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A NOVEL HYBRID ALGORITHM FOR STITCHING OF SPINE MAGNETIC RESONANCE IMAGES

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Abstract:

The technique of merging several overlapping images from the similar viewpoint into a superior one without defeat of information is known as an image stitching. The utilization of scale invariant feature transform (SIFT) and Random Sample Consensus (RANSAC) techniques to stitch the C-T-L (cervical-thoracic-lumbar) spine magnetic resonance (MRI) images to provide the entire view of spine in a solo flawless image is the rationale of this study. All MRI images were obtained by the fast spin echo (FSE) pulse sequence using MRI scanners. Because of the limitations of MRI scanners, whenever Patients go through spinal cord examination, three different images of C-T-L sections of spine are generated. For diagnostic purpose, it is desired to have single flawless image of entire spinal cord.

For the improvement of diagnosis of spine the proposed approach can be performed best. We believe that our approach can be supportive for the medical purpose and extension of other medicinal imaging modalities for image stitching. The stitching process for every section of spine MRI image were performed and implemented on a graphic user interface (GUI) configuration.

Keywords **— Image stitching, SIFT, RANSAC, MRI**

I. INTRODUCTION

Image stitching is the method that combines various images to structure a single image with a broad field of vision. To figure one exclusive image it fundamentally combines more than two dissimilar images that is called panorama. Panoramic images can be created in a variety of manners. The purpose of the stitching is to increase the resolution of the image as well as the field of vision. A camera is normally proficient of capturing films contained by the span of its visualization only; it cannot take a big picture with all details mounted in a solitary frame. This problem leads to the use of the panoramic camera and use of these types of cameras increases the overall costing. Panoramic imagery solves this problem by combining images taken different sources in a single image. The soaring resolution film mosaics produced using Image stitching algorithms. In this article, the focus is on the image stitching of spinal cord MRI Images

Magnetic resonance imaging (MRI) was built-up in 1980s and enhanced the doctor's capability to distinguish between normal and abnormal structures of the spine and assist in diagnosis. The Doctor needs some spatial information from MRI scan that is the position of the spine, the stature of the disc, vertebral body configuration and irregularities, etc. MRI Scanners which has capacity 3 Tesla that cannot scan the whole body in solitary stroke. The majority MRI Scanners in India are 0.2 to 3 Tesla. Accordingly these are unable to obtain a complete view of the body at once. Even though a small number of MRI scanners in the world which have capacity 4 Tesla and more than that can capture full picture at a one stroke. But the cost of these scanners is uneconomical. This provoked us to use an image stitching on images obtained by MRI scanners available. And generate a full vision of the interested body part

There are different methods for feature extraction techniques. SIFT algorithm is more vital

and robust than Harris corner detection algorithm. The matching keypoint from Harris detection can be obtained with high elapsed time and is very difficult to get highly correct and exact match keypoint. Where using SIFT features we can get high exactness and robustness match keypoints. SIFT can give better performance compared with Harris corner detection method for exact keypoints matching. The main aim of this work is to stitch three C-T-L section images of spine to form single flawless image of whole spine using SIFT and RANSAC.

A. *Main objectives*

1) To develop Data base for MRI Images.
2) To extract Feature Points called "Keypoints" using SIFT algorithm.
3) To match the Keypoints with other image Keypoints using RANSAC algorithm.
4) To Stitch three images using reference of match feature points.
5) To study the performance of novel algorithm developed by fusing specific parameters of SIFT and RANSAC algorithm.

II. HUMAN SPINE STRUCTURE

One of the fundamental sciences of medicine that deals with the study of the basic structure of body parts is the Human anatomy.

TABLE I
DETAILS OF SPINAL SECTION

Sr. no	Name of Section	No. of Vertebrae	Notation
1	Cervical	7	C1 - C7
2	Thoracic	12	Th1 – Th1
3	Lumbar	5	L1 – L5
4	Sacral	5(fused)	S1 – S5
5	Coccygeal	3-5(fused)	Tailbone

The most important structure between the body and the brain is the spinal cord. The central nervous system is constituted the brain and spinal cord together. The human spinal cord is sheltered by the bone spine which consists of bones called vertebrae. There are five subdivisions of the spinal cord analogous to the diverse grouping of vertebrae, as shown in table 1.

III. METHODOLOGY

The image stitching method that made a single image using the separate images was broadly used to perform the combining images. The different stages involved in process of image stitching method can be explained with the help of block diagram as shown in figure no 1.
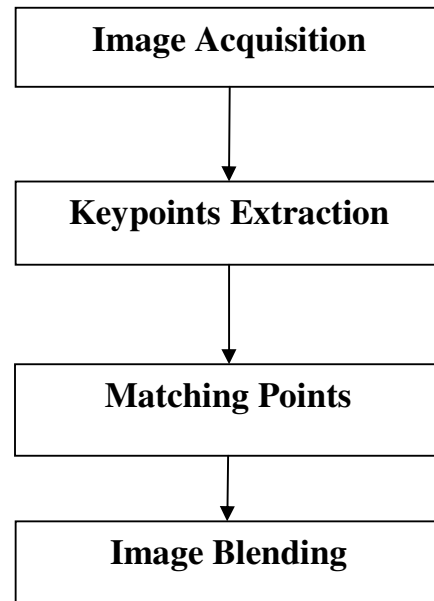
```
┌─────────────────────────┐
│   Image Acquisition     │
└─────────────────────────┘
            │
            ▼
┌─────────────────────────┐
│   Keypoints Extraction  │
└─────────────────────────┘
            │
            ▼
┌─────────────────────────┐
│    Matching Points      │
└─────────────────────────┘
            │
            ▼
┌─────────────────────────┐
│    Image Blending       │
└─────────────────────────┘
```

Fig. 1 Block diagram

The widely used image stitching method for stitching two or more images can be performed with the following Procedure.

A. *MRI Image acquisition*

The first stage of image stitching is the image acquisition stage. Image acquisition can be broadly defined as the action of retrieving an image from some sources. The three images are required (C-T-L) Spine MRI.

B. Features detection and Keypoints Extraction

The SIFT algorithm will used to detect the feature points created from an edge or corner of an object for vector calculation. Features point can be defined as the elements in the three input images.

C. Feature Matching

The SIFT detected Feature points of three images can be compare as C and T image feature points compared and T and L Feature Points are compared using RANSAC and match points are retrieved.

D. Blending

After Match point finding by RANSAC are blended referring the Match Points. And finally it can give the One Full C-T-L Spine Image and stitching is done.

IV. SIFT – FEATURE EXTRACTION AND FEATUREVMATCHING

In 1999 the David G Lowe first introduced the SIFT. SIFT stands for Scale Invariant Feature Transform. With the scaling, rotation or refinement transformation the SIFT algorithm is very invariant and robust for the characteristic or feature matching.

Detection of the extrema of the scale space

↓

Accurate keypoint localization

↓

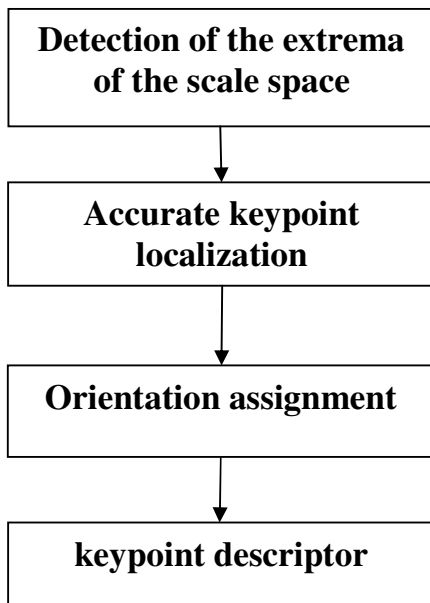**Orientation assignment**

↓

keypoint descriptor

Fig. 1 Steps of SIFT

We use the SIFT features to find matching keypoints between two successive images. The SIFT algorithm can be explained with main steps as shown in Fig. 2.

A. Scale space extrema detection

By progressively blurring the original image Scale space is constructed. After that the original image is reduced to half size. Next blurred out images are generated again then the same process is repeated. Mathematically, the convolution of input image and Gaussian operator as given in Eq(1) results in blurring of images. Expression of Gaussian blur is given in Eq(2) which gives blurred image when applied to each pixel in image. With a Gaussian mask we initially construct the image pyramid by continuous smoothing. Difference Gaussian which is DoG pyramid of the image will be obtained by subtracting the smoothed adjacent images. [17]The expression for DOG pyramid is given in Eq(3).

$$L(x, y, \sigma) = G(x, y, \sigma) * I(x, y) \qquad (1)$$

$$G(x, y, \sigma) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2 + y^2}{2\sigma^2}} \qquad (2)$$

G: The Gaussian blur operator.
L: The blurred image.
I: Input image.
σ: The scale parameter.
x, y: The location coordinates of pixels in image.

$$D(x, y, \sigma) = \big(G(x, y, k\sigma) - G(x, y, \sigma)\big) * I(x, y)$$
$$= L(x, y, k\sigma) - L(x, y, \sigma)$$
$$(3)$$

The local extrema which is maxima or minima of Difference of Gaussian pyramid is determined by using the locations of feature points. A 3 x 3 neighborhood area is considered around region of each pixel. First in the same scale the center pixel is compared with its 8 neighboring pixels. Further it is compared with its 9 consequent neighbors from the superior scale and 9 corresponding neighbors from the inferior scale if it is found an extrema. If it is not extrema then it is discarded. This reduces calculations significantly rather than comparing each pixel directly with 26 neighboring pixels. [3]

B. *Accurate keypoint localization*

The initial result of this algorithm assumes that at the center of the sampling point there is the location of the keypoint. Nevertheless, it is not the correct maximum position of the keypoint. So that we require 3D quadratic function to fit the local sampling points in order to determine the actual location, that is, the sub-pixel precision level of the maximum value. Shifting of the Taylor expansion of the space scale function is done so that the original is at the sampling point.

$$D(X) = D + \frac{\partial D^T}{\partial X} X + \frac{1}{2} X^T \frac{\partial^2 D}{\partial X^2} X \qquad (4)$$

At the sampling point and x = (x, y, σ), D along with its derivative is estimated. From this point T is the offset. By taking the derivative of this function with respect to x and fixing it to zero, the location from the extremum, $\hat{X}$ is determined.

$$\hat{X} = -\frac{\partial^2 D^{-1}}{\partial X^2} \frac{\partial D}{\partial X} \qquad (5)$$

The keypoints having a low contrast or which are poorly located on one edge are eliminated in this step. We evaluate the value D($\hat{X}$) with threshold for the search for points of low contrast. By substituting two equations above, we have: $\hat{X}$

$$D(\hat{X}) = D + \frac{1}{2} \frac{\partial D^T}{\partial X} \hat{X} \qquad (6)$$

This point will be excluded if the value of D (x) is less than a threshold. We use the reality that in these cases there is a huge principle curvature across the edge but a miniature curvature in the perpendicular direction in the difference of Gaussian function in order to eliminate extrema which is poorly localized. H which is a 2x2 Hessian matrix is computed at the location. To find the curvature scale of the key point is used. The ratio of the curvature of the principle can be confirmed proficiently using these formulas.

$$H = \begin{bmatrix} D_{xx} & D_{xy} \\ D_{xy} & D_{yy} \end{bmatrix} \qquad (7)$$

$$\frac{(D_{xx} + D_{yy})^2}{D_{xx}D_{yy} - (D_{xy})^2} < \frac{(r+1)^2}{r} \qquad (8)$$

The keypoint is removed from the contender list if inequality in above equation (8) fails.

C. *Keypoints orientation assignment*

A foremost orientation is assigned to each feature based local image gradient after the stable features are determined. This gives the rotation invariance characteristics. The gradient magnitude $m\ (x, y)$ and orientation $\theta\ (x, y)$ are computed for each pixel $(x,)$ of the region around the feature location. This is given in Eq (16) and Eq (17).

$$m(x,y) = \sqrt{((L(x+1,y) - L(x-1,y))^2 + (L(x,y+1) - L(x,y-1))^2}$$
$$(9)$$

$$\theta(x,y) = \tan^{-1}((L(x,y+1) - L(x,y-1))/(L(x+1,y) - L(x-1,y))$$

$$(10)$$

For each feature point from the weighted magnitude and orientation of each pixel around the feature point an orientation histogram is created.

D. *Keypoint Descriptor*

The m x m region about the keypoint is conked out into n x n windows where n<m. Gradient magnitudes are weighted by appropriate Gaussian window and orientations are calculated inside each n x n window. Also these are put into an 8 bin histogram. This is done on all the windows in order to obtain n x n x 8 dimensional vector which is SIFT descriptor. In order to achieve illumination invariance the descriptor is normalized to unit length. Using the feature vector a keypoint is exclusively identified.

Feature Matching

Next step subsequent to extracting the probable keypoints is to match them. To institute accurate feature correlation between two images in order to ensure precise registration is known as Keypoints or features matching. The Euclidian distance based approach is used to find corresponding keypoints in two images.

Lowe anticipated use of threshold. This threshold is the ratio of Euclidian distance to the nearest neighbour and to the second nearest neighbour. If Euclidian distance to nearest neighbour is significantly smaller than that of second nearest neighbor then a match is accepted.

V. RANSAC

After the initial set of feature correspondences has been established, next step is to find a set of homography parameters (also called projective transform) that will produce a high accuracy alignment between two images.

Least square fit traditional method for homography estimation. It is more restraint algorithm in the intellect that all the keypoints are considered to fit a model. [2] Disadvantage of Least square fit method is that it can't deal with the outliers i.e. false keypoints correspondences. If outliers be present then anticipated homography is sternly imprecise than the preferred one. To conquer this problem, excellent initial set of correct keypoints correspondences i.e. inliers should be sort out from all matched feature keypoints. And unwanted outliers should be discarded. The extensively used solution to this problem is Random Sample Consensus (RANSAC).

Random sample consensus (RANSAC) is an iterative method. It is used for estimation of factors for a mathematical model from a set of pragmatic data that contains outliers, if outliers are to be concurred no influence on the values of the estimates. Consequently, it is also known as an outlier detection method. The algorithm was earliest published by Fischler and Bolles at SRI International in 1981.The basic steps of RANSAC algorithm are discussed below:
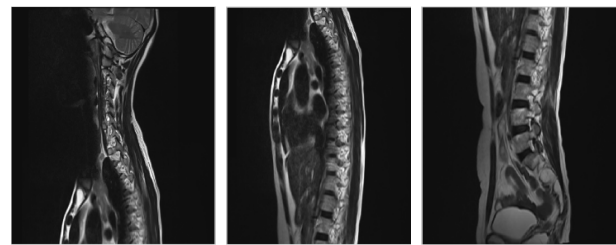
1) Select a random subset of keypoints from recognized feature keypoints correspondences.
2) Using selected subset of feature keypoints estimated in step 1, homography matrix is to be anticipated.
3) Count number of feature keypoints adapting this anticipated model with predefined tolerance. These feature keypoints structure the consensus set.

4) A novel homography matrix is estimated if adequate number of keypoints falls in consensus set, using all these inliers.
5) Or else, re-estimate homography by repeating steps 1 through 4 (for prescribed number of iterations).

The main advantage of RANSAC is its capability to dynamically approximate the homography between two images with soaring exactness even in presence of large number of outliers that is up to 50% outliers. Also, RANSAC permits us to put problem explicit thresholds depending upon the relevance and experimental evaluation.
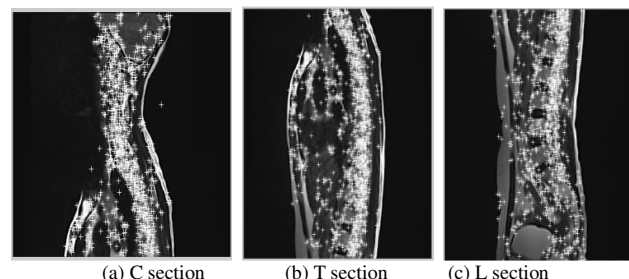
VI. RESULTS

In turn to execute the image stitching of C-T-L sections of spine SIFT and RANSAC methods have been executed using Matlab R2013a. The testing has been performed on a sample of C-T-L images of a patient. The sample images of patient 1 are shown in Fig. 3. The difference between two different images can be seen from the figures and the complication of the stitching problem.

(a) C section   (b) T section   (c) L section
Fig. 3The sample images of C-T-L sections of a patient

We discover first the equivalent keypoints from both pairs of images to be stitched from the C-T-L sections of spine using SIFT method which is shown in Fig. 4.

(a) C section   (b) T section   (c) L section
Fig. 4 The keypoints detected for images of C-T-L sections of a patient using SIFT method

Finally, after detection of keypoints the matching of keypoints is done. From the set of detected keypoints the perfectly matched keypoints are extracted and matched using Feature Matching. Feature Matching of keypoints is shown in Fig. 5.

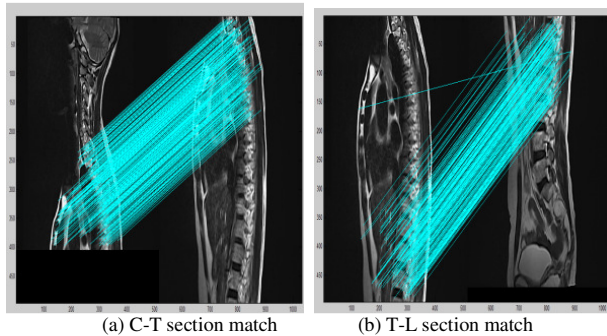(a) C-T section match   (b) T-L section match

Fig. 5 The keypoints matching of images of C-T-L sections of a patient

Finally, after matching of keypoints the C-T-L sections images of spine are stitched into a single flawless full spine image using RANSAC. All these processes are implemented on GUI. The GUI for whole work is shown in Fig. 6. And full stitched C-T-L image of spine is shown in Fig. 7.

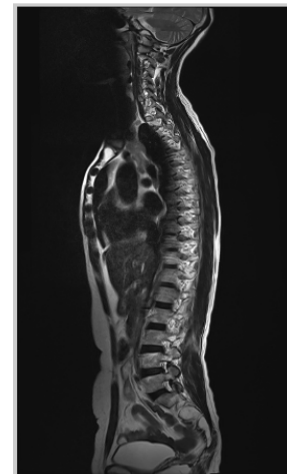Fig. 6 Developed GUI configuration program for C-T-L spine MRI stitching

Fig. 7 The full stitched image of C-T-L sections of spine

VII.   CONCLUSION

In this paper, a novel hybrid algorithm for stitching of spine magnetic resonance images to generate solitary flawless image of human spine is presented. As Scale Invariant Feature Transform is robust to changes in illumination, it makes our system robust to changes in illumination. As well as the system proposed in this paper is robust to input image sequence. Still in presence of outliers the RANSAC makes the system robust. The proposed approach is implemented using real images of a spine C-T-L sections which are obtained with a MRI scanner.

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