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Liver Image Mosaicing System Based on Scale Invariant Feature Transform and Point Set Matching Method

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Abstract: Image mosaic is an important research content in digital image processing, and could be used to solve the problem of observing large objects with narrow view, such as 360 degree panorama stitching. Microscopic observation of liver biopsy is a commonly used method in diagnosing liver diseases, which are always rely on the whole liver slice. Therefore, the liver pathological microscopic image mosaic is the best way to formulate it. This paper proposes a liver image mosaicing system based on scale invariant feature transform and point set matching method, which includes the feature point selection and location process to find the extremum point, screen them, and precisely position them. This system takes the affine transformation as the motion model, and adopts a new matching algorithm for the rigid transformation to accelerate solving the motion parameter. The design and implementation of the liver image mosaicing system have completed more than 100 cases successfully, which shows the effectiveness and robustness of our algorithms.

Keywords: Liver microscopic slice, mosaicing system, point set matching, scale invariant feature transform.

1. INTRODUCTION

In China, liver disease is a common disease, which hazards and involves a wide range. In fact, Chinese government has invested a lot of manpower, financial resources to start research work on viral hepatitis. Quantitative analysis of pathological features of liver biopsy is often required by the observation of liver tissue cell morphology under the microscope. Under the microscope, one can only observe a part of liver slices, observation results of this part are not representative of the entire sections of the situation. The purpose of this paper is to provide an automatic splicing tool, fast and accurately stitch the pieces of partial liver biopsy images together into a complete image, providing a good supporting environment for the pathological features of liver biopsy analysis.

Image mosaic is an important research topic in image processing. Image stitching technology can be divided into two kinds of methods, such as regional based methods and characteristics based methods. Regional based stitching technology realizes image mosaicing through direct elimination of pixels' dissimilarity, which always needs long search time, and sometimes requires manual intervention. Characteristics based stitching technology comes from the theory of pattern recognition, by utilizing the structure information of interesting defined in the image and the image feature to find the transformation model between the images. Therefore, These heuristic methods can reduce the scope of the search and can realize the automatic mosaic on real significance, and become the mainstream of the technology of image mosaic field.

The feature descriptor matching is always used in characteristics based stitching technology, for the similarity comparison between the obtained neighborhood feature point. Description method of feature points obtained extensive research last years. Zabih *et al.* used the complementary relationship between rank histogram and neighborhood pixel feature values as the feature descriptor [1], and the descriptor is brightness invariance. Johnson *et al.* statistics neighborhood feature point gray value of each pixel to the image center of gravity and distance, obtained a two-dimensional histogram as the feature descriptor [2], and the descriptor is rotation invariance. Lowe using weighted gradient direction feature as feature point descriptor (SIFT descriptor) [3], the descriptor has the affine invariance and scale invariance. Belongie *et al.* proposed shape descriptor which is similar to the SIFT descriptor (Shape Context), by using the Canny edge detection operator, statistics the number of different position and gradient direction of the edge point, get a 3 dimensional histogram as a feature descriptor [4]. Y. Ke *et al.* proposed PCA-SIFT descriptors, by using principal component analysis (PCA) methods, SIFT descriptors transform from 128 dimensions to 36 dimensions, speeding up the matching speed [5]. Krystian Mikolajczyk proposed a method of extending SIFT - GLOH method (Gradient Location-Orientation Histogram) [6], which added the global information into account, enhancing the descriptor's separability.

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2. THE ACQUISITION OF LIVER PATHOLOGICAL IMAGES

The acquisition of digital pathology of liver slice image can be from two ways, the first one is using digital camera to take pictures of the liver sections under the microscope, which is direct access of digital image; the second one is using the common camera to take image by the photographic film, and getting digital image through high resolution scanner. The cost of the latter one is low and widely used. The paper adopts the second method.

In the image acquisition process, the microscope is fixed above the loading platform; the optical axis of the microscope is vertical to the photograph surface. Due to the lens vision limitations, not the whole section could be shot completely one time. We always need to manually turn the mobile carrier platform, and sequence acquisition the image section. The acquisition microscope images have basically no serious distortion. There are translation, rotation, and some small tension between the changes in image sequences. In addition, due to the manual operation, the overlap size of two adjacent images is not fixed, and there are differences in exposure, and a certain degree of ambiguity.

3. LIVE IMAGE MOSAICING SYSTEM FRAEWORK

Biopsy liver image mosaicing system is to provide support for the analysis of pathology of liver slices. Pathological analysis is mainly focused on hepatic fibrosis and hepatic cell division, calculating fibrosis liver cell and normal liver cell proportion, so as to judge the degree of liver fibrosis. Accurate and efficient liver pathology analysis requires the mosaicing image must be able to reflect the liver biopsy perspectively, in addition, the operator can only guarantee the image sequence stitching, and require no manual intervention.

Because the liver slice image sequence is known, the left problem is the adjacent image stitching. Furthermore, we assume one image is fixed, so we only have to move and transform the other image to the right position, the former is called fixed image, while the other is referred as the floating image. The overall mosaicing flow includes two parts.

First part is the acquisition of adjacent image transforming parameters which determine the transform position in image sequence of every two adjacent images.

Second part is the image synthesis, namely according to the transform parameters of two adjacent images, aligning and fusing the image sequence to formulate the synthesis mosaic image.

To obtain adjacent image transform parameters is a key problem of the whole process. In order to adapt to the complex pathological splicing sequence liver images, as well as to ensure the veracity of stitching, we adapt the feature based method which is from coarse to fine calculation to formulate the image transformation parameters. The transform parameters calculation is roughly first in a small image sampling, *i.e.* the coarse registration, according to the coarse registration results in the original image to adjust, and realize the precise registration at last.

4. FEATURE POINT SELECTION AND LOCATION

Feature point selection and location process include finding the extremum point, screening of candidate feature points, and precisely positioning feature points.

First step is finding the extremum point. For each sample point in the Difference of Gaussian (DoG) space of each image, finding the extremum point is the judgment of the points in its neighborhood space whether it is extreme point. If it is the extreme point, then it is regarded as a candidate feature point. Turn on each scale image with the exception of both two external processing, get the initial set of candidate feature points.

As shown in Fig. (**1**), each point is determined by its adjacent points. The adjacent 8 points of the same scale and the surrounding 18 points of the upper and down of two scale image formulate a total of 26 neighborhood points compared to the size of the gray value. If the point of gray value is the maximum or minimum value, then the point is designated as a candidate feature point.

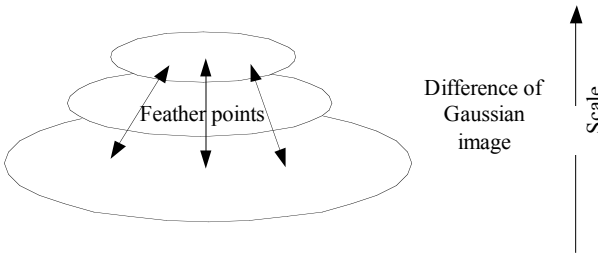


Fig. (1). Neighborhood point in image space of DoG scale.

Second step is screening of candidate feature points. In one image, the initial number of feature points is very large. in order to ensure significant feature points, we need further screening them. Because the DoG image reflects the contour of image gray value, small place is generally smooth regions of the image, and the larger value is concentrated at the edge of the image. If the candidate points are in the edge area of the image smoothing area or small curvature area, then feature neighborhood distinction degree is small, which is not conducive to the effective feature description, needs to be filtered. We set a threshold, if the gray feature value is less than the threshold value, we filter them. For the rest on the edge of the points, we filter them according to their curvatures.

Thirdly step is refining the position of feature points.

In the detection process above, we can only get the positioning accuracy with the pixel level. To achieve a better matching effect, we often require the location precision of sub-pixel level. This requires the detected feature points for further processing on the last step. We treat the scale space as a continuous space, the scale factor σ as one dimensional, defined objective function $D(X)$, where $X=(x,y,\sigma)$.

By Taylor expansions $D(X)=D+\frac{\partial D^T}{\partial X}X+\frac{1}{2}X^T\frac{\partial^2 D}{\partial X^2}X$, For the derivation, and the derivative X is set to 0, we get $0=\frac{\partial D}{\partial X}+\frac{\partial^2 D}{\partial X^2}\Delta X$.

Solving it we get $\Delta X = -(\frac{\partial^2 D}{\partial X^2})^{-1}\frac{\partial D}{\partial X}$, ΔX is a vector, where $\Delta X = (\Delta x, \Delta y, \Delta\sigma)$

We could use the fitting method, the derivation of its exact position in the image space is to get it in the plane of the sub-pixel precision position ($x+\Delta x$, $y+\Delta y$).

The process of solving the problem can be described by the following formula:

5. POINT SET MATCHING METHOD

In the acquisition process of liver pathology in a sequence of images, image relative to the imaging equipment is a planar motion, two adjacent images transform basically is in the same plane, which have only a very small distortion.

$$\begin{bmatrix} \frac{\partial^2 D}{\partial \sigma^2} & \frac{\partial^2 D}{\partial \sigma y} & \frac{\partial^2 D}{\partial \sigma x} \\ \frac{\partial^2 D}{\partial \sigma y} & \frac{\partial^2 D}{\partial y^2} & \frac{\partial^2 D}{\partial y x} \\ \frac{\partial^2 D}{\partial \sigma x} & \frac{\partial^2 D}{\partial y x} & \frac{\partial^2 D}{\partial x^2} \end{bmatrix} \begin{bmatrix} \Delta\sigma \\ \Delta y \\ \Delta x \end{bmatrix} = -\begin{bmatrix} \frac{\partial D}{\partial \sigma} \\ \frac{\partial D}{\partial y} \\ \frac{\partial D}{\partial x} \end{bmatrix} \tag{1}$$

where, $\frac{\partial D}{\partial \sigma} = \frac{D_{k+1}^{i,j} - D_{k-1}^{i,j}}{2}$, $\frac{\partial^2 D}{\partial \sigma^2} = \frac{D_{k+1}^{i,j} - 2D_k^{i,j} + D_{k+1}^{i,j}}{2}$,

$$\frac{\partial^2 D}{\partial \sigma y} = \frac{(D_{k+1}^{i+1,j} - D_{k-1}^{i+1,j}) - (D_{k+1}^{i-1,j} - D_{k-1}^{i-1,j})}{4}$$

Affine model (Fig. (**2**)) is adapted in the following test, which could be defined as: after the transformation, if the transformation of the linear image is still linear, and keeping the parallel relationship, this kind of transformation is called the affine transformation. The affine transformation can be decomposed into a linear transformation and translation transform, rigid transformation is a special case of affine transformation.

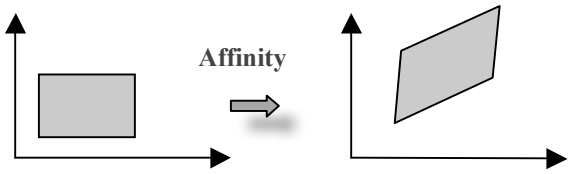


Fig. (2). Schematic diagram of the affine transformation.

In the two-dimensional plane, the affine transformation can be expressed by the following formula.

$$\begin{pmatrix} x' \\ y' \end{pmatrix} = B^* \begin{pmatrix} x \\ y \end{pmatrix} + M = \begin{pmatrix} b_{11} & b_{12} \\ b_{22} & b_{21} \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} t_x \\ t_y \end{pmatrix} \tag{2}$$

Where, $\begin{pmatrix} x \\ y \end{pmatrix}$, $\begin{pmatrix} x' \\ y' \end{pmatrix}$, is the each pixel transform coordinate in the image Respectively, matrix $B = \begin{pmatrix} b_{11} & b_{12} \\ b_{22} & b_{21} \end{pmatrix}$ is a non-zero matrix, vector *M* is the offset, *B* and *M* is the calculated parameters need to transform for model fitting.

The relative motion transform function is

$$A_{i-1} \circ a_i' = a_i * B_i + M_i, a_i' \in A_i, a_i \in A_i$$

The next problem is: point set geometric coordinates are known, we need to solve the corresponding geometric transform parameters.

We proposed a new matching algorithm (Fig. **3**) for the rigid transformation:

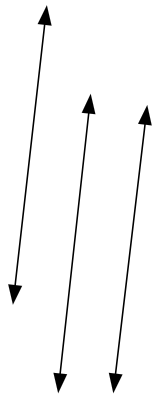


Fig. (3). Picture above (**a**) has a total of 27 points, below (**b**) has a total of 16 points. At least 10 points are matched.

First we construct adjacent distance matrix of the point set. Fig. (**a**) construct the matrix for 27×27 dimension, while Fig. (**b**) construct the matrix for 16×16 dimension. Where,

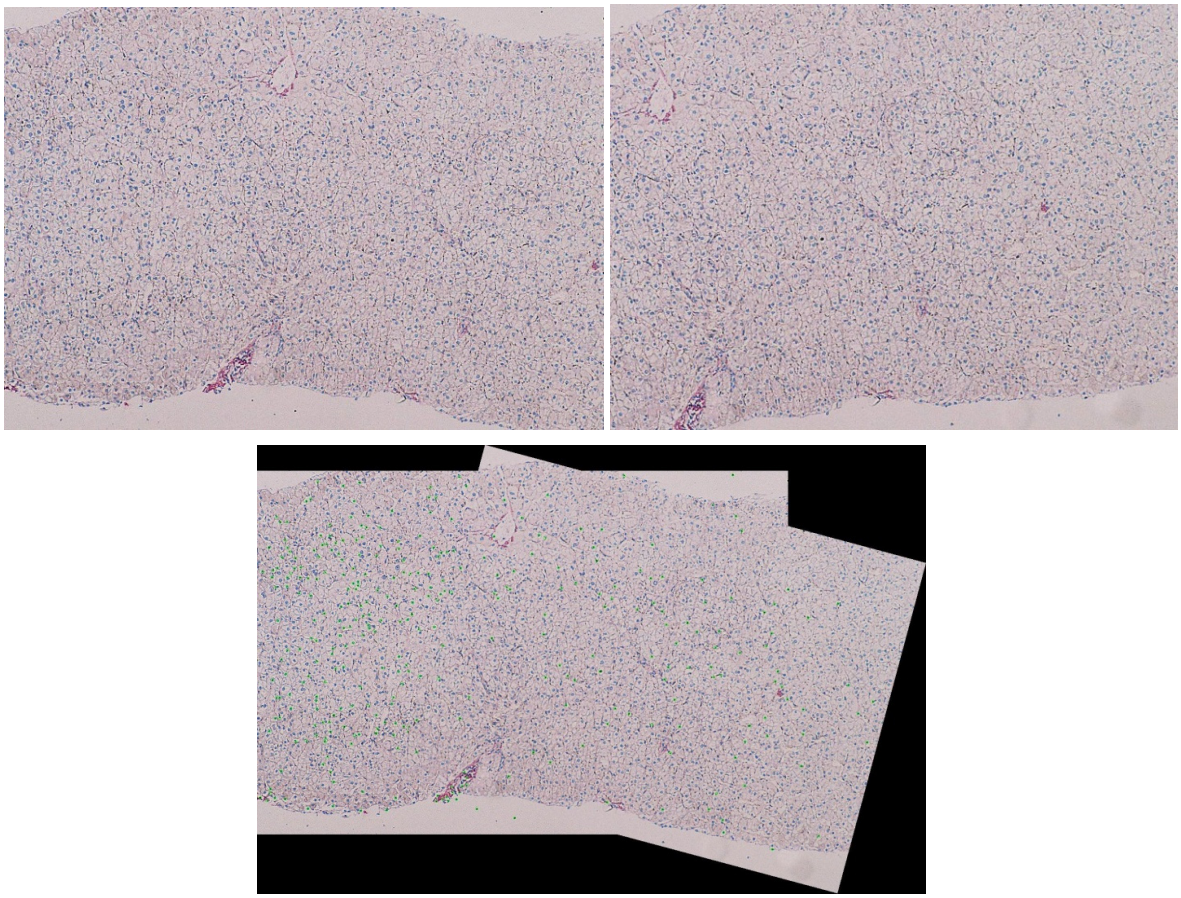
$$A = \begin{bmatrix} a_{11} & a_{12} & & a_{1,27} \\ a_{21} & a_{22} & \cdots & a_{2,27} \\ & \vdots & \ddots & \\ a_{1,27} & a_{2,27} & & a_{27,27} \end{bmatrix}, \quad B = \begin{bmatrix} b_{11} & b_{12} & & b_{1,16} \\ b_{21} & b_{22} & \cdots & b_{2,16} \\ & \vdots & \ddots & \\ b_{1,16} & b_{2,16} & & b_{16,16} \end{bmatrix}$$

At the same time to construct effective element matrixes,

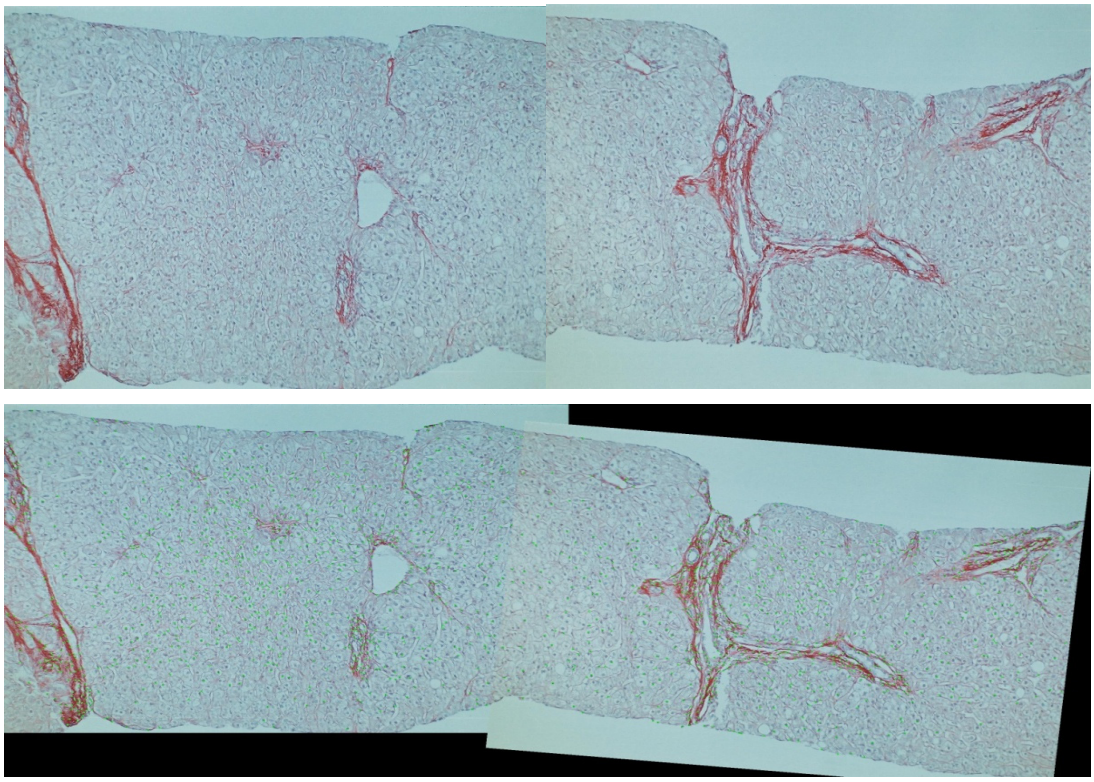
$$\overline{A} = 0_{27\times27}, \overline{B} = 0_{27\times27}$$

$a_{i,j}$ represent the distance of point *i* and the point *j*, and the diagonal elements of the default is 0. Apparently the matrix *A* and *B* are symmetric matrixes.

1) We take matrix A of the upper triangular elements (351 in total) are in ascending order, form a vector α , consequently, the upper triangular element B in the matrix (120 in total) are in ascending order, form a vector β .
2) All values of the matching pairs of vectors α and β are calculated, if the absolute value of a difference value of the two elements is less than a positive number ε , then we put the corresponding position of the effective elements in the matrix from 0 to 1.
3) Complete steps 3, we obtain a new effective element matrix $\overline{A}$ and $\overline{B}$; then, calculating each row (or a column) element for the number of 1, if the number 1 less than a positive number ζ , then the row of the matrix and the corresponding column are deleted, the corresponding points are also be deleted.



(**a**) example 1



(**b**) example 2

Fig. (4). Some liver image mosaicing results.

4) Complete steps 4, to obtain the effective element matching matrix $\overline{A}$ and $\overline{B}$. Of the two matrix to select three points, set of transform coefficients are calculated, and then the two matrices of each selected another three points, transform coefficients set, if the two sets of coefficients for the same problem, the problem is complete; if different, then take another three points, calculation of transform coefficient sets, two are equal comparison the line number set and whether the front. This process is repeated until finding the same transform coefficient sets.

The algorithm by deleting the useless point (no matching point) method to compute the matching point set. According to the three points form a triangle (that is, to determine a set of transform coefficients to calculate the transform coefficient method). The two parameter ε and ζ are determined according to the data quality.

6. ANALYSIS OF INCLINATION

Liver biopsy images have a large number of similar hepatic cells and fibers. There is no obvious visual feature. Furthermore, there is brightness change, coupled with the acquisition sequence image is rotated in the sampling process, and the fuzzy effect in scanning, all of them lead to the difficulty in mosaicing. This paper proposes the design and implementation the liver pathological image mosaicing system, which completed more than 100 cases (Fig. (**4**)). It shows that the experiment of this system has high robustness and adaptability for the mosaic.

CONFLICT OF INTEREST

The authors confirm that this article content has no conflict of interest.

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