SAKARYA UNIVERSITY JOURNAL OF COMPUTER AND INFORMATION SCIENCES
http://saucis.sakarya.edu.tr/
e-ISSN: 2636-8129
Publisher: Sakarya University
Vol. 8, No. 3, 510-517, 2025
DOI: 10.35377/saucis...1754835

RESEARCH ARTICLE

Artificial Intelligence-Based Screening for Diabetic Retinopathy: Model Comparison and Interpretability

Muhammed Telçeken[1,*], **Şeyma Değirmenci**[2]

[1]Department of Computer Engineering, Sakarya Applied Sciences University, Sakarya, Türkiye, ror.org/ 01shwhq58
[2]Institute of Graduate Education, Sakarya Applied Sciences University, Sakarya, Türkiye, ror.org/ 01shwhq58

Corresponding author:
Muhammed Telçeken,
Sakarya Applied Sciences University,
Sakarya, Türkiye
muhammedtelceken@subu.edu.tr

Article History:
Received: 31.07.2025
Revised: 18.08.2025
Accepted: 29.08.2025

ABSTRACT
Diabetic Retinopathy is one of the common complications of diabetes and can lead to permanent vision loss if left untreated. This study examined the performance of different AI-based methods for DR classification. Deep learning-based models, ResNet-50, DenseNet-121, U-Net, and classical CNN structures, along with traditional machine learning algorithms, SVM, Decision Trees, and k-Nearest Neighbor, were evaluated on the APTOS 2019 dataset. To optimize model performance, image data were subjected to various preprocessing steps, such as resizing, contrast correction, and denoising. Augmentation techniques were used to increase data diversity. According to experimental results, the most successful model was DenseNet-121, with an accuracy rate of 87% and an F1 score of 86%. In contrast, while classical machine learning methods produce lower accuracy values than deep learning, they exhibit consistent performance under certain conditions and offer a more computationally cost-effective alternative. The comparisons indicate the applicability of classical methods, especially in scenarios with limited data. This evaluation process creates a basic framework that will enable the integration of explainable artificial intelligence (XAI) approaches in later stages and is a preparation for adapting interpretation techniques such as SHAP and LIME to clinical decision support systems.
Keywords: Diabetic Retinopathy, CNN, K-NN, SVM, Decision Trees

1. Introduction

Diabetic retinopathy (DR) is one of the microvascular complications of diabetes. This serious disease affects approximately one-third of diabetic patients worldwide and can lead to blindness if left untreated [1]. DR is a pathology that occurs when small blood vessels on the retina are damaged and can cause irreversible deterioration in the retina over time. The fact that the disease is mostly asymptomatic in the initial stages makes early diagnosis even more important. In fact, vision loss due to DR can be prevented to a significant extent with correct diagnosis and treatment in the early stages [2]. Nowadays, ophthalmologists usually perform DR diagnosis through manual evaluation of fundus images. However, this process poses several challenges in clinical practice due to the high expertise required, openness to interpretation differences, and time-consuming nature [3]. In this context, artificial intelligence-supported automatic diagnosis systems stand out as a promising solution to provide faster, more consistent, and more accurate analysis of images. Deep learning techniques, in particular, have demonstrated impressive success in medical image analysis in recent years and have become widely used in DR diagnosis [4]. Convolutional Neural Networks (CNNs) are one of the most preferred deep learning architectures in this field due to their capacity to detect DR symptoms (microaneurysms, hemorrhages, exudates, etc.) from fundus images with high accuracy [5]. Studies in the literature show that different CNN-based models, such as EfficientNet, ResNet, Inception, and DenseNet, are successful in DR classification [6]. However, the structure of these models and the lack of direct understanding of the rationale behind their decisions by healthcare professionals constitute a significant obstacle in the clinical acceptance process [7]. Model explainability is critical in integrating medical decision support systems into clinical practice. Being able to show which image regions the model focuses on when making a decision can increase the trust and acceptance of healthcare professionals, especially in high-risk clinical decision processes [7]. In this regard, explainable artificial intelligence (XAI) techniques such as LIME (Local Interpretable Model-Agnostic Explanations) [8] and SHAP (SHapley Additive Explanations) [9] allow model decisions to be made understandable by humans.

This study aims to systematically compare the classification performance of various convolutional neural network (CNN) architectures, along with different machine learning algorithms (SVM, Decision Trees, and k-Nearest Neighbor) used in the diagnosis of Diabetic Retinopathy (DR). Depending on the dataset and task definition, the applied methods will be compared across algorithms based on accuracy, sensitivity, specificity, and F1 score metrics. This analysis will not be limited to performance-based analysis alone but will also evaluate behavioral differences in model outputs. This comparative analysis, by enabling the examination of decision processes as well as model accuracy, aims to lay a solid foundation for the application of explainable artificial intelligence (XAI) methods such as SHAP (SHapley Additive Explanations) and LIME (Local

Cite as: M. Telçeken and Ş. Değirmenci, "Artificial intelligence-based screening for diabetic retinopathy: Model comparison and interpretability" *Sakarya University Journal of Computer and Information Sciences,* vol. 8, no. 3, pp. 510-517, 2025. doi: 10.35377/saucis...1754835

Interpretable Model-Agnostic Explanations) in future studies. While the study does not directly implement XAI techniques, it provides preliminary evaluations to understand the behavior of models into which these techniques can be integrated. In this respect, a systematic comparison is made of the applications of both classical machine learning algorithms and modern deep learning architectures in the diagnosis of DR, while also providing an empirical reference framework for research prioritizing the explainability of these models. Given the necessity of achieving high accuracy and interpretability in clinical decision support systems, the findings are expected to guide the development of transparent and reliable artificial intelligence systems in future studies.

2. Related Work

Traditional image processing methods, deep learning approaches, and hybrid methods are used in the early stages of diabetic retinopathy diagnosis. Some of these studies include: Atila et al. [10] proposed a method based on traditional image processing for detecting exudate lesions in diabetic retinopathy diagnosis. Lesion regions were isolated using color space transformations, adaptive thresholding, and morphological operations. The method showed high accuracy in comparison with manual labels. Tanyıldızı and Okur [11] developed a method based on conventional image processing techniques to segment retinal vascular structures in diagnosing diabetic retinopathy. They successfully separated the vascular structures using gray-level transformation, histogram equalization, edge detection, and morphological operations. The method successfully distinguished small vessels and had a stable performance in different image conditions. Şehirli [12] developed a computer vision-based method to detect retinal vascular structures and microaneurysm lesions in diagnosing diabetic retinopathy. Automatic detection of microaneurysms was aimed at with vessel segmentation, contrast enhancement, and lesion zoning techniques. His study demonstrated that conventional image processing methods can provide effective and consistent results in determining early-stage DR findings. Çakar [13] developed a method based on conventional image processing to determine choroidal thickness in OCT images. Choroidal borders were detected using gray level transformation, edge detection, and morphological operations, and the measurements showed high consistency in manual evaluations. Özçelik and Altan [14] presented a study to diagnose diabetic retinopathy by classifying undistorted images with deep learning-based methods. The model developed with a CNN architecture classified retinopathy findings at different stages with high accuracy and provided effective results, especially in early-stage detection. Yalçın et al. [15] developed a model aiming to classify fundus images with deep learning for the early diagnosis of diabetic retinopathy. Automatic feature extraction was performed with a CNN-based structure, and the stages of the disease were classified with high accuracy. Budak [16] comparatively examined the performance of deep learning-based classification approaches in diagnosing diabetic retinopathy. In the study, classification was performed using different CNN architectures after the preprocessing steps, and the models were evaluated with metrics such as accuracy, precision, sensitivity, and F1-score. Ağca and Takcı [17] proposed a hybrid model that combines deep learning with traditional machine learning methods in diabetic retinopathy classification. Deep features obtained from fundus images were evaluated with classical classifiers such as support vector machines and decision trees. The study revealed that the hybrid approach provides higher accuracy and generalization performance than single methods. Ciran and Özbay [18] developed a hybrid model that combines deep learning and feature selection techniques to detect eye diseases. Statistical selection methods applied after CNN-based automatic feature extraction both increased the accuracy and reduced the computational cost. Ramaha and Imad [19] comparatively analyzed deep learning and traditional machine learning methods in diabetic retinopathy diagnosis. In experiments conducted on fundus images, deep learning models provided higher accuracy in large datasets, while classical methods provided more consistent results in small datasets. Çavlı and Toğaçar [20] comparatively examined the effectiveness of artificial intelligence-based methods in diabetic retinopathy diagnosis. In the study applied to fundus images, deep learning and traditional machine learning algorithms were evaluated in terms of performance. The results showed that deep learning was superior in accuracy and F1-score, but in some cases, classical methods could provide sufficient success at a lower cost. Polater and Işık [21] developed a deep learning-based model for classifying diabetic retinopathy stages. The classification performed using a CNN architecture on fundus images reached high accuracy rates with hyperparameter optimization.

3. Materials and Methods

In this study, the APTOS 2019 Blindness Detection dataset was used for diabetic retinopathy detection [22]. The dataset includes color retina fundus images of five classes: normal, mild, moderate, severe, and proliferative retinopathy. In the preparation process of the dataset, preprocessing steps widely used in the literature and aimed at improving image quality were performed. In this context, all images were resized to the specified input dimensions (224x224 pixels), CLAHE was applied to increase contrast, and Gaussian blur and median filter techniques were used to reduce image noise. In addition, various data augmentation methods such as rotation, reflection, and zoom were applied to increase the model's generalization ability and reduce the risk of overfitting.

After the data preprocessing process, four different deep learning architectures were used for diabetic retinopathy classification. The classical CNN model was applied to establish the basic comparison standard, then ResNet-50, DenseNet-121, and U-Net architectures were used as more advanced models. Compared with deep learning models, the results of classical machine learning algorithms such as Support Vector Machine (SVM), Decision Trees (DT), and k-Nearest Neighbor (k-NN) were examined on the same dataset and compared with deep learning models.

3.1. Dataset

In this study, the APTOS 2019 Blindness Detection dataset was used to train and evaluate diabetic retinopathy classification models. This dataset, provided by the Asia Pacific Tele-Ophthalmology Society (APTOS), consists of color retinal fundus images containing different diabetic retinopathy findings [22]. The dataset, which contains 3,662 high-resolution images, also includes diagnostic labels corresponding to each image. Comprehensive data augmentation strategies were implemented to improve the model's generalization ability and reduce the risk of overfitting. To this end, the diversity of the training data was increased using geometric transformations such as rotation, reflection, and zoom. Samples in the dataset were labeled into five classes based on disease severity: healthy (0), mild (1), moderate (2), advanced (3), and proliferative (4) retinopathy. However, the images' illumination differences, blurriness, and inter-class imbalance necessitate preprocessing steps before model training. Class imbalance was specifically compensated for through resampling and data augmentation techniques, increasing the representativeness of minority classes and ensuring the model learned more fairly and consistently across all classes. These approaches expanded the dataset in volume and diversity, aiming to provide a more robust and generalizable performance for the deep learning-based model. The distribution of classes in the dataset is shown in Table 1.

Table 1. APTOS 2019 Blindness Detection dataset

Class ID	Diabetic Retinopathy Level	Number of Images	Percent (%)
0	No DR	1805	49.3
1	Mild DR	370	10.1
2	Moderate DR	999	27.3
3	Severe DR	193	5.3
4	Proliferative DR	295	8.1
Total		3662	100

3.2. Convolutional Neural Network (CNN)

Convolutional Neural Network (CNN) is a deep learning-based artificial neural network architecture that stands out with its high success, especially in image processing and computer vision fields [23]. CNNs can automatically extract low-level (edge, texture) and high-level (shape, structure) features through convolution layers designed to learn spatial and regional relationships in image data. The convolution, pooling, and fully connected layers in these architectures provide an effective learning process in tasks such as image classification [23]. Especially in medical image analysis, it eliminates the need for manual feature extraction and enables automatic identification of complex images. In this respect, CNN is frequently used as a preferred method in diagnosing retinal diseases such as diabetic retinopathy, and its effectiveness has been proven in the literature. An example structure of the general structure of CNN algorithms is shown in Figure 1.

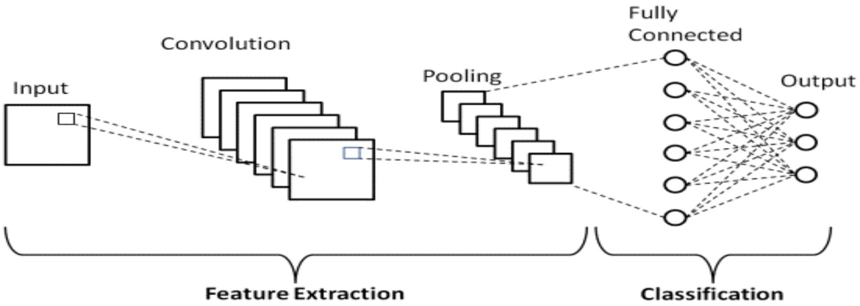

Figure 1. General structure of the CNN algorithm

The classical CNN model used in this study has a simple but effective architecture for diabetic retinopathy diagnosis. The model starts with two convolution layers that extract relevant features from fundus images. The first layer has 16 filters, and the second layer has 32 filters, and the dimensions of the feature maps are preserved in both. Then, a max pooling layer is added to reduce the feature map dimensions and preserve the dominant features. A dropout layer is used to prevent overfitting during training. The resulting feature map is flattened and transferred to the fully connected layer. At this stage, batch normalization accelerates and stabilizes the model training. In the last layer, a dense layer separates the images into five different classes. The architectural structure of the classical CNN model is shown in Table 2.

Table 2. Layer structure of the architecture of the classical CNN model

Layer	Output Size	Number of Parameters	Explanation
Conv2D	(224,224,16)	448	Basic feature extraction from an image
Conv2D	(224,224,32)	4,640	Obtaining more detailed features
MaxPooling2D	(112,112,32)	0	Reducing the size of the feature map
Dropout	(112,112,32)	0	Regulatory layer to prevent overfitting
Flatten	(401408,)	0	Converting feature maps to a one-dimensional vector
BatchNormalization	(401408,)	1,605,632	Increasing training speed by normalizing input values
Fully Connected	(5,)	2,007,045	The output layer that performs the classification process

3.2.1 ResNet-50

ResNet-50 is a deep convolutional neural network architecture proposed by [24]. The bottleneck block, which is the basic component of the model, consists of three convolution layers. First, there is a 1x1 kernel contraction convolution, then a 3x3 kernel feature extractor convolution, and finally a 1x1 kernel expansion convolution. The residual connection at the end of each block facilitates the gradient flow by directly adding the input of the block to the output. It greatly reduces the optimization problems that arise as the network gets deeper. ResNet-50 contains 50 layers and has achieved over 76% accuracy in ImageNet classification tasks with approximately 25.6 million parameters [24]. Each residual block in the model is supported by an identity connection or a 1x1 projection connection when the size is different. The Batch Normalization layer and ReLU activation after each convolution layer stabilize the learning process and increase the accuracy. To avoid training difficulties as the depth increases, the connection structure allows the network to be deepened up to 152 layers, thus setting a new standard in multi-layered architectures.

3.2.2 DenseNet-121

DenseNet-121 is an architecture that uses the dense connection structure introduced by Huang et al. [25], which connects each layer to the outputs of all previous layers. The model is divided into four dense blocks. A bottleneck unit consisting of 1x1 and 3x3 convolution layers is repeated in each block. Each added layer generates new feature maps with a fixed growth rate (usually k = 32), which are reused throughout the chain. This way, parameter efficiency increases, and gradients are transmitted through the network via short paths. DenseNet-121 has approximately 8 million parameters and offers lower memory requirements and computational cost than other architectures of the same depth [25]. Studies have shown that DenseNet's feature reuse mechanism helps prevent over-learning, especially on small datasets, and strengthens its generalization ability. Additionally, the transition layers in the model keep the computational load under control by reducing the feature map dimensions with 1x1 convolution and 2x2 average pooling operations.

3.2.3 U-Net

U-Net is an encoder-decoder architecture that Ronneberger et al. [26] developed for medical image segmentation. In the encoder path, blocks consisting of four pairs of convolution and max pooling layers extract increasingly rich features from the image. In the decoder path, after each upsampling step, feature maps from the corresponding layer in the encoder are combined with a skip connection to preserve fine structural details. The symmetric structure of the U-Net enables the integration of spatial information with features. Thus, it performs accurate and sharp segmentation of organ or lesion boundaries. The model starts with 64 filters and doubles the number of filters in each contraction step, halving the number of filters in expansion steps. This arrangement supports the effective capture of both local and global context information. Since the U-Net can exhibit high performance even with very little labeled data, it is especially preferred in the medical field.

3.3 Support Vector Machine (SVM)

Support Vector Machine (SVM) is a powerful supervised learning algorithm that provides effective classification and regression performance, especially on high-dimensional and complex data. Its main purpose is to determine the optimal decision boundary that separates examples belonging to different classes from each other with the widest margin [27]. For this purpose, SVM performs the classification process by considering only the data points closest to the bounding surface. While a flat hyperplane can separate linearly separable data sets, in nonlinear cases, the data is projected to a higher-dimensional space using kernel functions and made separable [28]. SVM is frequently preferred in medical image analysis due to its high generalization ability, especially on small and imbalanced data sets.

3.4 Decision Trees (DT)

Decision Trees (DT) are an intuitively understandable and interpretable supervised learning method used for data classification or regression analysis [29]. Organized in a tree structure, this model separates the data into branches according to their features and produces a class or prediction value at each leaf node. Each internal node of the decision tree contains a decision rule according to a specific feature in the dataset. This way, data samples are divided into branches and homogeneous subsets are reached. Measures such as the Gini index, information gain or entropy are generally used in creating the model [30]. Decision Tree algorithms are preferred, especially in classification problems, due to their high interpretability and computational efficiency. However, they may require careful parameter adjustments due to their high variance and tendency to over-fit.

3.5 K-Nearest Neighbor (k-NN)

K-Nearest Neighbor (k-NN) is an instance-based classification method among supervised learning algorithms, particularly notable for its simplicity and intuitive structure [31]. This algorithm decides by looking at the class label of the k nearest neighbors of the example to be classified according to a distance metric, such as Euclidean distance, in the training dataset [32]. The K-NN model has no training process; all calculations are made during testing, placing it in the algorithm group called lazy learning.

If the parameter settings are correct, k-NN can provide effective results, especially in low-dimensional datasets. In medical image analysis, it is frequently preferred, especially in small datasets, since it can be classified directly from previously extracted feature vectors. However, the algorithm may lose effectiveness in high-dimensional data, and the computational cost may increase significantly, especially in large datasets. In addition, the choice of k value and distance metric is an important factor directly affecting the model's success. When combined with deep learning-based architectures, the classification of deep features obtained from the last layers with k-NN can offer an interpretable and flexible alternative.

4. Experimental Results

During the training of the models, hyperparameters such as learning rate, batch size, and epoch number were experimentally optimized. Model performances were evaluated via accuracy, sensitivity, specificity, and F1-score metrics. Figure 2 shows the Accuracy and F1-score graphs of classical CNN, ResNet-50, DenseNet-121, U-Net, SVM, Decision Tree, and k-NN models used for diabetic retinopathy detection. The highest accuracy and F1 scores were obtained with the DenseNet-121 model, with 87% accuracy and 86% F1 score. In classical machine learning algorithms, SVM, Decision Tree, and k-NN exhibited lower but consistent performances than deep learning models. These results reveal the superiority of deep learning algorithms in large data sets and the applicability of classical algorithms in small or limited data sets. The graph is also visually supported with dot connection lines to emphasize the trends in model performance.

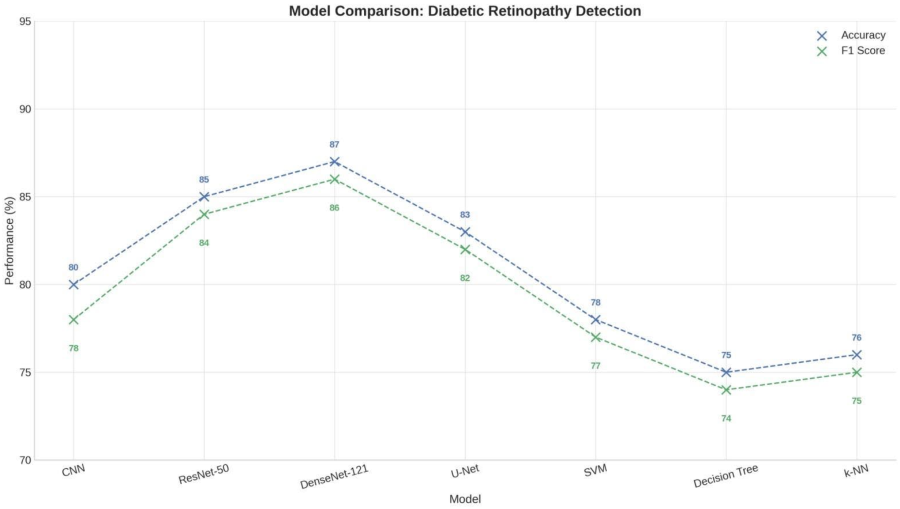

Figure 2. Comparison graph of model results used for diabetic retinopathy detection

Table 3 shows the success levels of each model in terms of multiple evaluations. The DenseNet-121 model achieved the best result with 87% accuracy and an ROC-AUC of 90%. The ResNet-50 model stood out with similarly high accuracy and balanced F1, Precision, and Recall rates. The U-Net model was evaluated as a strong alternative due to its segmentation ability in biomedical image analysis. The SVM model's most successful results were achieved among classical machine learning algorithms. However, experiments have shown that deep learning-based models exhibit a significant superiority over classical methods in overall performance. Especially on large and complex datasets, the automatic feature extraction and nonlinear relationship learning capabilities of deep learning architectures provide a significant advantage in improving classification accuracy. However, classical methods remain a valuable benchmark due to their lower computational costs and effectiveness on small datasets. This table guides which algorithms should be preferred regarding the study's clinical applications.

Table 3. Confusion matrix for DenseNet121, which performs the best classification on the APTOS 2019 dataset

Model	Accuracy	F1-Score	Precision	Recall	ROC-AUC
CNN	80	78	79	77	81
ResNet-50	85	84	86	83	88
DenseNet-121	**87**	**86**	**88**	**85**	**90**
U-Net	83	82	84	81	85
SVM	78	77	76	78	79
Decision Tree	75	74	73	75	76
k-NN	76	75	74	76	77

A confusion matrix is a widely used evaluation tool to evaluate the performance of classification algorithms. This matrix is created by comparing the classes predicted by the model with the real classes of the data. The matrix rows represent the real classes, and the columns represent the classes predicted by the model. In this way, it is possible to clearly observe which classes the model is more successful in and which classes it confuses. Critical performance metrics such as accuracy, precision, sensitivity, and F1-score can be easily calculated from the confusion matrix, thus comprehensively evaluating the model's performance. The confusion matrix of the model performance on the data series with the DenseNet121 architecture is shown in Figure 3.

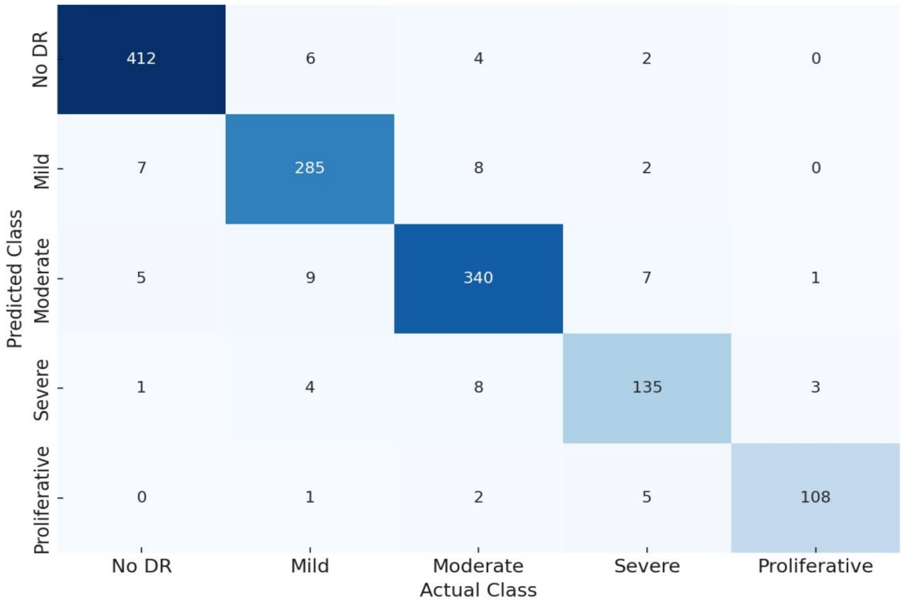

Figure 3. Confusion matrix of DenseNet121 architecture

5. Conclusions

This study confirms the results of the reference studies in the literature and prepares the ground for the research to be carried out in the next stage. It is aimed to increase the interpretability of the outputs of deep learning and machine learning algorithms, especially in the field of explainable artificial intelligence. In the following study, SHAP and LIME methods will be applied to gain a deeper understanding of the decision-making processes of the developed models. These methods will reveal the features or image regions the model bases its classification decisions on, allowing for a transparent examination of the decision mechanisms. Heat maps, generated specifically on fundus images, will visualize regions that play a critical role in the model's retinopathy diagnosis, allowing for the consistency of the pathological areas considered by the model with clinical findings. Furthermore, feature importance ratings will be used to analyze which structural or pixel-based parameters the model prioritizes in its decisions. This step makes the performance of the models explainable. It constitutes a critical step toward developing transparent, reliable, and interpretable AI systems for clinical use, which is the most significant contribution of this study.

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Article Information Form

Authors Contributions

The artificial intelligence studies, code development, literature review, and the writing of the manuscript were carried out by Muhammed Telçeken and Şeyma Değirmenci.

Acknowledgments

There is no person or institution/organization that has made contribution to the study.

Conflict of Interest Notice

The authors declare that no conflicts of interest are associated with this article's publication.

Ethical Approval

It is affirmed that the preparation of this study was conducted under scientific and ethical standards, and all referenced sources have been duly cited in the bibliography.

Artificial Intelligence Statement

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