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A new segmentation method for retinal pathologies detection in optical coherence tomography images

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Abstract: Diabetic macular oedema (DME) and age-related macular degeneration (AMD) are the leading causes of blindness in adults. The most significant signs of these diseases are appearance of exudates and change of retinal layer structure. Screening of these diseases is very important to prevent vision loss. In this work, a new method based on a genetic k-means algorithm for lesions detection is proposed. From the selected region of interest (ROI), four textural features are extracted and used to classify these two retinal diseases against the normal subjects using the SD-OCT images. From the experimental results found, the SVM gives better results for AMD and DME recognition. The mean accuracy, sensitivity and specificity values for the macular region's classification are 99.67%, 100% and 99.51% respectively.

Keywords: OCT images; age-related macular degeneration; AMD; diabetic macular oedema; DME; features extraction; classification; genetic algorithms.

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1 Introduction

AMD is an eye disease known by a progressive loss of central vision; it results from macular deterioration. AMD is the leading cause of low vision in the elderly since it affects nearly 10% of 65–75 years old and 25% to 30% of those over 75 years old (https://www.sante-sur-le-net.com/maladies/ophtalmologie/dmla/). There are usually two forms of AMD, dry AMD and wet AMD. The dry AMD is the less serious and most frequent (approximately 90% of cases). But, the second form is rarer but most often appears suddenly and progresses much faster (Ferris et al., 1984).

DME is a diabetic retinopathy complication. Macular oedema affects 5% to 10% of diabetic patients (Ferris et al., 1984) and causes the visual impairment of these patients. It is result of an increase in vascular permeability which leads to an accumulation of fluid as well as a deposition of a protein in the macula followed by swelling and damage of the retina.

Compared to fundus photography, optical coherence tomography (OCT) provides detailed information on the retina anatomy with high resolution. The OCT technology has given considerable improvements in the understanding of the pathophysiology of certain diseases and has enabled clinicians to characterise the disease state (Zhang et al., 2008). The ophthalmologists face several major problems such as the workload where they must treat dozens or more patients. For this purpose, the automatic screening for retinopathies can be very useful and effective, which facilitates clinical decisions and will greatly contribute to the early detection of the disease and to the preservation of vision.

In the literature, many approaches have been proposed to identify different macular disorders. Using OCT images, some groups of researchers have developed software algorithms classifying patients into various diseases or normal. Alsaih et al. (2016) proposed an automatic detection method of DME on OCT volumes. A set of different feature vectors was created using the histogram of oriented gradients (HOG) combined with local binary patterns (LBP) which are fed to a linear-SVM Classifier. Their results in term of sensitivity and specificity are 75% and 87% respectively. Sankar et al. (2016) based on the appearance modelling of normal OCT images, a semi-supervised strategy was used to classify DME vs. normal OCT volumes by using Gaussian Mixture Model (GMM). Both intensity and LBP features are employed. Their found results are SE and SP of 93.8% and 80.0% respectively. For AMD detection, Albarrak et al. (2013) propose a Bayesian network classifier using the LBP-TOP and HOG characteristics combined with LBP-TOP. Their performance results in terms of SE and SP reached 92.4% and 90.5% respectively. Otherwise, there are other studies are focused on the multi classification, i.e., the classification of AMD, DME and normal cases (three classes). Yu et al. (2016) proposed a computer-aided diagnosis (CAD) model to discriminate AMD, DME and healthy macula. Using the correlation-based feature subset (CFS) selection algorithm, the linear configuration pattern (LCP) based features were screened. They reached an accuracy of 99.3% using the sequential minimal optimisation (SMO)

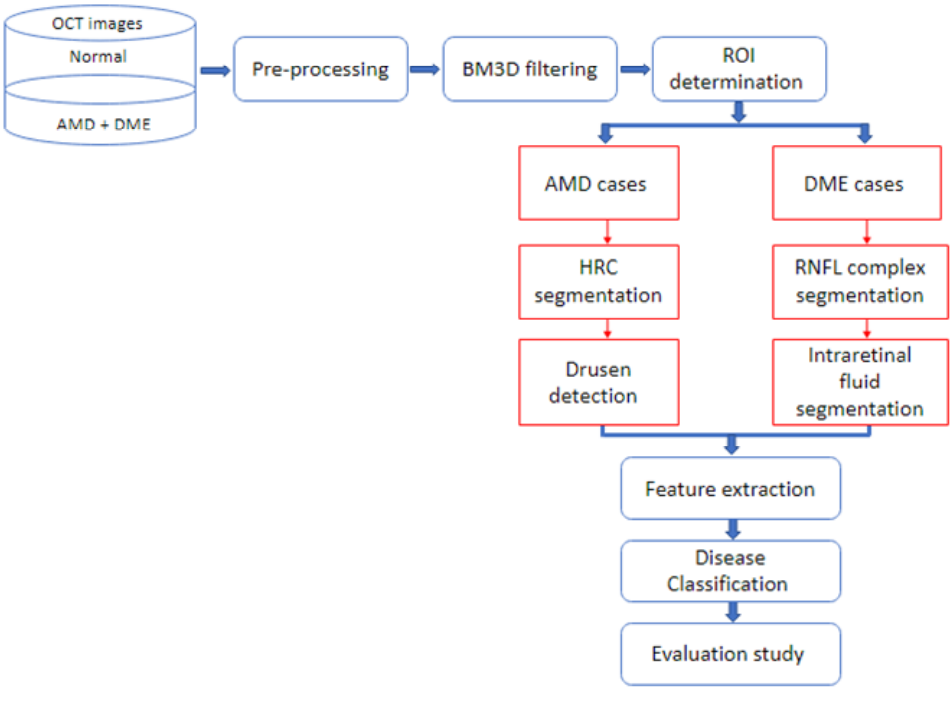
algorithm. Using HOG descriptor and SVMs, in Srinivasan et al. (2014), have reported an accuracy of 97.78%for the AMD and DME identification.

The majority of these mentioned methods use feature extraction techniques in the characterisation step, which increases the computation time and complicates the classification algorithms. Therefore, we propose a new automatic image analysis approach for quantitative assessment of AMD, DME and healthy OCT images. The proposed approach includes two fundamental steps: in the first step, the genetic K-means algorithm, is used to detect automatically the site of these pathologies. Its main advantage is that it is a simple and fast algorithm. Then in the second step, different classifiers are used in order to perform a comparative study, using the meaningful extracted features. Our results are very interested in the classification of three cases.

1.1 Material used

The SD-OCT images used in this work have been collected from (http://people.duke.edu/~sf59/Srinivasan_BOE_2014_Dataset.htm). This database contains multiple scans of SD-OCT images obtained from 15 normal patients, 15 AMD patients and 15 DME patients (Srinivasan et al., 2014). In this work, 200 images of AMD, DME patients and 100 images of normal patients with varying degrees of disease have been used.

Figure 1 Block diagram of the proposed method (see online version for colours)



2 Experimental method

A block diagram of the main steps involved in the proposed method is presented in Figure 1. An automatic denoising step is performed based on a filtering model using a block matching and 3D filtering (BM3D) algorithm. In the second step, the ROI detection and feature extraction. A new automatic segmentation approach is performed using the genetic K-means algorithm. The resulting ROI are used for extracting statistical features. These features are used for macular characterisation in the subsequent evaluation approach. In the last, a classification step in order to separate subjects into three classes (AMD, DME and normal).

2.1 Preprocessing

All OCT images are generally affected by speckle noise (Sudeep et al., 2016) that inherently exists and degrades the images quality which makes retinal images analysis a hard task. Since this process is strongly dependent on the image quality, a pre-processing step is required for quality enhancement and equalisation of the OCT images. In the literature, several categories of methods have been explored for image denoising (Dabov et al., 2007; Hassouni et al., 2006; Rital et al., 2002). In this paper, a BM3D algorithm is applied as a solution to reduce speckle noise in OCT images (https://webpages.tuni.fi/foi/GCF-BM3D/). BM3D is a collaborative filtering process presented in Figure 2. Firstly, a group of similar blocks are extracted from the image. All blocks in a group are then stacked together to form 3D cylinder-like shapes. Then, filtering is done on every block group. Linear transform is applied followed by Wiener filtering, then transform is inverted to reproduce all filtered blocks. Eventually the image is transformed back into its 2D form. So, we can basically look at the denoised image as shown in Figure 3.

Figure 2 Explanatory diagram of the block matching 3D filtering (see online version for colours)

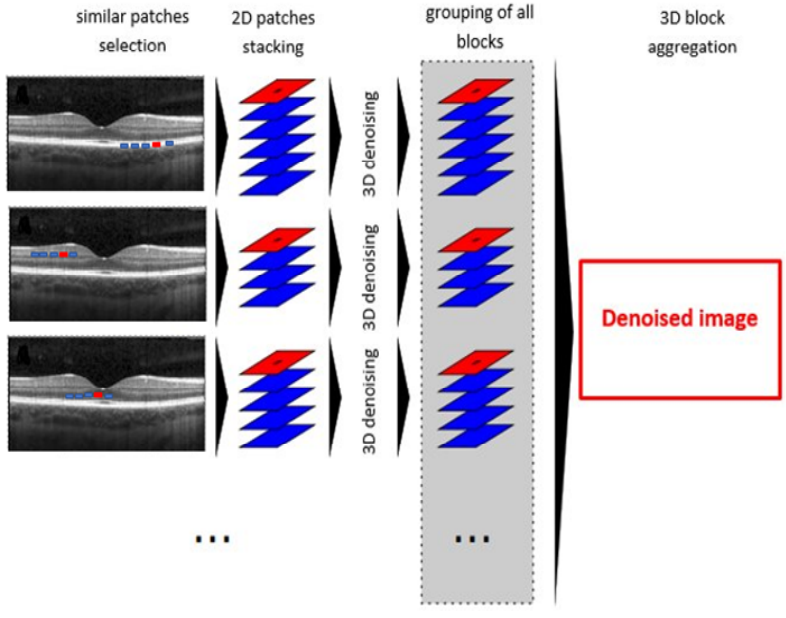
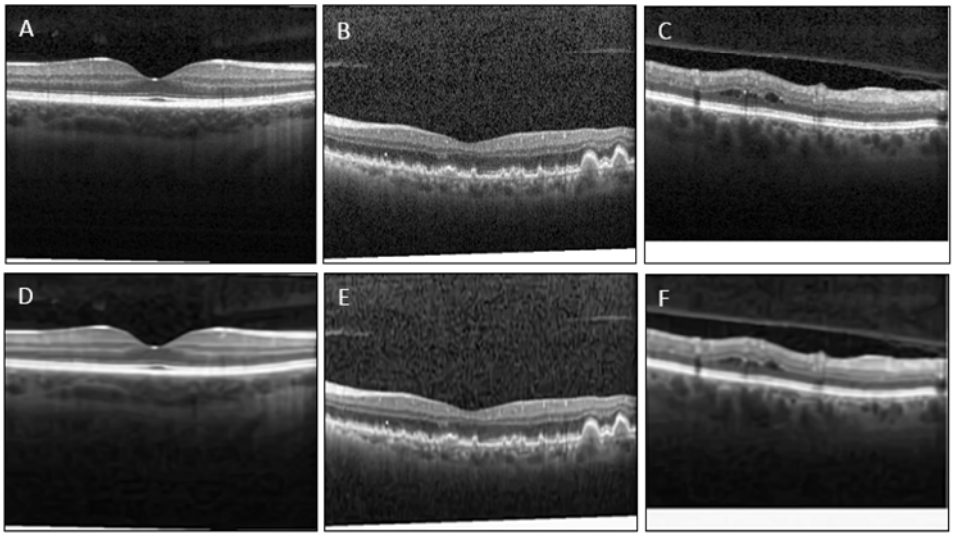


Figure 3 Oct images filtering, (a) the original healthy image (b) the original AMD image (c) the original DME image (d) the filtered healthy image (e) the filtered AMD image (f) the filtered DME image



2.2 ROI selection

In this phase, we aim to identify the meaningful and important regions in the images where the primary signs of diseases are localised. These structures are very helpful in the AMD and DME screening.

2.2.1 Hyper reflective complex (HRC) segmentation

At an early stage, AMD is characterised by an accumulation of an asymptomatic and amorphous extra cellular material, called drusen. Drusen are focal yellowish-white deposits located between RPE and the inner collagenous zone of Bruch's membrane. The RPE layer fused with the Bruch's membrane and choriocapillaris is formed a complex named as the hyper-reflective complex (HRC). It is about the high intensity image band above the choroid. Therefore, the ROI for AMD images is determined by extracting the HRC layer, since most of the symptoms appear at the level of this complex.

2.2.2 Retinal nerve fibres layers (RNFL) complex segmentation

Macular oedema is the accumulation of fluid in the macula causing it to thicken. It occurs when the blood retinal barrier is ruptured. Leaking blood passes the RPE layer and the internal photoreceptor (IS/OS) segment of the choroid in the RNFL complex. In OCT images, the oedema is considered as a hypo-reflective in the outer plexiform layer (OPL) and inter nuclear layer (INL) with multiple intra retinal cystoids and sub retinal fluid, it looks like a spongy form. In this case, the ROI is determined by identifying the RNFL complex that fused five distinct layers such as: OPL, INL, inner plexiform layer (IPL), ganglion cell layer (GCC) and RNFL layer. At this level, the fluid bubbles are concentrated which represent the signs of diabetic maculopathy and caused the oedema.

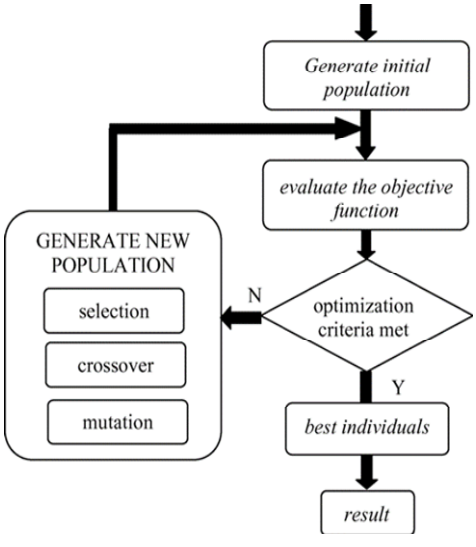
According to the definition of the HRC band and RNFL complex in the OCT images, there are several methods in the image processing domain that can be used to select the right ROI. The most popular and simplest are that based on data clustering, like k-means, Fuzzy c-means, Hierarchical clustering algorithm…, etc.

K-means is an unsupervised non-hierarchical clustering algorithm. It allows observations in the dataset to be grouped into K distinct groups based on the feature similarity. Thus, similar data will be found in the same cluster. K-means is an iterative algorithm which minimises the sum of the distances between each individual and the centroid. Although k-means is a simple and scalable method with the ability to process very large databases, but it suffers from some drawback such as:

- K-means algorithm is time consuming, because it needs to pass observations several times
- optimisation can result in a local minimum of intra-class inertia. Therefore, for the same dataset, we can have different partitions
- the solution depends on the initial choice of class centres
- the number of clusters needs to set beforehand.

To override the above limitations, the traditional K-means clustering algorithm is optimised using genetic algorithm (GA). Using this technique, we can easily select the right ROI without errors.

Figure 4 Block diagram of the GA



Source: Aydogan et al. (2005)

2.3 GA-based clustering

2.3.1 Genetic algorithms

GAs belongs to the family of evolutionary algorithms. Their main goal is to obtain an approximate solution to an optimisation problem, when there is no exact method (or the solution is unknown) to solve it within a reasonable time, using techniques inspired by natural evolution and genetics. The search space parameters are encoded as strings (called chromosomes). A collection of these strings is called a population. To solve an optimisation problem, GAs use a fixed population size. A solution consists of a string of binary symbol. The fittest members of this population are more likely to mate and produce the next generation. Over the generations, members of the population come closer and closer to the solution. The principal outline of GA is represented in Figure 4.

2.3.2 Genetic K-means clustering

The principle of the genetic k-means clustering algorithm is based on the following main genetic operators:

Initialisation	The data objects behave as candidates for the centre cluster.
Fitness computation	The main object of this step is to evaluate all the instances in order to compute the fitness value using the objective (fitness) function provided by the system.
Selection	On the basis of Charles Darwin's principle 'survival of fittest', the selection process is used to achieve the optimal solution giving preference to chromosome with high fitness (Angeline, 1998).
Crossover	This phase is a probabilistic process that exchanges information between two parent chromosomes to generate two child chromosomes (Season, 2005).
Mutation	The mutation process normally changes the structure of chromosomes, cancelling out a randomly chosen bit (https://github.com/KendallPark/genetic-algorithm).
K-mean operator	Over the generations, the final result represents the fittest chromosome which is selected in this case as the centroid of the further k-means clustering.

After the application of the different steps of this algorithm the result of region selection for both normal and abnormal sets are represented in Figure 5.

Figure 5 ROI selection final results, (a) HRC complex extraction in healthy image (b) Drusen detection in AMD image (c) intra retinal fluid segmentation in DME image (d) HRC complex superimposed on the original image (e) Drusen result superimposed on the AMD image (f) intra retinal fluid segmentation result superimposed on the DME image (see online version for colours)

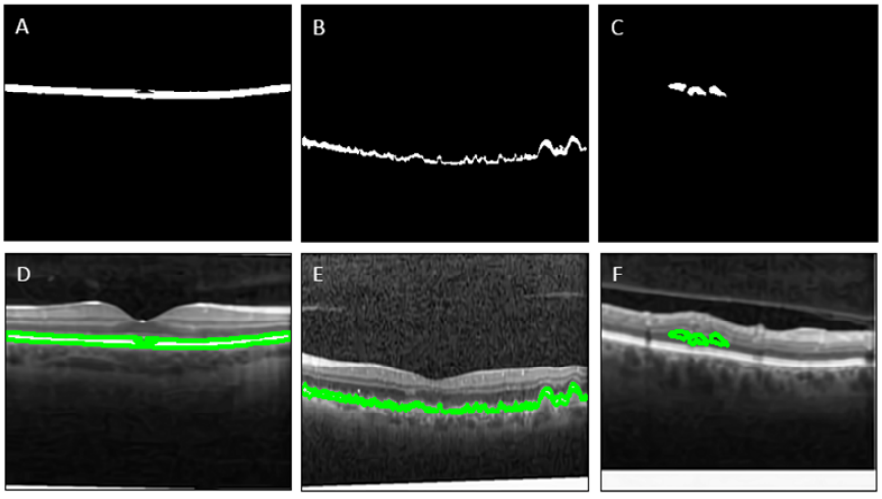


Table 1 Textural feature equations

Eq. no.	*Equations*
1	$contrast = \sum_{i=0}^{M-1}\sum_{j=0}^{N-1}\lvert i-j\rvert^2 p(i,j)$
2	$Energy = \sum_{i=0}^{M-1}\sum_{j=0}^{N-1} p(i,j)^2$
3	$Correlation = \frac{\sum_{i=0}^{M-1}\sum_{j=0}^{N-1}(ij)\,p(i,j) - \mu_x\mu_y}{\sigma_x\sigma_y}$
4	$Homogeneity = \sum_{i=0}^{M-1}\sum_{j=0}^{N-1}\frac{p(i,j)}{1+(i-j)^2}$

Notes: p (i, j) is the normalised co-occurrence matrix coefficients; μ_x and μ_y are the mean of p_x and p_y, respectively; σ_x and σ_y are the standard deviation of p_x and p_y respectively.

2.4 Features extraction and classification

The features of Haralick (Robert et al., 1973) have been widely used in many image analysis applications such as medical image segmentation. In this work, the co-occurrence matrices are calculated from all the ROI images preprocessed to extract four textural characteristics, namely: contrast, energy, correlation, homogeneity. We chose to work with textural characteristics that because of the effects of AMD and DME on the

retinal layer reflectivity. The early stage of dry AMD is characterised by changes in the macula pigment. And for DME is presented as a hypo-reflective in the inner retinal layers. The characteristics are expressed by the following equations successively.

Using the selected features, the images classification is done by various classifiers like SVM (Demirkesen and Cherifi, 2008), K-nearest neighbour (KNN) (Rao and Basavaraj, 2018), decision trees (DT) (Saxena et al., 2019), Naïve Bayes (NB) (Zhang, 2004) and discriminant analysis (DA) (Jia et al., 2019). The goal is to perform a comparison study between these classifiers to find the most accurate to identify AMD and DME pathology.

2.5 Performance evaluation

In order to significantly clarify our experiences, a common performance is evidently established. From each ROI image a set of four textural features are extracted. Since we have a limited number of datasets, cross-validation is an important step in evaluating performance. The features are given to classifier and tested by a 10-fold cross-validation technique. The feature set is split into ten equal-sized subsets. Using k−1 of the folds as training data, the classifier is trained. The resulting model is validated the on the rest part of the data. This process is repeatedly done ten times by taking each subset for testing once. The final result is obtained by averaging the results of all the ten evaluations.

Table 2 Classifier performance index equations

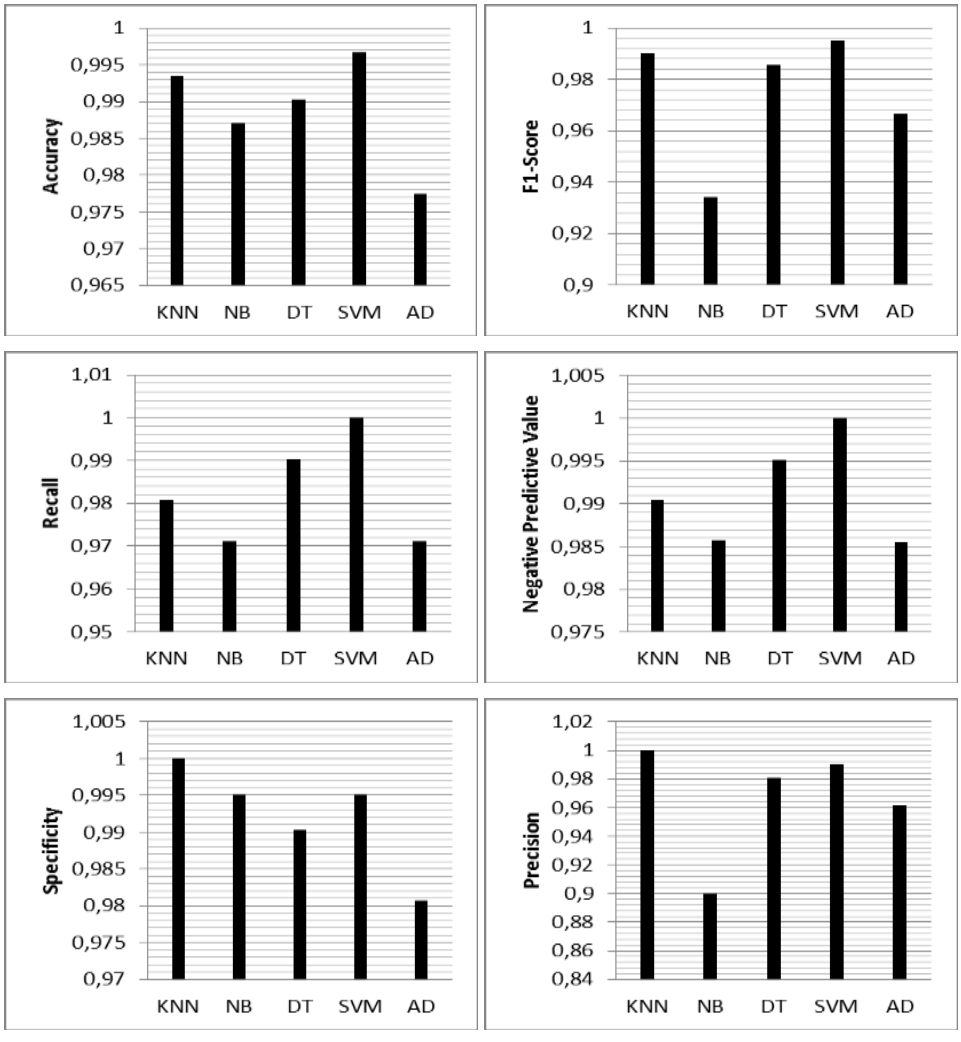
Eq. no.	*Equations*	*Definition*
5	$Acc = \frac{TP + TN}{(TP + TN + FP + FN)} \times 100$	This metric simply indicates the percentage of correct
6	$PPV = \frac{TP}{(FP + TP)} \times 100$	This metric means the probability that patients with a positive screening test really have the disease.
7	$NPV = \frac{TN}{(FN + TN)} \times 100$	This parameter represents the probability that patients with a negative screening test do not really have the disease.
8	$Sen = \frac{TP}{(TP + FN)} \times 100$	This metric represents the rate of true positives. It is the index that assesses a classifier's ability to correctly classify abnormal cases.
9	$Spe = \frac{TN}{(TN + FP)} \times 100$	It is the index that assesses the ability to correctly classify normal cases.
10	$F1 - Score = \frac{2 * TP}{(2 * TP + FP + FN)} \times 100$	The F1 score reflects the balance between precision and recall of a classifier. It is useful for measuring the precision and robustness of the classifier.

A confusion matrix is a tool for measuring the performance of a machine learning model by checking in particular how often its predictions are accurate compared to reality in classification problems (Hussain et al., 2018). The matrix indicates the number of correct and incorrect predictions for each class organised according to the predicted class. Each row in the table corresponds to a predicted class, and each column corresponds to an actual class. Four types of classification results are generally provided by the confusion

matrix including: true-negative (TP), true-positive (TN), false-positive (FP) and false-negative (FN).

From these four outcomes, a quantitative evaluation of the classifier performance is carried out using six indexes, namely, accuracy (Acc), sensitivity (Sen), specificity (Spe), positive predictive value (PPV), negative predictive value (NPV), and F1-Score. They are defined as follows:

Figure 6 Histogram of performance metrics evolution for the different classifiers



3 Results and discussion

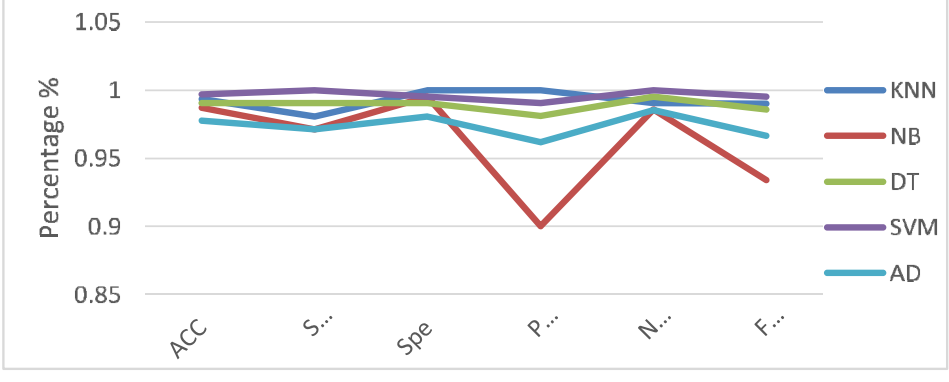
The performance of our method is that it helps to overcome all the limits of the traditional clustering method (K-means) and it allow to detect exactly the site of the pathology. The

extracted HRC and RNFL complex images is then used to extract the features needed to classify pathological and normal images using different types of classifiers to determine the most efficient method by performing a comparative study based on the evaluation parameters mentioned previously. The performance parameters mentioned above are computed for both of healthy and pathology 2D OCT images and represented in the following histograms.

The obtained results are very important in confirming that the extracted features are the most qualified to perform a classification study. As indicated in the histograms, the five used classifiers achieved a good result until it reached 100%. And this is what confirms also that using the genetic K-means algorithm is the appropriate method for feature extraction. Thus, we can conclude that our algorithm is a reliable and applicable method to identify the right ROI from OCT images.

In order to compare the relative performance of different classifiers, the following curve (Figure 7.) is represented. The comparative study is carried out based on accuracy, specificity and sensitivity, as they are considered to be the most significant parameters of medical probability. We notice that there is not a big difference between the results obtained by the two classifiers SVM and KNN; however, the SVM classifier gave better performance compared to the KNN classifier. In the term of accuracy, SVM accurate 99.67% followed by KNN with 99.35%. SVM still remain the powerful classifier in term of sensitivity with 100% compared with KNN (98.07). And SVM show also a very high result in term of NPV is which is equal to 100%. These results indicate that the SVM classifier has a very good ability to correctly predict abnormal images and confirm that the patient does not really have the pathology. An important observation about KNN is that it has 100% specificity. So, it can contribute in the prediction of the normal cases. This demonstrates the effectiveness of the proposed scheme that can be helpful for the doctors in the process of ophthalmologic diagnosis.

Figure 7 Curve representation for comparison of classifiers performance (see online version for colours)



Additionally, the advantage of the proposed approach is highlighted by comparing its performance against the existing models that used the same dataset, as shown in Table 3. Our proposed method achieves the highest value for all the evaluation metrics using the different classifiers. This analysis clearly demonstrates the promise of the developed approach for the classification of AMD, DME, and healthy OCT images.

Table 3 Comparison with the existing studies

Classifier used	*Authors*	*ACC%*	*Se%*	*Sp%*	*PPV%*	*NPV%*	*F1–score*
NB	Other (Yu et al., 2016)	95.70	95.70	97.40	–	–	–
	Other (Hussain et al., 2018)	91.11	–	–	–	–	–
	Our approach	*98.72*	*97.11*	*99.51*	*90.01*	*98.57*	*93.42*
SVM	Other (Yu et al., 2016)	93.30	93.30	96.30	–	–	–
	Other (Hussain et al., 2018)	87.56	–	–	–	–	–
	Our approach	*99.67*	*100*	*99.51*	*99.04*	*100*	*99.52*
DT	Other (Hussain et al., 2018)	93.56	–	–	–	–	–
	Our approach	*99.03*	*99.03*	*99.03*	*98.09*	*99.51*	*98.56*

4 Conclusions

One of the most effective ways to prevent the spread of DME and AMD is the early detection of their clinical signs by analysing OCT images. The development of methods for lesions detection linked to these two diseases was one of the main objectives of this paper to aid in the diagnosis and screening of DME and AMD. It is about blood bubbles area in RNFL complex and drusen in HRC complex respectively. To reach this goal, a new method based on the genetic K-means algorithm is proposed. Extraction of textural features followed by a classification process based on different machine learning algorithm has been performed on a benchmark dataset. The experimental results prove that the SVM is very efficient compared to the other approaches studied in view of its accuracy (99.67%), sensitivity (100%) and specificity (99.51%). These percentages express the capacity of the method to detect diseases in their early stages. The results obtained are very encouraging, they have the potential to help prevent vision loss and blindness in patients with diabetes and age-related macular degeneration. This work can make interesting contributions if used for the development of an OCT application.

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