Ensemble Disease Learning Algorithm (EDL) for Retinal Diseases Detection

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Abstract
Retinal diseases pose a significant threat to global eye health and require accurate and efficient diagnosis for effective treatment. Fundus images, obtained through non-invasive methods like fundus photography, provide valuable insights into the condition of the retina. In this study, fundus images are used to automatically detect and classify retinal illnesses using an Ensemble Disease Learning Algorithm (EDL). The EDL increases the robustness and accuracy of illness diagnosis by combining the predictive capability of several base classifiers. The diverse feature extraction techniques capture various aspects of retinal pathology, including optic disc morphology, blood vessel abnormalities, and lesion characteristics. These features are used to train a collection of base classifiers, such as Capsule Networks (CapsNets) for disease detection and disease classification using support vector machines (SVM). To create a robust ensemble approach, a weighted voting strategy that combines the decisions of individual base classifiers. The weights are determined through cross-validation and are adjusted to maximize overall accuracy. The proposed EDL algorithm enhances diagnostic accuracy and increases generalization by reducing the risk of overfitting. EDL on a comprehensive dataset comprising fundus images with various retinal diseases, including diabetic retinopathy (DR), age-related macular degeneration (ARMD), glaucoma, and typical cases. The experimental results demonstrate the superiority of the ensemble approach over individual classifiers, with an accuracy exceeding state-of-the-art methods. Finally, EDL presents a robust and accurate solution for the automated detection and classification of retinal diseases from fundus images. By harnessing the strengths of multiple base classifiers, we provide a reliable tool that can assist ophthalmologists in making well-informed decisions and thus contribute to early disease detection and timely intervention. This research signifies a substantial step towards enhancing the efficiency of retinal disease diagnosis and promoting better eye care on a global scale.

Keywords: support vector machines (SVM) Convolutional Neural Networks (CNN), Diabetic Retinopathy (DR), Age-Related Macular Degeneration (ARMD), Glaucoma.

INTRODUCTION

The human eye is a complex organ responsible for our sense of vision and plays a vital role in our daily lives. Retina is the thin layer of tissue that placed at back of the eye that capture and process the visual data. However, the retina is susceptible to various diseases that if not detected and treated early, can significantly impair vision or lead to blindness. Retina transforms light into neural impulses that are delivered to the brain, enabling humans to perceive visual images. Retinal illnesses are disorders that affect this tissue. If left untreated, these diseases can cause vision impairment and even blindness. Retinal diseases are a group of ocular conditions that affect the retina, the delicate tissue at the back of the eye. If not diagnosed and treated promptly, these diseases can cause vision impairment and even blindness. Ophthalmologists conduct manual examinations as part of traditional techniques of diagnosing retinal disorders. This can be time-consuming and sensitive to variances in competence. When it comes to automating the diagnosis process, increasing accuracy, and facilitating early intervention in the detection of retinal diseases, deep learning (ML) approaches have demonstrated encouraging outcomes.

Developing methods that enable computers to learn from data and make predictions or judgments based on that data is known as DL, a subset of ML. ML models can analyze medical retina images, such as fundus photographs or optical coherence tomography (OCT) scans, to identify patterns and anomalies associated with various diseases in the context of retinal disease detection. Image processing (IP) with DL in detecting retinal diseases has several advantages. For starters, it can help medical professionals by providing consistent and objective image analysis, reducing the possibility of human error. Second, DL models can process a large volume of data in a short period, allowing for the rapid identification of potential issues. Finally, the automated screening process can aid in prioritizing patients needing immediate attention, thereby optimizing healthcare resources. This work mainly aimed to process the retinal fundus images to analyze the disease-affected regions between the blood vessels. The proposed approach follows several steps to process the Fundus images and classifies the input images based on the retinal diseases. The first step is a pre-trained model DeepMind used to train the retinal fundus images. Next, the preprocessing step removes the noise from the input images using Z-score Normalization (ZSN) and Anisotropic Diffusion (AD) integrated and sent to the segmentation process—the segmentation random walks segmentation (RWS) and U-net combined segment the input images. Finally, the proposed approach identifies the abnormal regions and classifies the input images based on retinal diseases.

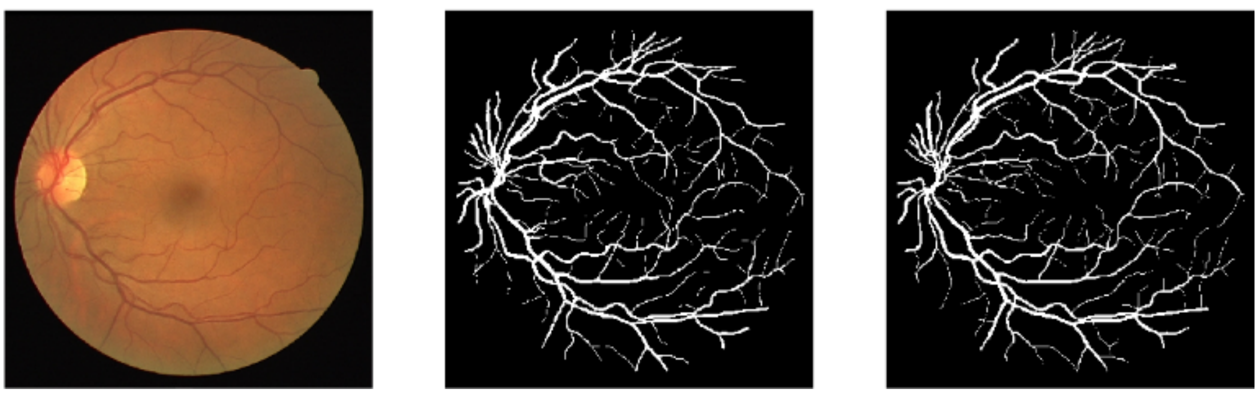
Figure 1: Sample RGB Fundus Image by Showing Vessels

LITERATURE SURVEY

Khan et al. [1] presented the novel DL model that expands the different versions of fully CNN. The proposed approach mainly focused on providing the convoluted challenges by utilising the skip connections that are shared through max-pooling from the decoder to the encoder stage for improving the resolution of the feature map. This approach, step-by-step, reduces the overloading and tunable hyper-metrics in the training and testing phases. The proposed approach focused on solving the retinal vessel segmentation that helps fill the gaps between the input fundus images. The performance of the proposed approach is demonstrated by using three publicly available datasets, and the proposed approach achieved high performance with 83.97% accuracy for the first dataset, 97.92% for the second dataset, and 98.1% for the third dataset. Nawaz et al. [2] introduced the new CNN approach that classifies the issues with efficient memory usage. The proposed approach analyses the Eye Net dataset, which contains 32 types of retinal diseases. The proposal focused on performing accurate memory management with high accuracy. The accuracy is about 95% for the proposed approach. The multi-scale attention module was introduced by Xingxin He et al. [3] to extract both local and global information for fundus images. The region-based attention model, which encodes information derived from the retinal layer and ignores the backdrop in OCT images, is used to analyze the background region. The suggested method extracts the modality-based characteristics for OCT and fundus image classification based on illness prediction in the last stage. Shanthi et al. [4] presented the classification model for DR using fundus images based on stage of the disease. The proposed approach is an integrated approach contains the CNN, Softmax, ReLU and selected Pooling layers which obtains high accuracy. The dataset is UCI repository dataset collected from Messidor database. The comparison between three stages accuracy is about 96.4%, 96.5% and 96.8% accuracy. Mahendran et al. [5] proposed the segmentation algorithm called as Otsu's threshold. The recommended segmentation method examines the tissues involved in macular edema and records the fluid that leaks and accumulates in the macula from injured blood vessels in the surrounding retina. The DML mainly affects the vision and patient may loss the vision. This can be observed based on the swelling caused in the eye. Finally, the proposed approach segments the accurate effected regions for better classification with the accuracy of 92%. Polamuri, et al. [6] discussed about various retinal diseases and the ML and DL algorithms that may used to segment the input images. The experiments are conducted by using fundus images that are collected from various hospitals. Finally, the segmentation and classification is evaluated based on the parameters. Jha et al. [8] introduced the detection of polyp present in various places in the human body. It is mainly used to detect the abnormal regions present in the ColonSegNet. An integrated method that combines the Hessian and intensity transformation approaches was presented by Alhussein et al. [9]. For CLAHE region tuning, the sophisticated PSO algorithm is employed. The noise in the input samples is eliminated using denoise filters like Wiener and Morphological. Lastly, the image is converted using Global Otsu threshold to identify the updated thick vessel image, and ISODATA local threshold is then applied to the updated thin vessel image. The automated diagnostic systems' overloading and computing complexity were decreased by the suggested method. Yan et al. [10] introduced automatic vessel segmentation that diagnoses retinal diseases based on thick and thin vessels and their features. The proposed segmentation is divided into three stages, such as thick, thin, and vessel fusion. Advanced, unique features are used to separate the segmentation vessels. The proposed approach reduces the negative impact that is caused by the huge imbalanced ratio. In the final step, fusion vessels extract the outcomes by finding the non-vessel pixels. The results show that the proposed model is highly compared with existing models. Liu et al. [11] discussed medical segmentation using DL algorithms. The author wants to challenge the drawbacks of existing approaches and introduce new models to provide better segmentation results. Hesamian et al. [12] presented several segmentation approaches that predict the most common and abnormal issues in detecting diseases. Wang et al. [13] presented the joint segmentation approach that helps to detect the early stages of glaucoma for retinal OCT images. In general, experts make decisions based on the stage of the nerve fibre layer. The proposed novel DL approach is used to combine layer segmentation and glaucoma classification. The segmentation mainly predicts the six retinal layers and the five boundaries among them. The classification mainly diagnoses glaucoma. Finally, the accuracy is about 81.6%, and the AUC is about 0.865. Chen et al. [14] proposed an attention-based model that classifies the diseases based on a multi-branch network with four different groups. The proposed approach contains the MSFF module and a dual attention module. This is also focused on finding small lesions based on the features that are extracted from the proposed MSFF model. A new approach that extracts features based on thick and thin vasculature was proposed by Tan et al. [15]. The suggested strategy concentrated on identifying the optic disc, which facilitates the easy identification of the vessels using the current techniques. Khandouzi et al. [16] presented various segmentation approaches that found an accurate disease detection rate. The comparison between various algorithms shows high performance. In comparative research, used manual segmentations from several human specialists to classify retinal pictures of both normal and glaucomatous eyes. Expert judgment on an image depicting a healthy or glaucomatous eye, as well as whether or not an image has a notch, is also provided by the dataset. This dataset is used to evaluate a number of cutting-edge techniques employing boundary-based assessment metrics, area, and cup-to-disc diameter ratio (CDR).

I. DEEPMIND PRE-TRAINED MODEL FOR TRAINING THE RETINAL FUNDUS IMAGES

DeepMind has significantly advanced in artificial intelligence, mainly using deep learning in healthcare. Among their noteworthy contributions is the development of a pre-trained model for the detection and diagnosis of retinal disorders. Globally, glaucoma, ARMD, and DR are the main causes of vision impairment and blindness. For prompt intervention and successful treatment, early identification and precise diagnosis of certain illnesses are essential. DeepMind's pre-trained model analyses medical images of the retina, such as fundus photographs and scans, using deep learning techniques, specifically CNNs. These images provide detailed information about the retinal structures and aid in identifying any abnormalities that may indicate underlying diseases. Retraining the model involves using a sizable collection of labeled retinal pictures. The model gains the ability to identify features, patterns, and abnormalities in photos during this training phase. Deep learning enables the model to automatically extract relevant information from images, identifying subtle changes and characteristics that human observers might miss.

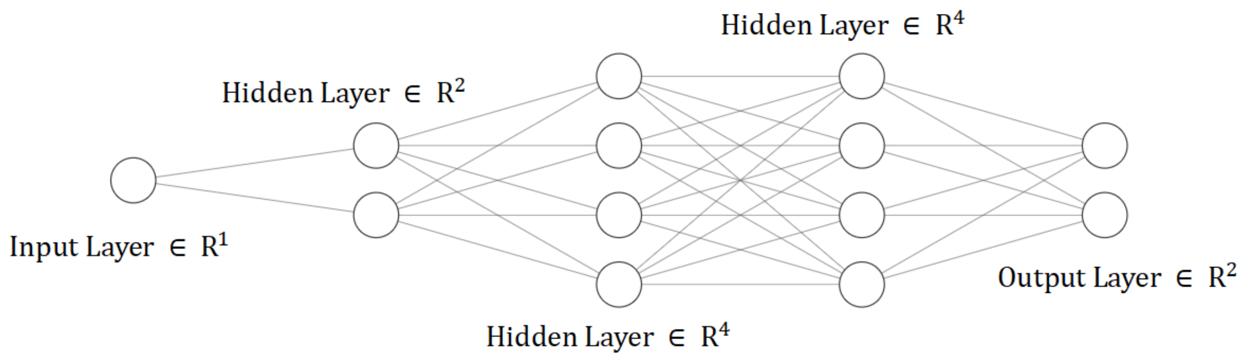

Figure 2: DeepMind Network for Training on Retinal Fundus Images

II. PREPROCESSING

A. Z-Score Normalization (ZSN) and Anisotropic Diffusion (AD)

ZSN, also known as standardization, is a technique for transforming data with a mean of zero and a standard deviation of one. Frequently done to bring various features or variables to a standard scale, which can be especially useful in machine learning and statistical analysis. ZSN is applied to pixel values within an image in the context of image processing. ZSN can help standardize the intensity values of pixels across retinal fundus images. It can help improve image comparability, especially when images come from different sources or have different lighting conditions. ZSN does not alter the image's overall structure or content but adjusts the pixel values to ensure consistency. The formula for ZSN is given in (1)

$$z = \frac{x - \mu}{\sigma} \qquad (1)$$

Where:
z initialize z-score of the data point.
x initialize actual value of the data point.
μ - Initialize mean.
σ - Standard deviation.
AD is an image processing technique used for image denoising and edge-preserving smoothing. It is especially good at reducing noise while keeping sharp edges. Noise reduction is critical because noise can obscure important structures and details in medical images, such as retinal fundus images. AD allows pixel values to diffuse across neighboring pixels, with diffusion being stronger along edges and weaker in flat regions. It helps to smooth out noise while keeping edges sharp. The diffusion coefficient is a parameter that governs the process.

In retinal fundus images, AD can reduce noise caused by camera flaws, lighting variations, and sensor noise. It can improve the clarity of essential structures in the images, such as blood vessels, lesions, and the optic disc.

$$\frac{\partial \mathrm{I}}{\partial \mathrm{t}} = \nabla * (\mathrm{c(r)}\nabla \mathrm{I}) \quad (2)$$

$\frac{\partial \mathrm{I}}{\partial \mathrm{t}}$ −Represents the rate of change of the image intensity with respect to time.
∇ -Represents the gradient operator, yielding the spatial derivatives of the image intensity.
c(r) is the diffusion coefficient, which controls the amount of diffusion at a given point in the image. It can be a function of spatial coordinates or the image gradient magnitude.

∇I is the gradient vector of the image intensity.

The diffusion coefficient c(r) is intended to be significant in areas of rapid intensity change (edges) and minor in areas of relatively uniform intensity (smooth regions). Because of this, the diffusion process is more robust along edges, preserving them and weaker in flat regions, allowing noise reduction. The specific form of the diffusion coefficient c(r) depends on the version of Anisotropic Diffusion used and the requirements of the problem. ZSN and AD are both valuable techniques in their respective fields. In image processing, ZSN is used for data normalization and comparison, whereas Anisotropic Diffusion is used for noise removal and edge-preserving smoothing.

B. Segmentation with random walks segmentation (RWS) and U-net

Image segmentation is a task that solves various issues and finds the significant regions belongs to similar content. It is also used to solves the content localization. RWS is a technique used in image segmentation. It's a graph-based algorithm that leverages the concept of random walks to partition an image into different segments. RWS treats the image as a graph, with edges signifying the similarity between pixels and each pixel acting as a node. The algorithm uses random walks to measure the probability of a random walker moving from one pixel to another within a certain number of steps. A limited, balanced, positive-definite set of linear equations that can be swiftly solved using a variety of techniques must be formulated in order to satisfy the RWS. By utilizing the previous result as the foundation for an iterative matrix solver, the technique can carry out quick editing. It is also possible to produce an arbitrary segmentation with sufficient user interaction. The user provides input in the form of "seeds" in this process, and the information obtained from the seeds is propagated throughout the image. The first step in this process is calculating the likelihood that a random walker will arrive at the seeded pixels from a particular pixel. The transition probability is inversely proportional to the contrast between pixels, preventing the walks from crossing the edges.

1. Constructing a Graph:
First, you need to create a graph representing the data you want to segment. Each data point becomes a node in the graph, and you establish connections (edges) between neighboring data points. The type of data you're working with will determine the nature of these connections. For example, in a 1D time series, adjacent points could be directly connected.

2. Simulating Random Walks:
Random walks are simulated on this graph to determine how likely it is for a walker to move from one point to another. A walker starts at a certain node and then follows edges to move between nodes. The probabilities of moving from one node to another can be based on various factors, such as the similarity between data points, the gradient, or other domain-specific criteria.

3. Segment Boundaries:
Segment boundaries are inferred from the behavior of random walks. When a random walker transitions from one segment to another, there's often a change in the properties of the walk. These changes could be in terms of the walker's speed, the frequency of node visits, or the variance in step sizes. These shifts can indicate potential segment boundaries.

4. Mathematical Equations:
The mathematical representation of the RWS process:

a. **Graph Construction:** Suppose you have a 1D time series data $X = [x_1, x_2, \ldots, x_n]$

b. **Random Walk Simulation:** Define a transition probability matrix P, where P(i, j) represents the probability of moving from node i to node j. This matrix can be based on similarities, gradients, or other metrics.

c. ***Random Walk Process:*** Given a walker's current position at node i, the probability distribution for moving to other nodes is given by a row of the matrix P. Let's denote the walker's position at time t as W(t).

Mathematically, the probability distribution for the walker's next step can be represented as:

$$P(W(t+1) = j \,|W(t) = i) = P(i, j)$$

d. **Segment Boundary Detection:** To detect segment boundaries, you can analyze various characteristics of the random walk, such as the mean displacement, variance in displacement, or the number of visits to nodes. Significant changes in these characteristics might.

C. U-Net:

A DL architecture called U-Net was created specifically for semantic segmentation tasks in the context of medical image analysis. The U-Net architecture has a U-shaped structure with an encoder and a corresponding decoder. It's particularly effective for tasks where you need to preserve spatial information while segmenting objects in images.

The following high-level steps of the U-Net architecture:

Encoder: The encoder is composed of multiple convolutional layers that successively reduce the spatial dimensions while increasing the number of channels (feature).After every convolutional layer, batch normalization and a nonlinear activation function like ReLU are commonly used.

Down-Sampling: In the encoder, downsampling operations (e.g., max-pooling) are used to reduce the spatial dimensions, which helps to capture higher-level features.

Decoder: The decoder is a symmetrical structure to the encoder. It consists of convolutional layers that increase the spatial dimensions while progressively decreasing the number of channels.

Skip Connections: It is key feature from U-Net. These connections allow information from the encoder's layers to be directly concatenated with the decoder's layers at corresponding spatial scales. This helps in combining low-level and high-level features.

Final Layer: The final layer often employs a 1x1 convolution followed by a suitable activation function (e.g., softmax for pixel-wise classification) to produce the segmentation map.
The exact formulas for U-Net's layers and operations involve convolutional operations, pooling operations, skip

connection concatenations, and activation functions. The specifics can vary based on the implementation and any potential modifications/extensions.

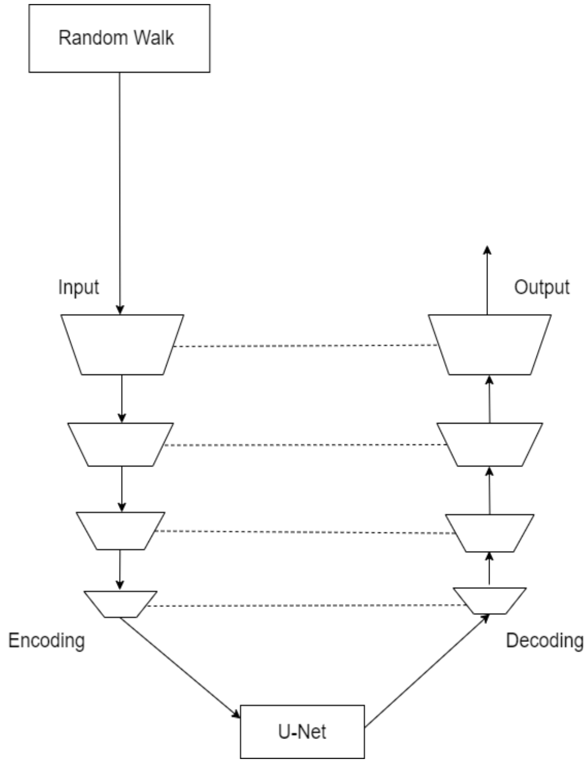

Figure 3: RWS and U-NET Structure

III. ENSEMBLE DISEASE LEARNING ALGORITHM (EDL)

Capsule Networks (CapsNets) are artificial neural network architectures developed to replace traditional Convolutional Neural Networks (CNNs). Geoffrey Hinton and his colleagues proposed them in a 2017 paper titled "Dynamic Routing Between Capsules." Capsule Networks seeks to address some of CNN's shortcomings, particularly its difficulties in dealing with hierarchical relationships and viewpoint variations in images. Capsule Networks are based on "capsules," which are groups of neurons that work together to detect specific features or patterns in an image. These capsules are intended to contain various characteristics of the detected entity, such as its pose, size, deformation, etc. Capsule Networks can capture more prosperous and spatially hierarchical information from images than traditional CNNs. Capsule Networks have been investigated as a potential tool for automated diagnosis and classification of retinal diseases. Diseases such as DR, ARMD, and glaucoma frequently cause subtle and complex changes in retinal images, necessitating a more in-depth understanding of spatial relationships and finer details within the images. The ability of Capsule Networks to capture hierarchical features and relationships may make them well-suited for such tasks.

Dynamic routing is a critical concept in CapsNets. It enables capsules in one layer to send information to appropriate capsules in the next layer based on their predictions and the incoming data. This dynamic routing mechanism aids in the development of hierarchical feature representations as well as the learning of relationships between parts and whole objects. The Capsule Network outputs can be used as feature vectors to capture the hierarchies and relationships in the input data. These feature vectors can then be classified using a Support Vector Machine (SVM). SVMs effectively locate a hyperplane in feature space that best separates different classes. Pass the data from training and testing datasets through the trained Capsule Network and extract the feature vectors from the final layer capsules for each data point. To train an SVM classifier, input the feature vectors obtained from the Capsule Network. For multiclass classification, binary SVMs can be used one-vs-all for each class. Pass a new, unknown data point through the Capsule Network to extract the feature vector, then classify it using the trained SVM. Using Capsule Networks in conjunction with SVMs takes advantage of CapsNets' ability to capture complex hierarchical features and relationships, while SVMs provide a well-established and robust classification mechanism. It should be noted that the effectiveness of this approach is dependent on factors such as dataset size, quality, and complexity, as well as proper hyperparameter tuning for both the Capsule Network and the SVM.

$$Squash(v) = \frac{||v||^2}{(1 + ||v||^2)} * (\frac{v}{||v||})$$

v is the input vector.
||v|| represents the Euclidean norm (magnitude) of the vector v.

Performance Metrics

Performance metrics provide information about different aspects of a classification model's behavior. They go beyond simple accuracy to assist how well the EDL performs on different classes, dealing with class imbalances and making informed decisions about model selection, parameter tuning, and potential trade-offs with retinal diseases. The following parameters analyze the model performance when evaluating the performance of EDL classification: Accuracy, Precision, Recall, F1-Score, and Sensitivity. EDL tunes the hyper parameters by leveraging these metrics and improving its predictive capabilities.

$$\text{Accuracy(ACC)} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FP} + \text{TN} + \text{FN}}$$

$$\text{Precision(Pre)} = \frac{\text{TP}}{\text{TP} + \text{FP}}$$

$$\text{Sensitivity (Sn)} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

$$\text{Specificity (Sp)} = \frac{\text{TN}}{\text{TN} + \text{FP}}$$

$$\text{F1} - \text{Score} = 2 * \frac{(\text{Precision} * \text{Recall})}{(\text{Precision} + \text{Recall})}$$

IV. DATASET DESCRIPTION AND EXPERIMENTAL RESULTS

Experiments are conducted using Keras and pandas libraries functions to run the initial Python program. TensorFlow, PyTorch, Caffe, and DL4J (Deeplearning4j) also show more potential to implement the proposed EDL algorithm. The dataset consists of 3600 Fundus images with 46 retinal diseases. This paper classifies the two retinal diseases such as DR, ARMD. Another dataset used for experiments is Drishti-GS1 dataset which contains Glaucoma Fundus images. There are 101 fundus photos in the Drishti-GS1 dataset [21], of which 31 are normal and 70 are sick. There are 51 photos in the test set compared to 50 in the training set. Four ophthalmologists with different levels of clinical expertise labeled the OD and OC regions on every photograph.

Table 1: Datasets used for Experiments

Datasets	Training	Testing	Total Images
Kaggle Retinal Dataset	500	500	1000
Drishti-GS1 dataset	50	51	101

Table 2: Performance of List of Algorithms over Kaggle Retinal Dataset

Algorithms	Acc	Pre	Sn	Sp	F1-Score
CNN	91.23	90.12	89.34	92.1	91.2

RNN	94.1	93.5	93.7	93.9	93.22
EDL	99.34	99.23	99.98	99.34	99.3

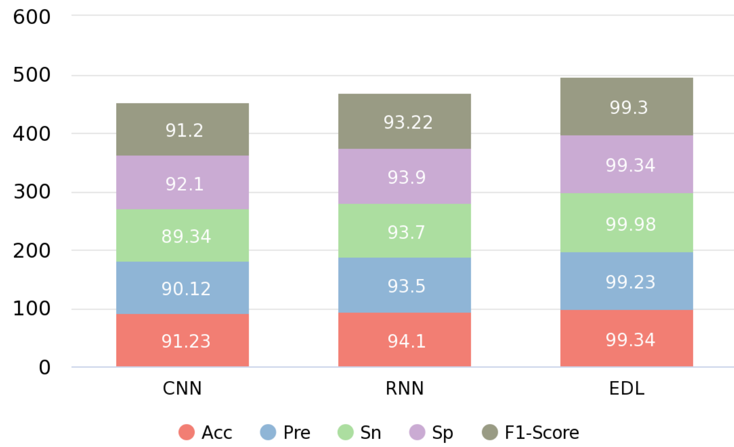

Figure 4: Comparative performance over Existing and Proposed Algorithms for Kaggle Retinal Data

Table 3: Analysis of optic cup (OC) model changes based on the Drishti-GS1 dataset

Algorithms	Acc	Pre	Sn	Sp	F1-Score
CNN	89.23	88.23	90.1	92.1	90.34
RNN	94.34	94.89	93.78	93.23	92.12
EDL	99.45	99.67	99.23	99.34	99.23

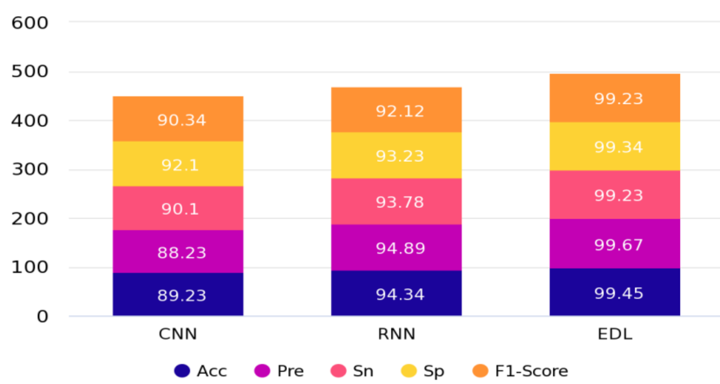

Figure 4: Comparative performance changes based on the optic cup (OC) model Drishti-GS1 dataset

Table 4: Visualize the optic disc (OD) model changes based on the second dataset.

Algorithms	Acc	Pre	Sn	Sp	F1-Score
CNN	88.98	89.23	90.23	90.45	91.23
RNN	94.23	94.98	93.89	94.23	93.45
EDL	99.67	99.67	99.12	99.45	99.78

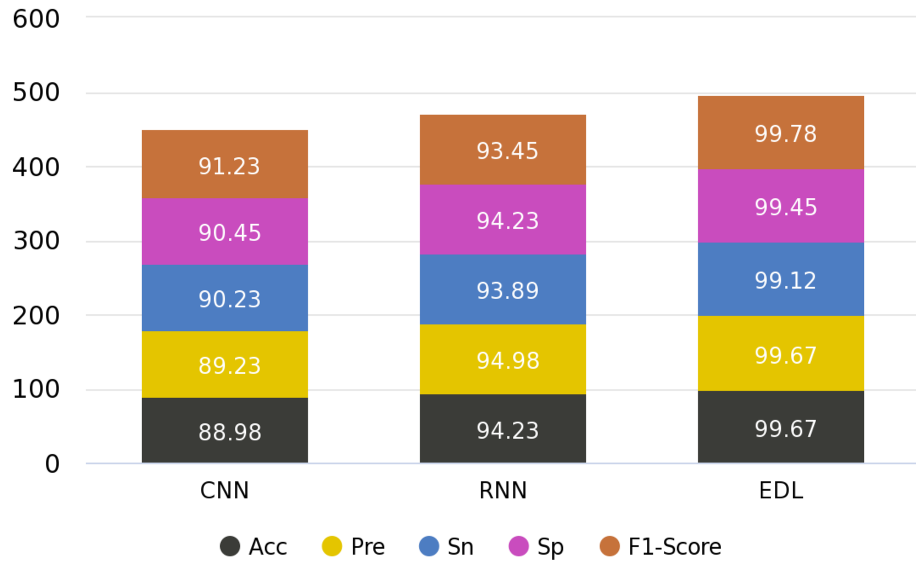

Figure 5: Comparative performance optic disc (OD) model changes based on the Drishti-GS1 dataset

V. CONCLUSION

When combined with Capsule Networks (CapsNets) and Support Vector Machines (SVM), the EDL provides a sophisticated and powerful approach to disease prediction, diagnosis, and classification tasks. This hybrid approach capitalizes on the strengths of each component to improve the system's overall performance and robustness. The following is a summary of this combination's key benefits and potential outcomes: Finally, combining the EDL with CapsNets and SVM holds great promise in medical diagnostics and disease prediction. This hybrid model offers several notable advantages by combining the predictive capabilities of CapsNets with the discriminative power of SVM and further boosting performance through the ensemble approach of EDL: CapsNets provides a mechanism for capturing hierarchical relationships among data features, allowing for improved representation learning, particularly in cases where spatial hierarchies or part-whole relationships are critical in disease diagnosis. SVM excels at determining non-linear decision boundaries, allowing the model to classify complex and intricate disease patterns in data accurately. By combining multiple base models, the EDL approach reduces the risk of overfitting and improves generalization. It improves disease prediction robustness and reliability even when noisy or ambiguous data points exist. However, potential challenges such as model interpretability, computational complexity, and the need for large amounts of labeled data for training must be considered. Furthermore, fine-tuning model hyperparameters and architectural choices will be critical in achieving optimal performance.

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