SIFT and Preserving Topology Structures of Local Neighborhood: Matching Feature Point in Deformation Measurement of Nonrigid Biological Tissues from Magnetic Resonance Images

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In this paper, we propose an integrated method SPTSLN (SIFT and Preserving Topology Structures of Local Neighborhood) for feature point matching in MR images of nonlinear and nonuniform deformation of nonrigid tissues. First, from the template and deformed images, the DoG detector and SIFT descriptor are used to extract and describe the feature points. Then the matching probability matrix of relaxation labeling is initialized according to the SIFT matching results of the feature points between the template and deformed images. Subsequently, the relaxation labeling is adopted to update the probability matrix and refine the matching based on preserving topology structures of local neighborhood of the feature points. Finally, the mismatching elimination method based on affine transformation and distance measurement is used to eliminate the residual mismatched points. The experimental results showed that the proposed SPTSLN method outperformed the single SURF and SIFT methods.

Keywords: SPTSLN, Matching, Feature Point, Nonrigid, Image.

1. INTRODUCTION

Deformation field measurements of nonuniform and nonrigid biological tissues from magnetic resonance (MR) images are often needed in clinical diagnosis, simulation and planning of surgery, and evaluation of the physical characteristics of biological tissues. It is important to accurately measure local, irregular deformations between initial and deformed images.¹–⁵ Deformation measurement aims at obtaining the displacements of a number of feature points, which are usually distributed on the inner parts, boundaries and separatrices of layers in the tissues. Generally, the deformations of the biological tissues are irregular. For example, the human body consists of various tissues, such as skin, muscle, organ, bone, and nail. The big differences among the physical parameters of these tissues result in different deformations even with the same force on them. Due to the nonlinear deformation of nonrigid and nonuniform tissues, it is difficult to measure the accurate displacements of a number of feature points distributed on the inner parts, boundaries and separatrices of layers of the tissues.

Deformation measurement of nonrigid tissues is not identical with nonlinear registration which aims at finding a transformation such that the transformed template is similar to the reference image. Usually, one cannot obtain the accurate displacements of many feature points by the intensity based registration techniques such as FFD (Free Form Deformation) B-Spline and Demons based registration methods.⁶–¹³ In feature point based registration methods, the matching of feature points is critical while difficult to be solved in nonlinearly deformed images.¹⁴–¹⁷ Current feature point based registration methods are usually combined with the intensity based registration methods.¹⁸–²¹

In this paper, we propose an integrated matching approach named SPTSLN (SIFT and Preserving Topology Structures of Local Neighborhood). According to SPTSLN method, the DoG and Harris detectors are adopted to extract both the corners and blob feature points from the nonrigid biological tissues. Then the SIFT descriptor is used to describe the local texture feature of
the neighbor region around the feature point. However, SIFT feature lacks global information on images which making it prone to mismatching when there are multiple similar local regions in the image. Unfortunately, similar local regions usually occur in the MR images of nonrigid biological tissue. Therefore, the characteristic that the topological structure of the feature points in the local neighborhood is usually preserved although the non-linear deformation of the nonrigid tissues is utilized to describe the global spatial information of the feature point. Further, the relax labeling method is adopted to optimize the matching of the feature points. Finally, the matching accuracy is improved by eliminate the potential mismatching points. In our experiments, the methods SIFT and SURF were compared with our method, and the results showed that our method is more feasible and effective.

The rest of this paper is organized as follows: The remainder of Section 1 gives a brief review of the literature, focusing on the differences between existing methods and ours. Section 2 contains an overview of the proposed approach. The optimization approach derived from the SPTSLN algorithm is developed in Section 3. Section 4 gives the validation experiments using synthetic examples and a preliminary evaluation of the algorithm on feature points between the template and the deformed MR images. Conclusions are drawn in Section 5.

1.1. Related Work
Extraction and matching of the feature points, which should be robust against the change in illumination, scaling, rotation, and noise or slight distortion, is one of the most important methods used to detect the correspondences between the images. A wide variety of feature point detectors and descriptors have already been proposed in the literature.22–33 Among them, the widely used Harris corner detector, which is based on the eigenvalues of the second-moment matrix, is not scale-invariant.24 Lowe introduced the Scale Invariant Feature Transform (SIFT) approach, which approximated the Laplacian of Gaussian (LoG) by a Difference of Gaussians (DoG) filter.22,25,26 Shown in the literature,27 SIFT outperforms other feature descriptors like Gaussian derivatives, moment invariants,26 and—phase-based local features. Various refinements on the SIFT scheme have been proposed, among which the PCA-SIFT (Principle Component Analysis-SIFT) and the GLOH (Gradient location-orientation histogram) methods are well-known.23,26 Bay presented the method SURF (Speeded-UP Robust Feature) in Ref. [29], which is more repeatable, distinctive, and robust than SIFT. In the experimental results, Bay also proved that SURF outperformed some other methods such as GLOH and PCA-SIFT.26,29,30 However, SIFT and SURF is not invariant to general deformations.23,31

Chui proposed a nonrigid point matching algorithm RPM (robust point matching) which can estimate the correspondence and nonrigid transformations between the two point-sets at the same time.23 However, according to Ref. [32], the optimal processing of the energy function used in the method could get trapped in bad local minima. Ling and Jacobs proposed a geodesic distance based deformation descriptor called GGH (Geodesic-Intensity Histogram).33 One drawback of this method is that it assumes the deformation along different directions is isotropic. This assumption is usually not true in practice.33 Tian proposed a low-complexity deformation by using Hilbert scanning.34 Unfortunately, if an interest point is located in the subdivision line of Hilbert scanning, the method would be disabled. In addition, this method assumes that only pixel locations change but their intensity does not change, which is not always practicable because the MR images taken at different times would not always have the same intensities. Cheng proposed a deformable local image descriptor called Local-to-Global Similarity (LGS) model.33 Unfortunately, the method only has a little improvement in recall precision when compared with SIFT, and there was no elimination method of wrong matching points proposed.

In our previous work, we proposed the TPS-SURF-SAC matching method and a mismatching elimination method of TPS clustering.35 The matching region is identified by TPS for every query point first, and then the SURF descriptors and the Spatial Association Correspondence (SAC) method are combined to match the feature points. Finally, by clustering the coordinate differences between the matching points obtained by the proposed method and the matching points calculated by TPS model, most of wrong match points are eliminated. Nevertheless we have to extract some landmarks manually to obtain the initial TPS transformation model between the template image and the deformed image, which would result in some measurement errors and the method could not be automatic. So far, the feature point matching of nonrigid biological tissues is still an open problem.

2. OVERVIEW OF THE PROPOSED APPROACH
The overview of the proposed approach is shown in Figure 1. According to the proposed method, the DoG and Harris detectors are used to extract the feature points, and then the feature points are described by SIFT descriptor. The matching probability matrix of relaxation labeling is then initialized according to the $\chi^2$ statistic distances of the SIFT feature vectors between the feature points. Then relaxation labeling is adopted to update the probability matrix and refine the matching. This is used to maximize the value of the object function deduced from the method of Preserving Topology Structures of Local Feature Points Extraction

Create Feature Point

Descriptor

Analyze Preserving Topology Structures of Local Neighborhood

Feature Points Extraction

Initialize Matching Probability Matrix

Relaxation Labeling

Mismatching Elimination

End

Fig. 1. The flow chart of SPTSLN method.
3. MATCHING

In this section we use the relaxation labeling process to solve the optimization problem of nonrigid point matching. The relaxation labeling is an iterative process to reduce ambiguities in assigning labels to a set of objects by incorporating the contextual information. The contextual information is usually represented as the compatibility coefficient.

3.1. Feature Point Detection and Description

To accurately measure a nonuniform deformation field, it is necessary to extract an adequate number of feature points in the MR images. In this paper, Difference of Gaussian (DoG) and Harris detectors are adopted to extract a number of feature points from the deformed tissues.

Lowe’s method for image feature generation transforms an image into a large collection of feature vectors, each of which is invariant to image translation, scaling, and rotation, partially invariant to illumination changes and robust to local geometric distortion. Since the SIFT method outperforms other point descriptors, it is adopted here to describe the feature points (keypoints). After the keypoints are detected, dominant orientations are assigned to localized keypoints. This step ensures that the keypoints are more stable for matching and recognition. The gradient magnitude and orientation are precomputed using pixel differences, and then an orientation histogram is formed from the gradient orientations of sample points within a region around each keypoint. The orientation histogram has 36 bins covering the 360 degree range of orientations. Peaks in the orientation histogram correspond to dominant directions of local gradients.

The next step is to compute a specific descriptor for the local image window around each keypoint. The descriptor is as invariant as possible to the remaining variations. First, the image gradient magnitudes and orientations are sampled around the keypoint, using the scale of the keypoint to select the level of Gaussian blur for the image. In order to achieve orientation invariance, the coordinates of the descriptor and the gradient orientations are rotated according to the keypoint orientation. These samples are then accumulated into orientation histograms summarizing the contents over 4x4 subregions of the window, and each histogram has 8 orientation bins. The descriptor of the keypoint is formed from a vector containing the values of all the orientation histogram entries with $4 \times 4 \times 8 = 128$ elements.

3.2. Preserving Topology Structures of Local Neighborhood of the Feature Points

Considering the spatial structures of several feature points in a small region, we observe that although the absolute distance between two points may change significantly under nonrigid deformation, the topological structure of a point neighborhood is generally well preserved due to the physical constraints. For example, although a human face is a nonrigid shape, the relative position of the chin, nose, mouth, and eyes, etc., cannot deform independently because of the underlying constraints of bones and muscles. These physical constraints restrict the deformation of the feature points extracted in a neighborhood. Zheng formulated point matching as an optimization problem of preserving local neighborhood structures. However, when selecting neighbors, the topological relations among the points such as distance, angle, and orientation were not considered, and hence mismatching still occurs.

Lee proposed the topology preserving relaxation labeling method to match nonrigid points in shapes. According to Ref. [38], the differences of the distance and angle among point pairs are calculated to refine the matching. The method preserves the topology structure of the whole shape during the matching of nonrigid points. Unfortunately, during the deformation measurement, the nonrigid and nonuniform biological tissues are deformed nonlinearly and irregularly with the force being added. Therefore, the topology structure of all the extracted feature points in the whole MR image is not preserved.

Preserving local neighborhood structures makes it more efficient and reliable for the human visual system to recognize shapes because the early stages of visual processing are basically local, parallel and bottom-up. In view of the above mentioned, we consider the spatial topology information such as distance, angle, and direction among the points in the local neighborhood, which leads to the preservation of the topology structures of local neighborhood.

Lee used topology preservation to match the point sets in the nonrigid deformed shapes. In this paper, we combine topology preservation of local neighborhood with SIFT to match the feature points from nonrigid deformed MR images. The details of the topology preservation of local neighborhood are given below.

Let $S = \{s_1, s_2, \ldots, s_i\}$ be a set of points in a model shape and $T = \{t_1, t_2, \ldots, t_j\}$ be a set of points in the target shape. Usually in a point matching problem, one-to-one matching is impossible because of the outliers. To handle this problem, we introduce the dummy points, $s_{nn}$ and $t_{nn}$, such that the two point sets are augmented to $S' = \{s_1, s_2, \ldots, s_i, s_{nn}\}$ and $T' = \{t_1, t_2, \ldots, t_j, t_{nn}\}$. The common points can be matched one-to-one and outliers can be matched to the dummy points. For a given point, $s_i \in S'$, one can select adjacent points $a_i^x$, $x = 1, \ldots, X$, which reside in the circle centered at $s_i$ and $X$ is the total number of adjacent points of $s_i$. We set the radius of a circle as the median value of all the Euclidean distances between point pairs in $S$. Similarly, for a point $t_j \in T'$, adjacent points are $a_i^y$, $y = 1, \ldots, Y$, and $Y$ is the total number of adjacent points of $t_j$.

In this paper, the point matching problem is formulated as the graph matching problem. Each point is a node of a graph, and a point and its adjacent point forms an edge of the graph. Then the problem is to maximize the number of matched edges between two graphs. For this purpose, we determine the fuzzy correspondence matrix $P$. Each entry of $P$ named $P_{ij}$ has continuous value between $[0, 1]$ that indicates the weight of the correspondence between $s_i$ and $t_j$. The optimal match $\hat{P}$ is found by maximizing the energy function as follows:

$$\hat{P} = \arg \max C(S', T', P)$$

where $C(S', T', P)$ is the energy function optimized by the probabilistic relaxation method.

Initially, each point $s_i \in S'$ is assigned a set of matching probability based on the shape context distance. After the initial probability assignment, the relaxation labeling process updates the
matching probability. The purpose of the subsequent process is to assign a matching probability that maximizes $C(S', T', P)$ under the relaxed condition as $p_{ij} \in [0, 1]$. At the end of the relaxation labeling process, it is expected that each point will have one unambiguous matching probability.

The determination of the compatibility coefficients is crucial because the performance of the relaxation labeling process depends on them. As a key contribution, we define a new compatibility coefficient to relax the binary value into multiple discrete values. The proposed compatibility coefficient quantifies the degree of agreement between the hypothesis that $s_i$ matches to $t_j$ and $a_i^s$ matches to $a_j^t$. It is measured by the set of vectors originating from a point and extending to all other sample points. The full set of vectors increases the algorithm complexity and processing time. To simplify and speed up the process, log distance and polar angle bins are used to capture the coarse location information. The bins are uniform in log-polar space, which makes the descriptor more sensitive to positions of adjacent points than to those of points far apart. In the diagram, the distance is defined as zero in the origin and increased by one toward the outer bins. More specifically, the bin distance measure quantifies the original Euclidean distance from 0 to 5, where 0 indicates the shortest Euclidean distance and 5 indicates the longest Euclidean distance. The Euclidean distance uses multiple digits. Because we use only one digit to represent the distance, the computational complexity of the distance measure is reduced compared to the arbitrary Euclidean distance measure.

Let $d_i(s, a_i^s)$ be the distance between an origin point $s_i$ and its nearest adjacent points. Then the distance set of the origin point $s_i$ is defined as $DS(s_i) = \{d_i(s, a_i^s), d_i(s, a_{i+1}^s), \ldots, d_i(s, a_{i-N}^s)\}$. For the computation of the angle between point pairs, the alignment of a diagram with a reference point is necessary. In this paper, the mass center of a point set is used as a reference point. The direction from a point to the center of mass is set as the positive x-axis of the descriptor. From this axis, the angle is incremented by 1 in a counterclockwise direction. Let $l_i(s, a_i^s)$ be the angle between an origin point $s_i$ and its nearest adjacent points. The angle set of an origin point $s_i$ is given as $ANG(s_i) = \{l_i(s, a_i^s), l_i(s, a_{i+1}^s), \ldots, l_i(s, a_{i-N}^s)\}$. Every point can be an origin and the origin varies with the points considered in the calculation of the location information.

In the nonrigid degradation of point sets, we note that a point set is usually distorted; however, the neighboring structure of a point is generally preserved because of the physical constraints. The displacement of a point and its adjacent point between two point sets constrains each other. Thus, if the distance and angle of a point pair $(s_i, a_i^s)$ in the model shape and its corresponding point pair $(t_j, a_j^t)$ in the target shape are similar, we say that they have high correlation. This is further strengthened if the points in a point pair $(s_i, a_i^s)$ in the model shape are close to each other. To quantify this observation, we introduce the similarity constraint, $\alpha$ and $\beta$, as well as the spatial smoothness constraint, $\gamma$.

The similarity constraint is related to the differences between the distances and angles of $(s_i, a_i^s)$ and $(t_j, a_j^t)$. This first constraint ensures that if $(s_i, a_i^s)$ has smaller distance and angle differences with $(t_j, a_j^t)$, then they are more compatible. The disparities between $(s_i, a_i^s)$ and $(t_j, a_j^t)$ are defined as follows:

$$\alpha(s_i, a_i^s; t_j, a_j^t) = 1 - |d_i(s, a_i^s) - d_j(t, a_j^t)| / \max|d_i(s, a_i^s), d_j(t, a_j^t)|$$  \hspace{1cm} (2)

The second constraint, spatial smoothness, is measured by the distance between $s_i$ and $a_i^s$:

$$\gamma(s_i, a_i^s) = 1 - d_i(s, a_i^s) / \max d_i(s, a_i^s)$$  \hspace{1cm} (3)

where $\max d_i(s, a_i^s)$ is the longest edge of point-adjacent point pairs. Two points $s_i$ and $a_i^s$ are called the most salient if $\gamma(s_i, a_i^s)$ is 1, or the least salient if $\gamma(s_i, a_i^s)$ is 0.

3.3. Relaxation Labeling

The relaxation labeling method is adopted here to search the optimal matching of the feature points between the template image and the deformed image. First, we define a total compatibility coefficient by

$$r_{ij}(a_i^s a_j^t) = \alpha(s_i, a_i^s; t_j, a_j^t) \cdot \beta(s_i, a_i^s, a_j^t) \cdot \gamma(s_i, a_i^s)$$  \hspace{1cm} (4)

Clearly, $r_{ij}(a_i^s a_j^t)$ ranges from 0 to 1. A high value of $r_{ij}(a_i^s a_j^t)$ corresponds to a high matching probability between $(s_i, a_i^s)$ and $(t_j, a_j^t)$, and a low value corresponds to a lower matching probability. The support function $q_{ij}$ in the $k$-th iteration is given by

$$q_{ij}^k = \sum_{i=1}^{X} \sum_{j=1}^{Y} r_{ij}(a_i^s a_j^t)p_{ij}^k$$  \hspace{1cm} (5)

Note that $r_{ij}(a_i^s a_j^t)$ is weighted by $p_{ij}^k$, because it depends on the likelihood of adjacent point pairs matching probability. Finally, $p_{ij}^k$ is updated according to

$$p_{ij}^{k+1} = p_{ij}^k q_{ij}^k \sum_{i=1}^{X} \sum_{j=1}^{Y} p_{ij}^k q_{ij}^k$$  \hspace{1cm} (6)

The optimization process is as follows: if a matching probability between $s_i$ and $t_j$ is supported from their adjacent points $a_i^s$ and $a_j^t$, then the probability of being matched increases. The probability decreases if they have relatively small support from their adjacent points.

Traditionally, the sum of rows (or columns) in the matrix $P$ is used as a constraint in the relaxation labeling process. In this paper, we use both the sum of rows and the sum of columns as a two-way constraints. In order to meet these constraints, alternated row and column normalization of the matrix $P$ is performed after each relaxation labeling updates. This procedure is known as Sinkhorn normalization and it showed that the procedure always converges to a doubly stochastic matrix.$^{[31]}$

After a predefined relaxation labeling iteration, the estimated matching probability is assigned to every point. To handle outliers, the points with the maximum matching probability less than a certain minimum probability (in our case, we set this to be $p_{lim} = 0.95$) are labeled as outliers by matching them to a dummy point. The outlier rejection scheme is performed throughout the relaxation labeling process.
3.4. Mismatching Elimination

Although the relaxation labeling is used to update the matching probability matrix of the feature points, and the dummy points are adopted to match the feature points that cannot be matched to the corresponding points, the mismatching cannot be avoided in the matching of the feature points from the blur, obscure and low resolution MR images.

Suppose \( U \) is the observation data set. In the initial matching set \( U \), part of the data conforms to the correct transformation parameters from the template image to the deformed image, namely inliers or true correspondence. The other data that doesn’t conform to the correct parameter are called outliers or gross error. The goal of the mismatching elimination algorithm lies in discovering correct transformation parameters \( \theta^* \) from the parameter space \( \Theta \), and in retaining inliers and rejecting outliers simultaneously.

In this paper, although the deformation results from the force added on the nonrigid biological tissues, the affine transformation could be adopted to approximate the deformation of the MR images. From \( U \) we randomly select three pairs of matching points, and calculate their affine transformation parameters to obtain \( C_{ij}^l \) sets of affine transformation parameters. Suppose \( \{\theta_k, k = 1, 2, \ldots, 5\}_l \) be the \( i \)-th set of the affine transformation parameters. Let \( V(N_{\text{match}}) = \{(x_i, t_j), i, j = 1, 2, 3, \ldots N_{\text{match}}\} \) be the set of matching point pairs obtained by the proposed method before mismatching elimination, where \( N_{\text{match}} \) is the amount of the matching point pairs, \( x_i \) and \( t_j \) are the feature points matching to each other in the template image and deformed image, respectively.

For any query point \( x_i \) in the template image, let \( x_i \) and \( x'_i \) denote the coordinate vectors of \( x_i \) and its matching point \( t'_j \) obtained by the affine transformation parameters \( \{\theta_k\}_l \) in the deformed image, respectively. If \( x'_i \) is the coordinate vector of \( t_j \), then let \( d \) be the distance between \( t'_j \) and \( t_j \).

\[
d = |x'_j - x_j|
\]  

(8)

Let \( T \) be the predefined threshold of the distance. If \( d > T \), then the matching point pair \((x_i, t_j)\) is regarded as the outlier and

![Fig. 2. Initial and deformed images of volunteers’ calves and abdomens. In each pair of images, the left image shows the initial natural posture, and the right image shows the deformed posture of the biological tissues under some force. (a) and (b) show deformations of calf when pushing the instep and pressing the toes, respectively. (c) and (d) show deformations of the abdomen when pushing and pressing on the kyte, respectively. (e) and (f) show deformations of the abdomen when pushing the kyte with the volunteer lying on the side.](image)

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<th>NCM</th>
<th>NWM</th>
<th>Ratio (%)</th>
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Notes: NM: Number of the matched pairs; NCM: Number of correctly matched pairs; NWM: Number of incorrectly matched pairs; Ratio: matching accuracy.
would be eliminated according to the parameters \( \{ \theta_i \} \). Then we can obtain the matching point pair set \( V(M_l) = \{(s_i, t_j), i, j = 1, 2, 3, \ldots, M_l \} \) corresponding to the affine transformation \( \{ \theta_i \} \), where \( M_l \) is the amount of the matching point pairs in \( V(M_l) \), and \( M_l \leq N_{\text{match}} \). Subsequently, we can obtain \( C_U^l \) matching point sets corresponding to the \( C_U^l \) sets of parameters \( \{ \theta_i \} \) \((l = 1, 2, \ldots, C_U^l) \). Finally, we compare the values of \( M_l \) \((l = 1, 2, \ldots, C_U^l) \). If \( M_{\text{max}} \) equals to the maximum of \( \{ M_l, l = 1, 2, \ldots, C_U^l \} \), then the matching point pairs of set \( V(M_{\text{max}}) \) are considered to be the correct matching points. Consequently, the residual matching point pairs are eliminated as mismatching.

4. EXPERIMENT RESULTS
We compared the methods of SIFT, SURF, and SPTSLN experimentally. The initial and deformed MR images of volunteers’ calves and abdomens are shown in Figure 2. The images are taken by the 0.5T open MRI device, of which the FOV is 24 × 24 cm. The distance between two adjacent slices is 2 mm. For the SIFT and SURF methods, each of the image pyramids consisted of 3 octaves, with every octave having 4 levels with different scales. After the feature points were extracted, the NN/SCN (the ratio of the nearest and second nearest neighbors) of SURF distance was adopted to match the feature points of the initial and the deformed MR images.

The experimental results of the three methods on the tested MR images are shown in Table I. The method SPTSLN has correctly matching ratios around 85% and many correctly matched
points. The correctly matching ratios of SIFT and SURF are lower than those of SPTSLN. Especially, much more correctly matching points are obtained by SPTSLN than that of SIFT and SURF methods, which is significant for the accurate deformation measurement of nonrigid deformed tissues. Fewer points were matched correctly with SIFT and SURF, and the correctly matched pairs of points in the MR images are less than 30, except for AbdPush and AbdPress, whose deformations on the bottom were very little. Due to the lack of global information in SIFT and SURF, the positions of wrongly matched points were usually far away from those of points correctly corresponding to the query points, as shown in the experimental results for CalPush in Figure 3.

The experimental results of the proposed method for CalPush are shown in Figure 4. Figure 4(a) shows all the feature points extracted by DoG and Harris detectors. There are 396 and 391 feature points extracted from the template and the deformed images, respectively. The matching probability matrix is initialized by $\chi^2$ statistic distances of SIFT descriptor. Then, after iterating the matching probability matrix using relaxation labeling, 352 pairs of points are obtained as shown in Figure 4(b). Subsequently, the mismatching elimination method is used to eliminate the potential mismatching pairs, leaving 63 pairs of matching points as shown in Figures 4(c) and (d). There are 51 pairs of points being correctly matched, and 12 pairs of points being mismatched as shown in Figure 4(e). The correct ratio of matching equals 80.59%. Since the mismatching elimination method is applied to the matching results of the relaxation labeling, although there are a small quantity of mismatching points, the displacement measuring errors resulted from the mismatching
From the experimental results, it is found that preserving local neighborhood topology structures can be used to describe the spatial information between the feature points, which is helpful to correctly match more feature points from the template and deformed images. When we combine SIFT descriptor and preserving local neighborhood topology structures we find that more correctly matching feature points are obtained than single SIFT method. Also the mismatching elimination method can improve the matching accuracy of the feature points.

MR images are usually low resolution, blurred and obscure. Especially, many similar local regions such as the muscle region usually occur in the MR images of nonrigid biological tissue. Therefore, various features combination is recommended to improve the matching accuracy and obtain more correctly matching feature points for deformation measurement.

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**References and Notes**


