

PAPER

Automatic 3D MR Image Registration and Its Evaluation for Precise Monitoring of Knee Joint Disease

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SUMMARY We describe a technique for the registration of three dimensional (3D) knee femur surface points from MR image data sets; it is a technique that can track local cartilage thickness changes over time. In the first coarse registration step, we use the direction vectors of the volume given by the cloud of points of the MR image to correct for different knee joint positions and orientations in the MR scanner. In the second fine registration step, we propose a global search algorithm that simultaneously determines the optimal transformation parameters and point correspondences through searching a six dimensional space of Euclidean motion vectors (translation and rotation). The present algorithm is grounded on a mathematical theory - Lipschitz optimization. Compared with the other three registration approaches (ICP, EM-ICP, and genetic algorithms), the proposed method achieved the highest registration accuracy on both animal and clinical data.

key words: registration, global optimization, corresponding points, articular cartilage, cartilage thickness

1. Introduction

Magnetic resonance imaging (MRI) is routinely used in the diagnosis of a wide variety of joint pathologies in human; it has been proposed for assessing cartilage volume and thickness in several human studies. Changes in the articular cartilage over time can indicate the progression of osteoarthritis (OA) and show particular promise for evaluating the efficacy of disease modifying OA drugs. There is evidence that cartilage changes (volume and thickness) in joint degeneration are rather a local than a global effect [1], [2]. Consequently, it is imperative to develop a three dimensional (3D) registration technique for tracking local cartilage changes over time.

Only a limited number of studies have applied the image registration to monitor quantitative changes of cartilage [3]. In literature [3], Stammberger et al. used a 3D elastic registration method to identify the corresponding points of the bone-cartilage interface for quantifying the local cartilage thickness changes. This has two noticeable problems: 1) the algorithm depends of the accuracy in normal vector of both surfaces; 2) there is a lack of evaluation of the registration accuracy using the anatomical mark points.

The more general problem of finding the registration

between two 3D data sets was considered in [4], where the iterative closest point (ICP) algorithm is proposed to solve the problem. The ICP algorithms can handle various types of data, which include point sets, line segment sets, triangle sets, and implicit surfaces. However, the ICP algorithms require a good initialization in order to converge to the globally optimal solution, otherwise only a local optimum is attained; moreover, their performances heavily depend on the spatial configuration (distribution) of 3D points. A number of approaches [5] have been devoted to make the ICP algorithm more robust to such difficulties, but in some cases the algorithms are still plagued by local minima problems, and lots of iterations are required. Chow et al. [6] presented a dynamic genetic algorithm to avoid local minima problems. The main problem of this algorithm is time required to converge.

The purpose of the present study is to find a global solution, meaning that the estimated transformation (translation and rotation) and correspondences should be globally optimal, i.e., giving rise to globally minimal objective function error. To our knowledge, no such efficient global method is available for registration of knee femur surface points on serial MR images obtained at different times yet.

In this paper, we present a new framework for globally solving the 3D registration problem of knee femur surface points. Our framework is grounded on a mathematical theory - Lipschitz optimization [7]. Based on this theory, we propose a global search algorithm that simultaneously determines the transformation and point correspondences. The main advantage of the proposed method is that our algorithm does not need any initialization and a lot of computation time. Additionally, we describe a six dimensional (6D) search space for simultaneously finding the optimal transformation parameters (translation and rotation), thus our algorithm can achieves arbitrarily high accuracy. Finally, our algorithm is independent of point configuration.

The accuracy of registration was evaluated using 20 fresh frozen knees from pigs and 15 knees of patients. The proposed method was more accurate than the conventional methods for registration of 3D knee joint femur surface.

2. Methods

The 3D registration method presented in this study consists of two stages: In the first pre-registration stage, the knee femur surfaces are registered using the direction vectors of the

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volume (3D cloud of points) given by the cloud of points of the MR image to align the sequence of MR images between them [8]. In the second stage, a global optimization algorithm is presented for obtaining the most accurate solution as possible. This method is grounded on a mathematical theory - Lipschitz optimization. After determining the corresponding points of both femur surfaces, different local properties (such as the cartilage thickness) can be compared. These are explained in the following section.

2.1 Coarse Registration

This registration step is based on using the direction vectors of a cloud of points, to compensate for different knee joint positions and orientations inside the MR magnet during the data acquisition [8]. The method involves calculating the covariance of each spatial point set as follows:

$$Cov = \frac{1}{n} \sum_{i=1}^n (x_i - \bar{x})(x_i - \bar{x})^T \quad (1)$$

where n is the number of points, $\bar{x}$ is the center of mass of cloud of points, and x_i is the i -th point of the surface. Then, the direction U_i of the main axis can be computed by singular value decomposition (SVD):

$$Cov = U_i D_i U_i^T \quad (2)$$

The rotation is determined by the product of the eigenvector matrices:

$$R = U_i U_i^T \quad (3)$$

Furthermore, the translation is determined by the distance between the centers of mass of both clouds of points.

2.2 Fine Registration

The goal of the fine registration is to obtain the most accurate solution as possible. This method is grounded on a mathematical theory - Lipschitz optimization. Moreover, we describe a 6D space to simultaneously find the optimal translation and rotation. In the 6D space, registration accuracy is improved.

2.2.1 Objective Function in the 6D Space

We want to find an optimal rigid motion that minimizes the objective function, where the motion is represented by a translation T and a rotation R . The translation vector and the rotation matrix are expressed as

$$T = \begin{bmatrix} t_1 \\ t_2 \\ t_3 \end{bmatrix} \text{ and } R = \begin{bmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{bmatrix} \quad (4)$$

To simultaneously find the optimal translation T and rotation R , we describe a 6D transformation space. The two

vectors (T and R) can be combined in a single transformation matrix $[R \ T; 0 \ 1]$ which is the 4×4 transformation matrix. Q belongs to Lie group $SE(3)$, which is given by [9]

$$SE(3) = \begin{bmatrix} 0 & -\omega_3 & \omega_2 & v_1 \\ \omega_3 & 0 & -\omega_1 & v_2 \\ -\omega_2 & \omega_1 & 0 & v_3 \\ 0 & 0 & 0 & 1 \end{bmatrix} \omega, v \in R^3 \quad (5)$$

Equation (5) demonstrates that the transformation space can be mapped into a 6D space. The transformation search space can be substituted by a 6D space in which the vector can be denoted by $[\omega_1, \omega_2, \omega_3, v_1, v_2, v_3]$. Each transformation matrix Q has the corresponding point $[\omega_1, \omega_2, \omega_3, v_1, v_2, v_3]$ in the 6D space by using the exponential map.

Let us assume that X and Y represent two 3D point sets, and x_i and y_i are coordinates of the i -th points in the sets, respectively. $\vec{x}_i^T$ and $\vec{y}_i^T$, ($i \in [1, \dots, n]$) are denoted as vectors from matrices $X \in \mathbb{R}^{n \times 3}$ and $Y \in \mathbb{R}^{n \times 3}$, respectively. Suppose $\vec{x}_i$ and $\vec{y}_i$ are matched, in the 6D space, the objective function can be defined by

$$d(X, Y|Q, P) = \frac{1}{n} \sum_{i=1}^n \|\vec{x}_i - Q\vec{y}_i\|^2 \quad (6)$$

where the correspondences are represented by a permutation matrix $P \in \mathbb{P}^{n \times n}$. The optimal combination P between X and Y that can be computed by Hungarian algorithm [10].

The distances between every point from X and every one from Y are calculated, and then the distance matrix $P^{n \times n}$ is regarded as the cost matrix in Hungarian algorithm, where the element in the i -th row and j -th column represents the distance of the j -th point from Y and the i -th point from X . The correspondence between X and Y , represented by an assignment matrix, is derived by using the Hungarian method. The size of the assignment matrix is also $n \times n$. The result of Hungarian method means that the position of the zero-value element in the assignment matrix is the position of the selected element in the distance matrix $P^{n \times n}$. For example, if the element in the i -th row and j -th column of the assignment matrix is zero, then the element in the i -th row and j -th column of distance matrix is selected, the i -th point from X and the j -th point from Y make a corresponding point pair.

2.2.2 Lipschitz Algorithm and Lipschization

Currently, the paper is aiming at simultaneously finding a truly globally-optimal combination Q . To achieve this goal, we should derive a global optimization algorithm to minimize Eq. (6). However, the global optimization method basically conducts an exhaustive search over all possible Q in the 6D search space. It seemed to be impossible, because the entire space to be searched is the space of $SE(3)$, which is extremely huge.

To overcome this, we present a new method based on

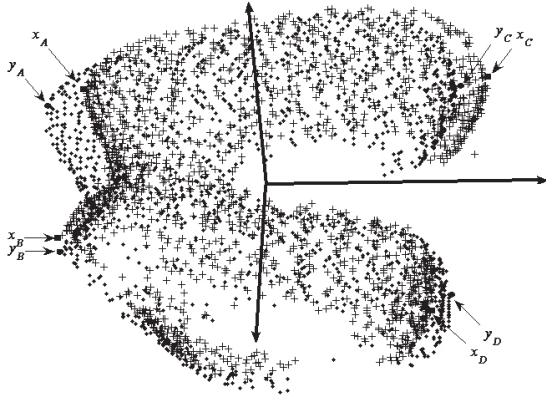


Fig. 3 Coarse registration of two femur surfaces, one (surface X) shown with the symbol “+” and the other (surface Y) with the symbol “·”. Graph shows the three principal axes of femur surface. Each femur surface is composed of 2037 points. x_A, x_B, x_C and x_D represent the four endpoints in the surface points of X , respectively. y_A, y_B, y_C and y_D represent the four endpoints in the surface points of Y , respectively. x_A and x_B lie on the trochlear line (TA), and x_C and x_D on the posterior condylar axis (PCX) in the femur of knee.

Branch-and-bound (minimization) works by recursively subdividing feasible transformation region into a set of sub-regions eliminating sub-region which cannot contain global minima by evaluating lower bounds over the considered sub-region. The process stops when the global minimum is bracketed into a small enough region that guarantees the desired accuracy.

Manipulating a set of ε -hyper-balls is not an easy task. Alternatively, we propose the use of hyper-cuboids. This results in a tree data structure -which is subsequently used to implement the branch and bound search. We call this tree data structure “Hexagram-64-tree data structure”. In the tree data structure, each of the tree nodes represents a hyper-cuboid in the 6D space. Each hyper-cuboid has a data member of a hyper-ball with radius ε . One node can be subdivided into 2^n sub-nodes in the n dimensional vector (transformation) space [11]. For visualization purpose we show a tree data structure in the 2D space Fig. 4 (a) and in the 3D space Fig. 4 (b). We concluded that in the 6D space, one hyper-cuboid (node) would result in 64 sub-hyper-cuboids (sub-nodes) for the tree data structure.

As such, we call our new method the Hyper-cuboid-and-hyper-ball (HCnHB) algorithm. It starts from a hyper-cuboid circumscribing the hyper-ball. Suppose f^* is the best function value obtained so far. Evaluate the function at the center point (denoted by x) of the hyper-cuboid currently under examination. Compute the radius ε of a neighboring hyper-ball, $\varepsilon = |f(x) - f(x^*)|/L$. If the ε -hyper-ball of the node encloses the entire volume of its own hyper-cuboid, then this hyper-cuboid can be eliminated safely; otherwise subdivide the hyper-cuboid into 64 sub-hyper-cuboids. Repeat this process until the desired accuracy is reached (see Fig. 4 (c) for a 2D slice of this process). Our algorithm is described in details below:

(1) (Preparation) Build a Hexagram-64-tree data structure,

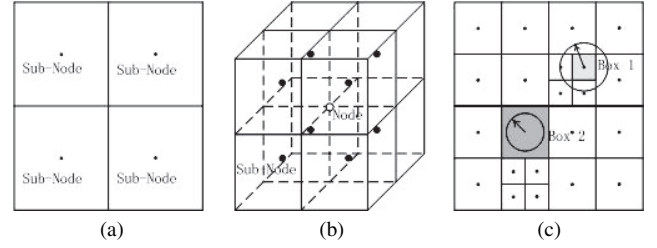


Fig. 4 (a) In the 2D space, the region is subdivided into four sub-regions, 4 sub-nodes are derived from one node. (b) In the 3D space, the region is subdivided into two 8-region, 8 sub-nodes are derived from one node. (c) A 2D slice of the branch-and-bound process. The black circles indicate the ε -balls. During a branch-and-bound process, the light gray (Box1) can be safely removed as its volume is contained entirely inside its ε -ball, but the charcoal gray (Box2) deserves further subdivision.

each node of which is a hyper-cuboid in the 6D space. At the very beginning there is only one hyper-cuboid which circumscribes the hyper-ball. Each hyper-cuboid has an associated ε -hyper-ball. Radii of these hyper-ball are initially set to 0, $\varepsilon = 0$. The center point x of hyper-cuboid is a 6D vector, each component of vector is the mean value of the upper bound and lower bound along the six directions. Make a rough estimate of the transformation by any available method (e.g., even a random guess). Denote the best function value obtained so far as f^* . Make a proper estimate to the Lipschitz constant L . The desired accuracy is set to γ .

- (2) (Implementation) Do repeated depth-first-search over the Hexagram 64-tree. For each node:
 - a. Calculate a transformation matrix $Q(R, T)$ using the center of point x the hyper-cuboid.
 - b. Calculate the best permutation matrix P for given $Q(R, T)$ by using the Hungarian algorithm. Output the current function $f(x) = d_l$. If $f(x) < f^*$, ($f^* = d_l^*$), then update f^* ; otherwise calculate the radius of its ε -hyper-ball by $\varepsilon = |f(x) - f(x^*)|/L$.
 - c. If the hyper-cuboid is entirely contained in its own ε -hyper-ball, then remove this hyper-cuboid from Hexagram-64-tree; otherwise, subdivide it into sixty-four sub-hyper-cuboids and insert these sub-hyper-cuboids at the current position in the Hexagram-64-tree. With the transformation matrix and Hungarian Algorithm, the optimal R, T and P so far is derived.
 - d. Stop the search when $f^* \leq \gamma$.
- (3) Report the center x_{opt} of one of the remaining hyper-cuboids that produces the least function value as the optimal $Q_{opt}(R, T)$, and the corresponding permutation P_{opt} as the optimal correspondences. End.

3. Experimental Setup

In the first experiment, 20 fresh frozen knees of pigs were used for the study. For each knee, 15 toothpicks made

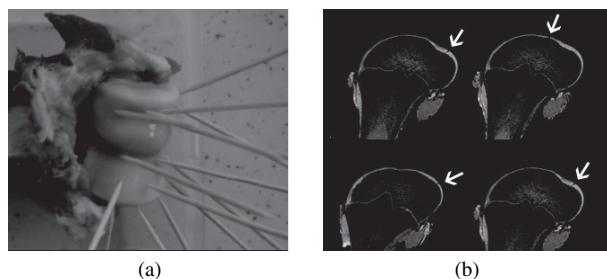


Fig. 5 (a) Pig knee. 15 toothpicks were inserted into the femur surface through the cartilage. 15 mark points of registration per pig knee are used for testing the registration accuracy. (b) MR image of pig knee. 15 points of toothpicks can be identified in the MR images. Four mark points on the femur surface (arrows) are shown.

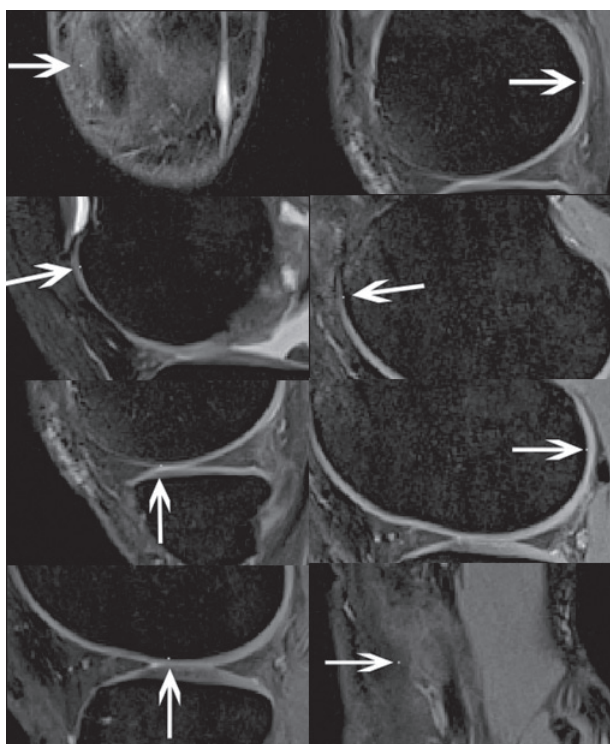


Fig. 6 Sagittal MR image of the knee joint in 47-year-old female patient. Eight mark points (arrows) were selected for evaluating the registration accuracy. The coordinates of landmarks was determined by using the method proposed by Mountney et al. [12]. A single person repeated this six times over three weeks and results were averaged to give a 3D location for the landmark. A radiologist confirmed the landmark selection.

of bamboo were inserted into the femur surface through the cartilage Fig. 5 (a). Each knee with toothpick markers was scanned twice Fig. 5 (b). In the second experiment, 15 knees of patients with borderline to mild OA (51.2 ± 6.3 years) were imaged twice over 3 months (Fig. 6). As shown in Fig. 5, 8 mark points were selected for evaluating the registration accuracy. The coordinates of landmarks was determined by using the method proposed by Mountney et al. [12]. A single person repeated this six times over three weeks and results were averaged to give a 3D location for the landmark. A radiologist confirmed the landmark selec-

tion.

All MR imaging was performed on a 1.5-T MR system (Horizon, General Electric). Image parameters were as follows: TR/TE, 24.4/5.7 ms; flip angle, 20° ; section thickness, 0.56 mm; in-plane resolution, $0.562 \text{ mm} \times 0.562 \text{ mm}$; image direction, sagittal.

Segmentation of the femur surface was performed semi-automatically using a combination of threshold and manual editing of the segmented region. After segmentation of two femur surfaces (two time-points), each femur surface is composed of the cloud of points.

4. Experimental Results

We compare the registration performances of the four approaches on the animal data and clinical data. The four approaches are respectively described as follows:

- 1) **ICP**: The ICP algorithm is the most widely used registration technique [4].
- 2) **EM-ICP**: A number of approaches have been devoted to increase the robustness of ICP. The EM-ICP algorithm is probably the most popular among those approaches [5].
- 3) **Genetic**: The ICP and improved ICP algorithms are the most common registration method used, and the results provided by authors are very good. However, these methods present problems of convergence, lots of iterations are required, and in some cases the algorithms converge to a local minimum. Some authors presented dynamic genetic algorithms to avoid local minima which is a common problem in registration, especially when the initial motion is not provide [6].
- 4) **Proposed**: The main problem of the genetic algorithm is the time required to converge. Thus, we propose a global algorithm that simultaneously determines the translation and rotation. Our algorithm is based on the rigorous mathematical theory-Lipschitz optimization.

4.1 Accuracy Tests

We evaluate the registration accuracy based on the concept of target registration error using fiducial markers in the animal experiment and using the landmarks in the experiment of clinical data. For each of the 20 selected pig knees, two sets of femur surfaces of 12272 points are registered. Also, the accuracy of registration is evaluated by measuring the root mean square distance (RMSD) error of 15 mark points between two femur surfaces (two time-points). In the experiment using clinical data, two sets of chosen femur surfaces of 25036 points per knee are registered; the accuracy of registration is evaluated by measuring the RMSD error of 8 landmarks as well.

Figure 7 shows the RMSD error using 20 knees of pigs for each of four different registration methods. The results using 15 knees of patient for each of four different methods are shown in Fig. 8. Also, the aver-

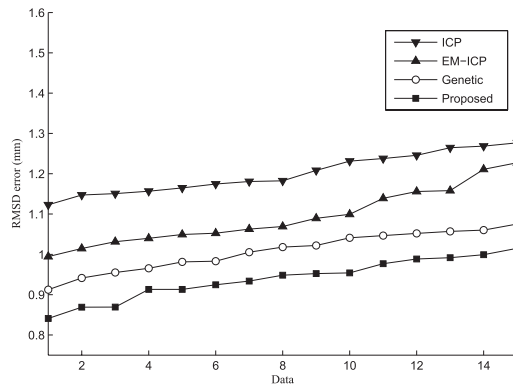


Fig. 7 Root mean square distance (RMSD) for each of four registration approaches using 20 knees of pigs. For each of 20 knees, the RMSD was estimated using 15 corresponding image points belonging to both femur surfaces.

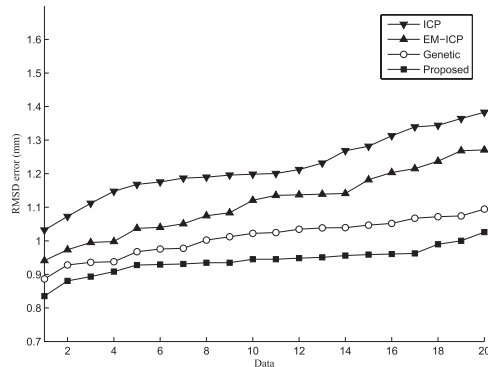


Fig. 8 Root mean square distance (RMSD) for each of four registration approaches using 15 knees of patient. For each of 15 knees, the RMSD was estimated using 8 corresponding image points belonging to both surfaces.

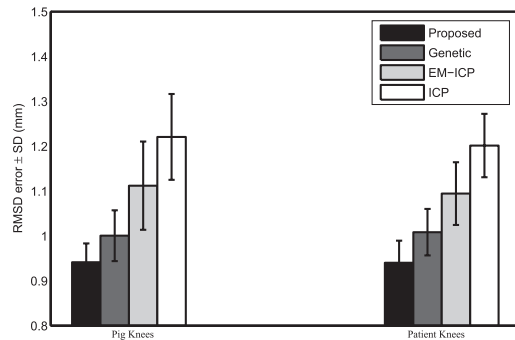


Fig. 9 The average RMSD and its standard deviation (SD) for each of our registration approaches Left: The results using 20 knees of pigs; right: the results using 15 knees of patients.

age RMSD and its standard deviation (SD) were calculated for each registration method, and displayed in Fig. 9. In the animal experiment, the average RMSD was 1.22 ± 0.10 mm (SD) (range, 1.03–1.39 mm) by ICP method, 1.12 ± 0.10 mm (range, 0.94–1.27 mm) by EM-ICP method, 1.00 ± 0.06 mm (range, 0.88–1.09 mm) by the genetic method, and 0.93 ± 0.04 mm (range, 0.83–1.02 mm) by the proposed method. In the experiment using clinical

Table 1 Experimental results using the pig knees obtained by four registration methods: The first column reports the 3D clouds of points. The last three columns report the RMSD, the number of iterations, and the computation time in seconds (Time).

Points	Method	RMSD	Ni	Time (s)
1000	ICP	1.39	27	221
	EM-ICP	1.35	31	242
	Genetic	1.22	39	276
	Proposed	1.15	28	229
5000	ICP	1.32	53	1072
	EM-ICP	1.28	65	1159
	Genetic	1.16	80	1325
	Proposed	1.07	56	1097
10000	ICP	1.26	83	9877
	EM-ICP	1.22	92	11552
	Genetic	1.05	99	12736
	Proposed	0.94	87	10325

Table 2 Experimental results using the clinical data obtained by four registration method.

Points	Method	RMSD	Ni	Time (s)
1000	ICP	1.38	24	180
	EM-ICP	1.25	27	201
	Genetic	1.21	32	235
	Proposed	1.16	25	187
5000	ICP	1.32	49	1037
	EM-ICP	1.28	58	1120
	Genetic	1.16	76	1287
	Proposed	1.06	51	1055
10000	ICP	1.28	78	9120
	EM-ICP	1.13	86	10722
	Genetic	1.08	95	11973
	Proposed	0.97	81	9632

data, the average RMSD is 1.20 ± 0.07 mm (range, 1.12–1.28 mm) by ICP method, 1.09 ± 0.07 mm (range, 0.99–1.23 mm) by EM-ICP method, 1.01 ± 0.05 mm (range, 0.91–1.08 mm) by the genetic method, and 0.94 ± 0.05 mm (range, 0.84–1.01 mm) by the proposed method. It can be shown in Figs. 7–9 that the proposed method was the best among the four approaches.

4.2 Computation Time

The RMSD errors for four registration methods have been estimated. The computation time has also been considered, which might be critical in some applications. Although the time required is very important, all the methods have been programmed using Matlab 6.5 in an Intel (R) Core (TM) 2 Duo E6550 computer, 2.33 Ghz, 2 G RAM because we are only interested in the comparison among the methods and Matlab guarantees a simple implementation.

Experimental results using the pig knees are summarized in Table 1. The last three columns give the average RMSD errors, number of iterations and computation time. Table 2 shows the results using the patient knees. In the genetic method, the RMSD errors were found to be better than the ICP and EM-ICP algorithms, while the computation time greatly increased. The executing time of the proposed method was considerably smaller compared to the genetic and EM-ICP methods. Thus, the proposed method

was highly efficient for computation time in the application of the 3D point clouds-based registration described above.

5. Discussion

The 3D registration techniques have become an important tool in medical image processing. They are useful for combining data from different image modalities, comparing spatial distribution patterns between different individuals, and displaying longitudinal changes in those distribution patterns, particularly in the context of monitoring disease progression.

Disorder of the knee joint, which is a load-bearing joint, can cause severe disability in walking. Detection of subtle physiological and anatomic changes in diseased knee joints is essential for predicting prognosis of the disease and planning therapy. Accurate evaluation of changes in lesions requires precise matching of rotation and translation of MR images, as well as high in-plane resolution and thin slice thickness. To this end, we developed a registration method of serial MR images of knee joints for precise monitoring of knee joint disease.

Several investigators have already reported on the changes in cartilage morphology over time [1], [2], [13], [14], and a few studies have reported the registration algorithms of 3D cartilage surfaces for detecting local cartilage morphology changes [15]. Until now, the authors could not find any report commenting on the registration accuracy of knee joint in terms of anatomical inspection. In the present study, we have quantitatively evaluated the accuracy of 3D femur surface matching using the three widely used registration approaches, and our proposed approach.

Although the global search algorithm can avoid the local minima, this algorithm basically conducts an exhaustive search. To overcome this, we introduced a "Lipschitzization" process to the objective function. After making the objective function globally Lipschitzian, global search algorithm was carried out effectively over the motion space. Moreover, a coarse registration method based on the principle component analysis (PCA) was used to reduce the bound to be searched. The experimental results by the proposed approach demonstrated the effectiveness for the computation time (see Tables 1 and 2).

It should be noted that the proposed method is different from the others such as the ICP algorithm. The ICP algorithm evaluates the correspondence between the two point sets, estimates the optimum (in the least squares sense) registration vector, that is, the set of translation and rotation parameters that lead to the optimum (in the least squares sense) registration of the two sets and then applies this transformation to one of the sets. This process is applied repeatedly until a certain dissimilarity measure (e.g., the mean square error) becomes smaller than a certain value. On the contrary, our proposed method obtained the translation and rotation parameters through searching a 6D space of Euclidean motions (rotation and translation) simultaneously. Then, this search is carried out by using a Hyper-cuboid-and-hyper-

ball (HCnHB) algorithm.

Wachowiak et al. [16] also used the Lipschitzian method for the registration of 3D medical image. In the Wachowiak's method, two optimization algorithms (DIRECT and MDS) were used for optimization problem. DIRECT (Dividing Rectangles) is a global technique, and the multi-directional search (MDS) is a local method. Wachowiak's method is a trade-off between the global and local optimization. DIRECT is a relatively recent algorithm for finding the global minimum of a multivariate function subject to linear bounds. It is essentially a Lipschitzian approach, but no Lipschitz constant needs to be specified. Like the Nelder-Mead method, MDS use a simplex of $n + 1$ vertices. A new simplex is generated at each iteration based on the current best point, the point attaining the lower function value in the simplex. Initial vertices are usually chosen as $[I_n - 1_{n \times 1}]$, where I_n is the $n \times n$ identity matrix, and $-1_{n \times 1}$ is column vector of $n - 1$'s. Since MDS is an iterative descent algorithm, it requires a good initial estimate in order to converge to the global minimum. In the present study, we described a Hyper-cuboid-and-hyper-ball (HCnHB) method for global optimization. This algorithm is based on the branch-and-bound method, a well-known technique in global optimization. Branch-and-bound technique was adapted for finding the optimal translation and rotation in the 6D space of Euclidean transformation. Our algorithm (HCnHB) of solving the mathematical optimization problem guarantees global optimality.

Current study has developed a 3D global optimization algorithm for the identification of anatomically corresponding points of the knee femur surface to quantify local cartilage thickness changes. Furthermore, the cartilage thickness must be measured. In the literature on thickness measurement of articular cartilage from MR images, the edge detection method has been widely used for thickness measurement [17], [18]. However, for the articular cartilage with a small thickness, its measured value is an overestimation relative to its true thickness. This is due to finite spatial resolution of imaging scanners and blurring involved in edge detections [18]. To improve the measurement accuracy, Cheng et al. [19], [20] proposed a method based on a model of the MR imaging process. Thickness measurement problem was formulated as the least square fitting of an actual gray-level profile observed in the MR data set to a modeled gray-level profile. Their results show that the model-based method gave thickness measurements with sufficient accuracy.

In the present study, registration of tibia images was not investigated. We have focused on registration of the femur because detection of subtle changes in the femur can help in predicting prognosis of the disease and planning therapy. However, detection of changes in the tibia is also important for precise monitoring of knee joint disease [14]. Further research is needed to use the proposed method for testing the accuracy of registration around the tibia.

6. Conclusion

We have presented a technique for the identification of anatomically corresponding points of the knee femur surfaces in the two MR image data sets. The technique can track local cartilage thickness changes over time. The present technique is grounded on a mathematical theory - Lipschitz optimization. Based on this theory, we propose a global search algorithm that simultaneously determines the optimal transformation parameters and point correspondences through searching a 6D space of Euclidean motion vectors (translation and rotation). Compared with the other three registration approaches (ICP, EM-ICP, and genetic algorithms), the proposed method achieved the highest registration accuracy on both animal and clinical data. In the future, we plan to apply our proposed registration method to track local cartilage thickness changes over time for the clinical application.

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