

Chapter 5

Fast and Efficient Segmented Retinal Image Registration to Identify the Changes in Vascular Structure

5.1 Introduction

The objective of segmented retinal image registration is to identify the disease progress by aligning two retinal images namely the source and target image. These images are taken at different time interval or different view points of the same retina. Retinal image registration is helpful for the detection and diagnosis of various retinal diseases such as hypertension [139], glaucoma [140], diabetes [26],[66],[27]. The variation of intensities with respect to time and poor quality of retinal images are the major challenges of retinal image registration. For example, registration of retinal image pair is difficult because the selected image pair is captured in between some years apart, may be acquired from different camera with different sensitivity or may be in different modality.

According to authors Brown [74], Maintz *et al.* [72] and Lester *et al.* [73] registration techniques are classified into two categories, namely area-based and feature-based technique. The area-based techniques [173, 174, 175, 80, 176, 177] compare the intensity differences of retinal image pairs by using mutual information [175, 80, 176] and nor-

malized cross-correlation [178, 179] as similarity metric and an optimization technique [176, 177] is used to achieve the optimum similarity metric which indicates the better registration. According to the author Chanwimaluang *et al.* [106], area-based techniques are not suitable in case of low overlapping area of registration. To overcome this problem, generally a region of interest within image pair is selected for evaluating the similarity metric [177].

Area-based techniques are also sensitive to illumination changes and significant initial-misalignment [93]. Therefore area-based techniques are susceptible to background changes due to their pathologies and changes to the view points of camera [93]. On the basis of exhaustive literature survey it is found that the feature-based techniques [180, 100, 181, 182, 149, 183, 93, 108, 184, 185, 186, 187] are more suitable for the segmented retinal image registration in comparison to area-based techniques. The main characteristic of feature-based techniques are their robustness against illumination changes.

Feature-based techniques generally extract the salient and distinct features for searching the appropriate transformation between image pair such as translation, rotation, and scaling [188], which optimizes the correspondence between selected features. However, it is difficult to extract the features in poor quality retinal images. To overcome this problem for retinal image registration, generally blood vessel structure of respective segmented retinal images are used to identify the matched feature points [108].

For extracting distinct matched feature point, a Scale Invariant Feature Transform (SIFT) has been used by various authors [189, 190, 191, 192, 193]. The SIFT features are scale and rotation invariant and provide robust matching across the change in viewpoint, changes in illumination and a substantial range of affine distortion [190], [193]. The SIFT features are highly efficient to sense a single feature that can be exactly matched with the large set of features of other images and specially designed for mono-modal image registration [189]. The main disadvantage of SIFT features are its scale invariance strategy, which is not able to provide sufficient control points in case of high order transformation [194]. Therefore author H. Bay *et al.* [194] proposed Speed Up Robust Features (SURF), which is more faster and robust with respect to SIFT features. The author Cattin

et al. [195] proposed SURF based retinal image registration method, which is based on Haar wavelet, and does not depend on vasculature; however, this method is applicable for mono-modal retinal image registration.

The authors Stewart *et al.* [93] and Tsai *et al.* [99] proposed general dual bootstrap iterative closest point algorithm (GDB-ICP) for registration of poor quality retinal images. To provide the initial matches before applying the GDB-ICP, there are two methods available in literature. In first method to identify the initial matches, various authors [189, 190, 191, 192, 193] used Lowe's multi-scale keypoint detector and the SIFT descriptor. In second method, the central line extraction algorithm [108] was used to extract the bifurcations point of the retinal blood vessels and generate the initial matches. After identifying the initial matches the GDB-ICP algorithm was applied to iteratively expand the area around initial matches by mapping the corner points. According to authors Stewart *et al.* [93] and Tsai *et al.* [99] only one initial match is sufficient for the iterative registering process. Further, author Chen *et al.* [196] state that for more poor quality images, having correct initial match, the GDB-ICP algorithm may fail because the corner points are affected due to their poor quality. Further, the author Taha *et al.* [179] and Li Chen *et al.* [197] proposed a feature-based retinal image registration schema by using SURF feature, to improve the quality of retinal image registration. The author G. Wang *et al.* [15] proposed a robust point matching method for multimodal retinal image registration based on speed up robust feature (SURF) detector. Authors G. Wang *et al.* [15], Li Chen *et al.* [197], and Taha *et al.* [179] claimed that the performance of their approach is good but still some improvement is required in thresholding techniques and vascular network detection phase, which gives an idea for our proposed approach.

On the basis of exhaustive literature survey, it was found that for the detection of suitable features from image, the main challenges are high quality description and low computational requirements which gives an another idea for our proposed approach. Author Leutenegger *et al.* [198] set a new milestone and proposed a BRISK methodology that handle the both challenges. The BRISK achieved comparable quality of feature matching at less computational time [198].

Therefore, we proposed a Binary Robust Invariant Scalable Keypoint (BRISK) feature-based registration approach of segmented retinal image, to achieve the better registration accuracy. The proposed approach is able to handle two major challenges of segmented retinal image registration which are as follows:

- Selection of suitable retinal vessels segmentation approach which helps for better segmented retinal image registration.
- Use of the BRISK framework for feature detection and matching because it is a high quality descriptor and require less computational time.

The detailed theoretical aspect related to proposed approach is discussed in section 5.2 methods and model and validated them through experimental result shown in results and discussions section.

5.2 Methods and model

Our proposed retinal image registration approach contains three steps, namely, pre-processing, Gumbel PDF based matched filter approach for retinal image segmentation, and BRISK feature based registration between the pairs of segmented retinal images. The block diagram of the proposed registration approach is shown in Figure 5.2.

5.2.1 Pre-processing

In retinal image the contrast difference between the blood vessels and their background is low and decreases, when one move away from the optical disk of the retinal image. Therefore, the contrast enhancement of gray scale retinal image is a prominent pre-processing task. The pre-processing module contains two sub-modules, first convert the color retinal image into gray scale image and then enhance the contrast of gray scale image. Most of the authors [149], [160, 161, 162, 12, 2, 163] used only green channel image of color retinal image for converting the gray scale image. Because the contrast of the green channel image is better with respect to the red and blue channels of color retinal image. The

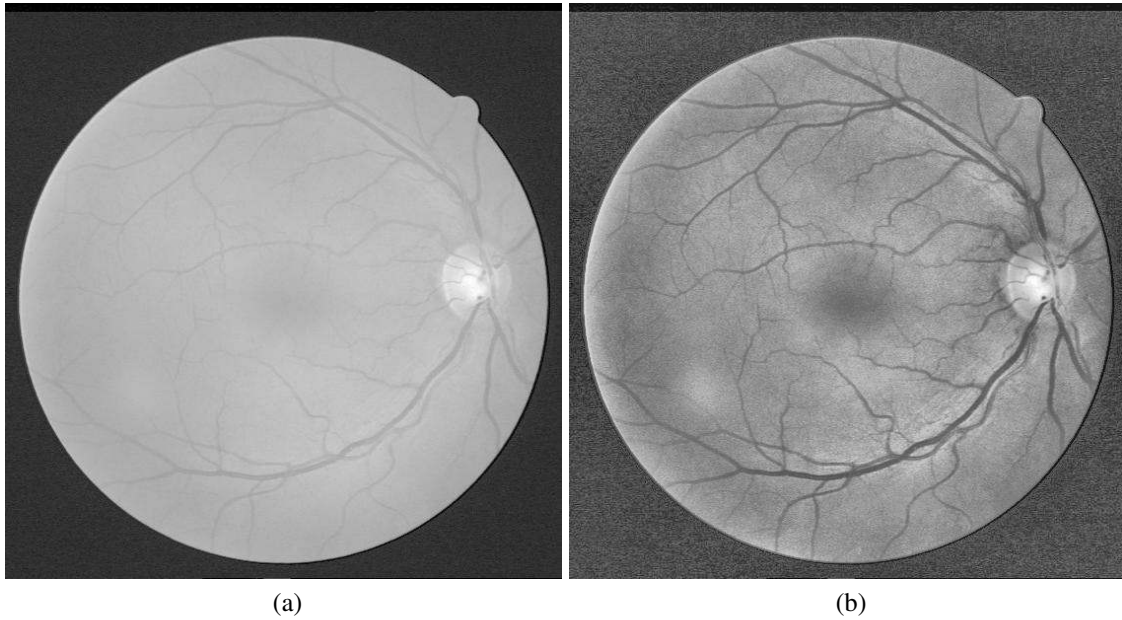


Figure 5.1: (a) Gray scale image of '20_test.tif' selected from DRIVE dataset (b) Contrast enhanced gray scale image of '20_test.tif' selected from DRIVE dataset

PCA based color-to-gray image conversion method is used to generate a gray scale image. Because, the PCA based color-to-gray conversion method effectively preserves both the texture and color discriminability by using simple linear computations in subspaces with low computational complexity [164]. The main steps used in PCA based color-to-gray conversion method are mentioned in Figure 5.2. In second step of pre-processing module, a Contrast limited Adaptive Histogram Equalization (CLAHE) is applied on the gray scale retinal image to generate the contrast enhanced gray scale image as shown in Figure 5.1(b).

5.2.2 Gumbel PDF based MF for Segmentation

The matched filter (MF) based retinal blood vessel segmentation approach compares the gray scale cross section profile of retinal blood vessels with the predefined kernel. Chaudhuri *et al.* [12] proposed a first matched filter approach based on Gaussian function and claimed the vessel cross-section profile is in approximate Gaussian shape. After that the author H. Zolfagharnasa *et al.* [14] proposed a Cauchy PDF based matched filter approach and claimed the vessel cross-section profile matched better with Cauchy PDF curve. The Gaussian and Cauchy PDFs both equally diminish towards their truncated values on both

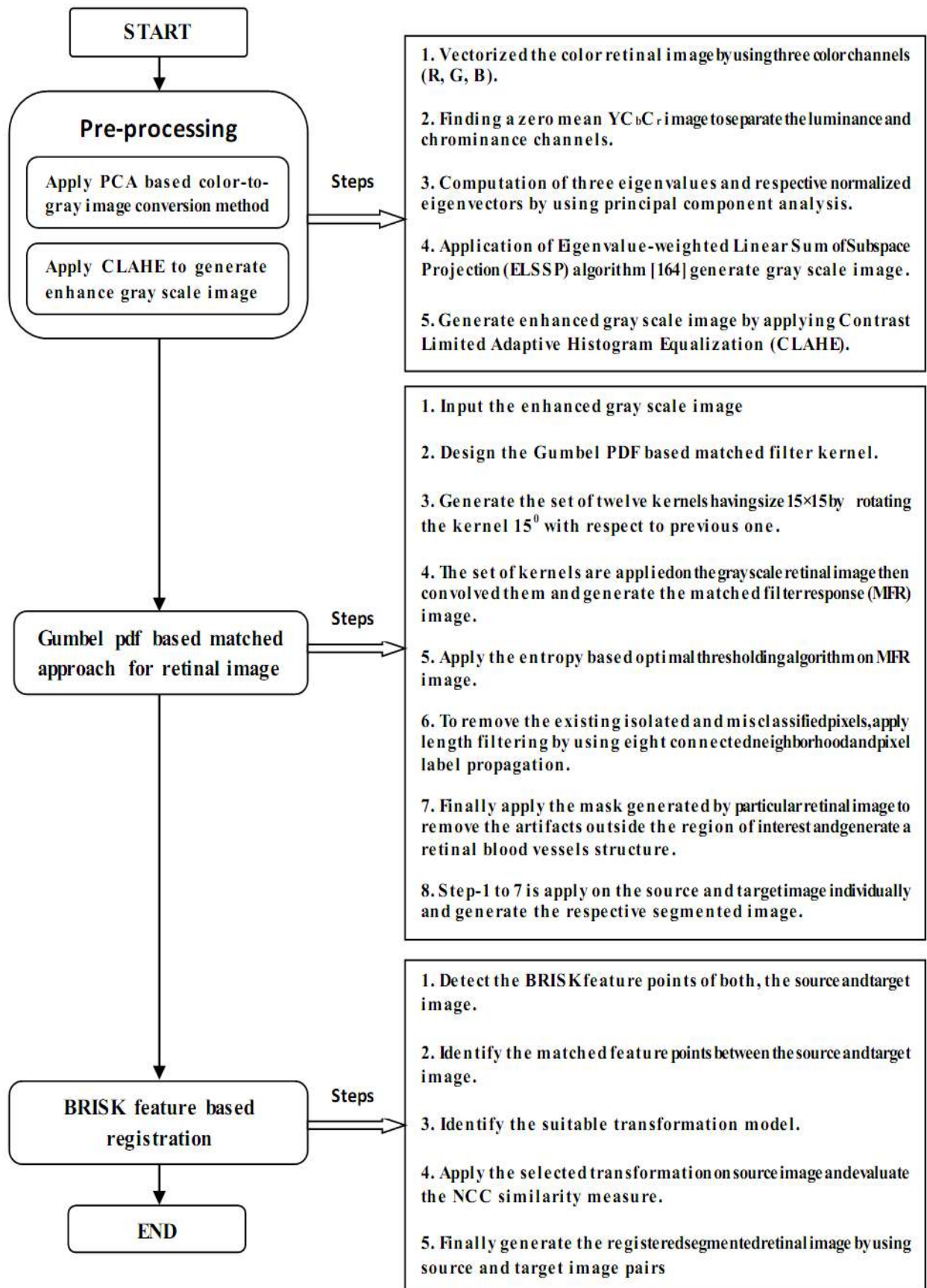


Figure 5.2: Block Diagram of proposed registration model.

sides of their peak value but the Gaussian curve reaches to its truncated value with faster rate in comparison to the Cauchy PDF curve.

If we analyze the vessel cross-section intensity profile of two marked regions with different color of lines (as shown in Figure 5.3) are shown in Figure 5.4(a) and Figure 5.4(b) by selecting 30 pixels between two points. According to the Figure 5.4(a) and Figure 5.4(b), it is clear that the cross-section intensity profile is moderately skewed not equally diminish toward their truncated values on both sides of their peak value.

Therefore, we use our recently proposed approach [199] as discussed in Chapter 4, the Gumbel probability distribution function based matched filter, for better retinal blood vessel segmentation. In paper [199], by using statistical analysis, we justified that the gray scale intensity profile curve of retinal image is slightly skewed and not an approximate Gaussian shape.

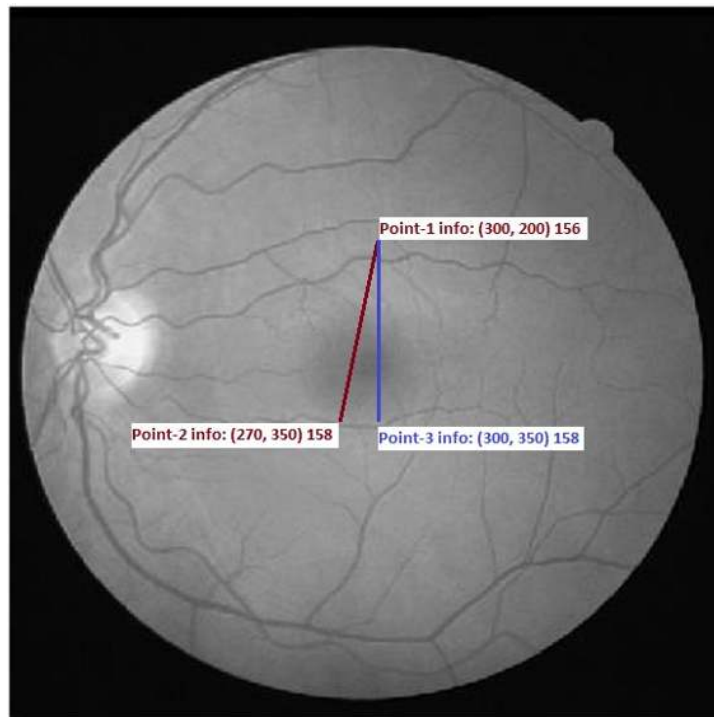
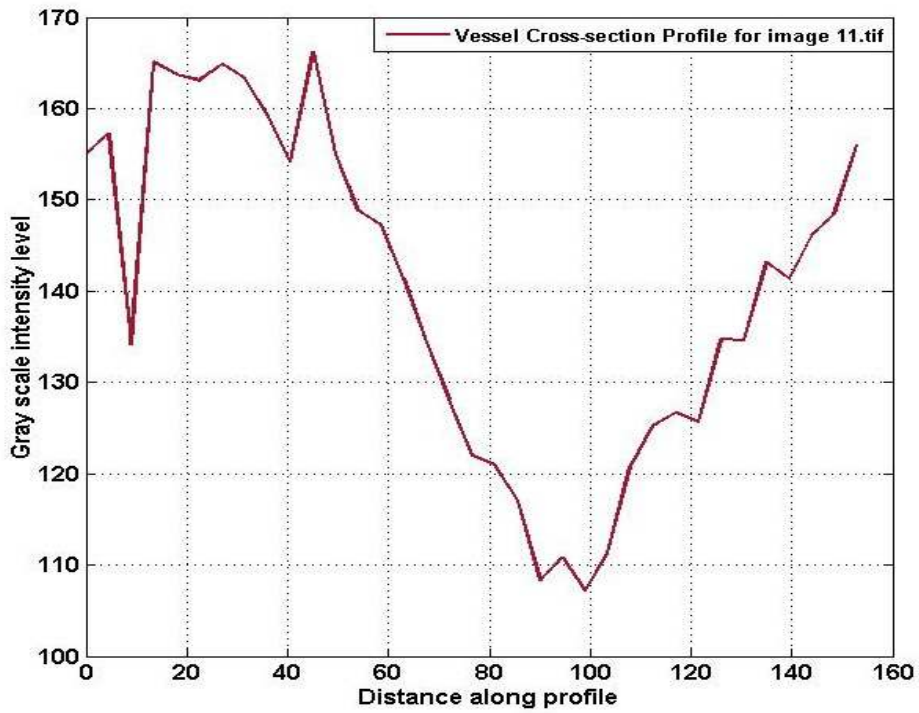


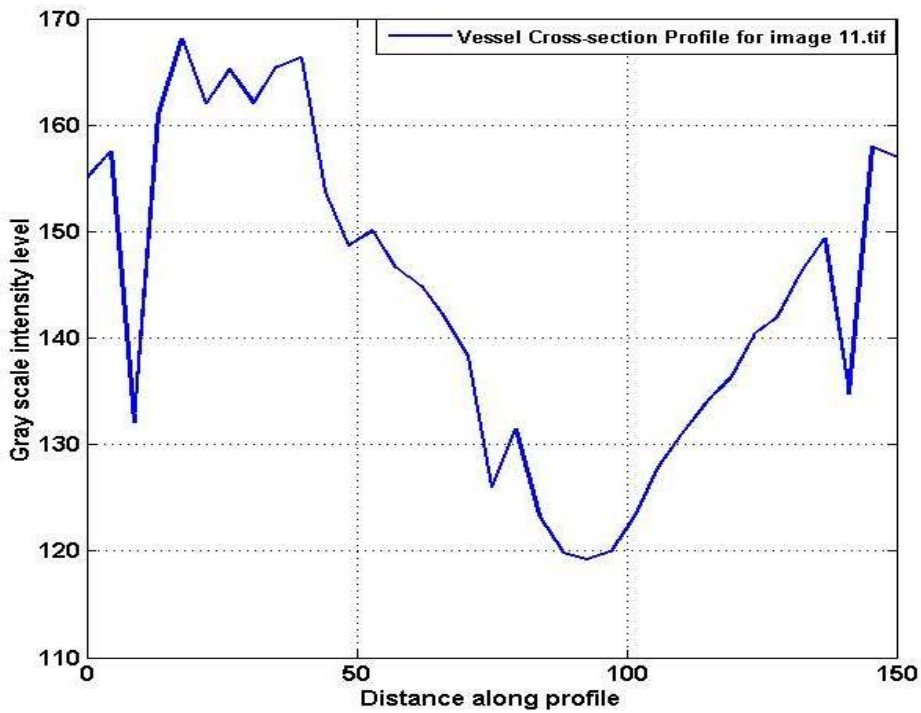
Figure 5.3: Gray scale retinal image '11_test.tif' selected from DRIVE database represents two marked region with claret color and blue color.

The Gumbel PDF having skewed characteristics is defined by the following Eqⁿ:-

$$f(x,y) = \frac{1}{\beta} e^{\frac{x-\mu}{\beta}} e^{-e^{\frac{x-\mu}{\beta}}} \text{ for } |y| \leq L/2 \quad (5.1)$$



(a)



(b)

Figure 5.4: (a) Cross-section intensity profile of the region marked by claret color in Figure 5.3 by selecting 30 pixels between two points, (b) Cross-section intensity profile of the region marked by blue color in Figure 5.3 by selecting 30 pixels between two points

where X is the perpendicular distance between point (x, y) and straight line passing through the center of retinal blood vessel, μ and β are the location and scale parameter respectively and L is the piece-wise line segment in the kernel. The main steps used in Gumbel probability distribution function based matched filter based segmentation approach are mentioned in Figure 5.2.

5.2.3 BRISK Feature base Registration

This sub-section, describe the main steps of BRISK framework [198], namely feature point detection, and construction of feature point descriptor.

5.2.3.1 Feature Points Detection

An efficient feature point detection is a prominent step for various tasks of computer vision. The corner detection plays an important role for the detection of interesting feature points because it provides important clue due to their two dimensional constraint and useful for fast algorithms to detect them [200]. The author Rosten *et al.* [201] proposed the Features from Accelerated Segment Test (FAST) feature detector approach which outperforms in both computational performance and repeatability with respect to previous existing algorithms in literature [200]. After that author Mair *et al.* [200] accelerated performance of the popular FAST feature detector approach and proposed Adaptive and Generic Accelerated Segment Test (AGAST) feature detector approach. Author S. Leutenegger inspired from the work of Mair *et al.* [200] and proposed a novel BRISK detector. The main objective of the BRISK detector is to achieve a invariance to scale which is difficult for high-quality key points and searching the maxima in the image plane as well as in scale-space [198]. The BRISK detector also estimates the true scale of each keypoint in the continuous scale-space [198].

For interest key point detection, the BRISK framework use the scale-space pyramid layer of n octaves O_i and n intra-octaves I_{o_i} for $i=0, 1, 2, \dots, n-1$ and assume the value of n is equal to 4. The first octaves are created progressively by half sampling the original image (O_0). The intra-octave I_{o_i} exists in between the two octave layers that means each

Io_i exist in between O_i and O_{i+1} . The first intra-octave Io_0 is obtained by down sampling the original image O_0 by a factor of 1.5. Remaining intra-octave layers are obtained progressively by half sampling. In the BRISK framework, initially, the FAST 9-16 detector is applied on each octave and intra-octave layers by using the same threshold T_h to identify the suitable region of interest (ROI). The 9-16 represents, at least 9 consecutive pixels in the circle of 16 pixels are either sufficiently darker or brighter than the central pixel. The points which exist in the ROI are subjected to non-maximal suppression in scale-space.

The non-maximal suppression in scale-space is required for removing the multiple interest points adjacent to one another. The algorithm for the non-maximal suppression is as follows:-

1. Calculate the sum of the absolute difference (SAD) between the pixels in the contiguous arc and the center pixel (say D).
2. Compare D value of two adjacent interest point and discard the interest point having lower value of D .

Above steps are mathematically summarized as follows:

$$D = \text{Max} \begin{cases} \sum(P_{arc} - P_{center}), & \text{if } (P_{arc} - P_{center}) > T_h \\ \sum(P_{arc} - P_{center}), & \text{if } (P_{arc} - P_{center}) < T_h \end{cases}$$

where P_{center} represents the value of center pixel, P_{arc} represents the values of contiguous pixels in the circle and T_h is the threshold for detection, which is determined by using the value of center pixel. The non-maximal suppression in scale-space is applied to identify the interest key points at octave layer and their immediate-neighboring intra-octave layers above and below the respective octave layer. Further, an image saliency is considered as a continuous quantity not only across an image but also along the scale dimension, and perform a sub-pixel and continuous scale refinement for each detected maximum. In all three layers of interest, the local saliency maximum refines the sub-pixel before a 1-D parabola is fitted along the scale-axis to determine the true scale of the keypoint. The location of the keypoint is then re-interpolated between the patch maxima closest to the determined

scale. The BRISK feature point detector is able to detect both the bifurcation and corner points presents in segmented retinal blood vessel structure as shown in Figure 5.5.

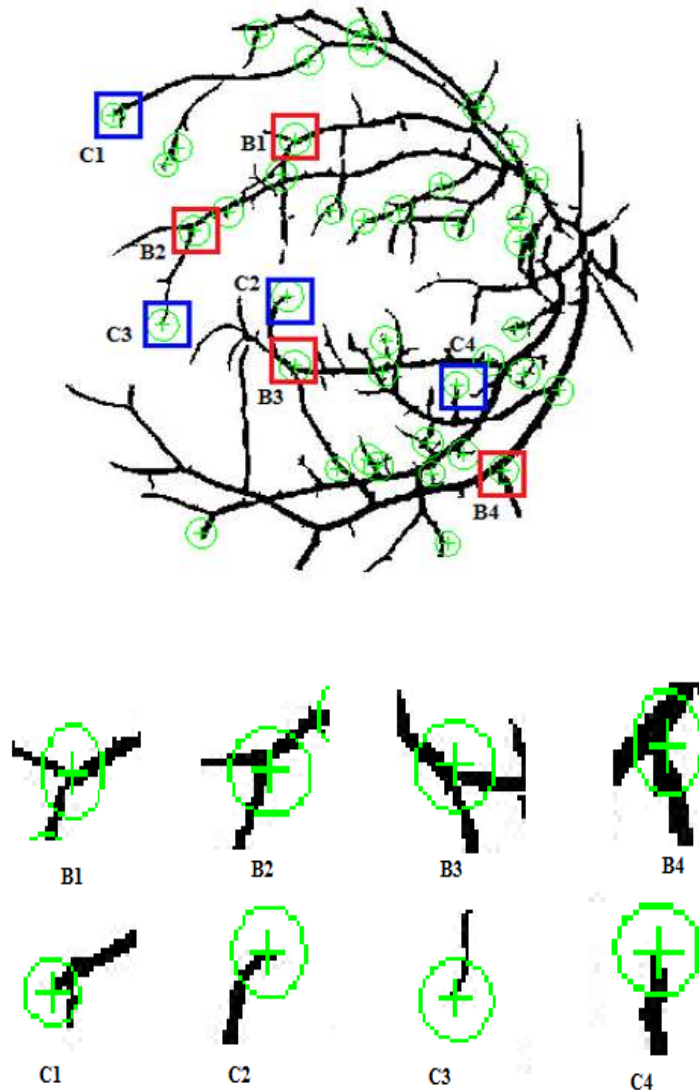


Figure 5.5: 40 interest points in segmented retinal image by using BRISK feature detection.

5.2.3.2 Feature Points descriptor

The set of interest points contains the refined sub-pixel image location and respective floating-point scale values. After identifying the set of interest points the BRISK descriptor is composed as binary string. The binary string is generated by concatenating the result of brightness comparison test which is described by author Chli *et al.* [202]. In BRISK

framework, to identify the characteristic direction of every interest point, the rotation and scale-normalized descriptors are used.

5.2.3.2.1 Pattern Sampling

Basic idea behind the BRISK descriptor is that, it uses the pattern for sampling the neighborhood of interest point. The BRISK sampling pattern, contains N locations equally spaced on concentric circles with the interest point. It was specifically built for dense matching and to capture more information [198]. In order to prevent aliasing effects when sampling the intensity of a particular point P_i in pattern, Gaussian smoothing with standard deviation σ_i proportional to the distance between the points presented on the particular circle is applied. For positioning and scaling the pattern to the particular point A in the image, we consider one sampling-point pairs (P_i, P_j) out of the total $N \cdot (N - 1) / 2$ sampling-point pairs. The smoothed intensity values of selected points $I(P_i, \sigma_i)$ and $I(P_j, \sigma_j)$ are used to estimate the local gradient $L_g(P_i, P_j)$ by using the following Eqⁿ :-

$$L_g(P_i, P_j) = (P_j, P_i) \cdot \frac{I(P_i, \sigma_i) - I(P_j, \sigma_j)}{\|P_i - P_j\|^2} \quad (5.2)$$

Let us consider the set S^a contains all sampling-point pairs, then two subsets of set S^a are defined that contains small-distance pairs and large-distance pairs which are represented by S^s and S^l respectively. The set S^a , S^s , S^l are mathematically defined as follows:-

$$S^a = \{(P_i, P_j) \in \mathbb{R}^2 \times \mathbb{R}^2 \mid i, j \in \mathbb{N} \text{ and } i < N \wedge j < i\} \quad (5.3)$$

$$S^s = \{(P_i, P_j) \in S^a \mid \|P_i - P_j\| < \delta_{max}\} \quad (5.4)$$

$$S^l = \{(P_i, P_j) \in S^a \mid \|P_i - P_j\| > \delta_{min}\} \quad (5.5)$$

where the δ_{max} and δ_{min} are known as maximum and minimum threshold distance respectively. The value of δ_{max} and δ_{min} are set to $9.75t$ and $13.67t$ where t is the scale of particular point A . Overall characteristic pattern direction vector ∇ of particular point A is estimated by adding the gradients of all point pairs in a set S^l by using the following

Eqⁿ:-

$$\nabla = \begin{pmatrix} \nabla_x \\ \nabla_y \end{pmatrix} = \frac{1}{L} \cdot \sum_{(P_i, P_j) \in S^l} L_g(P_i, P_j) \quad (5.6)$$

The large-distance pairs S^l are used for the computation of an overall characteristic pattern direction vector ∇ , by assuming that the local gradients annihilate each other therefore, it is not necessary in the global gradient determination [198].

5.2.3.2.2 Rotation Estimation and Construction of Descriptor

To construct the rotation and scale-normalized descriptor in a BRISK framework, we sampling the pattern, rotated by θ degree around the particular point A and θ is defined by the following Eqⁿ :-

$$\theta = \arctan2(\nabla_x, \nabla_y) \quad (5.7)$$

Then bit-vector descriptor D_a is assembled by performing all the small-distance intensity comparisons of point pairs $(P_i^\theta, P_j^\theta) \in S^s$ such that each bit correspond to as follows:

$$b = \begin{cases} 1, & \text{if } (P_j^\theta, P_j^\theta) > (P_i^\theta, P_i^\theta) \\ 0, & \text{otherwise} \end{cases} \quad (5.8)$$

$$\forall (P_i^\theta, P_j^\theta) \in S^s$$

5.2.3.3 Feature Matching and Transformation Model Estimation

After identifying interest/feature points of two segmented retinal images, we start the process of registration. Registration of two retinal images (source and target images) from their segmented image is a tedious task. In a feature based registration, the main tasks are feature matching and estimation of transformation model. According to authors Chen *et al.* [197] and Taha *et al.* [179] the performance of the registration will be improved when more robust feature points are adopted. The BRISK framework is used to provide the robust and fast feature points detection and their description. The BRISK feature detector is able to detect the bifurcation points as shown in Figure 5.5. The bifurcation

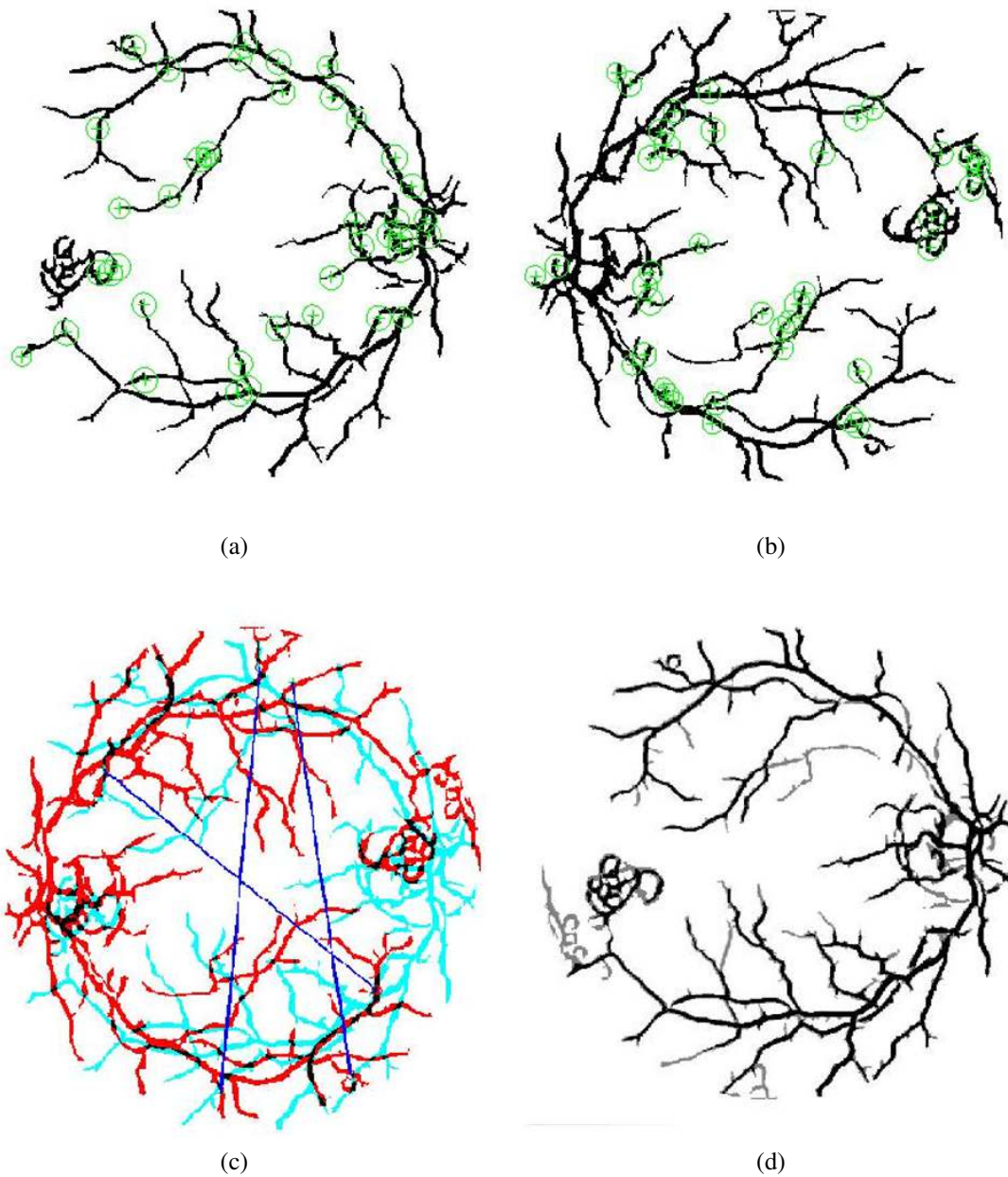


Figure 5.6: (a) represents 40 feature points of two segmented source retinal images, (b) represents 40 feature points of respective segmented target retinal image, (c) represents the respective matched feature points between source and target image pairs, (d) represents the registered retinal images of respective source and target image pairs

point contains three surrounding branches and angles and each branch is connected to a neighboring bifurcation points or closed at end point. Most of the end points are detected as corner points. Each bifurcation structure is represented by characteristic vector V_c . The bifurcation structure contains any one of the following characteristic:

- Bifurcation structure contains three branches and three angles.

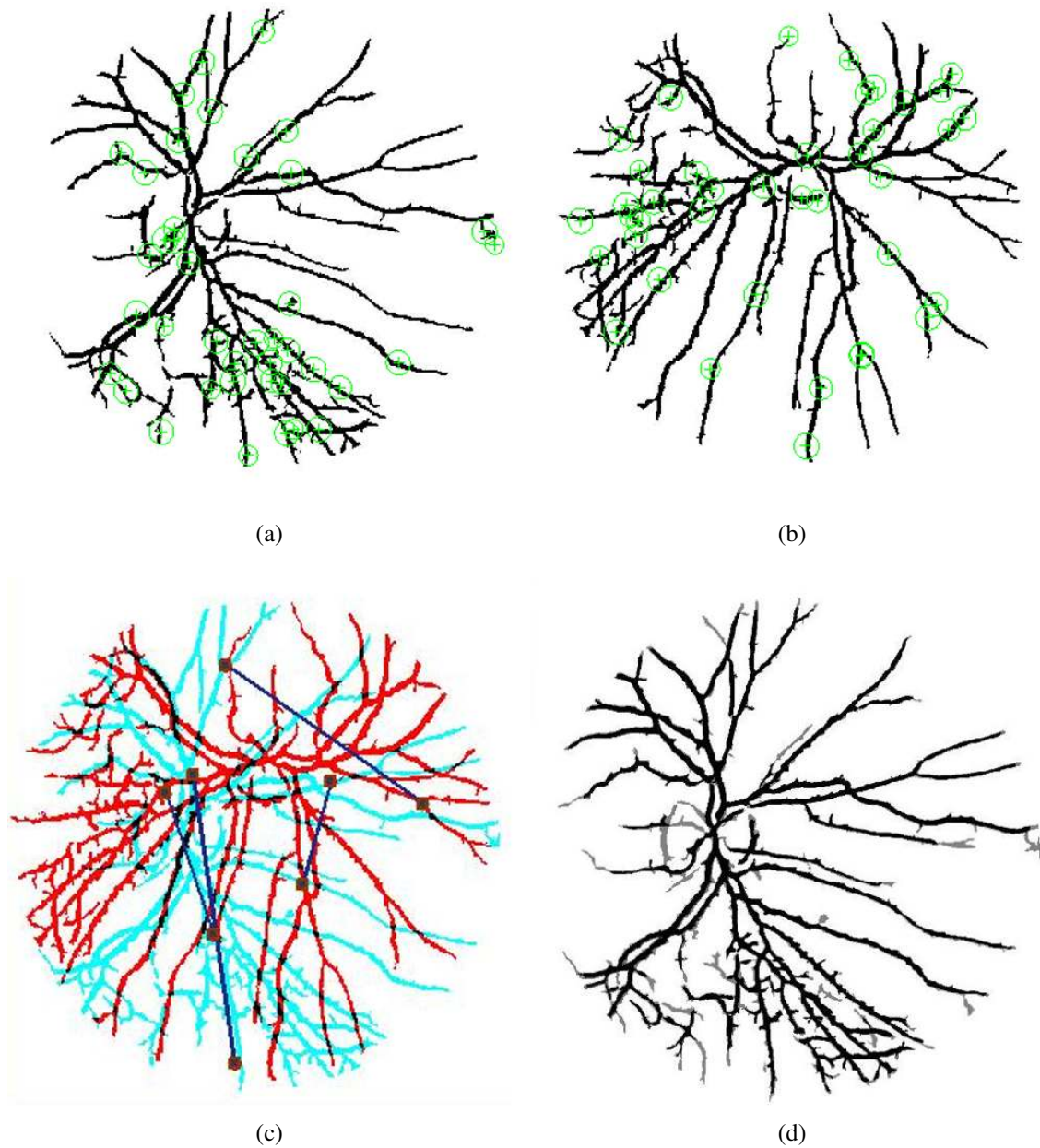


Figure 5.7: (a) represents 40 feature points of two segmented source retinal images, (b) represents 40 feature points of respective segmented target retinal image, (c) represents the respective matched feature points between source and target image pairs, (d) represents the registered retinal images of respective source and target image pairs

- Bifurcation structure contains three branches and six angles.
- Bifurcation structure contains three branches and nine angles.
- Bifurcation structure contains three branches and twelve angles.

Therefore to handle all the possibilities of bifurcation structure the characteristic vector V_c contains three branches having various length and twelve angles which is invariant towards the translation and scaling. The process of feature matching between two images search for better similarity among all structure pairs. Let us consider S_f, T_f are the feature groups of the source image and target image and contains N_s, N_t bifurcation structures respectively. The similarity S is the distance between the characteristic vectors of two bifurcation structure pair which is evaluated by using the following Eq^n :

$$S_{(i,j)} = D(V_{ci}, V_{cj}) \quad (5.9)$$

where V_{ci} and V_{cj} are the characteristic vectors of i^{th} and j^{th} bifurcation structure of the source and target image and D is sum of absolute difference. After identifying associated matched features between the source and target image (as shown in Figure 5.6(c) and Figure 5.7(c)), the next critical issue for feature based image registration is, the estimation of the transformation model. On the basis of literature survey it was found that the minimum points required for linear and affine transformation is 2 and 3 pairs of points respectively. Hence, one matched bifurcation pair is sufficient to identify the transformation model. The estimation of transformation model is done by using the following Eq^n :

$$E_{(pq,mn)} = D\left(M_1(V_p, V_q), M_2(V_m, V_n)\right) \quad (5.10)$$

where $M_1(V_p, V_q)$ and $M_2(V_m, V_n)$ are the transformation model estimated from the matched pairs (V_p, V_q) and (V_m, V_n) respectively and having good similarity according to $Eq^n - 5.9$. The correspondence pairs are used together to estimate the transformation models such as linear, affine, and quadratic transformation. For the estimation of appropriate transformation model, we experimentally evaluated the performance of proposed registration approach by using linear, affine, and quadratic transformation and found that affine transformation is performing better with respect to linear and quadratic transformation. Therefore in the proposed approach, an affine transformation is used for registration of segmented retinal images. The registered retinal images of two different source and target

image pairs are shown in Figure 5.6(d) and Figure 5.7(d). In registered retinal image, the changes in vascular structures of image pairs are represented in gray color which is clearly visible in Figure 5.6(d) and Figure 5.7(d). The performance of proposed registration approach is evaluated by using the normalized cross correlation (NCC) which is commonly used similarity measure between two registered images. The normalized cross correlation between the source and target image is evaluated by using the following Eq^n :

$$NCC(S, T) = \frac{\sum_X S(X).T(X)}{\sqrt{\sum_X S(X)^2.T(X)^2}} \quad (5.11)$$

where S and T represent the source and target image and X represents the two matched points between the S and T . According to the author Tsai *et al.* [203], the value of NCC closed to one indicates better degree of similarity.

5.3 Results and Performance Analysis

The DRIVE retinal database [2] is used to evaluate the performance of the proposed approach. All 20 retinal images of DRIVE database are used as a source image. The target image for respective source image is produced randomly by rotating, scaling, and translating with different angles, scaling, and translation factors respectively. Some target

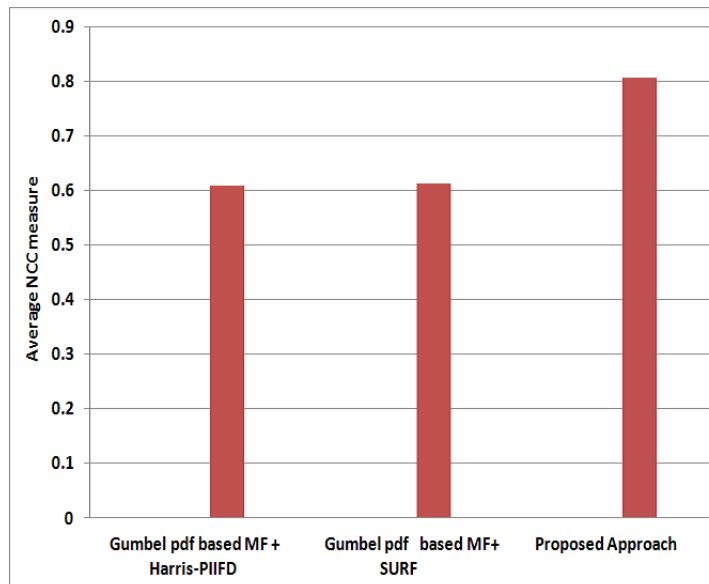


Figure 5.8: Comparative analysis of average performance measure (Average NCC).

Table 5.1: Normalized Cross Co-relation Coefficient (NCC) and Computation time of segmented retinal image registration approach based on SURF, Harris-PIIFD feature and proposed registration approach based on BRISK feature.

Source Image	Target Image	NCC (Gumbel pdf based MF + Harris-PIIFD)	NCC (Gumbel pdf based MF+ SURF)	NCC (Proposed Method)	Harris-PIIFD Time (Sec.)	SURF Time (Sec.)	Proposed approach Time (Sec.)
S1	T1	0.8101	0.8033	0.8098	29.37	8.41	6.97
S2	T2	0.8331	0.8410	0.8418	32.18	9.78	3.84
S3	T3	0.1155	0.0021	0.8005	19.79	8.16	3.64
S4	T4	0.6585	0.6836	0.7263	19.78	8.74	3.96
S5	T5	0.7400	0.7351	0.7715	26.20	8.31	3.65
S6	T6	0.1104	0.0015	0.7685	19.24	10.81	3.58
S7	T7	0.1160	0.1885	0.8197	19.16	5.76	3.63
S8	T8	0.6770	0.6974	0.7661	23.29	5.96	3.83
S9	T9	0.7285	0.7029	0.7354	23.77	6.04	3.50
S10	T10	0.9454	0.9437	0.9870	29.92	5.59	4.23
S11	T11	0.7747	0.7918	0.8235	33.02	8.23	3.86
S12	T12	0.1169	0.1230	0.8376	21.54	7.95	3.98
S13	T13	0.7507	0.7550	0.7792	25.12	6.31	3.97
S14	T14	0.1083	0.2130	0.7445	21.52	7.33	4.34
S15	T15	0.8054	0.8103	0.8194	28.65	9.56	4.15
S16	T16	0.7756	0.7890	0.8297	27.29	9.64	4.35
S17	T17	0.7022	0.7333	0.8098	24.37	10.29	4.64
S18	T18	0.8340	0.8385	0.8355	33.21	9.16	4.06
S19	T19	0.8021	0.8199	0.8319	29.49	7.92	4.55
S20	T20	0.7705	0.7624	0.7666	26.76	6.46	4.41

images are also produced by flipping (horizontal/vertical) the source image. The set of all 20 pairs of source and target images are used for experimental analysis. The performance (NCC) and the computation time of proposed approach are evaluated for all 20 image pairs as mentioned in Table 5.1. According to the experimental results presented in Table 5.1, it is observed that the performance of proposed approach is close to 1, which indicates that the registration accuracy is acceptable with less computation time.

Furthermore, we evaluate the performance and computation time of SURF feature based registration approach proposed by Taha *et al.* [179] and Harris partial intensity invariant feature descriptor based registration approach proposed by Chen *et al.* [196] by using same set of 20 image pairs which is also mentioned in Table 5.1. In both cases all

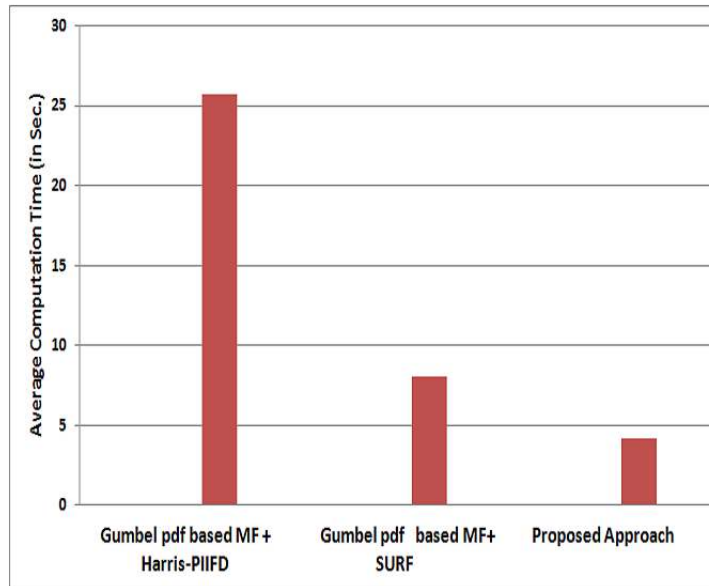


Figure 5.9: Comparative analysis of average computation time (Average Time in Sec.).

pairs of images are segmented by the Gumbel pdf based matched filter approach proposed in paper [199].

On the basis of comparative analysis of proposed, BRISK feature based segmented retinal image registration approach with SURF feature based [179] and Harris partial intensity invariant feature based segmented retinal image registration approach[196], it is observed that the performance and computation time of proposed approach is better with respect to other two approaches. The average performance measure (Average NCC) and computation time (average time) of all three approaches is also evaluated and their comparative analysis are mention in Figure 5.8 and Figure 5.9 respectively. On the basis of that, it is again observed that the overall average performance and computation time of proposed approach is better with respect to other two approaches. The performance of a proposed approach is better due to the following reasons:

- The Gumbel Probability distribution function based retinal image segmentation approach proposed by us [199] is used to achieve the better segmented vascular tree structure. According to the authors G. Wang *et al.* [15], Chen *et al.* [197] and Taha *et al.* [179], the main limitation of feature based retinal image registration using bifurcation structure is that it require better segmented vascular tree structure. Therefore the Gumbel Probability distribution function based retinal image

segmentation approach is used to overcome the limitation of feature based retinal image registration approach [15], [197], [179].

- The BRISK framework proposed by [198] is able to handle the main challenges (high quality description and low computational cost) for detection of suitable feature points from image. The BRISK framework is also able to handle translational, rotation and scaling of the vascular tree structures of source and target image pairs. Therefore, the BRISK framework is used for feature detection and matching, which improve the performance of registration and reduces the computation time.

5.4 Conclusion

The various retinal diseases such as hypertension, diabetes, glaucoma, etc. are diagnosed by identifying the changes in the retinal vessels structure, therefore fast and accurate registration of segmented retinal images is a prominent task. So, we proposed a novel BRISK feature-based segmented retinal image registration approach because the BRISK framework is an efficient keypoint detector, descriptor and matching approach. The Gumbel pdf based matched filter approach is used for segmentation of source and target image because the Gumbel pdf based matched filter approach provided a better segmentation result with respected to other existing matched filter approach [199]. The performance of the proposed approach was demonstrated by evaluating the normalized cross correlation similarity measure for image pairs. On the basis of comparative analysis of proposed approach with the SURF and Harris partial intensity invariant feature descriptor based segmented retinal image registration approach, it was found that the performance of proposed approach was better in both aspect, the performance as well as computation time.