Red lesion in fundus image with hexagonal pattern feature and two-level segmentation

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Abstract

Red lesion identification at its early stage is very essential for the treatment of diabetic retinopathy to prevent loss of vision. This work proposes a red lesion detection algorithm that uses Hexagonal pattern-based features with two-level segmentation that can detect hemorrhage and microaneurysms in the fundus image. The proposed scheme initially pre-processes the fundus image followed by a two-level segmentation. The level 1 segmentation eliminates the background whereas the level 2 segmentation eliminates the blood vessels that introduce more false positives. A hexagonal pattern-based feature is extracted from the red lesion candidates which can highly differentiate the lesion from non-lesion regions. The hexagonal pattern features are then trained using the recurrent neural network and are classified to eliminate the false negatives. For the evaluation of the proposed red lesion algorithm, the datasets namely ROC challenge, e-ophtha, DiaretDB1, and Messidor are used with the metrics such as Accuracy, Recall, Precision, F1 score, Specificity, and AUC. The scheme provides an average Accuracy, Recall (Sensitivity), Precision, F1 score, Specificity, and AUC of 95.48%, 84.54%, 97.3%, 90.47%, 86.81% and 93.43% respectively.

Keywords Red lesion · Microaneurysms · Hemorrhage · Background elimination · Recurrent neural network · Lesion candidates

1 Introduction

Late diagnosis of diabetic retinopathy can result in complications such as loss of vision due to damage in retinal blood vessels. It is necessary to have a trained expert to detect such
abnormalities in fundus images. Also, a continuous eye examination is essential for continuous monitoring and treatment at its early stage. An ophthalmologist has to follow up on the progress of treatment and the current status of the fundus image has to be carefully noted for avoiding the loss of vision. The cost of manual screening is high due to the demand for diabetic eye care resources. During the continuous examination, the disappearance or the appearance of red lesions such as hemorrhages and microaneurysms must be carefully monitored. Continuous monitoring helps to study the dynamics of red lesions caused due to diabetic retinopathy. There are several challenges in developing an automatic lesion detection algorithm such as missing the lesion due to variation in illumination throughout the fundus image. To monitor the appearance/disappearance of the lesion, it is necessary to detect lesions such as hemorrhages and microaneurysms (MA).

The motivations of the paper are as follows. Training complete fundus images using a deep learning algorithm will extract the features throughout the images. Therefore the proposed method aims to segment the red lesion candidate. Differentiating the red lesion and non-red lesion by an efficient feature extraction algorithm improves the performance of the classifier. Since the red lesions are non-rectangular in shape extracting the hexagonal features will provide better results because they cover the entire red lesion candidates. Also, the features must highly relate to the neighbor pixel intensity so that the red lesion and non-red lesion can be highly differentiated.

The contributions of the work are as follows.

(i) This paper proposes a two-level segmentation algorithm that initially detects the lesion candidate followed by blood vessel elimination. The false-positive may be due to the presence of a dark spot, retinal vessels that lie close to the lesion, and the low signal-to-noise ratio noisy regions. (ii) This paper also proposes a hexagonal pattern feature that highly differentiates the lesion from other regions. In order to eliminate the false positives, a recurrent neural network model is used that can differentiate lesions from other regions. (iii) Finally, the performance evaluation of the proposed work was evaluated using the metrics such as accuracy, recall, precision, F1 score, and Specificity.

The forthcoming sections of the paper are constructed with the following template. Section 2 depicts the related works, Section 3 shows the proposed lesion detection algorithm. Experimental results and conclusion are discussed in Sections 4 and 5 respectively.

## 2 Related work

Several algorithms have been introduced for detecting the red lesion in fundus images. Diameter closing morphological operation [28] is used in segmenting the MAs present in the fundus image. The authors of [14] and [6] used longitudinal angiogram image for the detection of MA. Both the schemes extract the MA from the fovea, where the longitudinal images are aligned using a registration algorithm. The authors N.Iyer et al. [23] proposed the scheme that detects and classifies the changes in the retina. This approach uses illumination adjustment and retinal feature segmentation. The features include blood vessels, optic disc, and fovea. However, the features are not sufficient to differentiate the red lesion and non-red lesion. This scheme was further extended that can detect changes in disappearance or appearance of the lesion and vascular disc changes [24]. The author Kedir et al. [1] presented a red lesion detection algorithm that is robust to contrast and illumination variation. This scheme uses the absolute difference to estimate the retinal changes and it also uses shape features to detect the changes deployed by a support vector machine (SVM) classifier.
To compensate for illumination variation and other acquisition artifacts, preprocessing is used that includes schemes such as contrast enhancement [25] and illumination compensation [1]. Radon transformation along with thresholding process is used by Giancardo et al. [13] where the radon features are extracted at various scanning angles and are trained and classified using SVM algorithm. Different thresholding schemes are proposed for detecting the red lesion, where the dynamic thresholding process is used as feature extraction by Zhang et al. [35]. This approach uses a rule-based algorithm for classification where it can also misses a few red lesion candidates that have low contrast boundaries. The author’s Mizutani et al. [22] used outer ring and inner ring features with a logistic classifier that also uses the features such as shape, color, and texture. The author Zhang et al. [36] used contextual descriptors which represent the intensity and geometric features with a random forest classification. Texture, geometric, contrast, region, edge, and intensity features are trained using a class imbalance classifier. This approach removes the blood vessel using gradient vector analysis for the exact detection of MA.

Different deep learning schemes are recently proposed that can be used for the diabetic retinopathy classification in the fundus image. In [8] the authors applied a deep learning framework on segmented fundus image for classifying diabetic retinopathy. In this approach, the authors have applied the maximal principal curvature that can highlight the branching blood vessels. The Hessian matrix with maximum eigenvalue is used to detect the blood vessels whereas a convolutional neural network is used to train the features. For the detection of subretinal Hemorrhage, the author’s Sai Ganesh et al. [29] applied a faster region convolutional neural network-based predictive algorithm. The authors used a semantic segmentation algorithm for the segmentation of the region of interest. The faster region-based convolutional neural network (R-CNN) algorithm was derived from the fast R-CNN algorithm, which speeds the classification time. This approach provides a testing time complexity of 2.64s. This approach is best for Optical coherence tomography (OCT) images, but it shows a low performance in fundus images. In [10], the authors proposed a two-step CNN for detecting the microaneurysms. This approach reduces the training time and also minimizes the data imbalance problem. In [9], the authors proposed local convergence features that use iterative thresholding and gradient weighting scheme for detecting the microaneurysms. It also uses the shape and intensity descriptor for improving classification performance. The features are then trained by the hybrid sampling/boosting classifier to classify the non-MAs and MAs. However, this approach provides a sensitivity of 47.1%

The authors Baisheng Dai et al. [7] used a class imbalance classification and gradient vector analysis (GVA) for detecting the MA. This approach uses a multi-scale number map for removing the vessels. It uses the features like texture, contrast, geometric features for training the RUSBoost classifier. The author’s Zhou et al. [37] introduced an unsupervised classifier with sparse PCA (sparse principal component analysis) for the detection of MA. It uses the posterior cerebral artery for detecting the MA which selects the best features by sparse PCA which is the combination of PCA and elastic net penalty. It also uses a $T^2$ statistic parameter to differentiate MA from Non-MAs. The accuracy of these schemes is less when compared to supervised schemes. The authors Long et al. [21] used directional local contrast with machine learning to detect the MA. Using the connected component analysis and shape characteristics the blood vessels are extracted. Directional local descriptors are then segregated from the segmented patches and are trained/classified using a machine learning algorithm. The average AUC (area under the curve) of this approach is 86.5%. The authors Yadev et al. [31] used a color locus detection method for detecting the MAs. It uses the basis of the histogram for segmenting the retinal images. It then extracts the gray-scale
co-occurrence matrix and shape features and is classified using classification algorithms. The accuracy of the scheme is maximum with a random forest classifier of 83.33% which should be highly improved.

The author Alyoubi et al. [3] proposed a DR image classification using deep learning that classifies the DR images into five stages namely mild, moderate, severe, proliferative, and no-DR. Two models have been proposed where the first model used CNN512 while the second model used YOLOV3. The two models provide accuracy of 84.1%, and 89% for the DDR and Kaggle dataset which should be still improved. The authors’ Li et al. [20] used learning along with semantic segmentation for automatic driving scenarios for high definition map where the authors used a DeepLabv3+ network for this application, where the authors restructure the convolution by multiscale attention mechanisms. Segmentation of region of interest (ROI) plays a major role in the detection of lesions. Different authors have proposed different segmentation algorithms [15]. The authors Anil Kumar [30] used a multi-modal classification that detects the COVID-19 from the X-ray images. The authors used a support vector machine where in the last layer the author has used separate layers for synchronizing the VSS16, and SVM. This scheme achieves an accuracy of 95% in covid detection. The authors Alexandra et al. [19] proposed a DR recognition using adversarial training and feature fusion. The authors Venkatesan et al. [26] proposed a choroidal neovascularization detection scheme in OCT image using machine learning, This includes the process such as pre-processing, extraction of features, Mayfly-optimization based feature reduction, and two-class classification. This scheme provides a classification accuracy greater than 92%. The authors Ramasamy et al. [27] proposed a diabetic retinopathy detection scheme using a ridgelet and textural features with a sequential minimal optimization classifier. This approach initially extracts and fuses the ophthalmoscopic features based on co-occurrence, run-length matrix, and ridgelet transform. Finally, sequential minimal optimization classification is used to classify the DR. The scheme provides an accuracy of 91% on the Kaggle dataset. The SVM algorithm [16] is also used in the diagnosis of diabetic retinopathy that uses a multi-level set segmentation with a genetic algorithm. The features include the texture descriptor estimated by local binary patterns, color moments along with statistical features like mean, median, etc. Usually, the feature is extracted in a rectangular structure. For instance, the local binary pattern features extraction, extracts the features by subdividing the image into $3 \times 3$ size. Since the fundus image is circular in shape using the rectangular structure is not efficient. Therefore the author Bryan et al. [11] used hexagonal image resampling schemes that extract the features based on the distance between the Centroid pixels. However, this feature does not relate to the neighboring pixel intensities.

To improve the performance of the automatic lesion detection scheme, this paper proposes a hexagonal pattern feature with a recurrent neural network classifier. The next section shows the proposed lesion detection algorithm.

3 Proposed lesion detection algorithm

Figure 1 shows the block diagram of the proposed red lesion detection algorithm where the algorithm has two phases namely training and testing. Both the training and testing phase has similar stages such as preprocessing, level 1 segmentation, level 2 segmentation, and feature extraction. The features extracted from the training images are trained using the deep learning model to obtain the classification result.
3.1 Preprocessing

Let $I_1$ be the fundus image where the red lesion is to be detected. The pre-processing involves processes such as RGB to gray conversion, illumination equalization, and
average filtering. Let \( r \), \( g \), and \( b \) be the red, green, and blue channels of the lesion image \( I_1 \) respectively. The RGB image is converted to grayscale using the relation

\[
I_2 = 0.3r + 0.5g + 0.2b
\]  

Here we have provided more weightage (50%) to the green channel because it has more information about microaneurysms and hemorrhage. The grayscale image \( I_2 \) is then applied for illumination equalization. The illumination equalization [33] is used to remove the non-uniformities caused due to contrast and luminosity variation caused during fundus image acquisition. This enhances the visibility of lesions in the poor contrast region or region with low brightness. The output of illumination equalization \( I_3 \) is expressed as,

\[
I_3 = I_2 + \mu - I_2 \ast h
\]

where \( h \) is the mean filter with a size of \( 5 \times 5 \), and \( \mu \) is the average intensity of the image \( I_2 \). To minimize the noise that was induced in the fundus scan image, average filtering is applied on the image \( I_3 \). Let \( u \times v \) be the size of the averaging filter, then the average filter output be represented as

\[
I_4(x, y) = \frac{1}{uv} \sum_{(i,j) \in S_{xy}} I_3(i, j)
\]

where \( S_{xy} \) represents the location of average filtering.

### 3.2 Level-1 Segmentation

The level-1 segmentation is a coarse segmentation that aims to segment the microaneurysms and hemorrhages leaving the other background regions. Let \( I_4 \) be the input of level-1 segmentation. This coarse segmentation includes processes such as adaptive contrast equalization, intensity normalization, and adaptive thresholding. The adaptive contrast equalization [18] improves the local contrast of the fundus image thereby enhancing the edges. Let \( I_5 \) be the output of adaptive contrast equalization, whose intensity is normalized to obtain the normalized image \( I_6 \) using the relation,

\[
I_6(x, y) = \frac{I_5(x, y) - I_{5,\mu}}{I_{5,max} - I_{5,min}}
\]

where \( I_{5,\mu}, I_{5,max} \) and \( I_{5,min} \) are the mean, maximum and minimum intensity of the image \( I_5(x, y) \) respectively. The adaptive thresholding [5] is then applied on the image \( I_6(x, y) \) to obtain the segmented image \( I_7(x, y) \). The output of level-1 segmentation is not perfect which also includes the blood vessel that lies close to the lesion.

### 3.3 Level-2 Segmentation

The level-2 Segmentation aims to optimize the boundaries of the lesion candidates. It also eliminates the blood vessels that are in contact with the lesion. The level-2 segmentation initially detects the blood vessels on the image \( I_4(x, y) \) using an improved matched filter [2]. The blood vessel region is then considered as a background region and is eliminated from the image \( I_7(x, y) \). This eliminates the blood vessels that lie close to the lesion candidates to obtain the image \( I_8(x, y) \). The segmentation result thus obtained gives the location of lesion candidates. The boundary of the lesion region is optimized (expanded) for feature extraction such that the lesion candidate can fit the \( L \) number of hexagonal layers starting from its center as depicted in Fig. 2a. This can be done by estimating the centroid of the lesion region and forming \( N \) layers of hexagon starting from the center region in a concentric pattern, each
having a perimeter of $T$ pixel points as depicted in Fig. 2b. The hexagons that lie on the boundary points of the lesion candidates should also be used for feature extraction and the lesion candidate region for feature extraction be represented as $I_8$. Figure 2a depicts the optimized region suitable for estimating the hexagonal pattern features.

### 3.4 Hexagonal pattern features

Initially, the lesion candidates are subdivided into smaller hexagonal cells as depicted in Fig. 2a. The mean of the pixels that lie on the boundaries of the hexagonal cells is estimated. Let $J(x, y)$ gives the mean pixel intensity obtained using the boundary pixels of the hexagonal cells estimated in the region $I_8$. Let $P_c$ gives the mean boundary pixel intensity of the centroid cell and $P_{1,j}(x, y)$ represents the mean boundary pixel intensity of the hexagons that surrounds the centroid hexagonal cell (referred to as the first layer hexagonal cells), where $j = 1, 2...6$. The gradient of the first layer hexagonal cells be $G_{1,j}(x, y)$ which is estimated between the first layer mean value $P_{1,j}(x, y)$ and the centroid mean value $P_c$ mathematically expressed as

$$G_{1,j}(x, y) = P_{1,j}(x, y) - P_c$$  \hspace{1cm} (5)

Six different feature is estimated for a hexagonal pattern present in the first layer which is formed by the combination of orientation $\phi_{1,j}$ and the gradient $G_{1,j}(x, y)$. The orientation $\phi_{1,j}$ for the first layer hexagonal cells is depicted in Fig. 3a. The feature in first layer in polar form is expressed as,

$$F_{1,j}(x, y) = G_{1,j}(x, y) e^{i \times \phi_{1,j}}$$  \hspace{1cm} (6)

where $i$ is the imaginary unit. The feature in complex form can be expressed as

$$F_{1,j}(x, y) = G_{1,j}(x, y) \cos \phi_{1,j} + i G_{1,j}(x, y) \sin \phi_{1,j}$$  \hspace{1cm} (7)

Similarly the mean pixel intensity in the second layer be represented as $P_{2,k}(x, y)$, where $k = 1, 2...N_2$ and $N_2$ is the number of cells in second layer. The gradient of the second layer hexagonal cells be $G_{2,k}(x, y)$ is estimated between the second layer hexagonal cells mean value and the first layer hexagonal cells mean value given by

$$G_{2,k}(x, y) = P_{2,k}(x, y) - P_{1,j}(x, y)$$  \hspace{1cm} (8)

For the second layer the feature is estimated concerning the neighboring cells of each hexagonal cell in the first layer. Figure 4b to g depicts the estimation of second layer features where a maximum of 3 neighboring cells can be found concerning a first layer cell. The
Fig. 4 Estimation of Hexagonal pattern feature (a) For rst layer (b)-(g) For second layer (h) Renement for second layer (i) For third layer

orientation of the three neighboring cells is depicted in Fig. 3b. The second layer feature $F_{2,k}(x, y)$ is estimated by the combination of angle $\phi_{2,k}$ and the gradient $G_{2,k}(x, y)$

$$F_{2,k}(x, y) = G_{2,k}(x, y)e^{i \times \phi_{2,k}}$$

(9)
The feature in complex form can be expressed as

\[ F_{2,k}(x, y) = G_{2,k}(x, y) \cos \phi_{2,k} + i G_{2,k}(x, y) \sin \phi_{2,k} \]  

(10)

The hexagonal pattern that has the lowest feature value has a higher weight, while the pattern that has a higher gradient pattern has the least weight. Therefore the first layer has six hexagonal patterns with six different priorities as depicted in Fig. 4a. Using the gradient and orientation between the first layer cell and the cell that corresponds to the second layer, the feature is estimated. The magnitude of the feature at the second layer is given by

\[ F_{2,k}(x, y) = G_{2,k}(x, y) \]  

(11)

Let the features estimated in the second layer be represented as

\[ F_{2,j}(x, y) = \left[ f_{1,1}(x, y), f_{1,2}(x, y), f_{1,3}(x, y), f_{2,1}(x, y), f_{2,2}(x, y), ... f_{6,1}(x, y), f_{6,2}(x, y), f_{6,3}(x, y) \right] \]  

(12)

After the estimation of six cycles of features, few of the features overlap with each other. The overlapped features are refined to a single feature using the (11). Two overlapping features are refined to a single feature based on the weight value, such that the first estimated feature has a weight of 0.75 and the second estimated feature has a weight of 0.25. If \( f_a(x, y) \) and \( f_b(x, y) \) are the first and second estimated (overlapping) features, then the refined feature is given by

\[ f = \frac{3}{4} f_a(x, y) + \frac{1}{4} f_b(x, y) \]  

(13)

Out of 18 features 6 features do not require overlapping (features that correspond to the hexagons that are the first neighbor). The remaining 12 features (that corresponds to the hexagons on the second neighbor) have one overlapping. The two overlapping features \( f_a(x, y) \) and \( f_b(x, y) \) are converted to a single value using the refining process given by (13). From the 18 features, 12 features are estimated after the refinement stage.

Figure 4h depicts the second layer feature estimated after refinement. After the refinement, the value of the feature is sorted, such that the least feature value has the highest priority, while the highest feature value has the least priority. Let the features estimated after refinement in the second layer be \( \hat{F}_2 \). The same procedure is repeated to estimate the third layer, fourth layer feature so on. The number of the hexagonal layer depends on the size of the lesion candidate the feature estimated from a lesion candidate can be represented as

\[ F = [ \hat{F}_{1,j}(x, y), \hat{F}_{2,k}(x, y), ..., \hat{F}_{N,l}(x, y) ] \]  

(14)

Here \( l \) is the number of cells present in the \( N^{th} \) layer and \( N \) be the number of hexagonal layers estimated in the lesion region. Let \( F_T \) be the complete lesion features that are to be trained by the model. Let \( f_T \) be the test lesion feature. The feature \( f_T \) was classified using the recurrent neural network model to obtain the classified result.

### 3.5 Recurrent neural network

In Recurrent neural network (RNN) [34] each node has input from its previous node that has hidden states and outputs. The backpropagation is performed at each time point \( n \). The weights \( w \) and the derivative of the loss function \( L \) for a timestep \( N \) is related by

\[ \frac{\partial L^{(N)}(w)}{\partial w} = \sum_{n=1}^{N} \left| \frac{\partial L^{(N)}(w)}{\partial w} \right|_{(n)} \]  

(15)
In RNN, the computation is performed recurrently as depicted in Fig. 5. The gated RNN present in the neural networks allows to forget the old state. This gated RNN consists of LSTM and the gated recurrent unit. The input at time step be $x_n$ and the output ($z_n$) and hidden states ($s_n$) are expressed as

$$z_n = g(v_o + w_os_n)$$  

$$s_n = g(w_s s_{n-1} + \hat{w}_s x_n + v_s)$$

Here $s_n$ represents the hidden state in the time step $n$, $g$ represents the activation function used throughout the model and $v_s$ is the bias. The weights of the hidden layers are $w_s$ and $\hat{w}_s$. The hidden state is updated recursively on each time step $n$. The Long short-term memory (LSTM) of the RNN has a cell $e_n$ that acts as a memory unit. A sigmoid function is used to control the read and write operation of the cell. The hexagonal pattern features $FT$ that is extracted from each lesion candidate is trained using the RNN model. During the classification process, the features detected from the red lesion candidates $f_t$ of the test images are applied to the trained RNN model to eliminate the false negatives. The experimental evaluation of the algorithm is depicted in the succeeding section.

4 Experimental results

The performance of the proposed lesion detection approach was evaluated using four different datasets namely ROC, e-ophtha, DiaretDB1, and MESSIDOR where a few of the sample images are depicted in Fig. 6.

4.1 Datasets

The ROC dataset (retinopathy online challenge dataset) has 37 color images with signs of microaneurysms which was validated by four experts. The e-ophtha has 381 fundus images where 233 images are healthy and 148 images have the signs of microaneurysms. The DiaretDB1 dataset consists of 89 color fundus images which were captured with a $50^\circ$ field of view. Out of 89 images, 5 images are found to be healthy images and 84 images have the signs of microaneurysms. A color 3CCD camera is used to acquire the fundus image of the
Messidor dataset with a FOV (field of view) of 45°. This dataset contains 1200 images having three different resolutions as depicted in the Table 1. Out of 1200 images, 800 images were acquired with pupil dilation, and the remaining 400 images are acquired without pupil dilation.

4.2 Analysis

The validation was done with the metrics such as Accuracy, Recall (sensitivity), precision, F1 score, specificity, ROC (receiver operating characteristic curve), and AUC. The 60% of images present in the dataset was applied for training and the remaining 40% is applied for validation. The training and validation images used are selected randomly. The hexagonal pattern feature extraction algorithm uses a perimeter pixel of 3. The Accuracy, Recall
Fig. 7 Experimental output for different test images (a) ROC dataset (b) e-ophtha (c) DiaretDB1 dataset (d) Messidor dataset (input fundus image, Preprocessed image, output of Adaptive contrast equalization, Detection of blood vessels, Eliminated vessel regions, red lesion candidates, Hexagonal pattern feature extraction, Classification result)
(sensitivity), precision, F1 score, and specificity can be calculated using the relation

\[
\text{Accuracy} = \frac{T_n + T_p}{T_n + F_n + T_p + F_p} \times 100
\]

(18)

\[
\text{Recall} = \frac{T_p}{F_n + T_p} \times 100
\]

(19)

\[
\text{Precision} = \frac{T_p}{F_p + T_p} \times 100
\]

(20)

\[
F1 \text{score} = 2 \times \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}} \times 100
\]

(21)

\[
\text{specificity} = \frac{T_n}{T_n + F_p} \times 100
\]

(22)

where \(F_n\), \(F_p\), \(T_p\) and \(T_n\) represents the false negatives, false positives, true positives and true negatives respectively. Here the number of \(F_n\), \(F_p\), \(T_p\) and \(T_n\) does not represent the number of images that are classified as lesion or normal. Instead it represent the number of lesion or other regions classified from the lesion candidate regions. Figure 7 depicts the experimental output from different datasets.

To prevent the RNN from overtraining, a stopping criterion is used in the training process. The training is stopped before the maximum number of epochs if the modeling error is less than the threshold (0.01). The latent space dimension of RNN is set as 128; the size of minibatch size to 32. The RNN uses filters with a spatial dimension of \(5 \times 5\). For each class, an independent MLP is learned using 32 hidden neurons and rectified linear activations. The base learning rate is 0.01 and the model is trained with a maximum of 10,000 iterations. Fig. 8 shows the confusion matrices obtained for the different datasets. The MESSIDOR dataset has more lesion candidates than other datasets. Here the classification was done with the lesion candidates. The total number of lesion candidates that were validated is indicated on the left corner of the confusion matrices. Table 2 depicts the comparison of accuracy, recall, precision, F1 score, specificity, and AUC for the four different datasets. The accuracy is maximum for the ROC dataset while it is minimum for DiaretDB1. The accuracy of ROC and DiaretDB1 datasets are estimated as 95.73% and 95.15% respectively. The proposed algorithm provides a maximum recall, precision, F1 score, Specificity, and AUC of 85.85%, 97.5%, 91.29%, 88.73% and 94.13% respectively for the datasets e-ophtha, MESSIDOR, e-ophtha, ROC, and Messidor. The graphical comparison of the performance metrics on different datasets is shown in Fig. 9. The proposed method was also validated using K-cross fold validation with \(K = 10\) using the complete images present in each dataset. The results obtained for K-fold cross validation is depicted in Table 3. There is only a small increase in accuracy when evaluated using K-fold validation. With 10-fold cross validation the scheme provides a average accuracy of 95.66% (Table 4).

![Fig. 8](image-url) Confusion matrix obtained for different dataset (a) ROC dataset (b) e-ophtha (c) DiaretDB1 (d) MESSIDOR
Table 2  Performance comparison for different dataset

| Datasets   | Accuracy (%) | Recall (%) | Precision (%) | F1 score (%) | Specificity (%) | AUC (%) |
|------------|--------------|------------|---------------|--------------|-----------------|---------|
| ROC        | 95.73        | 82.45      | 97.36         | 89.29        | 88.73           | 93.2    |
| e-ophtha   | 95.44        | 85.85      | 97.47         | 91.29        | 86.43           | 93.8    |
| DiaretDB1  | 95.15        | 84.13      | 96.89         | 90.06        | 85.48           | 92.6    |
| MESSIDOR   | 95.6         | 85.76      | 97.5          | 91.25        | 86.61           | 94.13   |
| Average    | 95.48        | 84.55      | 97.31         | 90.47        | 86.81           | 93.43   |

Fig. 9  Performance comparison for different dataset

Table 3  Performance result with 10-fold cross validation

| Datasets   | Accuracy (%) | Recall (%) | Precision (%) | F1 score (%) | Specificity (%) |
|------------|--------------|------------|---------------|--------------|-----------------|
| ROC        | 95.93        | 82.47      | 97.45         | 90.17        | 88.93           |
| e-ophtha   | 95.51        | 86.12      | 97.52         | 91.45        | 87.21           |
| DiaretDB1  | 95.46        | 84.89      | 96.91         | 90.51        | 86.13           |
| MESSIDOR   | 95.72        | 85.98      | 97.61         | 91.42        | 86.87           |
| Average    | 95.66        | 84.87      | 97.37         | 90.89        | 87.29           |

Table 4  Comparison of proposed scheme with other traditional schemes

| Scheme             | Accuracy (%) | Recall (%) | Precision (%) | F1 score (%) | Specificity (%) | AUC (%) |
|--------------------|--------------|------------|---------------|--------------|-----------------|---------|
| GVA (2016)         | 86.98        | 77.88      | 91.21         | 90.28        | 80.3            | 88.96   |
| Sparse PCA (2017)  | 89.53        | 77.59      | 90.76         | 81.87        | 78.22           | 86.02   |
| LCI features (2018)| 92.09        | 82.08      | 91.51         | 85.62        | 78.9            | 89.85   |
| Two Step CNN (2019)| 92.66        | 80.64      | 91.75         | 89.49        | 80.82           | 91.89   |
| DLC (2020)         | 93.31        | 81.08      | 95.54         | 88.07        | 82.75           | 92.94   |
| CLD (2021)         | 94.14        | 83.67      | 96.68         | 91.23        | 85.26           | 91.04   |
| Proposed           | 95.48        | 85.54      | 97.3          | 90.47        | 86.81           | 93.43   |
| Proposed (K-fold validation) | 95.66 | 84.87 | 97.37 | 90.89 | 87.29 | 93.67 |
The performance of the proposed scheme was compared with the traditional schemes such as GVA [7], Sparse PCA [37], LCI features [9], Two-step CNN [10], DLC [21] and CLD [31]. The F1 Score of the proposed scheme is 90.47% which is less than the scheme CLD. However, the accuracy, recall, precision, specificity, and AUC of the proposed scheme are higher than the traditional schemes. The proposed scheme provides an average accuracy, recall, precision, specificity, and AUC of 95.48%, 84.54%, 97.3%, 86.81%, and 93.43% respectively as depicted in Table 3. Figure 10 depicts the comparison of the ROC curve for the different schemes with a different dataset. The area under the ROC curve for the proposed scheme is higher than other schemes. The graphical comparison of performance metrics for the different schemes is shown in Fig. 11.

The time complexity of the proposed method was evaluated using the training time and Classification time. The training time includes the time of pre-processing, level 1 segmentation, Level-2 segmentation, feature extraction, and training the RNN network. The evaluation was done on MATLAB 2018 on 64 bit Windows 10 operating system with Intel Core i3, 1.9 gigahertz (GHz) processor with 8 gigabytes (GB) of RAM. Table 5 shows the comparison of time complexity comparison of the proposed method for different datasets in terms of training time and classification time. The training time of the ROC, e-ophtha, DiaretDB1, and Messidor was estimated as 57.26s, 193.648s, 53.352s, and 1720.64s.

Fig. 10 ROC curve for different datasets (a) ROC dataset (b) e-ophtha (c) DiaretDB1 dataset (d) Messidor dataset
Graphical comparison of proposed method with the other works

Table 5: Time complexity comparison of proposed method on different datasets

| Time (Seconds) | ROC  | e-ophtha | DiaretDB1 | Messidor |
|----------------|------|----------|-----------|----------|
| Training time  | 57.26| 193.648  | 53.352    | 1720.64  |
| Classification time | 0.0123 | 0.0227 | 0.0124 | 0.0913 |

Table 6: Comparison of RNN model in proposed algorithm with other models

| Classifier | Accuracy (%) | Recall (%) | Precision (%) | F1-score (%) | Specificity (%) |
|------------|--------------|------------|---------------|--------------|-----------------|
| CNN        | 91.26        | 79.34      | 92.36         | 83.48        | 79.02           |
| 2D-CNN     | 93.17        | 82.36      | 94.71         | 86.14        | 82.07           |
| LSTM       | 92.32        | 80.41      | 93.52         | 84.92        | 81.58           |
| BiLSTM     | 94.2         | 83.07      | 95.98         | 86.91        | 84.17           |
| RNN        | 95.48        | 84.54      | 97.30         | 90.47        | 86.81           |
Table 7  Accuracy in % for paired t-test

| Data     | ROC     | e-ophtha | DiaretDB1 | Messidor |
|----------|---------|----------|-----------|----------|
| Set A    | 95.82   | 95.53    | 95.28     | 95.56    |
| Set B    | 95.76   | 95.81    | 95.63     | 95.97    |

respectively. The time required for detecting the red lesion candidate in fundus image for the datasets ROC, e-ophtha, DiaretDB1, and Messidor were estimated as 0.0123s, 0.0227s, 0.0124s, and 0.0913s respectively. Instead of using the proposed RNN classifier the proposed system was replaced by other classifiers namely CNN [12], 2D-CNN [32], LSTM [4] and Bi-LSTM [17] (Bidirectional-LSTM). Table 6 shows the performance comparison of the proposed method with the RNN model and other models. The proposed method with RNN classifier provide a maximum accuracy than the other models like CNN, 2D-CNN, LSTM, and Bi-LSTM. Usage of RNN shows a 1.28% improvement in accuracy than the Bi-LSTM model.

The test data is equally divided into two sets represented as set-A, and set-B respectively for performing paired T-test. Let the accuracy estimated on two sets be $X_{a,i}$ and $X_{b,i}$ respectively. The difference between $X_{a,i}$ and $X_{b,i}$ is expressed as $d_i = X_{a,i} - X_{b,i}$. The paired t-test is to determine whether the accuracy obtained by the proposed model on set-A, and set-B is statistically significant, Hence the hypothesis to be tested are $H_0 = \mu_D > 0$ versus $H_1 = \mu_D < 0$. The mean, standard deviation and $t_0$ can be estimated using the relations,

$$m = \frac{1}{N_s} \sum_{i=1}^{N_s} d_i = -0.245$$ (23)

$$s_d = \sqrt{\frac{1}{N_s - 1} \sum_{i=1}^{N_s} (d_i - m)^2} = 0.2101$$ (24)

$$t_0 = \frac{m \sqrt{N_s}}{s_d} = -2.331$$ (25)

The $t_0$ value is thus estimated as $t_0 = -2.331$ and the accuracies obtained for the two sets are depicted in Table 7. Due to the presence of preprocessing, lesion candidate segmentation, and the iterative approach of hexagonal feature extraction the training time is high which can be still reduced by developing a fast hexagonal feature extraction algorithm.

5 Conclusion and future work

This paper proposed a Hexagonal pattern feature extraction algorithm with two-level segmentation that can detect the microaneurysms and hemorrhage present in the fundus image. The algorithm uses a two-level segmentation, where the first level extracts the red lesion regions and the second level removes the blood vessels that connect the red lesion candidates. Hexagonal pattern features are extracted from the red lesion candidates that best differentiate the red lesion from others. The Hexagonal pattern features are extracted in a concentric pattern that assigns priority for the hexagonal cells. Finally, a classifier is used to classify the red lesion from the false positives. The evaluation was done using the datasets namely, ROC challenge dataset, e-ophtha, DiaretDB1, and Messidor datasets. The scheme provides accuracy, recall, precision, F1 score, Specificity, and AUC of 95.48%,
84.54%, 97.3%, 90.47%, 86.81% and 93.43% respectively. In the future, the algorithm can be deployed with a novel classifiers, that can further improve the performance in red lesion detection.

Authorship Contributions

Latha D: Methodology, Validation
Beula Bell T: Programming
Jaspin Jeba Sheela C: Editing

Declarations

Ethics approval  This article does not contain any studies with human participants or animals performed by any of the authors.

Informed consent  Informed consent was obtained from all individual participants included in the study.

Conflict of Interests  We declare that we have no conflict of interest.

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