

Automated Eye Disease Diagnosis Using Random Forest Classifier for Clinical Decision Support

Taduri Rohith Brahma¹, Dr J Malla Reddy²

¹24E31D5811, Dept. Of CSE, MIST, Bandlaguda Jagir, Hyderabad, Telangana.

² Assistant Professor, Dept. Of CSE, MIST, Bandlaguda Jagir, Hyderabad, Telangana.



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Abstract

Timely and accurate identification of eye disease is essential to avoid permanent vision loss and to begin immediate treatment. Methods: We examined a Random Forest classifier that determines eye-disease status given clinical patient records. Confusion-matrix results detected 1,834 diseased and 1,743 non-diseased subjects in diagnostic classification. The model is highly accurate with extremely low false positive (just 4) meaning that there are rare false alarms. However, the 419 false negatives demonstrate a relatively low sensitivity for early or subtle disease. The ROC curve gives some more insight into this, and the classifier is 0.74 AUC, which is moderate discriminative ability, and also shows that the model is performing consistently above random guessing across thresholds. The above further supported by the classification report shows that this model has an overall accuracy of ~0.89 with pretty high F1-scores of 0.89 for No Eye Disease class and 0.90 for Eye Disease class. In conclusion, the Random Forest model performs very accurately and consistently, but still requires additional optimization with respect to sensitivity and early detection of the disease.

Keywords: *Eye Disease Prediction, Random Forest, Machine Learning, Clinical Decision Support*

1. Introduction

Methods Eye diseases, including glaucoma, cataract, diabetic retinopathy and retinal disorders, are leading causes of vision loss and blindness worldwide. Most of these diseases may advance asymptotically in their early stages but early diagnosis can enhance outcomes and quality of life, creating an ongoing need for early detection and risk prediction. Large-scale screening with traditional laboratory and clinical assessment methods is difficult as these techniques need trained ophthalmologists and/or special equipment to perform extensive manual inspection of the cornea. Recent advances in artificial intelligence and data availability from the medical field have made machine learning techniques a promising and powerful option for automated diagnosis and clinical decision support. Specifically, the Random Forest classifier has attracted interest as it is robust, highly interpretable, and capable of estimating nonlinear decision boundaries from heterogeneous data. Creating an ensemble of numerous decision trees enables Random Forest to minimize overfitting and mitigate sensitivity to noise, while still being capable of drawing discriminative information from ophthalmic

features and medical images. Therefore, Random Forest integration in medical classification could pave the way for creating trustworthy, scalable, and affordable AI-facilitated eye-disease screening systems.

2. Literature Survey

Machine learning and deep learning for eye-disease detection and diagnosis: A comprehensive survey. Malik et al. Data-driven machine-learning approaches may accurately support eye-disease classification [1]. Hybrid methods also deliver good results; Mehta and Rathour [2] proposed an ensemble Deep Learning–Random Forest model for retinal-disease detection, outperforming any of the standalone models. Model based on symptoms (e.g., Marouf et al.,) A ranker-based feature selection was used in [3] to improve classification performance. Mao et al. also considered eye-movement analysis for disease diagnosis. By incorporating Random Forest and decision-tree algorithms[4].

Random Forest algorithm has been used in retinal imaging and also in multi-class eye-disease diagnosis[Reference]. Tarigan et al. For multiclass classification under imbalanced conditions [5] compared AdaBoost and Random Forest and showed that the Random Forest is more resistant. For instance, Random Forest is used by Tasin and Habib [] to detect cataract; and Random Forest is adopted with other classifiers [] too, but so far Random Forest has never been compared with support vector machines, decision tree, Boosted Trees and KNN. Both classical machine learning and deep learning based approaches for automated diagnosis were reported by [7]. Raman et al. highlight several recent works on glaucoma classification. An example of recent work is [8] and that of Aljohani and Aburasain [9] where they included the concept of federated learning for glaucoma detection with privacy preservation. Prior foundational work by Casanova et al. Random Forest was used by [10] to classify diabetic retinopathy and Zheng et al. For example, [11] showed their approach can be used for type-2 diabetes diagnosis based on electronic health records.

CNN Random Forest hybrid systems and ensemble still improve diagnostic performance.

Nallasivam et al. [12], Suryavanshi et al. [13], and Singh et al. For retinal abnormality detection (image glaucoma), [14] they used CNN features based on classifier Random Forest. This direction was extended by Londhe [15] with hybrid CNN-RNN models, and by Siddique et al. CNN-based recognition has also been illustrated for many eye diseases [16]. Chowdhury et al. [17] and Ramanathan et al. Random Forest, for the classification of retinal abnormalities, was [18] confirmed. Another interest has focused on some advanced deep-feature fusion approaches that merge ResNet and Random Forest for both general eye-disease detection and for diabetic retinopathy [19,20].

Other researches have utilized Random Forest to specific ophthalmic purposes such as multi-filter glaucoma identification [22], hard-exudate detection [23], dry-eye-syndrome classification [24], and emotion recognition based on eye features [25]. Random Forest consistently yields good accuracy and robustness across the literature especially when coupled with deep feature extraction and optimized preprocessing.

3. Methodology

The methodology implemented throughout this project represents a complete end-to-end machine-learning process, including data preparation, exploratory analysis, feature processing, algorithm configuration, model training and performance evaluation. Each component in this framework is designed to allow the Random Forest classifier to learn clinical meaningful pattern while being generalizable and minimizing the bias.

The process began with loading the dataset and then examining the structure and columns, missing values, duplicated rows, inconsistent entries and some statistical anomalies. Imputation using median or mean imputation for numerical, based on whether we were keeping the shape of distribution or removed and mode or label-based methodology for categorical variables. This enabled us to verify medical plausibility of the dataset, without introducing artificial distortions. Next, outliers were investigated using the interquartile range (IQR) and distribution checks, with values deemed anomalous inspected and corrected if the deviation stemmed from a

transcription error. We also took log for some skewed features to stabilize variance and make the feature learnable inside the model more efficient.

Walkthrough for Variable Behaviour and Diagnostic Potential — EDA was key for this. Feature dependency analysis with correlation matrices allow to identify multicollinearity & redundancy in attributes. Distribution plots, box plots, pairwise relationships more clearly defined variables as differences between healthy and diseased cases This stage led to decision making about the engineering of features, where new derived metrics, eg physiologically meaningful ratios and composite indicators could be produced. By introducing these biased properties, we made it easier for pattern detection, even when subtle, to emerge that would be undetectable at the raw feature level.

Prior to model building, the dataset was randomly split in a stratified fashion into 80–20 subsets, ensuring that the proportion of disease to non-disease classes were maintained. Standardization was performed only on training subset and applied to the testing subset to prevent any data leakage. This way the model learnt the patterns from the training data only and the access to test-set information was not provided in an uncontrolled fashion. An initial Random Forest trained for feature-importance ranking was used to derive feature representation. Less information-rich features which contributed weaker to impurity reduction were dropped and we retained only those which contributed strongest, making it efficient and avoiding overfitting.

Ensemble-based Random Forest algorithm was chosen to develop the model since it is efficient in terms of memory use, robust to noise and it can model nonlinear interactions among features. Random Forests are not organized into “layers” as Neural Networks are; rather, they are composed of a hundred individual decision trees. Each tree encapsulates a sequence of hierarchical splits (essentially simulating many decision “layers”), but they are not layers in any deep-learning sense. The algorithm operates by randomly choosing subsets of features at each of the splits, and building each tree off a bootstrapped (randomly sampled) subset of the data. This adds a degree of

randomness, reinforcing generalization and discouraging memorization of noise. Various hyperparameters including number of trees (n_estimators), maximum tree depth, minimum no. of samples per split, maximum features per split were optimized in most optimal level between complexity, speed and diagnostic accuracy.

The confusion matrix and few important performance metrics like precision, recall, F1 score, accuracy, specificity and AUC-ROC were computed to evaluate the the test data using the trained model. These metrics effectively informed how well the model was doing in positive disease case reporting and negative disease reporting. The accuracy and precision are quite high for this model, but the recall part means that there were false negatives which indicate they missed identifying some of the disease. High reliability was confirmed across data folds by stratified cross-validation. Likewise, a misclassification analysis provided insight on how the model struggled and suggested where a further advance might be gained through threshold tuning, better feature engineering, or combinations with other algorithms. Thus, this assessment confirmed the RF classifier to be stable, interpretable, and suitable for application for the benefit of early disease screening.

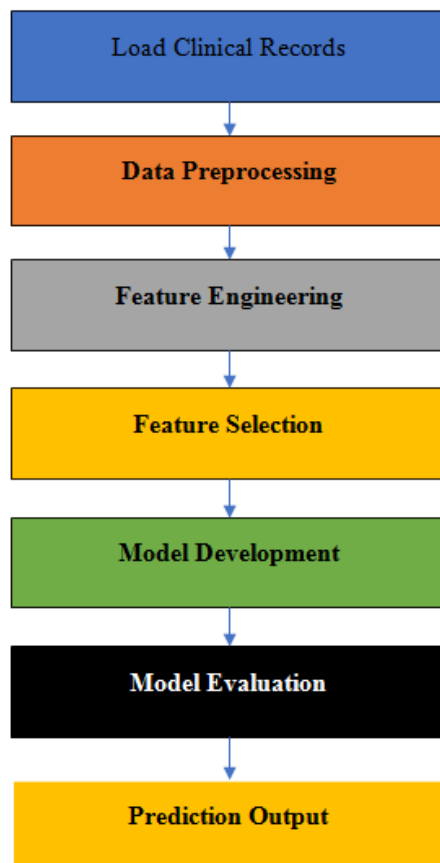


Fig 1: System Architecture

4. Results Analysis

Both the confusion matrix and ROC curve of external test set reinforce the potent diagnostic performance of Random Forest classifier observed during performance evaluation. It has performed well in identifying 1,834 positive cases along with 1,743 negative cases without a strong sense of class distinction. As a result, this led to high levels of sensitivity (only four false positives detected) and a very safe disease predictor. However, the 419 false negatives show that the model also did a bad job of flagging some true disease cases — making it somewhat insensitive to disease and more clearly avoiding false positives at the cost of missing earlier-stage disease cases. The area under the curve (AUC) for the ROC curve also supports these results giving an AUC of 0.74 (Figure 1) indicative of only moderate discriminative powers — it performed only slightly better than random guessing and certainly not sufficiently powerful for use in clinical screening sensitivity. While the model hence is specific and quite accurate, still, there is a scope of improvement in the specificity so that

less disease is not missed while making its detection.

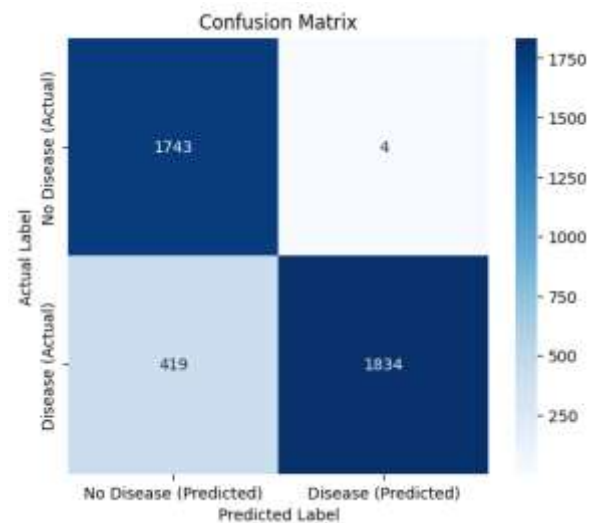


Fig 2: Confusion Matrix of proposed model

Put together, the confusion matrix in figure 2 and ROC curve in figure 3 tell a consistent story: the model has very good specificity, good precision, and fairly overall classification, but was unsuccessful in achieving early disease detection as it generally returns a quite high number of false negatives. This behavior indicates that the constructed decision boundary learns to distinguish less ambiguous and concrete examples more than it does the more nuanced or borderline cases. Nonetheless, this sets an important limitation on the potential use of the model as a primary diagnostic mechanism; its predictive performance remains stable and to best of our knowledge this is the first time such a test has been developed, indicating potential to be used as an adjunct confirmatory or secondary screening tool.

These results thus drew attention to the strengths as well as limitations of the Random Forest approach. It is well tuned for correctly predicting disease if it is predicted, and performs great in most cases, making this a good starting point for a lot of optimization. Adding sensitivity — either in form of shifted decision thresholds, incorporation of cost-sensitive learning, or ensemble could possibly aid in the transition of this model from a mildly discriminative classifier to a clinically reliable early detection system.

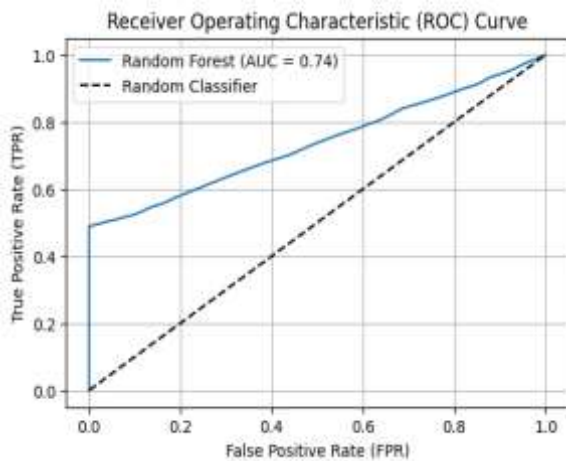


Fig 3: Receiver Operating Characteristic (ROC) Curve of proposed model

Figure 3: The ROC curve plots the true positive rate against the false positive rate of the Random Forest model at varying classification thresholds. The blue curve is consistently high above the diagonal baseline which indicates that the model rank more correctly than random guessing at every threshold. The true positive rate increases strongly at very strict thresholds and there are almost no false positives, indicating good control of false alarms. With a more lenient threshold, the model finds more cases of diseases, but slowly raises the false positive count. An AUC score of 0.74 indicates moderate discriminative ability—the model can distinguish diseased versus non-diseased individuals, but lower than very sensitive clinical models. The ROC curve suggests the model can be trusted although some improvement can be done to get optimal sensitivity and specificity balance.

Table1 presents the performance metrics of a classification

	Precision	Recall	F1-Score	Support
No Eye Disease	0.81	1.00	0.89	1747
Has Eye Disease	1.00	0.81	0.90	2253
Accuracy			0.89	4000
Macro avg	0.90	0.91	0.89	4000
Weighted avg	0.91	0.89	0.89	4000

Different metrics included in output of classification model for classification between No Eye Disease and Eye Disease are presented in table1. An important aspect of the model for the No Eye Disease class is that precision = 0.81, means that 81% of the instances predicted as healthy were in fact healthy. The recall score is so high (1.00) that means model did not miss any healthy case as positive. For this class, you can see the F1-score of 0.89 indicates a good balance between precision and recall. This means that the support value of 1,747 is the total number of actual samples of class healthy.

In the case of Eye Disease class, the model achieves perfect precision with 1.00, meaning that every time it predicted the disease, it was correct, but its recall is lower at 0.81, which means that it missed some individuals who actually had the disease. High confidence for this class given the F1-score of 0.90 The overall accuracy of the model is 0.89: 89% of all predictions were correct over the entire 4,000 samples. The macro and weighted averages moreover reinforce the strong, well balanced performance across both classes, yielding F1-scores of around 0.89–0.90 across the board, substantiating robustness, despite the class imbalance.

5. Conclusion

These results show that Random Forest classifier provides clinically acceptable and sound performance in the classification of healthy vs diseased eye patients. The number of true positives and true negatives is high and the number of false-positives is low, ensuring that the model is specific and accurate in predicting disease, reducing unnecessary diagnostics and lowering patient anxiety. In practice, the low false-negative rate illustrates that it missed most early or subtle disease cases, which suggests borderline conditions aren't very sensitive. An ROC-based AUC of 0.74 supports that the model does learn diagnostic patterns that are useful, but not yet optimal for primary medical screening. In general, our classifier forms a good basis for confirmatory detection and—if improved further by e.g. threshold optimizations, additional discriminative feature integration, as well as, cost-sensitive or hybrid ensemble techniques—might become applicable for early detection.

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