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A Soft Computing Approach towards Segmentation of Blood Vessels in Retinal Images

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ABSTRACT

Segmentation of blood vessels in the eye is used to diagnose optical impairments such as glaucoma and diabetic retinopathy. This paper proposes an efficient approach for blood vessel segmentation in retinal images adopting extensive feature set and soft computing technique. The soft computing technique utilized in our method is Genetic Algorithm (GA). GA is used for optimizing or selecting best features which give a reduced feature set eventually resulting in high classification accuracy. Reducing the dimensions of the feature space not only reduces the burden of computational complexity, but also improves the estimated performance of the classifiers. The proposed method aims at evaluating the efficiency of the applied descriptors and proves that this scheme will be capable of rendering accurate results, even when these types of features are used independently. Thus some more gray level and moments invariants features were added for better efficiency. The expected outcome of our research is good segmented image suitable for diabetic detection. The sensitivity, specificity and accuracy of the proposed method will be remarkable for the application.

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INTRODUCTION

Medical imaging is a technique and process used to create images of the living body for clinical purposes or medical science. The special nature of medical images derives as much from the method of acquisition as it does from the subjects whose images are being acquired. While surface imaging is used in some application, for example, in the examination of the properties of skin, medical imaging has been distinguished primarily by its ability to provide information about the layer beneath the surface. Medical imaging proves vital for large number of medical applications such as X-ray, CT (computed tomography), MRI (magnetic resonanceimaging), US(ultrasound), electroencephalography (EEG), magnetoencephalography (MEG), ECG (electrocardiography) and so on. The imaging modalities can be divided into two global categories: anatomical and functional. Anatomical modalities depict primarily the morphology. Anatomical modalities include X-ray, CT, MRI, US images, Tim McInerney (1998).Functional modalities depict, primarily, information on the metabolism of the underlying anatomy. These include (planar) scintigraphy, SPECT (single photon emission computed tomography).

Diabetic retinopathy (DR) is the leading ophthalmic pathological cause for blindness among people of working age in developed countries H. R. Taylor *et al* (2001).About 2% of the patients affected by this disorder are blind and 10% undergo vision degradation after 15 years of diabetes Diego Marín *et al* (2001), P. Massin *et al* (2000) as a consequence of DR complications. The total number of diabetic patients is forecasted to rise from 171 million in 2000 to 366 million in 2030 Diego Marín *et al* (2001). The main cause of DR is abnormal blood glucose level elevation, which damages vessel endothelium, thereby increasing vessel permeability. The first manifestations of DR are tiny capillary dilations known as micro-aneurysms. Although DR is not a curable disease, laser photocoagulation can prevent major vision loss if detected in early stages H. R. Taylor *et al* (2001), Diego Marín *et al* (2001). DR patients perceive no symptoms until visual loss develops, usually at the later stage. So, to ensure the treatment is received on time, diabetic patients need annual eye-fundus examination D. S. Fong *et al* (2003). Therefore, DR also becomes a great economic issue. Only in U.S., cost of ophthalmic

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chronic complications caused by diabetes exceeded 1 billion dollars in 2007, Economic costs of diabetes in the U.S.(2007)," in Diabetes Care.

The accurate diagnosis of this disease depends upon some features which have to be analyzed in order to quantify the severity level of the disease. Retinal blood vessels are important for the detection of DR, Marwan D *et al* (2011). The main features of a fundus retinal image are the optic disc, fovea and blood vessels. The optic disc is the entrance and exit region of blood vessels to the retina. Its localization and segmentation is an important task in an automated retinal image analysis system. The fovea corresponds to the region of retina with highest sensitivity. So far several methods have been developed for vessel segmentation, but visual inspection and evaluation by ROC analysis shows that there is still room for improvement. In addition, it is important to have algorithms that do not critically depend on configuring many parameters so that untrained community health workers may utilize this technology. These limitations of state of the arts algorithms have motivated the development of the framework described here, which depends on the manually segmented images for training purposes only, A. O.Sareh 2009).

Because of multifarious nature of the vascular network, the manual vessel segmentation is very difficult and time consuming, so the researchers have proposed several automated methods for retinal vessel segmentation which are classified as supervised and unsupervised based on the vessel classification techniques. The supervised methods require a feature vector for each pixel and manually labeled images for training the algorithm. To classify the pixel as vessel or non-vessel the supervised method uses different classifiers such as neural networks, support vector machine, Bayesian classifier with class-conditioned probability density function, k-nearest neighbor classifier and Ada boost classifier.

The rest of the paper is organized as follows. Section II explains the researches that are related to our proposed method. Section III shows our proposed method for developing efficient method for blood vessel segmentation in retinal images using extensive feature set and soft computing techniques. Section IV explains the result of the proposed methodology and finally Section V concludes our proposed method with suggestions for future works.

Literature Review:

A lot of research is being done in the area of blood vessel segmentation and feature extraction techniques. A brief review of some of the recent researches is as follows.

Yong Yag *et al*. presented a novel hybrid automatic approach for the extraction of blood vessels in retinal images. Morphology operators are applied to smoothen and strengthen thus the blood vessels are enhanced. Fuzzy clustering followed by a purification procedure is applied to remove theweak edges and noise and the results obtained when compared with some existing techniques found to be promising.

Chih-Chin Lai *et al*. have presented a hierarchical evolutionary algorithm for automatic medical image segmentation. The segmentation approach could automatically determine the proper number of regions. On the other hand, the representative gray levels of regions were also determined, and then a partitioning of the given image was done. The segmentation results were more continuous and smoother than dynamic thresholding, CHNN methods, k-means and fuzzy c-means. These results were convenient for doctors in recognizing organs and tissues correctly, thus enhancing their diagnostic efficiency and minimizing their workload in medical image analysis.

Diego Marín *et al*. have presented a supervised method for blood vessel segmentation in retinal images by using gray-level and moment invariants-based features. Its effectiveness and robustness with different image conditions, along with its simplicity and fast implementation, make this blood vessel segmentation proposal suitable for retinal image computer analyses such as automated screening for early diabetic retinopathy detection.

Elahe Moghimirad *et al* proposed a a multi-scale method to segment retinal vessels based on a weighted two-dimensional (2D) medialness function. The output from the medialness function are multiplied by the Eigen values of the Hessian matrix .The centerlines of vessels are extracted using noise reduction and reconnection method and thus vessel radius vessels were extracted .The main advantage of the method is to overcome the false detection arising due to noise and abnormality found in pathological images.

Marwan D. Saleh *et al*. have presented an Automated Blood Vessel Segmentation Algorithm Using Histogram Equalization and Automatic Threshold Selection. The segmentation algorithm which takes advantage of the powerful preprocessing techniques such as the contrast enhancement and thresholding offers an automated segmentation procedure for retinal blood vessels. To evaluate the performance of the algorithm, an experiment was conducted on 40 images collected from DRIVE database. The results show that the proposed algorithm performs better than the other conventional algorithms in terms of accuracy. Furthermore, the proposed algorithm was easy to implement, best suited for fast processing applications.

David Calvo *et al* (2011) presented a reliable and efficient method that is able to overcome the problems of classifying the feature points, specially crossovers, after preprocessing the structure, it has been eroded to obtain the skeleton and obtain the feature points. Local features and the relations

between points have been analysed for classification. Thus a high sensitivity and specificity in the classification of feature points is achieved allowing to control the number of misclassified points according to the application domain

A. Youssif *et al.* have presented optic disc detection from normalized digital fundus images by means of vessels. In this paper a simple matched filter is implemented to roughly match the direction of the vessels at the OD vicinity. The retinal vessels were segmented using a simple and standard 2-D Gaussian matched filter. Consequently, a vessels direction map of the segmented retinal vessels was obtained using the same segmentation algorithm. The segmented vessels are then thinned, and filtered using local intensity, to represent finally the OD-center candidates. The difference between the proposed matched filter resized into four different sizes, and the vessels' directions at the surrounding area of each of the OD-center candidates was measured. The minimum difference provided an estimate of the OD-center coordinates. The OD-center was detected correctly in 80 out of the 81 images (98.77%). In addition, the OD-center was detected correctly in all of the 40 images (100%) using the publicly available DRIVE dataset.

Jestin V.K *et al.* have presented a genetic algorithm for retinal image analysis. In this paper, Genetic Algorithm (GA) for best feature selection from retinal images was proposed. The features that improve the classification accuracy were selected by Genetic Algorithm and termed as optimized feature set. The others that degrade the performance were rejected at the end of specified generation.

Proposed Methodology For Developing An Efficient Method For Blood Vessel Segmentation:

Image segmentation can be defined as a process of partitioning an image into meaningful parts, mainly consisting of an object and background. In any imaging application, the design of robust and fast segmentation algorithms is a major requirement. Generally the need for accurate segmentation tools in medical applications is due to the increased capacity of the imaging devices. Here we have proposed a method for blood vessel segmentation in retinal images with the aid of Genetic Algorithm. Proposed scheme performs image preprocessing, feature extraction and optimization using GA. In feature extraction we have extracted statistical features as well as the disease based features. These features are then optimized using the Genetic algorithm which results in the better outcome.

Image Preprocessing:

The first step in our method is the image preprocessing. In order to reduce the imperfections and generate images more suitable for extracting the pixel features demanded in the classification step, preprocessing steps are applied. The different steps involved in our proposed method are shown in flow diagram given in Fig 1. In this, the input retinal images are converted into black and white images for better segmentation of the images. A data set is created with the retinal images which are manually segmented in order to compare the segmented output for better result. After the conversion, the images are filtered to remove the noise which is present in the output. The noise removal is done with the application of filter and here we utilized median filter for the noise removal which is explained in detail in the below section.

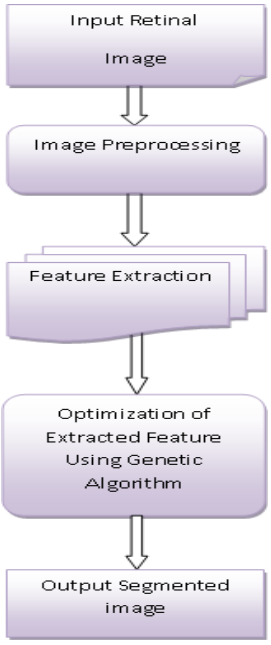

Fig. 1: Flow Diagram of our proposed methodology

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Noise removal Using Median Filter:

Anything apart from the hand forming the gesture was considered as noise. Sometimes when only one hand was being used to form the gesture, then the second hand when comes into the picture would be treated as noise. In our proposed method we utilize median filter for noise removal. Noise suppression or noise removal is an important task in image processing. The median filter is often applied to gray value images due to its property of edge preserving. In the median filtering operation, the pixel values in the neighborhood window are ranked according to intensity, and the median becomes the output value for the pixel under evaluation. Thus following steps were used to remove the noise from images,

The neighboring pixels are arranged according to brightness and the median value becomes the new value for the central pixel. Median filters can do an excellent job of rejecting certain types of noise, in particular, "shot" or impulse noise in which some individual pixels have extreme values. The general expression for the median filter is given as per the below eqn,

$$M_f(t_1, t_2 \ldots\ldots t_N) = MIN\left(\sum_{i=1}^{N}\|t_1 - t_i\|, \ldots\ldots \sum_{i=1}^{N}\|t_N - t_i\|\right) \quad (1)$$

Using Eqn 1, the median filtering is performed to remove the noise from the acquired image. The output image from the median filter is blurred image and these images are subtracted from the black and white image obtained in the preprocessing stage to obtain the output image. These images are further processed for feature extraction.

Feature Extraction:

When the input data to an algorithm is too large to be processed and suspected to be notoriously redundant then the input data will be transformed into a reduced set of features. Transforming the input data into a set of features is called feature extraction .Feature extraction is the process by which image features are extracted and used to represent concisely the image visual content J. Fernandeza (2009). It involves downsizing the amount of resources required to describe a large set of data accurately. Various features are present in the images which can be extracted for proper differentiation of any objects from its background such as the texture, color, edges etc. In our proposed method we have used two different set of feature like statistical feature and disease based features. The feature included in these are explained below,

Statistical Features:

The various statistical features used in our proposed method is explained in the sections below,

Mean:

It is the mean of pixel in the image. The n^{th} moment of mean is

$$\mu_0 = \sum_{i=0}^{L-1}(z_i - m)^n\, p(z_i) \quad (2)$$

where

z is the gray level value

m is the mean value of z.

Inverse differential moment:

This measure relates inversely to the contrast measure. It is a direct measure of the local homogeneity of a digital image. Low values are associated with low homogeneity.

$$I_D = \sum_i \sum_j \left\{ \frac{p(i,j)}{1+(i-j)^2} \right\} \quad (3)$$

where i, j is the number of rows and columns respectively and $p(i,j)$ is the mean of GLCM of the image.

Skewness:

It is a measure of skewness of the histogram

$$S(z) = \sum_{i=0}^{L-1}(z_i - m)^3\, p(z_i) \quad (4)$$

where z_i is the i th gray level and $p(z_i)$ is the mean of the GLCM of the image.

Angular Second Moment:

This is a measure of local homogeneity and the opposite of Entropy. High values of ASM occur when the pixels in the moving window are very similar.

$$A_s = \sum_i \sum_j \{p(i,j)\}^2 \quad (5)$$

where i, j is the number of rows and columns respectively and $p(i,j)$ is the mean of GLCM of the image.

Disease based features:

The various disease based features are as given below,

Area:

It gives the area of the disease spread and objects in the eye

$$\rho(i,j) = \frac{1}{M-N}\sum_{m=0}^{M-1}\sum_{n=0}^{N-1} b_i(i-m, j-n) \quad (6)$$

which supports M, N region for every (i, j) point of the image.

Minimum intensity:

It gives the minimum intensity of the abnormality present in the retinal image. It is actually a pixel value measurement

Mean intensity:

It gives the mean intensity of the pixels present in the retinal image. It is also a pixel value measurement.

Genetic Algorithm for our proposed blood vessel Segmentation:

In Genetic algorithm, initially chromosomes are generated in which genes are the indices of the database images. These genes are generated without any repetition within the chromosome and the values of the genes depend on the number of images in the database to be queried. The extracted features of each image are grouped as a feature set and the feature set of the query image is also extracted. Then the chromosomes are subjected to the genetic operators, crossover and mutation, and hence the new chromosomes are generated. Then the fitness is determined for the newly generated chromosomes. The various steps involved in our proposed GA is given below,

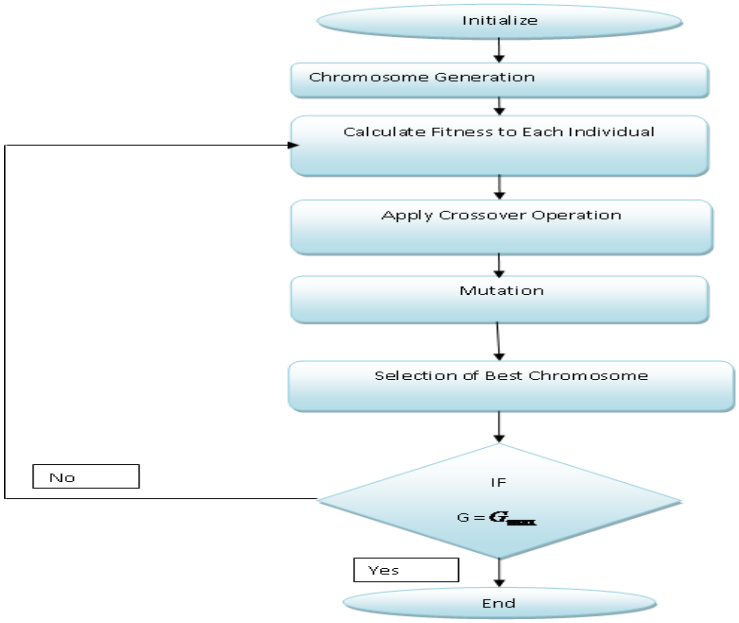

Fig. 2: Flow diagram for our proposed method.

Generation of Chromosomes:

Initially generate N_s number of random chromosomes and the number of genes in each chromosome rely on the number of images required which are similar to the given query image. As discussed earlier, the generated genes are the indices of the database images,

$$G^{(i)} = \{G_0^{(i)}, G_2^{(i)}, G_3^{(i)}, \cdots, G_{n-1}^{(i)}\}$$

$$0 \le j \le N_s - 1, 0 \le m \le n-1 \qquad (7)$$

n - Number of similar images to be retrieved

In eq.5, $G_m^{(i)}$ represents the m^{th} gene of the i^{th} chromosome. The features considered in the images are shape, texture, contourlet and color histogram; these features are extracted from all the images in the database. Once the features are extracted then they are stored in a separate vector for each image. After determining all the aforesaid set of features from the database images, the individual feature sets are concatenated into a single feature set and then each feature set is normalized.

Fitness Function

Evaluate fitness function (it will give best input that will satisfy the best or actual solution). Higher fitness function means better solution. Following are the purpose of fitness function.

- The fitness function is used for Parent selection
- Fitness function measure for convergence
- For Steady state: Selection of individuals to die
- Should reflect the value of the chromosome in some "real" way

Fitness function is a type of objective function, which is the leading target parameter to the optimized value. The fitness function is calculated by using the following formula.

$$F_i^1 = \sum_{i=0}^{N_L} ((C_i + W_i)/2)$$

$$\mathrm{F}_{\mathrm{j}}^2 = \sum_{i=0}^{N_L} ((F_i + T_i)/2) \qquad (8)$$

$$\mathrm{F_i} = F_i^1 + F_i^2$$

Here the fitness value of each chromosome is calculated based on the coverage and weight of the genes.

Selection of Optimal Solution:

After the process is repeated $I_{\max}$ times, best chromosomes are selected from the obtained group of chromosomes. Here, the best chromosomes are the chromosomes which have maximum fitness. The best chromosome obtained is used to retrieve the similar images from the database. In other words, the database images that are represented by the indices, which are obtained from the genes of the best chromosomes, are the images similar to the given query image and they are retrieved in an effective manner. For selection, various methods can be utilized. In our proposed method we used Roulette-Wheel Selection.

Roulette-Wheel Selection:

The *i* th string in the population is chosen with a probability proportional to f_i. The probability for selecting the *i* th string is

$$p_i = \frac{f_i}{\sum_{i=1}^{n} f_i} \tag{9}$$

where n is the population size.

The average fitness of the population is calculated as

$$f = \sum_{i=1}^{n} f_i \tag{10}$$

Here we will check our constraints are satisfied or not. If constraints are satisfied then we will select this output else we will use genetic algorithm operator for obtaining actual output which is described below,

Crossover and Mutation:

Among different types of crossovers, the two point crossover is selected with the crossover rate of C_R. In the two point crossover, two points are selected on the parent chromosomes using the eq. (11) and (12). The genes in between the two points c_1 and c_2 are interchanged between the parent chromosomes and so $N_s/2$ children chromosomes are obtained. The crossover points c_1 and c_2 are determined as follows

$$c_1 = \frac{\left|G_m^{(i)}\right|}{3} \tag{11}$$

$$c_2 = c_1 + \frac{\left|G_m^{(i)}\right|}{2} \tag{12}$$

Now, we have the children chromosomes which are stored separately and their corresponding indices from $G_m^{(i)}$ are stored in $G_{newm}^{(i)}$. Then, the mutation is accomplished by replacing N_M number of genes from every chromosome with new genes. The replaced genes are the randomly generated genes without any repetition within the chromosome. Now the chromosomes which are selected for crossover operation, and the chromosomes which are obtained from the mutation are combined, and so the population pool is filled up with the N_s chromosomes. The process is repeated iteratively until it reaches a maximum iteration of $I_{\max}$. The final step is the convergence process where it decides when to stop. Convergence step can be defined previously at a given threshold or maximum iteration can be calculated when above steps repeat the same value

After segmentation of the image I by adjusting the contrast and intensity of the image using threshold segmentation the morphological operation is performed on the image. In a morphological operation, the value of each pixel in the output image is obtained by comparison of the corresponding pixel in the input image with its neighbors. By choosing the size and shape of the neighborhood, we can construct a morphological operation that is sensitive to specific shapes in the input image. Here we are taking two morphological operations such as dilation and area opening.

Dilation:

In dilation, the value of the output pixel is the maximum value of all the pixels in the input pixel's neighborhood. In a binary image, if any of the pixels is set to the value 1, the output pixel is set to 1. It is used to increase the object in the image. It has the equation:

$$\delta_B(X) = \{x \mid B_X \cap X \neq \phi\} \tag{13}$$

where B_x means B translated with x, X is the image and B is the structure element.

Area opening:

From a binary image **t**he filter with its connected components having area smaller than a parameter λ is called area opening. From a morphological perspective, this filter is an algebraic opening, and it can be extended to grayscale images. In particular, the area opening of parameter λ of an image I is the supremum of the grayscale images that are smaller than I and whose regional maxima are of area greater than or equal to λ.It can be defined as:

Let $X \subset M$ and $\lambda >= 0$. The area of opening of parameter λ of X is given by

$$\gamma_\lambda^a(X) = \{x \in X \mid Area(C_x(X)) >= \lambda\} \tag{14}$$

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Apparently, if $(X_i)_{i\in I}$ denote the connected components of $X, \gamma_\lambda^a(X)$ is equal to the union of X_i's with area greater than or equal to λ:

$$\gamma_\lambda^a(X) = \bigcup\{X_i \mid i \in I, Area(X_i) >= \} \quad (15)$$

By using these morphological operation maximum intensity pixels of the image alone is selected. Thus, the contrasting and intense image is further enhanced by utilizing the morphological operation. The output image obtained from the morphological operation is then compared with the black and white image of the input. The regional probe's operation is followed by the morphological operation in order to group the image. This segmented image is then compared with the manually segmented input image to check for the mean square error value. The expected outcome of our research is a good segmented image. The sensitivity, specificity and accuracy of the proposed method will be significant for the application.

RESULT AND DISCUSSION

The proposed blood vessel segmentation of the retinal images based on Genetic Algorithm was implemented in the working platform of MATLAB (version 7.11) and databases that we have used are STARE and DRIVE. The result shows that our approach has an admirable performance.

Drive Database:

(Digital Retinal Images for Vessel Extraction):

DRIVE (Digital Retinal Images for Vessel Extraction) database was obtained from a diabetic retinopathy screening programme in the Netherlands. The screening population subjects range between 31 to 86 years of age. The database consists of 40 images which were supplied as training and test set, each containing 20 images; 7 contain pathology, namely exudates, hemorrhages and pigment epithelium changes. The training set has 3 images with pathology while test set has 4 images with pathology.

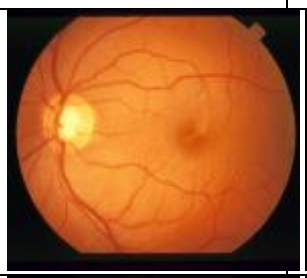
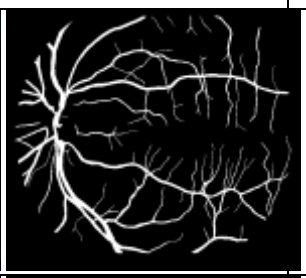
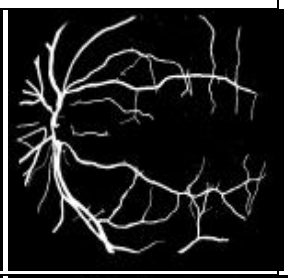
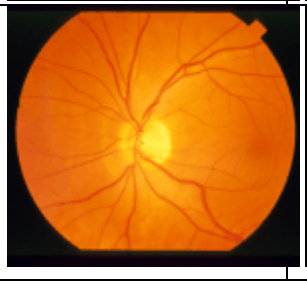
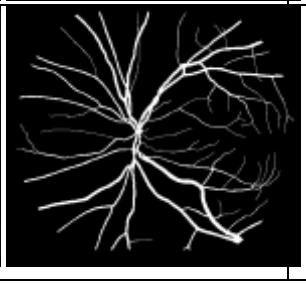
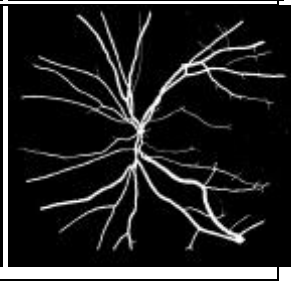
Stare:

(Structured Analysis of the Retina):

The STARE database contains 20 images for blood vessel segmentation; ten of these contain pathology.

The digitized slides are captured by a TopCon TRV-50 fundus camera at 35^0 field of view. The slides were digitized to 605 x 700 pixels, 8 bits per color channel. Two observers manually segmented all images. The observers were able to classify most of the pixels without any ambiguity. However, the human observers were uncertain about some pixels, such as those of vessels near pathology, those of small vessels and those on the vessel boundaries.

The input images are fed to our proposed technique where various steps like preprocessing, noise removal, and feature extraction are performed. Fig 3 shows the input and the output we obtained along with the morphological operation based images. . Finally the GA operation is performed to obtain the final extracted output. The extracted vessel output provides an accurate segmented output as it shows accurate value when compared with that of the manually segmented images.

Database	Input images	Manual Segmented images	Images after Morphological operation
STARE			
			

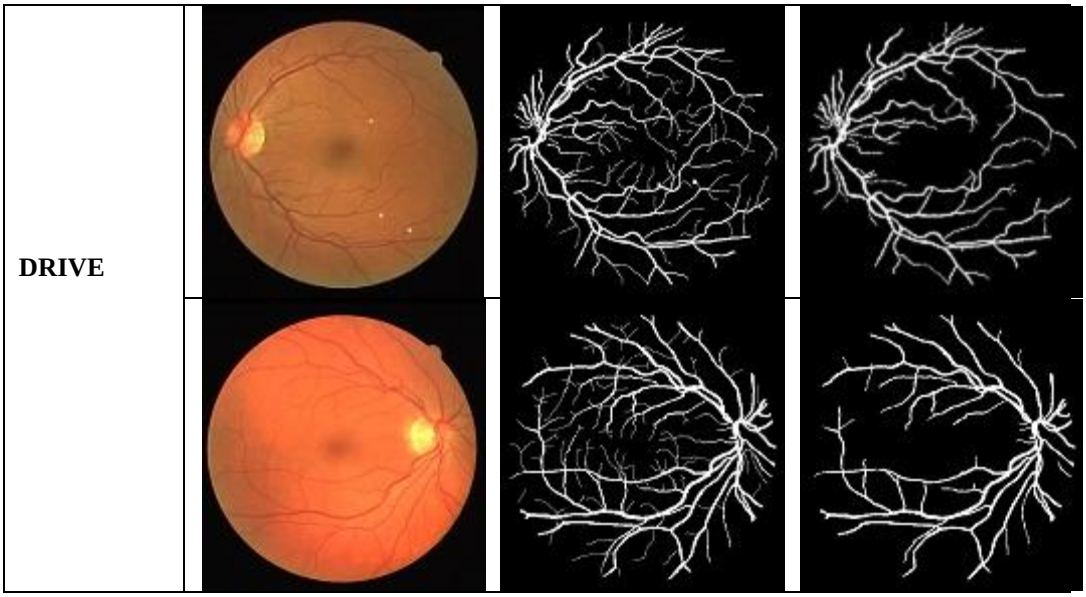


Fig. 3: From left to right :Input image, Ground truth image and segmented output.

Table 1: Comparison of: Sensitivity (Se), specificity (Sp), and accuracy (Acc) of the methods tested on the DRIVE database.

Algorithm	Se	Sp	Acc
Proposed	0.6382	0.9794	0.9458
Chaudhuri *et al*	0.6168	0.9741	0.9284
Martinez-Perez *et al*.	0.7246	0.9655	0.9344
Staal *et al*	0.7194	0.9773	0.9442
Espona *et al*. (subpixel accuracy	0.7313	0.9600	0.9325
Dizdaroglu *et al*.	0.718	0.974	0.941

Table 2: Comparison of: Sensitivity (Se), specificity (Sp), and accuracy (Acc) of the methods tested on the STARE database.

Algorithm	Se	Sp	Acc
Proposed	0.6876	0.9783	0.9467
Chaudhuri *et al*	0.6134	0.9755	0.9384
Martinez-Perez *et al*.	0.7506	0.9569	0.9410
Staal *et al*	0.6970	0.9810	0.9516
Hoover *et al*.	0.6751	0.9367	0.9267
Mendonca and Campilho	0.6996	0.9730	0.9440

Conclusion:

In this paper we have proposed an efficient method for blood vessel segmentation in retinal images with the aid of Genetic algorithm as a soft computation technique. GA is used for optimizing or selecting best features which gives a reduced feature set eventually results in high classification accuracy. This method is based on the optimization method where the feature that suits accurately for segmentation process are selected using GA. The proposed method aims at evaluating the efficiency of the applied descriptors prove this method will be capable of rendering accurate results, even when these types of features are used independently. From Table 1 and 2 our proposed method proved to be an efficient method for blood vessel segmentation.

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