

# Feature-Based Retinal Image Registration Using Bifurcation Structures

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***Abstract*** — This paper presents a new structural feature for feature-based retinal image registration. The conventional point-matching methods largely depend on the branching angles of single bifurcation point. The feature correspondence across two images may not be unique due to the similar angle values. In view of this, structure-matching registration is favored. The bifurcation structure is composed of a master bifurcation point and its three connected neighbors. The characteristic vector of each bifurcation structure consists of the normalized branching angle and length, which is invariant against translation, rotation, scaling, and even modest distortion. This can greatly reduce the ill-posed nature of the matching process as long as the vasculature pattern can be segmented. The simplicity and efficiency of the proposed method make it readily to be applied alone or incorporated with other existing methods to formulate a hybrid or hierarchy scheme.

***Index Terms*** —Retinal image, bifurcation structure, image registration, feature extraction

## I. INTRODUCTION

Image registration is the process of establishing pixel-to-pixel correspondence between two images of the same scene. The registration methods can be classified into several categories including feature-based techniques, gradient approaches, and correlation methods [1]. In feature-based methods, salient and distinctive objects (e.g. edge and corner) are manually or automatically selected for estimating the transformation between image pair, such as translation, rotation, scaling, and distortion [2]. Gradient approaches, originated from optical flow, estimate the translation parameters using linear partial difference equations [3]. The idea behind correlation methods is quite straightforward as that the cross-correlation between the delayed signal and the reference will have a peak at the delayed time. According to Fourier shift property, the Fourier transform of a shifted function is the transform of the un-shifted function multiplied by the phase. Hence, phase correlation method identifies the translation from the normalized cross-spectrum [4]. In similar fashion, rotation and scaling can be estimated with the aid of polar Fourier representation [5].

Retina image registration is challenging due to the difficulties of modality- and time-varying intensities of retinal images. The first difficulty refers to multimodal registration which means medical imaging with different modalities, such as *Fluoroscein Angiography*, *Indocyanine Green Angiography*, and *Red-Free*. The second is temporal registration of images taken at different times. These motivate the exploitation of robust features such as vasculature and optic disk instead of intensity in retinal image registration [6]-[8]. Generally speaking, the feature-based techniques can be classified into region- and point-matching categories. The region-matching approaches consider all the features in a region as a whole and identify the transformation parameters by minimizing the similarity measures. For example, the cost function in [9] is defined as the error between two binary vessel images with consideration of affine, bilinear, and projective transformation models. In [10], the similarity measure is formulated as the entropy-based mutual information. The shortcomings of region-matching methods lie in their huge searching space and local convergence when involving of high-order transformation models and inconsistent features.

Point-matching methods, on the other hand, rely on the matched features in both images. The technique consists of two steps: feature matching and transformation estimation. The feature matching process establishes

the correspondence between two feature groups. Once the matched feature pairs are reliable, the transformation parameters can be identified easily and accurately. Most of the point-matching methods use bifurcation point as landmark since it is a prominent indicator of vasculature. In [11], the branching angles of each bifurcation point are used to produce a probability for every point pair. Since some bifurcation points may have more than one matched counterpart, a hierarchical method is proposed to solve this dilemma in [12]. The correspondences are refined gradually from the coarse translation model to the fine quadratic model. This idea is extended to the dual-bootstrap iterative closest point (ICP) algorithm [13]. The location, branching angle and width of landmarks are taken as the similarity metric. Starting from low-order initial estimates that are only accurate in small bootstrap regions, the dual-bootstrap ICP iteratively decides the optimal transformation model from simple to complex, and expands the bootstrap region from local to global. Another possible way is to search the minimal error by imposing the transformation to any combination of feature points [14]. This exhausted search needs huge computations when the number of feature points increases. The self-organizing maps (SOM), an unsupervised neural network that can train itself, provides promising results for multimodal registration [15]. It is well known that when more robust landmarks can be obtained with less computational complexity, the performance of feature-based methods will be improved greatly. However, the aforementioned methods largely depend on the branching angles of single bifurcation point. As such angles have coarse precision leading to similar bifurcation points, the correspondence may not be unique and reliable for registration purpose.

In view of this, we present a new structural feature for feature-based retinal image registration. Different from point-matching techniques, the proposed method is a structure-matching approach. The bifurcation structure is composed of a master bifurcation point and its three connected neighbors. The characteristic vector of each bifurcation structure consists of the normalized branching angle and length. It is invariant against translation, rotation, scaling, and even modest distortion. Further analysis and simulation demonstrate that it can greatly reduce the ill-posed nature of the matching process.

The rest of this paper is outlined as follows. In Section II, the feature-based registration algorithm using the proposed bifurcation structure is developed and analyzed. Experimental results are reported in Section III and concluding remarks are given in Section IV.

## II. BIFURCATION STRUCTURE FOR RETINAL IMAGE REGISTRATION

### A. Bifurcation Point Matching

Consider retinal imaging in a 3-D machine vision scenario and the camera's optical axis as the reference coordinate, the main factors that will cause the difference between images are: (1) change of eye position including movements along X-, Y- and Z-axis (horizontal and vertical translation, and scaling); (2) change of eye pose including rotations around X-, Y- and Z-axis (horizontal and vertical quadratic spherical distortion, and rotation); (3) change of camera interior parameters, such as focal length and resolution; (4) change of imaging modality; and (5) change of retinal tissue in the progression of diseases. It is commonly assumed that some constraints will be imposed onto (1)-(3) to limit the misalignment in a controlled condition. However, the unpredictable (4) and (5) make the registration a challenging clinical practice.

It is a nature way to explore and establish the vasculature relationship between image pair because blood vessels are robust towards geometrical transformation and intensity changes. In most retinal images, the bifurcation points are prominent visual features and can be recognized by their T-shape with 3 surrounding braches, as shown in Fig. 1. Assuming the vessel centerlines are given, the bifurcation points can be detected if 3 neighbors in a  $3 \times 3$  window belong to the foreground. There are other types of points in vasculature. For example, the terminal and trifurcation points are characterized by their 1 and 4 foreground neighbors. The dummy bifurcation points are defined as those bifurcation points with a short branch or too close to another feature point.

In point-matching methods, the characteristic vector of each bifurcation point is mainly composed of its three branching angles. The matching process will search the best similarities among all pairs of characteristic vectors. However, the calculated branching angles have coarse precision around  $10^\circ \sim 20^\circ$ , the correspondence may not be unique due to similar bifurcation angles. To analyze this ill-posed problem of multiple-correspondence, 3 branching angles of each bifurcation point are assumed to be randomly distributed on a scale  $1 \sim N$ , where each scale represents  $15^\circ$  precision and the corresponding  $N$  is  $360^\circ / 15^\circ = 24$ . It is worth mentioning that the

number of combinations to satisfy  $a + b + c = N$ , subject to  $a, b, c > 0$  is  $\sum_{i=1}^{\lfloor N/3 \rfloor} \lfloor (N - 3i + 1)/2 \rfloor$ . Thus, the number is 48 for all the possible combinations of 3 branching angles. In other words, each bifurcation point will have, on average, two counterparts with the same angles when each image contains 100 bifurcation points.

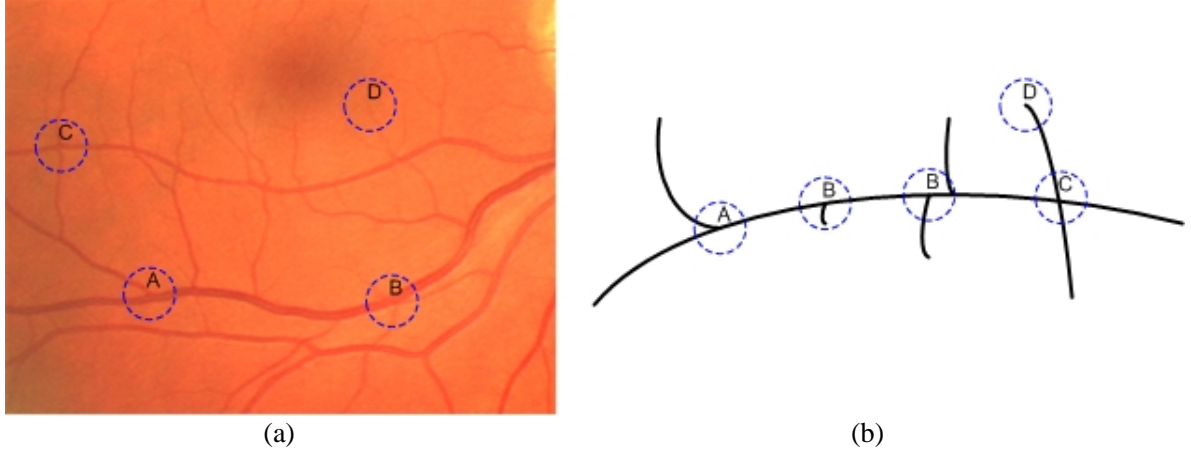


Fig. 1. The illustration of different point types in retinal images. A: Bifurcation point; B: Dummy Bifurcation point; C: Trifurcation point; D: Terminal point. (a) Real-life retinal vasculature. (b) Vessel centerlines.

### B. Bifurcation Structure Matching

In feature-based registration, the problem of feature matching and transformation estimation is the chicken and egg dilemma. The two issues can be solved gradually by trial and error approach. The basic idea is simple that one imposes a transformation model obtained from the matched features onto the image pair. If it doesn't work, another solution should be tried to minimize the error. This iterative scheme can be trapped by local minima when it solely depends on the bifurcation angles to establish the feature correspondence. On the other hand, it is well known that the registration performance will be greatly improved when more robust features are adopted. The better solution for feature matching will provide a solid foundation for the subsequent estimation of the transformation model. Moreover, a good feature should be invariant to different transformation models and robust under noisy conditions.

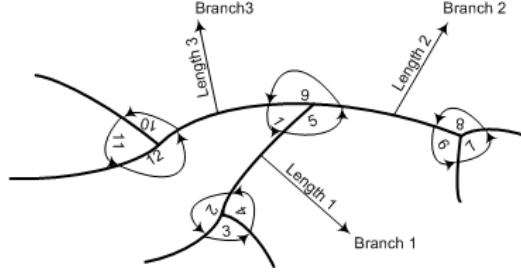


Fig. 2. Bifurcation structure is composed of a master bifurcation point and its three connected neighbors.

As shown in Fig. 2, a bifurcation structure, composed of a master bifurcation point and its three connected neighbors, is proposed for feature-base retinal image registration. The master bifurcation point has three surrounding branches with lengths numbered 1, 2, 3 and angles numbered 1, 5, 9, where each branch is connected to a neighboring bifurcation point. The characteristic vector for each bifurcation structure is:

$$\tilde{\mathbf{x}} = \{lengths, angles\} = [l_1, l_2, l_3, \alpha_1, \alpha_2, \alpha_3, \alpha_4, \alpha_5, \alpha_6, \alpha_7, \alpha_8, \alpha_9, \alpha_{10}, \alpha_{11}, \alpha_{12}] \quad (1)$$

where  $l_i$  and  $\alpha_i$  represent the normalized length and angle, respectively:

$$\begin{aligned} l_i &= i\text{-th branch length} / \text{sum}\{length\ 1, length\ 2, length\ 3\} \\ \alpha_i &= i\text{-th branch angle in degree} / 360^\circ \end{aligned} \quad (2)$$

Since there are some redundant elements in (1) as the summation of branching angles and length will be 1, we use a simplified characteristic vector in this work:

$$\mathbf{x} = \{l_1, l_2, \alpha_1, \alpha_2, \alpha_3, \alpha_5, \alpha_6, \alpha_7, \alpha_{10}, \alpha_{11}\} \quad (3)$$

It is worth mentioning that  $\mathbf{x}$  should be arranged that the longest branch is taken as the first element. This mechanism ensures that the characteristic vector is invariant towards the translation and scaling. The feature matching process will search the good similarity among all structure pairs. Let  $X$  and  $Y$  represent the feature groups of the two images that contain the number of  $M_1$  and  $M_2$  bifurcation structures, respectively. The similarity measure  $s_{i,j}$  for any bifurcation structure pair is

$$s_{i,j} = d(\mathbf{x}_i, \mathbf{y}_j) \quad (4)$$

where  $x_i$  and  $y_j$  denote the characteristic vectors of  $i$ -th and  $j$ -th bifurcation structure in two images. The term  $d(\cdot)$  denotes the distance measure between the characteristic vectors.

In contrast to 3 angles of single bifurcation point, the characteristic vector for the proposed bifurcation structure contains ordered length and angle elements. The extended feature facilitates the matching process in that the occurrences of multiple-correspondence can be reduced as shown in Fig. 3. It is worth mentioning that in the proposed bifurcation structures, dummy bifurcation, trifurcation and terminal points are excluded as they may not be consistent and be more easily error-prone in practical situations. Another minor technical point is that only the connected neighbors are considered instead of the spatial nearest neighbors. The connected bifurcation points indicate the physical relationship of the vessels when numerous bifurcation points are surrounded the master point or the geometrical distortion is present.

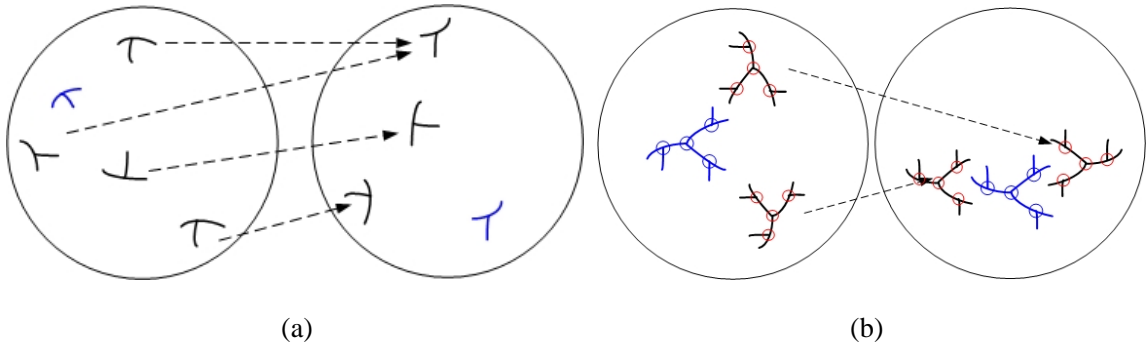


Fig. 3. The illustration of feature-based method. (a) Point-matching based on branching angles. (b) Structure-matching based on bifurcation structures.

### C. Correspondence Verification

Associating features across two images is critical to image registration, where features may be matched with one-, none-, or multiple-correspondence. To verify and correct the initial correspondence, the eigen-decomposition methods exploit spatial relations between features with the aid of the coordinate proximity matrices [16], [17]. The technique works well on simple shape matching, but suffers from the spurious feature points in the inexact matching. Several approaches are proposed to correctly resolve the ambiguous matches, such as Bayesian framework [18], region-based cross-correlation [19], and intensity profile [20]. In the following part, we are interested in developing an efficient correspondence verification scheme.

It is well known that the minimum points requirement for linear transformation is 2 pairs, and affine is 3 pairs. Therefore, one matched bifurcation structure pair is enough to estimate the parameters of low-order transformation model for it provide 4 point pairs. The correspondence refinement and transformation estimation can be simultaneously achieved by:

$$e_{(pq, mn)} = d(M(\mathbf{x}_p, \mathbf{y}_q), M(\mathbf{x}_m, \mathbf{y}_n)) \quad (5)$$

Here  $M(\mathbf{x}_i, \mathbf{y}_j)$  and  $M(\mathbf{x}_m, \mathbf{y}_n)$  are the transformation models estimated from the matched pair  $\mathbf{x}_p$  and  $\mathbf{y}_q$ ,  $\mathbf{x}_m$  and  $\mathbf{y}_n$ , respectively. In this verification step, the structure candidates must be those with good similarity in (4). Through this way, we can remove the spurious correspondence when it yields different model than others. At the final stage, the refined bifurcation structures can be used together to estimate the transformation models, such as quadratic spherical transformation [12], [13].

### III. EXPERIMENTAL RESULTS

The performance of the proposed algorithm is demonstrated using retinal images provided by Prof. Stewart's group at Rensselaer Polytechnic Institute. The dataset contains retinal images with various pathologies, where each image has approximate FOV of 1024×1024. Firstly, the vascular trees are segmented using ridge-based vascular tree segmentation [21]. Secondly, the structure-matching method is run using (3) and (4) to find the initial correspondence. These initial matched candidates are used to estimate the transformation model and retrospect refine the correspondence. Fig. 4(a) and (b) depicts a pair of retinal images taken at different time. For this image pair, 107 and 77 bifurcation structures are detected and yield 8 good matched pairs. The 3 best matching structures are highlighted in Fig. 4(d) and (e) using square boxes. We have tried the linear, affine and quadratic transformation and found that the affine model is enough and robust to describe the transformation. The mosaic image aligned by the affine model is shown in Fig. 4(c) and (f). It is observed that most of vessels are aligned well except a few local vessel centerlines with 1-pixel shift. In contrast, the point-matching method yields 797 matched point pairs with angle difference less than 1% among 145 and 136 bifurcation points. It needs further constraints such as location or vessel width to refine the results [12]- [14]. This will add the



complexity of the whole algorithm. Fig. 5(a)-(c) shows the registration results for another image pair in the dataset. After testing all image pairs, we observe that the only limitation is that it requires the vascular tree to be successfully segmented. This constraint is common for point-matching registration as bifurcation point detection is prerequisite. To overcome the failure of vascular tree segmentation, the proposed method can be incorporated with other existing methods to formulate a hybrid or hierarchy scheme.

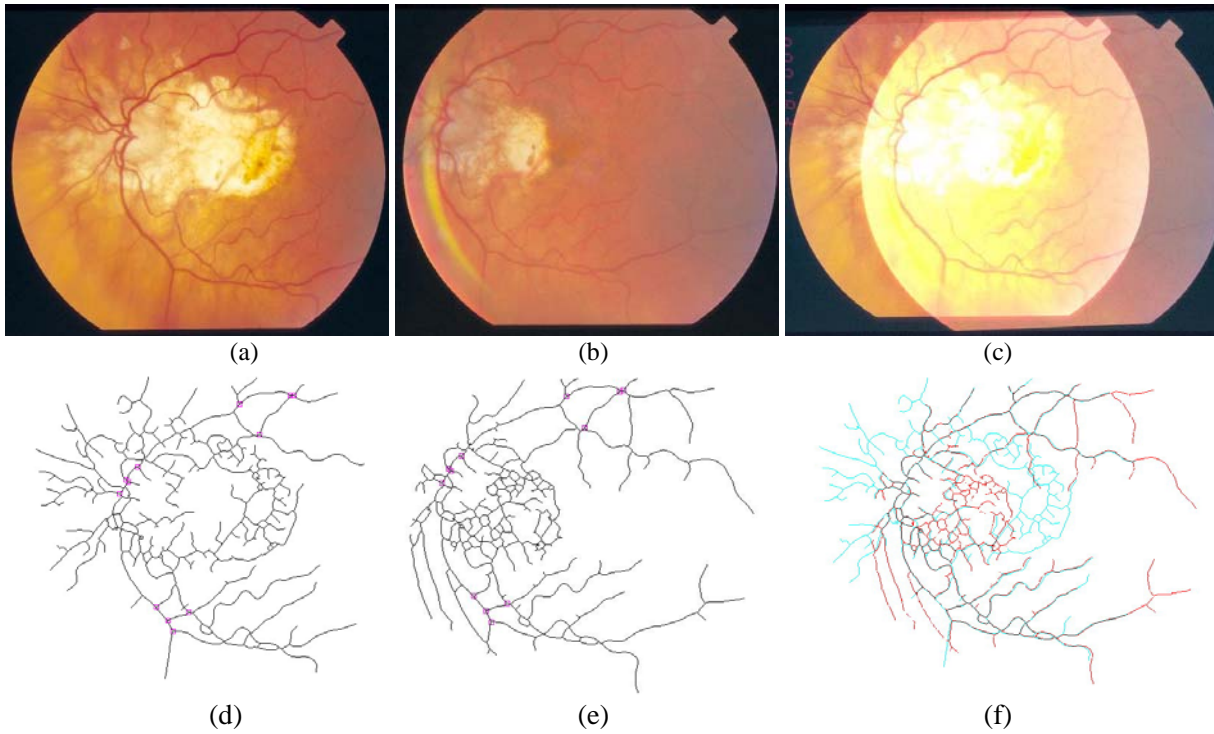


Fig. 4. Image registration results. (a) One retinal image. (b) Another retinal image captured at different time. (c) The mosaic retinal image. (d) Vascular tree and matched bifurcation structures of (a). (e) Vascular tree and matched bifurcation structures of (b). (f) The mosaic vessel image.

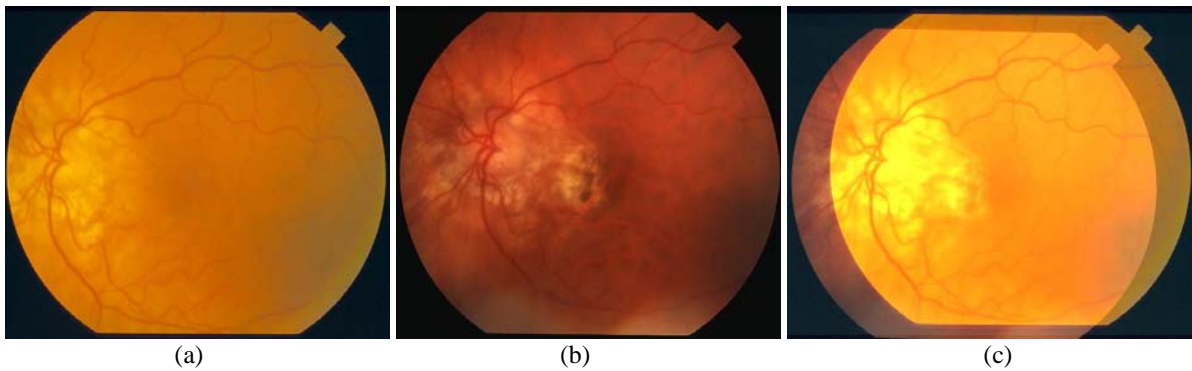


Fig. 5. Image registration results. (a) One retinal image. (b) Another retinal image captured at different time. (c) The mosaic retinal image.

Another advantage of the proposed structure-matching approach is the ability to handle translation, rotation,

and scaling provided the vascular trees of image pair are available. Fig. 6 presents a registration example of a pair of vascular tree. The partial view image in Fig. 6(b) is simulated by  $90^\circ$  rotation, 0.8 downsampling, and 70% overlap of Fig. 6(a). The 4 best matched structures are used to estimate the affine model to fuse the images. The mosaic vessel image in Fig. 6(c) clearly demonstrate the effectiveness of the proposed method in dealing with vasculature-like pattern registration.

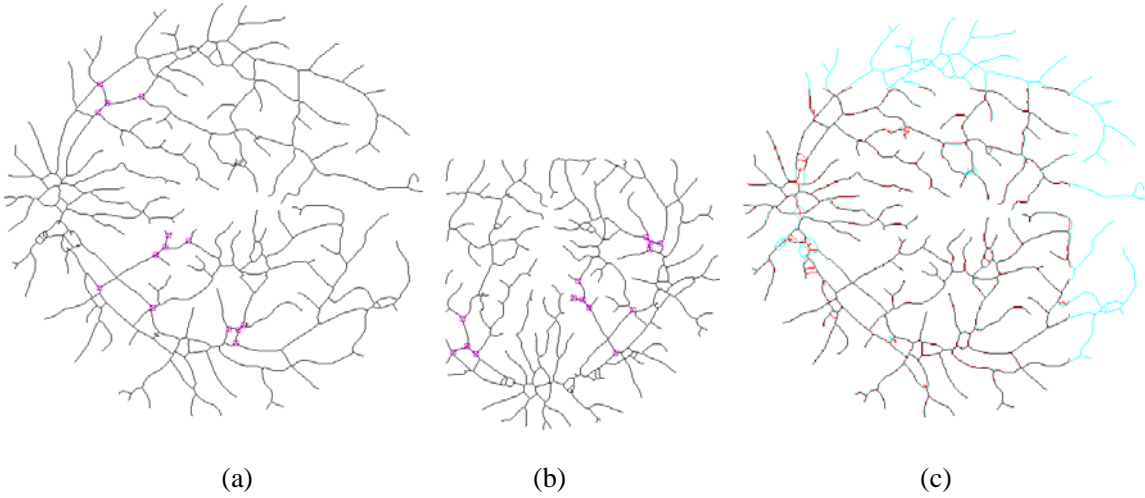


Fig. 6. Image registration results. (a) One vessel image. (b) Partial view vessel image. (c) The mosaic vessel image.

#### IV. CONCLUSIONS

This paper presents a feature-based retinal image registration method based on bifurcation structure-matching. The bifurcation structure is composed of a master bifurcation point and its three connected neighbors. It is invariant against translation, rotation, scaling, and even modest distortion. It can deal with the registration of retinal images when vasculature-like pattern is identifiable, even partially. The simplicity and efficiency of the proposed method make readily to be applied alone or incorporated with other existing methods to formulate a hybrid or hierarchy scheme.

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