



## A REVIEW ON SCLERA VEIN RECOGNITION

Delna K.V. and Caren Babu

SCET Kerala, India

E-Mail: [delnakv@gmail.com](mailto:delnakv@gmail.com)

### ABSTRACT

The vein structure in the sclera, the white and opaque outer protective covering of the eye, is anecdotally stable over time and unique to each person. As a result, it is well suited for use as a biometric for human identification. Sclera recognition poses several challenges: the vein structure moves and deforms with the movement of the eye and its surrounding tissues; images of sclera patterns are often defocused and/or saturated; and, most importantly, the vein structure in the sclera is multi-layered and has complex non-linear deformation. Here proposed a new method for sclera recognition, a line descriptor along with WPL descriptor based feature extraction, registration, and matching method that is scale, orientation, and deformation invariant, and can mitigate the multi-layered deformation effects and tolerate segmentation error. The use of Y shape descriptor along with WPL descriptor will unanimously increase matching speed.

**Keywords:** sclera vein recognition, feature matching, sclera matching.

### INTRODUCTION

In the present scenario it is very important to authenticate a person's identity to prevent the fraudulent activity such as accessing sensitive information, creating false identities etc. The most widely used method for this is passwords or other personal information. According to statistics, it states that Interpol has data on 40M of travel documents are stolen/lost. And the stolen documents are further misused by terrorists and fraudsters. Same happens for credit cards also. 88% of stolen data of credit cards is used within minutes. There is an increasing need to find a way to solve user identification issues and cut costs for password administration. A more sophisticated method of authentication is to have a unique system that must be capable of identify a person and these identities cannot be stolen and used by other individuals. Biometrics is a promising technology that is being touted as the solution to these problems. At present, biometrics technology holds a Biometrics is the identification of humans using intrinsic great deal of promise for doing just that, but is not without its limitations and certainly not without its critics.

Physiological, biological, or behavioral characteristics, traits, or habits. Biometrics has the potential to provide this desired ability to unambiguously and discretely identify a person's identity more accurately and conveniently than other options. Different parameters of an individual can be used for identification. Ocular biometrics comes under one of the classification among Biometrics. Out which Sclera vein pattern has got its unique features so as to use as a biometric trait.

This work is a review on one of the biometric method which is Sclera vein recognition. Sclera is the white region of the eye. And the vein pattern in the sclera is unique to each person. There are several methods to extract the sclera vein pattern. This paper compares two methods a parallel approach and line descriptor based sclera recognition.

### ISCLERA Recognition

Sclera recognition is identification of a human using the sclera, the 'white of the Eye.' It offers several benefits over other eye-based biometrics that makes it well-suited for non-compliant recognition situations.



**Figure-1.** Sclera.

The sclera is the white and opaque outer protective covering of the eye. The sclera completely surrounds the eye, and is made up of four layers of tissue — the episclera, stroma, lamina fusca, and endothelium [2]. The conjunctiva is a clear mucous membrane, made up of epithelial tissue, and consists of cells and underlying basement membrane that covers the sclera and lines the inside of the eyelids. Figure 1 shows an image of an eye under visible wavelength illumination with identification of the sclera vein patterns. In general, the conjunctival vascular is hard to see with the naked eye at a distance. For young children, the blood vessels in sclera area could be blue, but for adults, the blood vessels are red in color. The structure of the blood vessels in the sclera are well suited to be used as a biometric — they are an internal organ that is visible without undue difficulty and they are anecdotally stable over time and unique for each person [2,3]. Therefore, the vein patterns in the sclera could be used for positive human identification.

In comparison to iris recognition, sclera recognition offers several benefits, especially for non-compliant or non-cooperative situations. First, sclera



recognition does not require imaging the eye in the near-infrared wavelengths. This allows for less constrained imaging requirements, including imaging at very long stand-off distances, may not require additional illumination, and, perhaps, enable the use of existing imaging systems to acquire and match individuals (such as using existing surveillance systems to acquire the images). Second, sclera recognition does not require frontal gaze images of the eye. For sclera recognition, assuming that the entire sclera region was enrolled for matching, off-angle eyes reveal more of the sclera vein pattern for matching. Thus, even an individual who was actively attempting to avoid detection or recognition by looking away from the matching system would be unable to avoid presenting a valid biometric pattern for identification.

### Previous Works On Recognition In The Sclera Region

Crihalmeanu *et al.* [4] used an semi-automated k-means clustering algorithm to estimate the sclera region from the RGB values of the pixels in the color sclera images, and used manual intervention to correct for misclassified boundaries (in particular, the lower eyelid boundary). They proposed a registration method that incorporates local affine and global smoothing transformations that locally deforms the template image to provide the best registration with the target image. Using the 'cross-correlation between non-specularity regions' in the registered images, they report an equal error rate around 25%, using their internally acquired database of 50 users. In particular, note that this most recent work is the first, and only, that does not use manual segmentation to ensure that the sclera regions to be matched are already well segmented and registered. But conjunctival vasculature in the biometric field is a fairly new idea. In the non-ideal environments system shows poor performance.

Derakhshani *et al.* first proposed using 'conjunctival vascular' patterns [5] for user identification. The conjunctiva is the thin top layer of the sclera region, and the conjunctival vasculature is the system of veins and arteries in this layer. They used contrast limited adaptive histogram equalization (CLAHE) to enhance the green color plane of the RGB image, and a multi-scale region-growing approach to identify the sclera veins from the image background. For matching, they proposed a multi-level matching approach — a coarse approach to sub divide the database, and a fine approach to specifically match a user from the preliminary sub-divided segment of the database, as found from the course approach. For the course approach, they utilize Hu's 7-th skew invariant moments to perform preliminary matching. For the fine approach, as described in the paper, they propose 2 methods — a minutiae based approach and a two dimensional correlation approach. In this work, they used a small database of 24 images composed of 2 images of the left and right eyes of 6 users. With manual segmentation, they reported 100% matching accuracy for both matching approaches.

In [7], Derakhshani *et al.* first described a vein extraction and enhancement technique. In this work, the authors first enhanced the green color plane of the image using a contrast-limited adaptive histogram equalization technique (CLAHE). CLAHE is a histogram equalization technique that enhances small regions, or 'tiles', of the image separately and uses bilinear interpolation to limit artificially introduced boundaries between adjacent tiles.

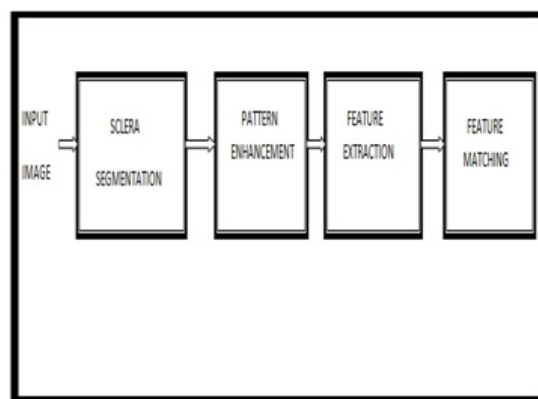


Figure-2. Complete block diagram.

A typical sclera recognition consists of four steps which include sclera segmentation, vein pattern enhancement, feature extraction, feature matching. Figure-2 shows the block diagram of sclera recognition. The registration of feature is a tedious task. Here the comparison is concentrated on feature registration.

### A New Parallel Sclera Vein Recognition Method

All the conventional sclera recognition systems lacks in matching speed. It is a matter of fact to consider the matching speed of the biometric system so as to make it useful for real time applications.

This approach reveals about a two-stage parallel approach for registration and matching by the use of Y shape descriptor-as feature to increase the matching efficiency. Parallel processing reduces matching time. A set of vessel segments combine to create Y shape branches often belonging to same sclera layer. Y shape branches are observed to be a stable feature and can be used as sclera feature descriptor. Within sclera there can be different layers of veins. According to the motion of layers blood vessels forms different patterns. And these blood vessels keep some of the form in same layer. The Figure-2 shows y shape vein pattern in same sclera layer.

When the number of branch is more than three vessel pattern comes from a different layer and deforms with the movement of eye. Y shape branches are observed to be a stable feature and can be used as sclera feature descriptor. To detect the Y shape branches in the original template, search for the nearest neighbors set of every line segment in a regular distance, classified the angles among these neighbors. If there were two types of angle values in the line segment set, this set may be inferred as a Y shape structure and the line segment angles would be recorded as



a new feature of the sclera. In order to measure orientation and relationship of every branch y shape vessels the angles between branch and iris radial direction is measured. In Figure-3.2  $\phi_1$ ,  $\phi_2$ , and  $\phi_3$  denote the angle between each branch and the radius from pupil center.  $\phi_1$ ,  $\phi_2$ , and  $\phi_3$  are quite stable even if the head tilts. The Y-shape descriptor is generated with reference to the iris center. Therefore, it is automatically aligned to the iris centers. It is a rotational- and scale- invariant descriptor (Figure-3).

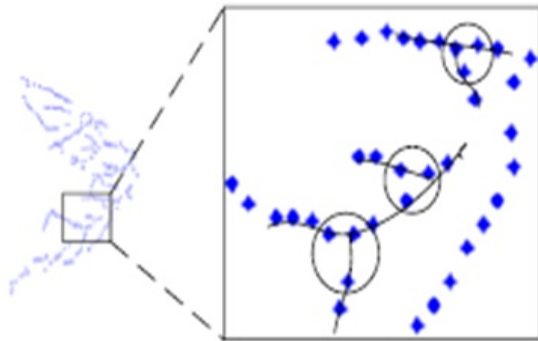


Figure-3. Y shape bran.

ch in sclera

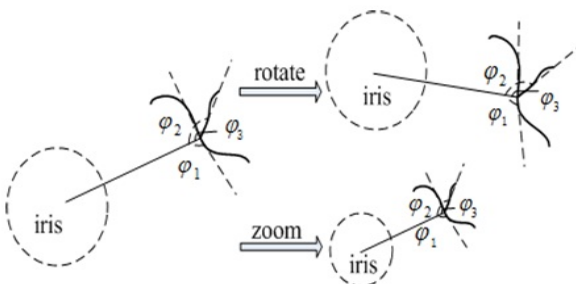


Figure-4. The rotation and scale invariant character of Y shape vessel branch.

### WPL SCLERA DESCRIPTOR

Due to poor segmentation accuracy, the descriptor in the edge may contain spur edges such as eyelashes, eyelids etc. Usually this is avoided with the help of mask files. The mask files will indicate whether descriptor belongs to edge of actual image sclera. But mask files will take large amount of memory to store them and it will slow down the data transfer. To avoid such heavy data transfer a new descriptor called weighted polar line descriptor developed which includes mask file information and can be automatically aligned for matching purpose. The geometric features of the descriptors are stored as a new descriptor. The weight of those descriptors who are beyond the sclera are set to be 0, and those who are near the sclera boundary are 0.5 and interior descriptors are set to be 1. In our work, descriptors weights were calculated on their own mask by the CPU only once. The calculating result was saved as a component of descriptor. The descriptor of sclera will

change to  $s(x, y, \varnothing, w)$ , where,  $w$  denotes the weight of the point and the value may be 0, 0.5, 1. To align two templates, when a template is shifted to another location along the line connecting their centers, all the descriptors of that template will be transformed. It would be faster if two templates have similar reference points. If we use the center of the iris as the reference point, when two templates are compared, the correspondence will automatically be aligned to each other since they have the similar reference point. Every feature vector of the template is a set of line segment descriptors composed of three variable (Figure-4): the segment angle to the reference line which went through the iris center, denoted as  $\theta$ ; the distance between the segments center and pupil center which is denoted as  $r$ ; the dominant angular orientation of the segment, denoted as  $\varnothing$ .

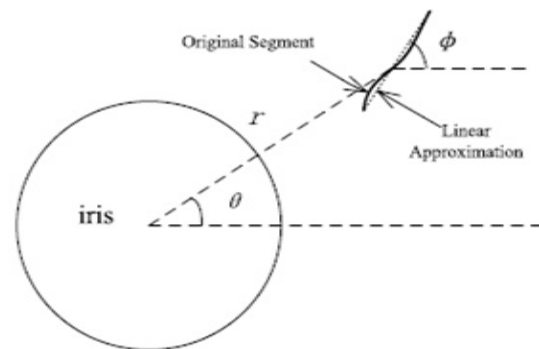


Figure-5. The key elements of descriptor vector.

### Line Segment Descriptor

This method uses an automatic segmentation approach both in color image and gray scale images. The segmentation step includes estimation of the glare area, iris boundary detection, estimation of the sclera region in color or grayscale images, and eyelid and iris boundary detection and refinement in the sclera region estimation step. Sobel filter applied to highlight the desired glare area. Pupil, and iris regions are segmented using greedy angular search on edge detected image. The line descriptor method can extract pattern at different orientation which helped to achieve orientation-invariant matching. Pupil, and iris regions are segmented using greedy angular search on edge detected image.  $S(x, y)$  is the edge detected image,  $(x_0, y_0)$  is the estimated pupil center,  $\theta$  is the angular search direction.

$$(u, v) = \arg \{(x, y) | \max S(x, y), \text{with } \arctan \left( \frac{y-y_0}{x-x_0} \right) = \theta \} \quad (1)$$

Due to physiological status of a person (for example, fatigue or non-fatigue, eye irritation, etc.), the vascular patterns could have different thicknesses at different times, due to the dilation and constriction of the veins. Therefore, vein thickness is not a stable pattern for



recognition. In addition, some very thin vascular patterns may not be visible at all times or in all situations. In this method, binary morphological operations are used to thin the detected vein structure down to a single-pixel wide skeleton, and to remove the branch points. This leaves a set of single-pixel wide lines that represents the vein structure. These lines are then recursively parsed into smaller segments. This is done until the line's maximum size ensures that the line segments are nearly linear, a property that is useful in feature extraction. In this work, the lines were parsed down to a size of 5 pixels. This small line segment size is small enough, in comparison to the matching distance, that the specific starting location of the line segment does not pose a significant cause of error for matching. For each segment, a least-squares line is fit to each segment. These line segments are then used to create a template for the vein structure. The segments are described by three quantities – the segments angle to some reference angle at the pupil center, the segments distance to the pupil center, and the dominant angular orientation of the line segment. The total descriptor for the sclera vein structure is the set of all of the individual segments' descriptors. Note that this implies that, while each segments descriptor is of a fixed length, the overall descriptor for a sclera vein structure can vary.

These line segments are then used to create a template for the vessel structure. The segments are described by three quantities the segment angle to some reference angle at the iris center, the segment distance to the iris center, and the dominant angular orientation of the line segment. The template for the sclera vessel structure is the set of all individual segments' descriptors. This implies that, while each segment descriptor is of a fixed length, the overall template size for a sclera vessel structure varies with the number of individual segments.

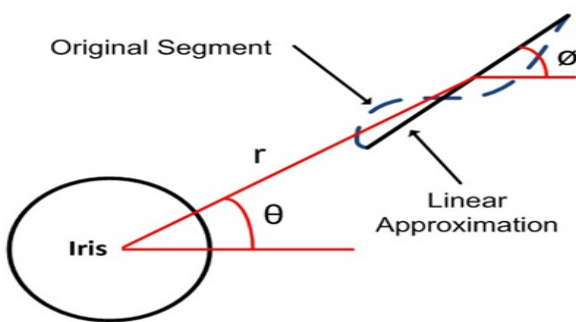


Figure-6. The sketch of parameters of segment descriptor.

A descriptor is  $S = (\theta r \phi)^T$ . The components are

$$\begin{aligned} \theta &= \tan^{-1}\left(\frac{y1 - yi}{x1 - xi}\right) \\ r &= \sqrt{(y1 - yi)^2 + (x1 - xi)^2} \\ \phi &= \tan^{-1}\left(\frac{d}{dx} fline(x)\right) \end{aligned} \tag{2}$$

Here,  $fline(x)$  is the polynomial approximation of the line

segment,  $(xl, yl)$  is the center point of the line segment,  $(xi, yi)$  is the center of the detected iris, and  $S$  is the line descriptor.

**Matching**

In general, the edge areas of the sclera may not be segmented accurately; therefore, the weighting image is created from the sclera mask by setting interior pixels in the sclera mask to 1, pixels within some distance of the boundary of the mask to 0.5, and pixels outside the mask to 0. This allows a matching value between two segments to be between 0 and 1 and allows for weighting the matching results based on the segments that are near the mask's boundaries. This reduces the effect of segmentation errors, particularly for under segmentation of the boundary between the sclera and eyelids. After the templates are registered, each line segment in the test template is compared with the line segments in the target template for matches. If there is a nonzero matching score, the segments are removed from future comparisons (one from the test and one from the target templates) and the matching result is recorded. The total matching score  $M$  is the sum of the individual matching scores divided by the maximum matching score for the minimal set between the test and target templates, i.e., one of the test or target templates has fewer points, and thus, the sum of its descriptor weights sets the maximum score that can be attained.

$$M = \frac{\sum_{(i,j) \in Matches} m(Si, Sj)}{\min(\sum_{i \in Test} W(Si), \sum_{j \in Target} W(Sj))} \tag{3}$$

Where  $Si$  and  $Sj$  are two segment descriptors,  $m(Si, Sj)$  is the matching score between segments  $Si$  and  $Sj$ .  $Matches$  is the set of all pairs that are matching,  $Test$  is the set of descriptors in the test template, and  $Target$  is the set of descriptors in the target template.

**Coarse-To-Fine Two-Stage Matching Process**

To further improve the matching process, the coarse-to-fine two-stage matching process. In the first stage, two images coarsely matched using the Y-shape descriptors, which is very fast to match because no registration needed. The matching result in this stage can help filter out image pairs with low similarities. After this step, it is still possible for some false positive matches. In the second stage, used WPL descriptor to register the two images for more detailed descriptor matching including scale and translation invariance. This stage includes shift transform, affine matrix generation, and final WPL descriptor matching.

Due to scale- and rotation- invariance of the Y-shape features, registration is unnecessary before matching on Y shape descriptor. To match two sclera templates, need to search the areas nearby to all the Y shape branches. The search area is limited to the corresponding left or right half of the sclera in order to reduce the searching range and time. The distance of two branches,



the angle between branch and the polar from pupil center in descriptor are defined. The number of matched pairs and the distance between Y shape branches centers are stored as the matching result. The decision is regulated by the threshold  $t$ : if the sclera's matching score is lower than  $t$ , the sclera will be discarded. The sclera with high matching score will be passed to the next more precisely matching process.

**Shift Parameter Search:** As discussed before, segmentation may not accurate. As a result, the detected iris center could not be very accurate. Shift transform is designed to tolerant possible errors in pupil center detection in the segmentation step. If there is no deformation or only very minor deformation, registration with shift transform together would be adequate to achieve an accurate result. First randomly select an equal number of segment descriptors in test template from each quad and find its nearest neighbors in target template. The shift offset of them is recorded as the possible registration shift factor.

**Affine Transform Parameter Search:** Affine transform is designed to tolerant some deformation of sclera patterns in the matching step. The shift value in the parameter set is obtained by randomly selecting descriptor and calculating the distance from its nearest neighbor. At end of the iteration, count the numbers of matched descriptor pairs from the transformed.

### Image Processing on the Compute Unified Platform

In the field of image processing intensive computation power is required to achieve high accuracy and real-time performance. Most of image processing and computer vision tasks perform the same computation on a number of pixels, a typical data parallel operations. Thus, they can exploit the single instruction multiple data (SIMD) architecture and be effectively parallelized on GPU. There is a strong desire to use GPU to accelerate computationally intensive tasks in the image processing and computer vision domain, mainly due to recent advances in the development of the compute unified framework, i.e., CUDA by NVIDIA. A CUDA compliant device is a set of multiprocessor cores, capable of executing a very high number of threads concurrently that operates as a coprocessor to the CPU or host. Each multiprocessor has a single-instruction multiple thread (SIMT) architecture; Image processing algorithms are too diverse to define a general aspect for parallel implementation. However, in practice, image processing involves independent processing of a massive pixel or feature set. This can benefit from SIMD-style GPU architecture. More importantly, image processing involves large memory buffers to store pixel data and needs frequent access to them, where the access pattern is often regular and sequential, as row-major or column-major order. The complexity of operations applied to the pixel data depends on the characteristics of the algorithm. However, the complexity is generally high due to intensive floating-point and logical operations. In addition, image processing algorithms consist of a mixture of sub algorithms, for which the efficiency of implementation on

the GPU is affected by the dependency of the task order and data exchange between consequent tasks.

There are multiple memory spaces in the CUDA memory hierarchy: register, local memory, shared memory, global memory, constant memory and texture memory. Register, local memory and shared memory are on-chip and could be a little time consuming to access these memories. Only shared memory can be accessed by other threads within the same block. However, there is only limited availability of shared memory. Global memory, constant memory, and texture memory are off-chip memory and accessible by all threads, which would be very time consuming to access these memories. Constant memory and texture memory are read-only and cacheable memory. Mapping algorithms to CUDA to achieve efficient processing is not a trivial task.

There are several challenges in CUDA programming: If threads in a warp have different control path, all the branches will be executed serially. To improve performance, branch divergence within a warp should be avoided. Global memory is slower than on-chip memory in term of access. To completely hide the latency of the small instructions set, we should use on-chip memory preferentially rather than global memory. When global memory access occurs, threads in same warp should access the words in sequence to achieve coalescence. Shared memory is much faster than the local and global memory space. But shared memory is organized into banks which are equal in size. If two addresses of memory request from different thread within a warp fall in the same memory bank, the access will be serialized. To get maximum performance, memory requests should be scheduled to minimize bank conflicts.

### RESULTS

The proposed system could accurately segment sclera from an RGB color image and extracted the Y shape descriptor as feature. The tools and simulation environments for development of applications are highlighted. Sclera appears to be a promising model especially focusing on standardizing APIs, security, interoperability, and dynamic application for complex services. Hence there is a scope for further research in these areas.

The UBIRIS database is a publicly available database with iris images acquired in color, in comparison with most iris databases which are acquired using NIR illumination. The database consists of 1877 images (1214 in Session1 and 663 in Session2), composed of 241 users in two distinct sessions. Both parallel and sequential approaches are done using this data base. The system can generate four possible recognition results: correctly matching (true positive: TP), correctly not matching (true negative: TN), incorrectly matching (false positive: FP), and incorrectly not matching (false negative: FN). The False Accept Rate (FAR), False Reject Rate (FRR), and Genuine Acceptance Rate (GAR) are calculated by



$$FAR = \frac{FP}{TN + FP} \times 100\%$$

$$FRR = \frac{FN}{TP + FN} \times 100\%$$

$$GARR = 1 - FRR$$

For the sequential method, the EER is 3.386%, the area under the curve (AUC) is 97.5% and GAR = 92.6% and 86.46% with FAR = 0.1% and FAR = 0.01% respectively. For the parallel computing, if all templates were used for the Stage II matching, the parallel approach would achieve better recognition accuracy than the sequential method with EER = 3.052%, AUC = 98.6%, GAR = 93% (when FAR = 0.1%) and 87.9% (when FAR = 0.01%). At the same time, the parallel computing

approach achieves a 769 times speed improvement. If we filter 23.3% of pairs from the Stage I, the speed would be further improved to be 805 times, while the accuracy still beats the sequential method using EER, AUC, GAR (when FAR = 0.1% and FAR = 0.01%) as measures. The receiver operating characteristic (ROC), a balanced plot of FAR and GAR, or FAR and FRR, can be used to evaluate the performance of the proposed system. Moreover, since FAR and FRR are in opposition to each other, when FAR = FRR, referred to as equal error rate (EER), it achieves the point which is also widely used to compare accuracy rates of two ROC curves.

The Figure-7 is the combined result obtained after applying morphological processing. After removing the exterior boundaries using structuring elements from the binarised image created a mask image.

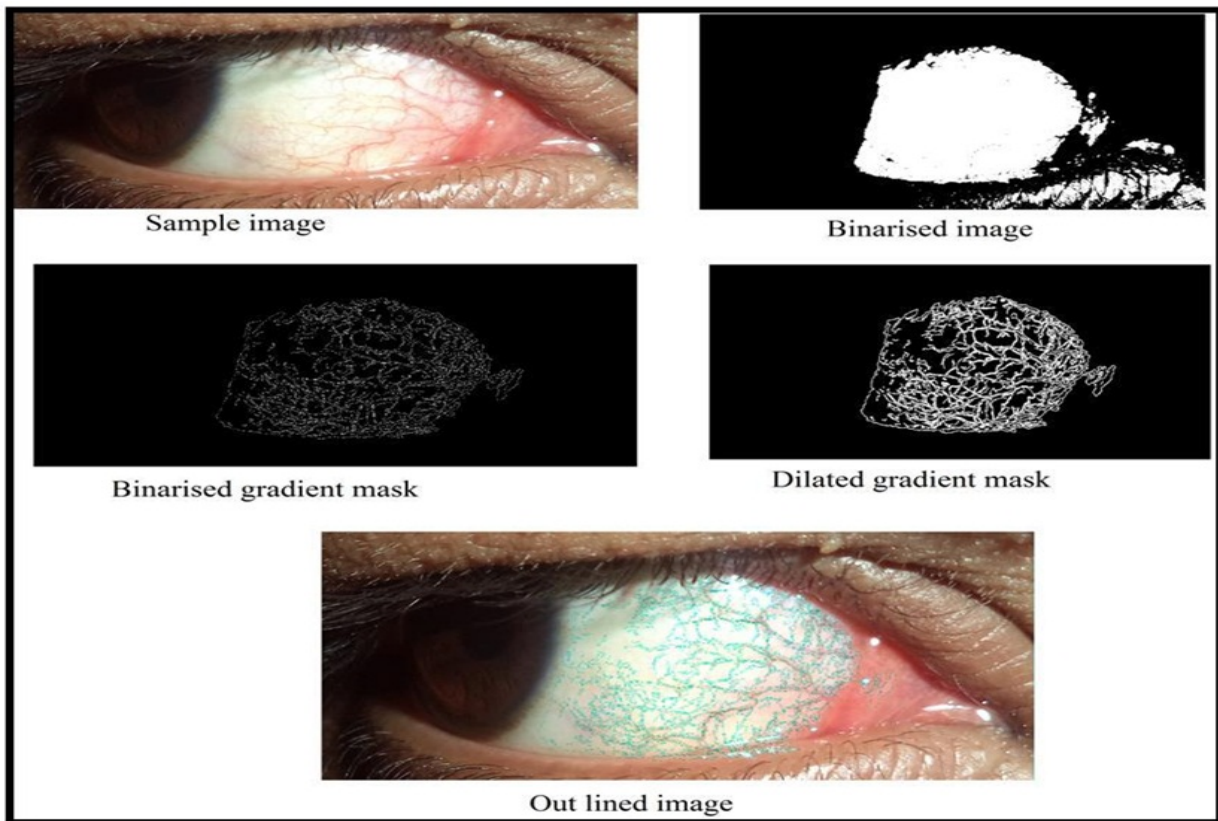


Figure-7. Segmentation results.

## CONCLUSIONS

The sequential method takes much time for matching. The new parallel sclera vein recognition method, which employees a two stage parallel approach for registration and matching. The Y shape descriptor can narrow the search range to increase the matching efficiency, which is a new feature extraction method to take advantage of the GPU structures. The WPL descriptor to incorporate mask information and make it more suitable

for parallel computing, which can dramatically reduce data transferring and computation.

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