy		Time (sec)	
	EX	GA	EX	GA
I	0.980757	0.957298	525.449255	92.28886
II	0.776215	0.724717	528.663203	67.39931
III	0.947717	0.89486	470.418922	86.56337

4 CONCLUSION

This paper addresses comparative result of registration methods using exhaustive affine transformation search and genetic algorithms. The results had shown that GA is a good searching strategy with acceptable accuracy compared to the traditional method (exhaustive). Even more, GA surpasses traditional method in the time consummation during the process. Our test proves that GA is 10 times faster than a conventional exhaustive registration method.
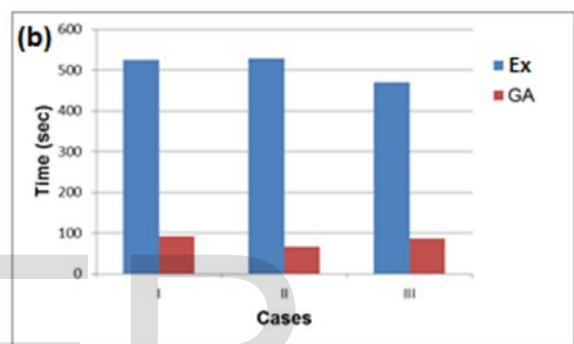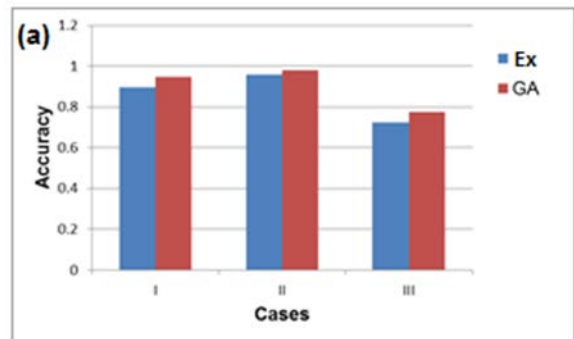
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Fig. 4. (a) The accuracy ratio between exhaustive affine transformation search and GA. (b) The time ratio between exhaustive affine transformation search and GA.

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