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ORIGINAL ARTICLE

Clustered Redundant Keypoint Elimination SURF Method in MRI Image Registration Based on Alpha-Trimmed Relationship

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Abstract

Purpose: The process of Magnetic Resonance Imaging (MRI) image registration is one of the important branches in MRI image analysis, which is a necessary pre-processing to use the information in these images. The purpose of this paper is to present a new approach for MRI image registration that can maintain the total number of initial matches and have the highest precision.

Materials and Methods: The Clustered Redundant Keypoint Elimination Method-Scale Invariant Feature Transform (CRKEM-SIFT) algorithm has recently been introduced to eliminate redundancies and upgrade the correspondence precision. The disadvantages of this algorithm include the high execution time and the number of incorrect correspondences. In this paper, to increase the accuracy and speed of MRI image registration, the CRKEM method is first used over the Speeded Up Robust Features (SURF) algorithm. Then, Spatial Relations Correspondence (SRC) and Alpha-Trimmed Spatial Relations Correspondence (ATSRC) methods are suggested to improve correspondences. These suggested methods, unlike conventional methods such as Random Sample Consensus (RANSAC), which only eliminates incorrect correspondences, detect incorrect correspondences based on spatial relationships and turn them into correct correspondences. Converting incorrect correspondences to correct ones can increase the number of correct correspondences and ultimately increase the precision of correspondences.

Results: The simulation results show that the suggested CRKEMSURF-ATSRC approach improves the mean by 28.92% in terms of precision and 37.58% in SITMMC compared to those of the SIFT-ARANSAC method.

Conclusion: The suggested SRC and ATSRC methods use the spatial relations of the initial correspondences to convert the incorrect correspondences into correct ones. The number of initial correspondences is maintained in these suggested approaches. These methods are better than other methods of improving correspondences such as RANSAC, and Graph Transformation Matching (GTM). These suggested methods can be used as a new and efficient approach to improve the correspondence of medical images.

Keywords: Brain Image Registration; Clustered Redundant Keypoint Elimination Method - Scale Invariant Feature Transform; Spatial Relations; Redundant Keypoints; Magnetic Resonance Imaging.

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1. Introduction

Magnetic Resonance Imaging (MRI) image registration is the process of co-referencing two or more images of a scene taken in different conditions such as different times, angles, sensors, and the type and nature of images [1]. This process geometrically aligns the two reference and corresponding images. Registration of medical images is an important preprocess in diagnosing the disease and the rate of disease progression and treatment plan [2]. MRI images consist of three dimensions (T1, T2, PD), the registration of each of which is called multimodal registration (for example, the registration of the T1 image and the T2 image). Multimodal registration is very effective in diagnosing and monitoring the progression of diseases [3]. The image registration process has four steps. First, feature extraction is carried out to identify features in two images. Secondly, correspondence is done to determine which feature in one image should be aligned with which feature in the other image. Thirdly, the calculation of transformation is done, which is the step where the mathematical operation that would be necessary to align the sets of correspondence is found. Finally, one image is re-sampled in another image space using an appropriate interpolation method. The correspondence process is a major preprocess in many MRI registration, including diagnosis [4], and image mosaicing [5].

MRI image registration methods can be mainly divided into three categories [6]: pixel--based algorithms [7, 8], feature--based algorithms [9, 10], and deep learning--based algorithms [11, 12]. The pixel-based algorithms mainly investigate the pixel relationship between two images. These methods have the disadvantages of low efficiency and sensitivity to noise. The deep learning--based methods for MRI image registration have not been widely developed in recent years [6]. These methods face poor applicability, high data volume, and registration problem assessment. Feature-based algorithms extract important image information as similar features in images. In general, the features in the images can be edges [13], keypoint [14], texture [15], and curvature [16]. This type of method has a much higher registration efficiency than pixel-level registration methods [17]. However, the registration accuracy of this type of method depends largely on whether the extracted features are invariant between different modal images [6].

The most effective feature--based method is Scale Invariant Feature Transform (SIFT) algorithm which is resistant to geometric deviations and radiometric deviations [18]. These advantages make this algorithm important in the correspondence process, but the complex nature of MRI images causes many incorrect correspondences [19].

Although there are many improvements in SIFT for MRI image registration, there are still challenges in registration, identifying redundant keypoints, and increasing runtime in the SIFT. The Redundant Keypoint Elimination Method (RKEM)-SIFT was introduced in 2017 to remove redundant features of SIFT. In the first step of the algorithm, SIFT keypoints are extracted. Afterward, distances between different points are computed. When a calculated distance is less than a certain threshold, the redundant keypoint is deleted, and the more important one is kept for the correspondence. One of the disadvantages of this method is that it eliminates unnecessary features, regardless of the details of the image. Recently, to solve the problem mentioned in RKEM-SIFT method, Clustered Redundant Keypoint Elimination Method (CRKEM) has been proposed [20]. The efficiency of the CRKEM in the SIFT for the registration of natural images has been proven. One of the disadvantages of this method is the increase in its execution time. In this paper, the CRKEM in SURF (CRKEM-SURF) is proposed for MRI image registration. This method has high accuracy and speed. In addition, due to the complex nature of MRI images, a large number of incorrect correspondences are created in the algorithm ultimately leading to interference in the process of MRI image registration. A great deal of research has been done to remove incorrect correspondences, examples of which include Graph Transformation Matching (GTM) [21] and RANdom Sample Consensus (RANSAC) [22], Classification-based Adaptive RANSAC (CAR) [23] and Adaptive Stopping Criteria A-RANSAC [24]. In these methods, maximum incorrect correspondences and minimum correct correspondences are eliminated, but these methods are not applicable in MRI images because the intensities of MRI images differ a lot due to different sensors and spectra, which causes a large number of incorrect correspondences and a small number of correct correspondences.

However, recent correspondence improvement methods, many correspondences are eliminated as incorrect correspondences. The number of output correspondences is not equal to the number of input matches in this method. These methods are not suitable due to the nature of MRI images because they reduce the initial correspondences and ultimately lead to the failure of subsequent processes. This motivates the use to propose a new way based on spatial relations to improve the correspondence process in MRI images that can convert incorrect correspondences into correct ones. In the suggested Spatial Relations Correspondence (SRC), the appropriate conversion model is selected based on the deviation between the images. In an iterative process, the best conversion parameters between the corresponding points are calculated. Finally, the corresponding points in the reference image correspond to the best conversion model in the target image. Despite the high capability of the SRC, when the number of initial incorrect correspondences is very large, the SRC does not work well. In this case, the conversion parameters may not be selected correctly. To overcome this problem, the Alpha-trimmed Spatial Relations Correspondence (ATSRC) is proposed. In this method, the Euclidean distance of the correspondence points is first calculated, and then arranged. Finally, the alpha percentage of correspondence points is removed and then three points are randomly selected from the remaining points for calculating the conversion parameters. The Suggested (SRC, ATSRC) methods can be used as an efficient method to eliminate incorrect matches. In this paper, the suggested methods try to identify incorrect correspondences and convert them into correct correspondences, while conventional methods such as RANSAC, ARANSAC, and GTM eliminate these incorrect correspondences and reduce the total number of correspondences. This advantage of the suggested methods improves the accuracy of correspondence and registration process in MRI images by increasing the correct correspondences.

The rest of the article is organized as follows. In the second part, the suggested methods for brain image registration are described. In the third and fourth sections, the results of experiments, and conclusions are discussed, respectively.

The SIFT algorithm and its improved versions are widely used to register medical images, and the RANSAC algorithm is commonly used to eliminate incorrect correspondences. Some of these methods used in medical image registration are described below.

In [25], a three-dimensional SIFT is suggested for Computed Tomography (CT) image registration. This method is effective in MRI image registration and has good function against light changes. In [26], SURF and RANSAC are used to identify keypoints, and eliminate false correspondences in the registration of MRI images. In [27], the parameters of the 3D SIFT adjusted to match MRI images. In [28], the geometric algebra-SURF (GA-SURF) is a suggested method that has improved the accuracy and speed of registration of CT and MRI images of the brain. In [29], SURF and Randomized RANSAC (R-RANSAC) are used to identify features and eliminate incorrect correspondences in the registration of brain MRI images. This method has improved the accuracy and speed of brain image registration compared to SIFT-RANSAC method. In [30], SURF and improved RANSAC are presented to identify keypoints and remove incorrect correspondences in medical image registration. This method works well in noisy medical images and medical images with nonlinear intensity. In [31], SIFT and RANSAC are used to extract features and eliminate incorrect correspondences in retinal image registration. In [32], SIFT and RANSAC are presented to identify features and eliminate incorrect correspondences in dental X-ray images, respectively. In [17], Uniform Robust (UR)-SIFT and RANSAC are used to identify features and eliminate incorrect correspondences in multimodal retinal image registration, respectively. In [33], SIFT is used to identify features in color retinal fundus image registration. In [34], the SIFT and the RANSAC are used to identify features and eliminate incorrect correspondences in eyeball image registration, respectively. In [1], the RKEM- Synthetic Aperture Radar Scale Invariant Feature Transform (SARSIFT) and Adaptive-RANSAC (ARANSAC) have been used to extract features and eliminate incorrect corresponding in retina image registration, respectively. In [35], the Redundant Keypoint Elimination method-Auto-Adaptive SIFT (RKEM-A2SIFT) is suggested for corresponding retinal images, which improves the accuracy of the registration. One of the main problems of this method is that it does not pay attention to the details of the MRI image to remove the redundant keypoints. In [29], SURF and R-RANSAC are used to identify features and eliminate false correspondences in the registration of brain images. This method has better accuracy and speed than SIFT-RANSAC method. In [31], the SIFT and the RANSAC algorithms are used to identify features and eliminate incorrect correspondences in retina image registration, respectively.

2. Materials and Methods

In this section, the process of MRI image registration is described in three steps of feature extraction using suggested CRKEM-SURF, initial corresponding using NNDR, and improved corresponding using suggested methods based on spatial relations according to Figure 1.

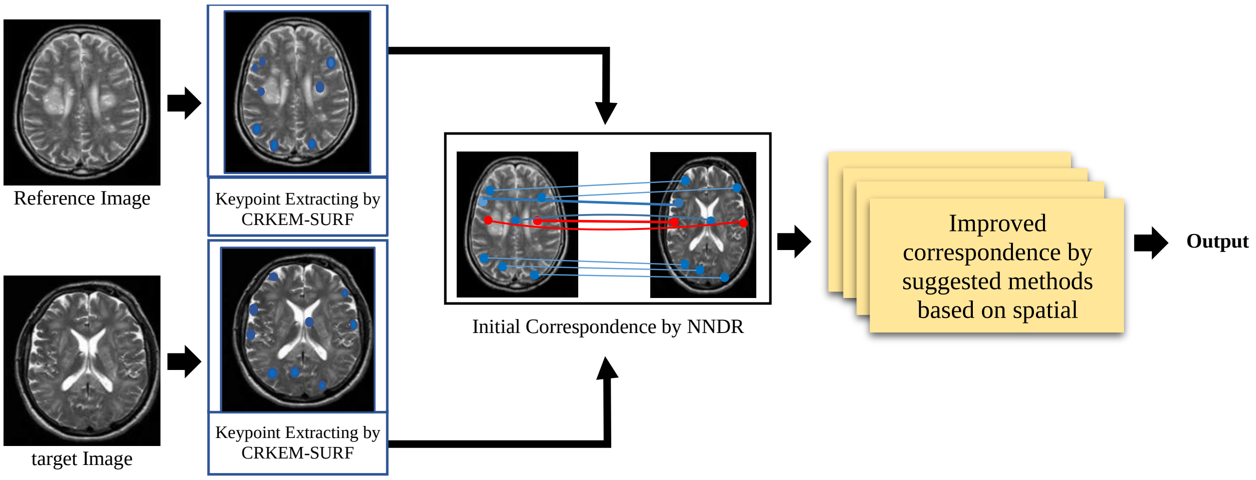

Figure 1. Proposed MRI Image Registration Flowchart

2.1. CRKEM-SURF

In this section, the CRKEM-SURF method is proposed to identify keypoints in MRI images. The details of the proposed CRKEM-SURF method are described in Algorithm 1.

Algorithm1: *The Clustered Adaptive Keypoint Elimination method-SURF (CRKEM-SURF)*

Input: *Reference and target images independently*

Output: *Essential SURF keypoints through removing redundant keypoints*

1- Compute of integral image [36]

$$I_{\Sigma}(x,y) = \sum_{x=1}^{X}\sum_{y=1}^{Y} I(x,y) \qquad (1)$$

2- Compute of Hessian Matrix and normalization to detect points [36]

$$H(x,y) = det\begin{bmatrix} A & B \\ C & D \end{bmatrix} = det\begin{bmatrix} \frac{\partial^2 f}{\partial x^2} & \frac{\partial^2 f}{\partial x \partial y} \\ \frac{\partial^2 f}{\partial y \partial x} & \frac{\partial^2 f}{\partial y^2} \end{bmatrix} \qquad (2)$$

3- clusters of keypoints are:

$$\{cluster(1), \ldots\ldots cluster(m)\}$$

4- Calculate threshold value for each cluster [20]

$$threshold = \frac{N_{ci}}{N_t} \qquad i = 1, \ldots, m \qquad (3)$$

5-Calculate Manhattan distance between each keypoint with other keypoints for each cluster as SD

$$SD(p_a) = \sum_{j=1}^{N}\sum_{i=1}^{k} \left| p_a(i) - p_j(i) \right| \qquad (4)$$

6- If the Manhattan distance of two distinct keypoints is less than the threshold value obtained according to Equation 1 in each cluster, the keypoint, according to Equation 3, whose redundancy is high is removed.

$$RI(p_a) = \frac{1}{SD(p_a)} \qquad (5)$$

7- Create an orientation for each keypoint

8- Create SURF descriptor vector for each keypoint

2.2. Initial Correspondence Using NNDR

In this part, the Euclidean distance criterion is used for the correspondence of the feature descriptors. In the NNDR method, the Euclidean distance ratio of the first nearest neighbor to the second nearest neighbor is calculated for each pair of keypoints. It must be less than the threshold value of 0.8 to be considered as the corresponding point. In this set, the initial correspondences generally include some incorrect and some correct ones. The incorrect correspondences will interfere with the next process.

2.3. Improved Correspondence Using Suggested Methods based on Spatial Relations

In this section, two suggested improved correspondence methods based on spatial relationships are presented for the registration of MRI images are proposed. Conventional methods such as RANSAC only eliminate incorrect correspondences, but this section proposes two methods that detect incorrect correspondences and turn them into correct correspondences. Converting incorrect correspondences to correct ones can increase their accuracy. The details of each of these suggested methods are discussed below.

Suggested Method 1: Spatial Relations Correspondence (SRC)

In this part, the suggested SRC method based on spatial relation is discussed. In this approach, three correspondence points are randomly selected from the set of initial correspondence to calculate the conversion parameters. In the following, the details of the suggested approach will be examined.

Step 1: The appropriate transformation model is selected based on the deviation between the MRI images. The number of correspondence points required to calculate the transformation parameters is according to Equation 6. Depending on the type of images and the deviations between the images, a suitable transformation type must be selected. The best conversion to use in these images is affine conversion [23].

$$m = \frac{n}{2} \tag{6}$$

The m is the minimum number of corresponding points required to calculate the conversion parameters. is the number of parameters in the conversion model. In this paper, the affine conversion based on the deviations between the images is used, which has six parameters. For this reason, three corresponding points are randomly considered.

Step 2: Three correspondence points are randomly selected to calculate the conversion parameters. Then the conversion model is calculated based on the conversion parameters according to Equation 7. This step is repeated a certain number of times [23].

$$\begin{bmatrix} a & b & c \\ d & e & f \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix} = \begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} \Rightarrow \begin{cases} x_1' = ax_1 + by_1 + c \\ y_1' = ax_1 + ey_1 + f \end{cases} \tag{7}$$

Step 3: To select the best transformation model in each iteration, for each correspondence point in the reference image, the distance between (P, RP_{ei}) is calculated in the target image according to Equation 8. The transformation model that has the lowest value according to Equation 9 will be selected as the best model.

$$T_p = \sum_{i=1}^{f} \|p_i - RP_{ei}\| \quad p = 1, \ldots., e \tag{8}$$

$$bestT = min(T_m) \tag{9}$$

In these relationships, f is the number of correspondence points, p_i is the i^{th} correspondence point in the target image, and RP_{ei} is the i^{th} conversion model of the reference correspondence point in the target image. e is the number of iterations and T_m is the sum of the conversion model distances in the m^{th} repeated.

Step 4: The correspondence points in the reference image correspond to the best transformation model in the target image obtained in the previous step.

Suggested Method 2: Alpha-Trimmed Spatial Relations Correspondence (ATSRC)

The suggested SRC approach introduced in the previous part is very applicable in improving correspondence compared to classical methods such as RANSAC, and GTM. However, this method is not suitable when there are many wrong correspondences in the images.

Step 1: Similar to the first step of the first suggested approach.

Step 2: The Euclidean distance of the correspondence points is calculated and arranged from highest to lowest. The alpha/2 percent maximum distances and alpha/2 percent minimum distances are not considered for calculating conversion parameters (Figure 2a).

Step 3: Three correspondence points are randomly selected from the rest of the distances set (according to Step 2) to calculate the conversion parameters (Figure 2b). Then, the conversion model is calculated based on the conversion parameters. This step is repeated a certain number of times. The other two steps are similar to steps 3 and 4 of the first suggested approach (Figure 2 c,d).

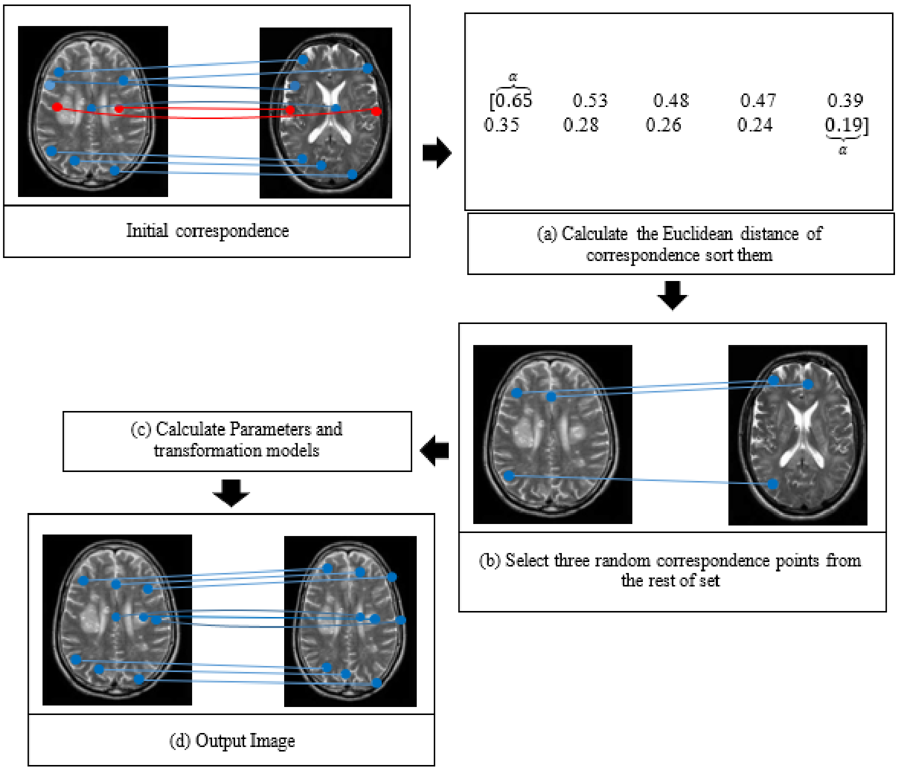

Figure 2. Proposed ATSRC Method Flowchart

3. Results

To evaluate the performance of the suggested approaches, three sets of experiments are performed with the classical SIFT [37], CRKEM-SIFT, SIFT-RANSAC [22], SIFT-GTM [21], SIFT-ARANSAC [1] and SIFT-Adaptive RANSAC [38]. The value of alpha in tests is considered 20. The database has used RIRE images [39] where each patient's MRI image includes three types of images: T1, T2, and PD. In the first experiment, the performance of the suggested CRKEMSURF method for extracting features is investigated. In the second test set, the performance of the suggested approaches is examined in the correspondence process. In the third set of experiments, the process of registering this set of images is performed and their performance is examined. The efficiency of the suggested approach was evaluated by the correspondence precision criterion according to Equation 10 [40]; the SITMMR, according to Equation 11 [40]: the SITMMC, according to Equation 12 [40]: and MAE [5].

$$precision = \frac{TP}{TP + FP} \tag{10}$$

$$SITMMR = \frac{FP + 1}{TP + FP} \tag{11}$$

$$SITMMC = \frac{TP - 1}{TP + FP} \tag{12}$$

In these relationships, TP is the number of correct correspondences and FP is the number of incorrect correspondences. The higher correspondence precision, and SITMMC and lower SITMMR, MAE and time indicate better MRI image correspondence performance.

3.1. Evaluating the Performance of the Suggested CRKEMSURF in the Extract Features

In this section, an experiment is performed to evaluate the performance of the suggested CRKEMSURF method in features extraction. The results of extracting the keypoints in the brain images can be seen in Figure 3.

As shown in Figure 3, SIFT detects more keypoints than SURF, so it can be concluded that this algorithm has more redundant points than SURF.In the RKEM-SIFT method, some of these redundancy keypoints have been removed, but in the suggested CRKEMSURF, the maximum redundancy keypoints have been removed, which increases the correspondence precision.

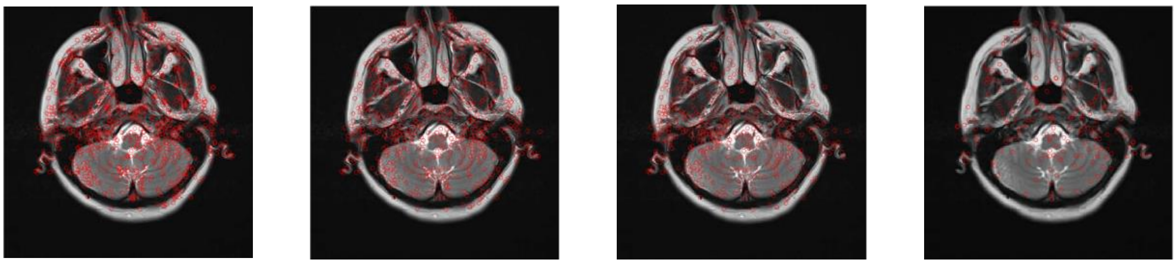
(a) (b) (c) (d)

Figure 3. Extract keypoints by different methods, (a) SIFT, (b) RKEM-SIFT, (c) SURF, (d) CRKEMSURF

3.2.Evaluating the Performance of the Suggested Approach in the Correspondence Process

In this experiment, brain images were used, the correspondence results of which are shown in Figure 4 and Table 1. As can be seen in Table1, the suggested CRKEMSURF-SRC and CRKEMSURF-ATRC approaches on the two pairs of brain images have the highest value compared to the SITMMC criterion and the lowest value compared to the SITMMR criterion, which indicates the success of its performance in the correspondence process. Other methods compared to SITMMC and SITMMR criteria are SIFT-ARANSAC, SIFT-GTM, SIFT-RANSAC, and finally SIFT for success in correspondence.

Table 1. Experiment results of methods

Method	Image type	SITMMC	SITMMR	precision
SIFT [37]	DATA1	0.723	0.276	0.736
SIFT-GTM [21]		0.730	0.269	0.746
SIFT-RANSAC [22]		0.666	0.333	1
SIFT-ARANSAC [1]		0.818	0.181	0.863
SIFT- Adaptive RANSAC [38]		0.80	0.20	0.816
CRKEMSURF-SRC		0.975	0.025	0..983
CRKEMSURF-ATSRC		**0.986**	**0.013**	**1**
SIFT [37]	DATA2	0.555	0.444	0.592
SIFT-GTM [21]		0.684	0.352	0.736
SIFT-RANSAC [22]		0.333	0.666	0.666
SIFT-ARNSAC [1]		0.705	0.294	0.764
SIFT-Adaptive RANSAC [38]		0.755	0.244	0.775
CRKEMSURF-SRC		0.956	0.044	0.970
CRKEMSURF-ATRC		**0.970**	**0.029**	**0.985**

3.3.Evaluating the Performance of the Suggested Approach in the Registration Process

In this experiment, a pair of brain images were used for registration that the registration results in Figure 5 and Table 2.

As can be seen in Figure 5, the registration is not well done (Figure 5 c,d). The unsuccessful registration of the SIFT-GTM algorithm and the SIFT-ARANSAC algorithm is due to incorrect correspondences. In the proposed methods, due to improving the accuracy of correspondence and increasing the correct correspondence, the correspondence process is well done (Figure 5.e, f).

Table 2. Experiment results of methods

Method	MAE	Time(s)
SIFT-GTM	2.861	11.31
SIFT-ARANSAC	2.207	**10.64**
CRKEMSURF-SRC	1.836	11.09
CRKEMSURF-ATSRC	**1.645**	13.21

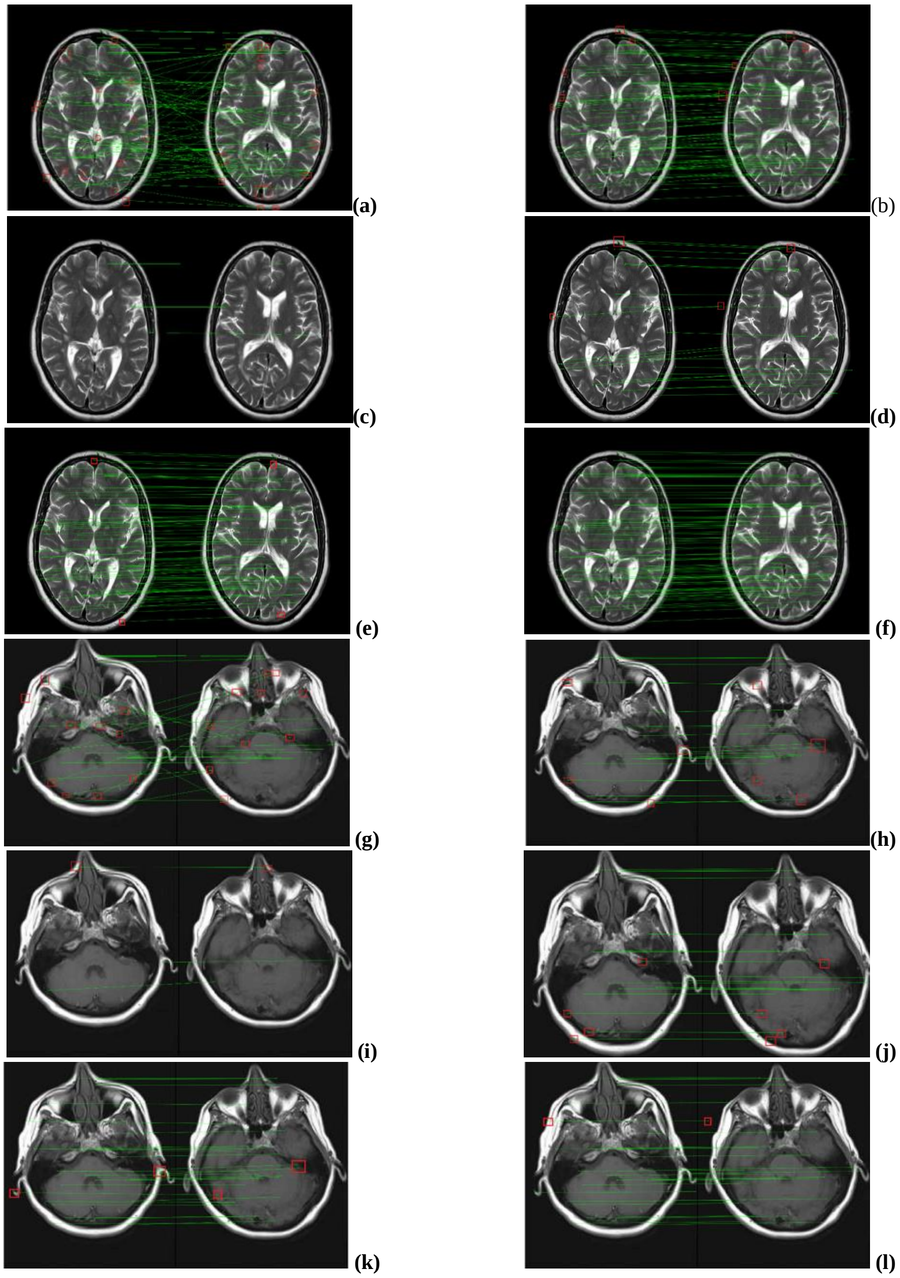

Figure 4. Brain image correspondence, (a)(g) correspondence by SIFT, (b)(h) correspondence by SIFT-GTM, (c)(i) correspondence by SIFT-RANSAC, (d)(j) correspondence by SIFT-ARANSAC, (e)(k) proposed CRKEM-SRC method, (f)(l) proposed CRKEM-ATSRC

According to Table 2, the performance of the suggested methods is better than other methods (SIFT-GTM, SIFT-ARANSAC). The suggested CRKEMSURF-ATSRC has a better performance than the CRKEMSURF-SRC.

4. Discussion

In order to evaluate the proposed methods, these algorithms are applied to RIRE images and their results are compared with the results of other algorithms by considering the visual criteria, precision, execution time, SITMMR, SITMMC, and MAE. Due to a better visual understanding of the efficiency of the suggested methods (CRKEM-SURF-SRC, CRKEMSURF-ATSRC) than other ones, the results of their correspondence process are shown in Figure 4. As it can be seen in Figure 4, the number of correct correspondences in the SIFT, SIFT-GTM, and SIFT-ARANSAC methods is less than that of the SIFT-RANSAC and the suggested methods. The total number of correspondences in SIFT-RANSAC is much less than the suggested methods (CRKEMSURF-SRC, CRKEMSURF-ATSRC), which indicates the inefficiency of RANSAC in subsequent applications.

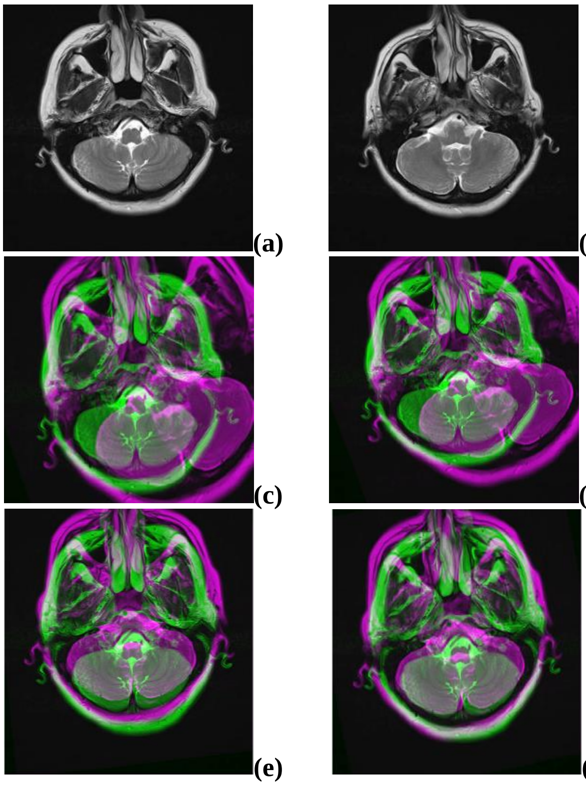

Figure 5. Brain image registration, (a) reference (b) target, (c) registration by SIFT-GTM, (d) registration by SIFT-ARANSAC, (e) suggested CRKEMSURF-SRC approach, (f) suggested CRKEMSURF-ATSRC approach

Therefore, the suggested methods using the improved correspondence method based on spatial relationships have led to the conversion of incorrect correspondences into correct correspondences and maintaining the total number of initial correspondences.

The registration process of the suggested methods compared to other methods is shown in Figure 5. The suggested CRKEMSURF-SRC and CRKEMSURF-ATSRC have been able to place the target image well on the reference image due to the improvement of correspondence, and these suggested methods have been able to have a successful registration process. SIFT-GTM and SIFT-ARANSAC could not have had successful registration due to their poor performance in the correspondence process.

The quantitative results of the correspondence process, in the suggested (CRKEMSURF-SRC, CRKEMSURF-ATSRC) methods and other methods such as SIFT, SIFT-RANSAC, SIFT-GTM, SIFT-ARANSAC, SIFT-adaptive RANSAC on the two pairs of MRI images are shown in Table 1. As can be seen, the suggested methods have better results in all images and for all criteria. The suggested methods have more ability to control the geometric and radiometric changes of MRI images by considering the spatial relationships of the corresponding points. This has led to the superiority of suggested SRC and the ATSRC methods in increasing correct correspondence (SITMMC), increasing precision, and minimizing incorrect correspondence (SITMMR) over GTM and ARANSAC algorithms. The RANSAC method is similar to the suggested methods with high precision, but the total number of correspondences and SITMMC is very small, which leads to poor performance.

The suggested CRKEMSURF-SRC and CRKEMSURF-ATSRC methods have a better performance in the image registration process than other methods such as SIFT-GTM, and SIFT-ARANSAC in terms of MAE criteria (Table 2). The suggested CRKEMSURF-ATSRC performs better than the suggested CRKEMSURF-SRC in registration process because the suggested ATSRC is more effective in complex deviations of MRI images that cause more incorrect correspondences. Suggested CRKEMSURF-SRC and CRKEMSURF-ATSRC have a longer execution time than SIFT-ARNSAC due to the step of removing redundant keypoints, but, the execution time of the suggested approaches is acceptable due to their effective performance. The SIFT-GTM has the longest execution time compared to other methods.

5. Conclusion

In this article, two methods are presented to improve the performance of the correspondence process in MRI images. The MRI image correspondence causes intensity changes due to differences in imaging sensors and imaging times, which reduces the accuracy of the correspondence. Features extraction is performed by the suggested CRKEM-SURF approach which eliminates redundant keypoints in the SURF method. This method improves the subsequent processes such as the correspondence process. Correspondence improvement methods such as RANSAC and GTM cause several initial correspondences to be omitted, including the removal of correct and incorrect correspondences. These methods are not suitable due to the nature of MRI images as they reduce the initial correspondences and ultimately lead to the failure of subsequent processes. In this paper, in order to solve the mentioned problem, two methods are suggested based on the spatial relationships of the initial corresponding points to maintain the initial correspondences and to convert the incorrect correspondences into corrections.

Then, the suggested correspondence approaches based on the spatial relationships of the SURF points are used to increase the correct correspondences. In the SRC method, the appropriate conversion model is selected based on the deviation between the images. In an iterative process, the best conversion parameters between the corresponding points are calculated. Finally, the corresponding points in the reference image correspond to the best conversion model in the target image. The SRC method was very effective in improving correspondence compared to RANSAC, GTM, and the improved RANSAC method, but this method did not work effectively when the number of incorrect correspondences is very high. To solve this problem, the ATSRC method was proposed. In the ATSRC method, the Euclidean distance of the correspondence points is first calculated, and then these distances are arranged. Finally, three points are randomly selected the (1-alpha) percentage of correspondence points. The main technique in the suggested approach is to improve the correspondence accuracy and improve the image registration process. Future studies will attempt to employ evolutionary algorithms to select the appropriate correspondence points to calculate the conversion parameters in the suggested ATSRC so that this approach can achieve more effective performance in multimodal images correspondence such as over CT-MRI image.

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