

# Electron Microscopic Sequential Images Stitching Based on Belief Propagation

Sheng Chang <sup>a,c</sup> Fangxu Zhou <sup>a,c</sup> Xi Chen <sup>c</sup> Hua Han <sup>b,c,d,e</sup>

<sup>a</sup> University of Chinese Academy of Sciences, Beijing, 100049, P. R. China;

<sup>b</sup> The School of Future Technology, University of Chinese Academy of Sciences, Beijing 101408, P. R. China.

<sup>c</sup> Institute of Automation, Chinese Academy of Sciences, Beijing, 100190, P. R. China;

<sup>d</sup> The Center for Excellence in Brain Science and Intelligence Technology, Chinese Academy of Sciences, Shanghai 200031, P. R. China;

<sup>e</sup> The National Laboratory of Pattern Recognition, Institute of Automation, Chinese Academy of Sciences, Beijing 100190, P. R. China;

## ABSTRACT

The precise stitching of microscopic images of large-scale biological sequence slices is of great significance for the study of biological structure and function, but the slight scale changes of microscopic images and the blank areas in the images seriously affect the accuracy of mosaic. In this paper, we propose a electron microscope sequence image stitching based on belief propagation algorithm, which basically solves this problem. Firstly, the relative scale of adjacent images is calculated by extracting the sift feature points of the images. Then the global optimization model is used to obtain the absolute scale of each image, and the image is scaled to obtain the microscopic image with consistent scale. Secondly, obtain the relative displacement relationship of adjacent images by template matching method, and then the global positions of all images are optimized by Belief Propagation (BP) algorithm to eliminate the influence of blank regions and repetitive structures on the stitching results. In the case study, the proposed method demonstrates high quality.

**Keywords:** Electron Microscope Image, Sequential Image, Image Stitching, Belief Propagation.

## 1. INTRODUCTION

The field of view of a single image is usually limited. It is difficult to get complete information about the target in high resolution, and only reflects part of the entire target scene. In order to solve this problem, image mosaic technology came into being. At present, image stitching has become an important research topic in image processing, and has been widely used in computer vision, video surveillance, virtual reality and so on.

The most important two steps in image stitching are adjacent image registration and global coordinate estimation. According to the different image information used in image registration process, the registration algorithms can be divided into three categories: based on gray information [1], transform domain [2] and feature [3]. These methods have their own advantages and disadvantages. Since the gray-based image registration method uses the gray information of the entire image, they are insensitive to noise errors, but the amount of calculation is large. The image domain registration method based on the transform domain is fast, but complex image transformation cannot be performed. The feature-based image registration method has good adaptability to different image transformation, but is sensitive to noise. For the global coordinate estimation, in order to reduce the global image stitching error, different global stitching models are adopted. Jong-Seung Park et al. [4] used least squares to correct local stitching errors to form a globally consistent panoramic image. Hui Zhou et al. [5] use graph theory-based methods to reduce stitching errors. For example, use the minimum spanning tree to minimize the error of the panoramic image [6], use the shortest path tree to determine the global position of each image [7], and use the minimum routing cost spanning tree to form the panoramic image [8].

These above methods for image stitching are mainly used for natural images, and these methods require 70% to 80% overlap between images to achieve better stitching results. But in the fields of biology, neuroscience, etc., in order to reduce the damage to biological tissues and speed up the shooting, the slice images of biological sequences taken by scanning electron microscopy usually only have 10% to 15% overlap regions, there are slight scale distortions between adjacent

images taken by scanning electron microscopes, and for further research and analysis, stitching images requires very high precision. Aiming at the above problems, this paper proposes a scanning electron microscope sequence images stitching method based on belief propagation algorithm. The method first estimates the absolute scale of each image using a least squares algorithm based on SIFT feature points. Then, the global position of each image is estimated by template matching and BP algorithm to reduce the error of global stitching caused by scale distortion and mismatch, thereby generating high quality panoramic image. The working flow chart of this method is shown in Fig. 1:

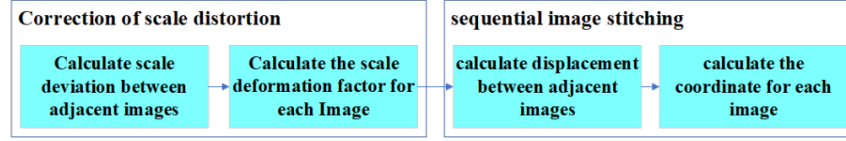


Figure 1. The work flow of sequential image mosaicing

The rest of the paper is organized as follows. The detailed method is described in Section 2. The preliminary results of the study are presented in Section 3, the followed Section 4 conclude the whole paper.

## 2. PROPOSED METHOD

In this section, we provide algorithmic details about our image stitching technique for scanning electron microscope sequence image. The proposed algorithm is divided into two parts. The first part is the correction of the scale distortion of the scanning electron microscope image. and the second part is the stitching of large-scale sequence image using BP algorithm.

### 2.1 Correction of Scale Distortion

Due to the presence of mechanical drift in the electron microscope, slight disturbances that cannot be completely avoided in the field, and occasional human error, there will be slight scale distortion between the scanning electron microscope images. The distortion is shown in Fig. 2. These small differences accumulate when stitching the image, which has a serious impact on the resulting panoramic image. In order to solve this problem, we propose a method for correcting scale distortion by using the matching relationship of SIFT feature points of adjacent images.



Figure 2. Scanning electron microscope image scale distortion. (a) Scale distortion of adjacent images taken with the same parameters. (b) Schematic diagram of scale distortion in stitching.

#### 2.1.1 Calculate the scale deviation between adjacent images

Give a set of images with scale distortion  $I = \{I_{ij} | i = 1, \dots, N, j = 1, \dots, M\}$  (where  $M$  and  $N$  respectively represent the total number of rows and columns of the images) that needs to be stitched. First extract the sift descriptor [9] ( $D_i$ ) of each image. And rough match the images by finding the closest pair of descriptors between the adjacent images. Then, in order to further ensure the matching result, the preliminary matching result is corrected by the random sampling consistency algorithm (RANSAC) [10]. The resulting exact matching descriptors ( $D'_1, D'_2$ ) are then used to estimate the relative scale of the two adjacent images. The main step is to calculate the similarity transform matrix ( $A$ ) of the matching descriptors pairs between the two adjacent images, namely:

$$D'_1 = AD'_2 \quad (1)$$

Since the similarity transformation is equivalent to a composite of translation transformation, rotation transformation and uniform scaling, after getting A, extracting the relative scale between two adjacent images from A by substituting (3)(4)(5) (6) into equation (2).

$$A = T \phi R_{ij} \text{ (or } A = T \phi C_{ij} \text{)} \quad (2)$$

$$A = \begin{bmatrix} a & b & e \\ c & d & f \\ 0 & 0 & 1 \end{bmatrix} \quad (3)$$

$$T = \begin{bmatrix} 1 & 0 & e \\ 0 & 1 & f \\ 0 & 0 & 1 \end{bmatrix} \quad (4)$$

$$\phi = \begin{bmatrix} \cos\theta & -\sin\theta & 0 \\ \sin\theta & \cos\theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \quad (5)$$

$$R_{ij} = \begin{bmatrix} r & 0 & 0 \\ 0 & r & 0 \\ 0 & 0 & 1 \end{bmatrix} \text{ or } C_{ij} = \begin{bmatrix} c & 0 & 0 \\ 0 & c & 0 \\ 0 & 0 & 1 \end{bmatrix} \quad (6)$$

Where T is the translation transformation matrix,  $\phi$  is the rotation transformation matrix, and  $R_{ij}$  (or  $C_{ij}$ ) is the relative scale transformation matrix of the two adjacent images we require.  $\{R_{ij}|i = 1, \dots, N, j = 1, \dots, M - 1\}$  represents the relative scale of two adjacent images in the horizontal direction,  $\{C_{ij}|i = 1, \dots, N - 1, j = 1, \dots, M\}$  represents the relative scale of two adjacent images in the vertical direction.

### 2.1.2 Calculate the scale deformation factor for each image

Based on the relative scale of the adjacent two images, the least squares method is used to solve the minimum scale error of two adjacent images to determine the scale deformation factor of each image. The specific solution formula is as follows:

$$\min_{S_{ij}} [\sum_{i=1}^N \sum_{j=1}^{M-1} (S_{ij} - R_{ij} S_{i+1j})^2 + \sum_{i=1}^{N-1} \sum_{j=1}^M (S_{ij} - C_{ij} S_{i+1j})^2 + \lambda \sum_{i=1}^N \sum_{j=1}^M (S_{ij} - 1)^2] \quad (7)$$

Where  $\{S_{ij}|i = 1, \dots, N, j = 1, \dots, M\}$  represents the scale deformation factor of the i-th row and the j-th column image, The third part limits the absolute scale of each image to around 1 and  $\lambda$  is the weight constant.

By solving the we can get the scale deformation factor  $S_{ij}$  of each image, then use the scale distortion factor to scale the image so that each image has a consistent scale.

## 2.2 Sequence Image Stitching

Due to local image stitching errors, the global stitching result will be seriously affected. When there is a blank or repetitive structure in the overlapping area, it is easy to cause local stitching errors of the image, and there are a lot of blank in the biological sequence slice images, as shown in Fig. 3. In response to this situation, we propose a method of using the global stitching image of the message transmitted between adjacent images--the image stitching algorithm based on BP algorithm.

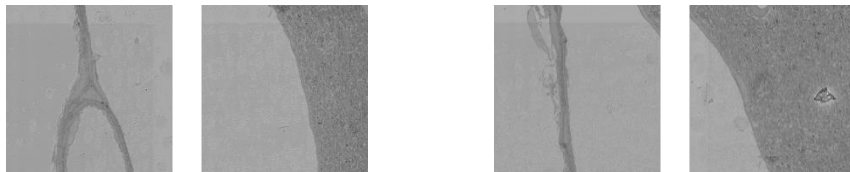


Figure 3. Blank areas in the Scanning electron microscope biological sequence slice images.

### 2.2.1 Calculate displacement between adjacent images

The template matching algorithm is simple, accurate, wide in application, good in noise resistance and fast. And there are 10%~15% overlapping areas between adjacent images, therefore, we select images which are located at the middle of the image boundary and occupy two-third of the entire overlapping area as templates to match their adjacent images to determine the relative displacement relationship ( $d_i$ ) of adjacent images.

### 2.2.2 Calculate the coordinate for each image

The adjacency relationship between images is represented by a graph  $G(V, E)$ , the vertex set  $V$  represents a set of images ( $g$ ), and the edge set  $E$  represents an adjacency relationship between images, as shown in Fig. 4.  $P_i$  is the global coordinate of the upper left corner of the image  $g_i$ ,  $P_j$  is the global coordinate of the upper left corner of the image  $g_j$  which is adjacent to the image  $g_i$ , and the global coordinate difference between them is recorded as  $d_i$ . The global spliced error model is expressed as

$$f = \min_p (\sum_{i,j \in V} \min[(p_j - p_i - d_i)^2, c]) \quad (8)$$

Where  $c$  is the truncation threshold, which is a pre-set constant that is introduced to handle possible mismatches in local splices.

$P_i, P_j$  are written in increments,  $p_i = p_i^0 + o_i$ ,  $p_j = p_j^0 + o_j$ , where  $o_i, o_j$  represents the difference between the new  $P_i, P_j$  and the initial  $p_i^0, p_j^0$ , Bring it into Equation (8):

$$f = \min_o (\sum \min[(o_j - o_i) + (p_j^0 - p_i^0 - d_i)]^2, c]) \quad (9)$$

The BP (Belief Propagation) algorithm [11] is used to solve the optimal solution of the above formula. The core of the BP algorithm is to continuously transmit local messages between adjacent nodes. For node  $I_i$  and its neighboring node  $I_j$ ,  $m_{i \rightarrow j}^t$  represents the messages sent from node  $I_i$  to node  $I_j$  at time  $t$ . During each iteration, the new message is calculated using the following formula:

$$m_{i \rightarrow j}^t(o_j) = \min_{o_i} (V(o_i - o_j) + \sum_{s \in N(I_i) \setminus I_j} m_{s \rightarrow i}^{t-1}(o_i)) \quad (10)$$

Where  $N(I_i) \setminus I_j$  represents all neighboring nodes of  $I_i$  except  $I_j$ ,

$$V(o_i - o_j) = \min((o_j - o_i) + (p_j^0 - p_i^0 - d_i))^2, c) \quad (11)$$

After  $T$  iterations, the confidence vector of node  $I_i$  can be calculated by:

$$b_i(o_i) = \sum_{s \in N(I_i)} m_{s \rightarrow i}^T(o_i) \quad (12)$$

On each node, the  $\hat{o}_i$  which minimizes  $b_i(o_i)$  is selected as the correction amount of the global coordinate value of the upper left corner of the image, so that we obtain the global position coordinates of all the images.

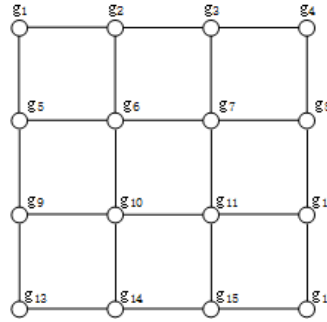


Figure 4. Schematic diagram of the adjacency relationship about the image

## 3. EXPERIMENTAL RESULT

In order to demonstrate the effectiveness of the proposed scanning electron microscope sequence images stitching based on belief propagation algorithm, we tested our method on scanning electron microscope biological sequence slice images.

### 3.1 Scale Distortion Correction

In order to verify the validity of the scale distortion correction algorithm, additional scale distortions were added to the scanning electron microscope sequence images. We could see that the image with the added scale distortion had been effectively corrected in Fig. 5. For scale distortion correction, the image with scale distortion is adjusted to a uniform scale. Therefore, for the artificially added scale distortion, the scale of each picture is consistent after the correction, but there is a slight difference from the added scale, the two curves in Fig. 5(a) are not completely coincident, and the calculated scale factor is always under the added scale distortion. In Fig. 5(b), compared with the uncorrected stitched image, the corrected stitched image has smaller average error and standard deviation which explains that the correction effect of scale distortion is obvious. We can see more intuitive results from Fig. 5(c)(d).

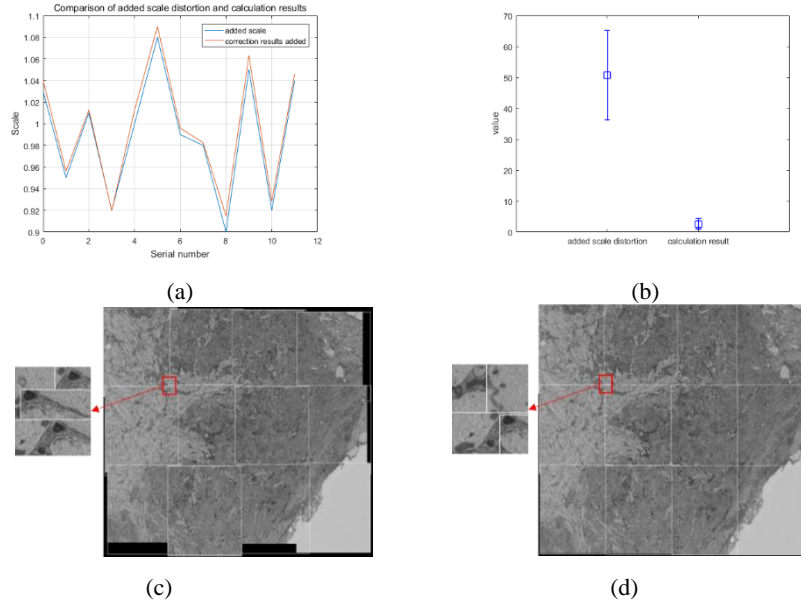


Figure 5. Results before and after scale distortion correction (a) Comparison of added scale distortion and calculation results (b) Comparison of stitching average error and standard deviation of adding scale distortion and correcting scale distortion (c) Mosaic result of uncorrected scale distortion. (d) Mosaic results of corrected scale distortion

### 3.2 Mismatched Area Detection and Global Optimization

In order to show the effectiveness of the proposed scanning electron microscope sequence images stitching based on belief propagation algorithm, we test our method on scanning electron microscope sequence images. For the detection of mismatches, we add extra displacement between the second row, the second column and the second row, the three columns of images in the case of correct matching, to cause mismatches. By observing the stitching results which are shown in Fig. 6, the method can effectively avoid this kind of erroneous matching in the global optimization process, and achieve the minimum stitching error compare with the least square, the shortest path and the minimum routing cost tree.

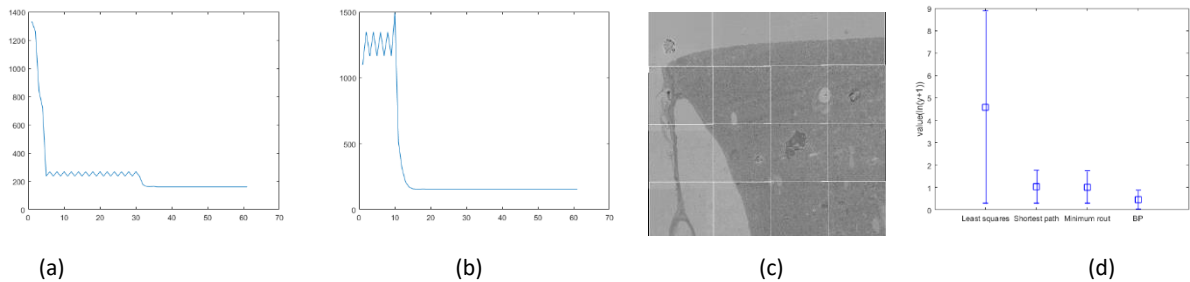


Figure 6. Schematic diagram of stitching results based on BP algorithm (a) (b) Schematic diagram of error convergence in x and y directions. (c) Stitching result schematic (d) Comparison of the average error and variance of least square, shortest path, minimum routing cost tree and BP(  $\mu$  represents the mean of the error,  $\sigma$  represents the variance)

#### 4. CONCLUSION

Aiming at the scale distortion in large-scale sequence images and the stitching errors caused by blank regions, a scanning electron microscopic sequential images stitching based on belief propagation algorithm is proposed. Experiments show that our algorithm effectively corrects the dimensional distortion present in the microscopic image and the global stitching failure caused by local stitching errors. The current BP algorithm-based scanning electron microscope sequence images stitching algorithm has higher time complexity, so improving the computational efficiency and real-time performance of the algorithm is the next research direction.

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