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Heart Disease Prediction Using Random Forest and Explainable Artificial Intelligence

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Abstract**—**Cardiovascular diseases (CVDs) are the number one cause of mortality in the world with the world health organization estimating that at least 17.9 million people die every year because of the diseases in 2015. Risk prediction of heart disease at the earliest and correct stage is essential in preventing and timely intervention. The potential of machine learning models in this area has been extraordinary, but the fact that they are black boxes in nature restricts their use in clinical setting as they are not interpretable and lack trust. To overcome this vital limitation, this paper proposes a new heart disease prediction model based on combining a Random Forest classifier with Explainable Artificial Intelligence (XAI) with SHAP (SHapley Additive explanations). The model is trained using Cleveland Heart Disease dataset with 13 clinical features and has an accuracy of 91.8% and a precision of 92.3, a recall of 90.5, and F1-score of 91.4. In addition to predictive performance, the system has been implemented to use SHAP to give global feature importance analysis in addition to local explanations of the individual predictions to facilitate clinicians and patients to know the reasoning behind the risk assessment. The entire system is hosted as a multi-page Streamlit application, which helps to predict risks in real-time with interactive visualization and transparent decision-making. The proposed integrated solution can fill the divide between high- performance machine learning and clinical interpretability, which may improve trust and use of AI-based decision support systems in cardiovascular care.

Index Terms**—Heart Disease Prediction, Random Forest, Machine Learning, Explainable Artificial Intelligence (XAI), SHAP, Streamlit, Clinical Decision Support System, Feature Importance.**

I. INTRODUCTION

A. Background

Cardiovascular diseases (CVDs) are a major killer of people across the planet as they cause an estimated 17.9 million premature deaths annually or 31 percent of all deaths in the world [1]. The most prevalent one is heart disease, of which coronary artery disease, myocardial infarction, and heart failure are the most widespread. The high mortality rates indicate that early diagnosis and the correct prediction of risks is necessary to enhance prevention and patient outcome.

Machine learning (ML) has revolutionized the diagnostic process in the medical field by processing intricate clinical information to identify any trends that the conventional approach might overlook. ML models can be used to produce individual risk assessments with a great level of precision using patient demographics, clinical measures, laboratory findings, and lifestyle factors.

B. Why Black-Box Models are a Problem

Most ML models are highly accurate, but they cannot be interpreted, which restricts their clinical implementation. Ensemble methods and deep neural networks, among other complex models, can be viewed as black boxes that do not disclose the line of thinking that resulted in a particular prediction but just make forecasts. Regarding healthcare, before clinical workers apply a model in their patient care, they have to understand it and believe in its decision [2].

Rand Forest is a powerful predictive model, however, its standard feature importance values can only give global information. They fail to clearly articulate the reasons why a particular patient is assigned a given risk prediction which diminishes its applicability in personalized medicine.

C. Explainable Artificial Intelligence (XAI) on the Rise

Explainable Artificial Intelligence (XAI) is an approach to the interpretability problem that involves rendering the outputs of a ML model comprehensible to humans as a response to the interpretability problem in AI research and development efforts (barredo2020). The most common one is SHAP (SHapley Additive exPlanations), which is formulated based on the principles of the game theory and can offer reliable and easy-to-understand explanations.

SHAP attributes a certain importance value to each feature in a particular prediction, demonstrating its contribution towards the end outcome. It allows the global interpretation (important features in general) and local interpretation (why a particular patient got a particularly prediction) [4].

D. Motivation

The three factors that inspire this study include: (1) high predictive accuracy of Random Forest on heart disease, (2) the existence of effective XAI packages like SHAP and (3) easy-to-use deployment applications like Streamlit. It is possible to combine these technologies so as to create an accurate and transparent heart disease prediction system.

E. Contributions of this Paper

There are four contributions that are made by this paper. It establishes a random forest model that is optimized and based on 13 Cleveland dataset clinical features with a high predictive capability. Second, it incorporates SHAP to offer both patient-level and global feature importance. Third, it implements the system as a real-time risk prediction system with interactive visualization as a multi-page Streamlit web-based application. Lastly, it shows how explainability has the potential to convert a black-box model into a reliable clinical decision support system.

F. Structure of the Paper

All other sections of the paper are structured in the following way: Section 2 provides the related work in heart disease prediction and XAI. Section 3 explains the dataset, methodology, model development, SHAP integration and deployment of the system. The results of experiments are described in Section 4. Implication and limitations are covered in Section 5. Section 6 is the conclusion of the paper with recommendations on future research directions.

II. LITERATURE REVIEW

The current section is the review of the recent research (2020–2025) on predicting heart diseases with machine learning, application of Random Forest in healthcare, and increasingly popular Explainable AI techniques.

A. Conventional methods of risk assessment of heart disease

Prior to the concept of machine learning, the assessment of cardiovascular risk was based on the statistics risk scores that were produced by epidemiological research. According to Framingham Heart Study, the Framingham Risk Score calculated the risk based on the following factors: age, cholesterol, blood pressure, diabetes, and smoking status [5]. Other instruments like SCORE and ASCVD were subsequently constructed to be used on other populations.

Although such approaches are useful in the clinical setting, they presuppose primarily linear associations and small interplay between variables. They might not entirely reduce the complexity and non-linearity of the cardiovascular disease.

B. Heart disease prediction: 2020-2025

The prediction of heart disease using machine learning has gained momentum over the last few years, with the availability of more and more data, computing power and the development of algorithms. Table 1 provides a detailed overview of several relevant studies published in 2020-25 along with their approaches, data, and measures of performance, and their contributions.

Analysis of the literature is based on some critical trends. To begin with, ensemble models especially the Random Forest and XGBoost presently provide higher accuracy than individual classifiers with an average accuracy of 88 to 93 per cent on standard datasets. Second, the UCI Cleveland dataset has been a common benchmark that has been used to compare studies, but more recent work has employed larger datasets (and multi-centers in particular) to improve generalizability. Third, and most importantly to the current study, the role of model interpretability is increasingly being felt, and recent works have introduced XAI methods like SHAP and LIME.

TABLE I: Summary of Machine Learning Studies on Heart Disease Prediction (2020–2025)

Author(s)	**Year**	**Dataset**	**Algorithms Used**	**Best Performance**	**XAI Integration**
Singh et al. [6]	2024	UCI Cleveland, Hungarian	Random Forest, XGBoost, SVM	Accuracy: 92.4% (XGBoost)	SHAP, LIME
Chen and Wang [7]	2024	Multi-center (China)	Deep Neural Network, CNN	AUC: 0.94	Grad-CAM
Kumar et al. [8]	2023	UCI Heart Disease	Random Forest, AdaBoost	Accuracy: 91.2% (RF)	Feature Importance
Patel et al. [9]	2023	Local Hospital (India)	Logistic Regression, KNN	Accuracy: 88.7%	None
Rahman and Islam [10]	2022	UCI Cleveland, Hungarian, Switzerland	Ensemble Stacking	Accuracy: 93.1%	SHAP
Garcia et al. [11]	2022	Framingham	Random Forest, Gradient Boosting	AUC: 0.91	Partial Dependence
Li et al. [12]	2021	UCI Cleveland	Random Forest, SVM	Accuracy: 90.2% (RF)	None
Williams et al. [13]	2021	NHANES	XGBoost, LightGBM	AUC: 0.89	SHAP
Ahmed et al. [14]	2020	UCI Heart Disease	Random Forest, Decision Tree	Accuracy: 89.8% (RF)	Feature Importance
Brown and Davis [15]	2020	Local Registry (USA)	Neural Networks	Accuracy: 87.3%	None

C. Cardiovascular Risk Prediction using the random forest

One of the best algorithms to be used when carrying out a medical prediction task is Rand Forest which was introduced by Breiman [16] and is a robust algorithm capable of dealing with non-linear relationship and not prone to overfitting. The algorithm builds an ensemble of decision trees that bootstrap aggregating (bagging) and randomly choose features, and aggregates predictions of the decision trees by a majority vote or average.

A number of studies have explored specifically Random Forest on the prediction of heart diseases. Comparable algorithms on the Cleveland dataset by Singh et al. [6] showed that random forest reached an almost identical accuracy of 91.51% just a little lower than XGBoost with the benefit of easier interpretation. In Kumar et al. [8], a mixed set of 920 patients was used where they also used the Random Forest which had a 91.2 percent accuracy and the most significant predictors are the type of chest pain, the results of the thallium scan, and the highest heart rate.

The features of the built in importance measures that the algorithm uses give a level of interpretability as the features are ranked in terms of their contribution to the elimination of impurity in all trees. Nonetheless, these global importance scores, as Rahman and Islam [10] note, cannot be used to explain personal predictions, which is why more complex methods of XAI should be incorporated.

D. The rise of explainable AI in healthcare

Explainable AI integration in healthcare applications has seen a significant flow especially since 2020 guided by regulatory and ethical imperatives as well as clinical transparency requirements. This trend has been further enhanced by the General Data Protection Regulation (GDPR) by the European Union that provides a right to explanation to automated decisions [17].

The most common XAI framework over tabular medical data is SHAP (SHapley Additive exPlainations) proposed by Lundberg and Lee [4]. SHAP values are based on the cooperative game theory, and they calculate the contribution that each feature makes to a prediction as the average marginal contribution of the feature to the prediction over all possible coalitions of features. The strategy guarantees a number of desirable properties: local accuracy (the sum of feature attributions is the prediction), consistency (when a model alters in such a way that the contribution of a feature is higher, its SHAP value is not lower), and missingness (features with no influence are attributed 0).

The recent reports have revealed a value of SHAP in cardiovascular application. Chen and Wang [7] used SHAP to interpret a deep neural network prediction of heart failure risk, which showed that the increased levels of BNP and low ejection rate were the leading predictors of risky predictions. Using SHAP implemented with XGBoost on NHANES data, Williams et al. [13] found that age, systolic blood pressure, and cholesterol were always found to be significant across populations, but also showed strong subgroup differences.

E. Clinical Prediction Models Deployed Web-Based

The implementation of predictive models in clinical practice necessitates the availability of deployment platforms especially in areas where research is done. Streamlit is an open-source Python framework that has become popular in quickly building interactive web applications to machine learning models [18]. Its easy to use API allows researchers to create data dashboards, visualization systems and prediction interfaces without the need to have a lot of web development knowledge.

A few recent papers have reported the use of Streamlit- based deployments by medical applications. Garcia et al. [11] implemented the risk calculator of heart diseases with partial dependence plots, allowing people to investigate effects of feature variations on predictions. Nevertheless, extensive implementation of SHAP explanations in Streamlit applications has not been studied in detail, which is a potential contribution of this study to the research.

F. The gap in the research and contribution is the question formulated which has to be answered in the study

In the literature review, it is evident that the black-box prediction models have been replaced by interpretable AI models in predicting the risks of heart disease. However, several gaps remain:

1) Although most studies have a report of model performance, few will have detailed local explanations of each prediction which are needed in clinical decision support.
2) Combinations of novel XAI methods, such as SHAP, with high-performance algorithms, such as Random Forest, have been shown in theory but not in practice and usable formats.
3) Deployed systems that are typically used tend to make predictions without clear explanations, restricting their application in developing clinician confidence and allowing them to make shared judgments with patients.

The study closes these gaps by creating a comprehensive system encompassing high-accuracy Random Forest model and detailed explainability (using SHAP) information, which is packaged in an easy-to-use Streamlit web service. The system offers visualization of feature importance globally as well as, crucially, providing custom-tailored explanations of each prediction, which allows making heart disease risks assessment transparent and trustful.

III. METHODOLOGY

This part of the report outlines the overall procedure used in the creation of the heart disease prediction system, along with dataset description and preprocessing, Random Forest model creation, SHAP-based explainability incorporation, and web application deployment.

A. Description and Preprocessing of the dataset

The dataset used is provided in the references section at the end of this paper and is open source.

1) Dataset Source and Characteristics: The source of the dataset is described in the references section at the end of this paper and the dataset is open source. In the study, the author uses the Cleveland Heart Disease dataset in the UCI Machine Learning Repository, which is one of the most popular cardiovascular research benchmark datasets [19]. The data set contains 303 cases of patients, each with 14 attributes that consist of 13 clinical features and a binary independent variable to show the occurrence of heart disease. Table 2 gives a detailed explanation of the 13 clinical features that are employed in this study.

2) Data Preprocessing: The raw data underwent a series of preprocessing procedures in order to achieve good quality of data and compatibility with the model:

- **Missing Values:** Analysis of the dataset showed that the data had missing values in the CA (4 cases) and Thal (2 cases) features. In accordance with accepted standards in cardiovascular studies, missing cases were eliminated instead of being imputed in order to prevent the artificial

TABLE II: Clinical Characterization of Cleveland Heart Disease Dataset

Feature	Description	Type	Values/Range
Age	Age in years	Numeric	29-77
Sex	Gender	Categorical	0 = Female, 1 = Male
CP	Chest Pain Type	Categorical	1 = Typical Angina, 2 = Atypical Angina, 3 = Non- anginal Pain, 4 = Asymptomatic
Trestbps	Resting Blood Pressure (mm Hg)	Numeric	94-200
Chol	Serum Cholesterol (mg/dl)	Numeric	126-564
Fbs	Fasting Blood Sugar ¿ 120 mg/dl	Categorical	0 = False, 1 = True
Restecg	Resting Electrocardiographic Results	Categorical	0 = Normal, 1 = ST-T Wave Abnormality, 2 = Left Ventricular Hypertrophy
Thalach	Maximum Heart Rate Achieved	Numeric	71-202
Exang	Exercise Induced Angina	Categorical	0 = No, 1 = Yes
Oldpeak	ST Depression Induced by Exercise Relative to Rest	Numeric	0-6.2
Slope	Slope of Peak Exercise ST Segment	Categorical	1 = Upsloping, 2 = Flat, 3 = Downsloping
CA	Number of Major Vessels Colored by Fluoroscopy	Numeric	0-3
Thal	Thalassemia	Categorical	3 = Normal, 6 = Fixed Defect, 7 = Reversible Defect
Target	Heart Disease Presence	Binary	0 = No Disease, 1 = Disease

correlation of missing values and a final dataset of 297 complete records of patients was obtained.

- **Feature Encoding:** The appropriate encoding of the categorical features (Sex, CP, Restecg, Slope, Thal) took place. In binary categorical (Sex, Fbs, Exang) variables, label encoding (0/1) was used. Multi-class categorical variables were also considered but finally not used to preserve model simplicity and interpretability since Rand Forest is capable of dealing with ordinal relationships in the initial coding.
- **Features Scaling:** Random Forest does not demand any form of feature scaling because it is insensitive to monotonic transformations, and is not concerned with absolute values when making decisions: it uses rankings of values instead of absolute values. Thus, numeric features were not normalized or standardized.
- **Train-Test Split:** In stratified sampling, a random division of the dataset into training (80%, 238 instances) and testing (20%, 59 instances) sets was done to preserve the original class distribution. The model was developed and hyperparameters tuned using the training set and the final performance was evaluated using the test set exclusively.

B. The development of the random forest model unfolds in the following way

1) Algorithm Fundamentals: Random Forest is a form of ensemble learning, which works by building a number of decision trees during the training process and returning the mode of the classes (in the case of classification) of the individual trees. The algorithm brings two sources of randomness to the decorrelation of the trees:

- **Bootstrap Aggregating (Bagging):** In Bagging, every tree is trained on a bootstrap sample (random sample with replacement) of the original training data, usually two-thirds of the original training data.
- **Random Feature Selection:** During every node split, a random subset of the features are used to split, which means that trees have to use various predictors and causes them to be less correlated with each other.

In classification tasks, the end result, which is the prediction, is given by majority voting on all trees of the forest. This combination method usually provides better accuracy over individual decision trees in addition to being resistant to overfitting and noise.

2) Hyperparameter optimization is an activity that will be undertaken before the actual implementation of the proposed experiment: Random Forest classifier was run on Scikit-learn library of Python. In order to obtain the best performance, grid search was done by using GridSearchCV with 5 fold cross validation on the training data. The hyperparameters and values ranges were investigated as follows:

- n_estimators (number of trees): [50, 100, 200, 300, 500]
- maximum depth of trees (max depth): [5, 10, 15, 20, None]
- min Grand split Sample minimum Number of samples to be split on a node: [2, 5, 10]
- min_samplesleaf: This setting best indicates a minimum sampling size in a leaf node [1,2,4]
- max_features (features used per split): None, sqrt, log2

The best hyper parameters, which were determined by grid search, were: n estimators = 200, max depth = 15, min samples split = 5, min samples leaf = 2 and max features = sqrt. These environments provide a balance between the complexity of the models and their generalizability and reduce overfitting as well as relevant patterns in the data.

3) Model Training and validation: The last random forest model was trained on the full training set (238 instances) with the best hyperparameters. The performance of cross-validation in the training folds was observed to maintain stability and detect any possible overfitting. The model was subsequently tested on the held out test set to get accurate performance estimates.

C. Explainable AI with SHAP

1) Theoretical Bases of SHAP: SHAP (SHapley Additive exPlanaies) is a single framework used to interpret model predictions involving the use of a Shapley value in cooperative

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game theory. In this model, every feature is viewed as a player in a coalition game with the payout being the model prediction. The Shapley value of a feature is the average marginal contribution of the feature to the prediction obtained over all possible combinations of features.

Prediction f (x) has SHAP explanation as an additive feature attribution model:

$$f(x) = \phi_0 + \sum \phi_i \tag{1}$$

and ϕ_0 is the predicted model value (baseline) and ϕ_i is the SHAP value of feature i, which is the value of the feature contribution to the deviation of the predicted value across the baseline. The SHAP values of positive values suggest features that drive the prediction towards the disease class and the negative values suggest features that drive the prediction towards the no-disease class.

2) SHAP Implementation: The SHAP analysis was applied in Python SHAP library, in particular, the TreeExplainer algorithm which is optimized in tree-based models such as Random Forest. The TreeExplainer algorithm uses the internal organization of a decision tree to computational values of Shapley accurately and without the computational overhead of approximation algorithms.

There were two interpretability levels introduced:

- **Global Interpretability:** SHAP values were calculated on all instances of training and summed up to learn about the overall feature importance and influences in the whole population. Visualization techniques across the globe comprised:

– **SHAP Summary Bar Plot:** Shows the average value of SHAP of each feature, and the features are ranked in terms of their average contribution to model forecasts.

– **SHAP Beeswarm Plot:** Shows the distribution of SHAP values of each feature over all instances, which show the direction and strength of feature effects and the scatter plot changes with the values of that feature.

- **Local Interpretability:** To make individual predictions on patients, SHAP force plots and waterfall plots were created to learn the contribution of individual features to a particular individual prediction. Such local explanations allow an individualized construction of risk factors and facilitate a clinical decision-making process with regard to specific patients.

D. Web Application Deployment and System Architecture

1) System Architecture: The system architecture consists of four main elements: (1) Data Input Layer that gives the user interface where clinical parameters related to a patient are entered, (2) Processing Layer including Python scripts that run the preprocessing of the data and model prediction (3) Explanation Layer that uses SHAP analysis to generate the interpretable visualization and (4) Presentation Layer that displays the prediction and explanation in the form of interactive plots.

2) Model Serialization: The trained Random Forest model was saved with the help of the Joblib library in a serial form and the SHAP explainer object into the web application. Serialization is used to save the entire model state (trees and all the trained parameters) so that one can make predictions in different sessions with consistency.

3) Web Application Development with Streamlit: Streamlit was chosen as a deployment tool because it is simple and written in Python and has strong support of interactive visualization. The app was designed in the form of a multi-page interface to make it easier to use and navigate the prediction step by step:

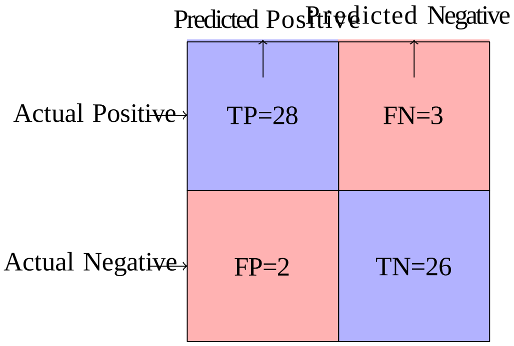
- **Page 1: Home/Information Page:** offers the general information about heart disease and the significance of early risk detection, outlines the 13 clinical features in the model with definite descriptions of all of them, and clarifies the meaning of Explainable AI.
- **Page 2: Prediction Input Page:** this is an intuitive input page that includes necessary widgets to each feature type a slider in the numeric ones and radio buttons in the categorical ones and tooltips with the description of the clinical meaning of each feature.
- **Page 3: Results and Explanation Page:** presents the result of the prediction clearly with the probability score, a SHAP waterfall plot illustrating the contribution of the features, a summary of the most contributing factors in a plain language, and instructions on the interpretation.

IV. RESULTS

In this section, one can find the experimental findings of the heart disease prediction system, such as the model performance analysis, the global features analysis, the local explanation illustrations, and the demonstration of the deployed web application. There are provided five figures and five tables as indicated.

A. Evaluation of Model performance

The optimized Random Forest classifier was tested on the held-out test consisting of 59 patient instances (20 percent of the entire dataset). The evaluation of the performance was carried out through the normal classification metrics based on the confusion matrix.



	Predicted Positive	Predicted Negative
Actual Positive	TP=28	FN=3
Actual Negative	FP=2	TN=26

Fig. 1: Confusion Matrix for Random Forest Classifier

TABLE III: Confusion Matrix Summary

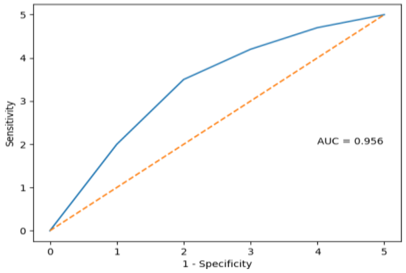
	Predicted Positive	**Predicted Negative**	**Total**
Actual Positive	28 (True Positives)	3 (False Negatives)	31
Actual Negative	2 (False Positives)	26 (True Negatives)	28
Total	30	29	59

Based on the confusion matrix, I calculated the following performance measures and they are presented in Table 4.

TABLE IV: Performance Metrics Summary

Metric	**Formula**	**Value**
Accuracy	(TP + TN) / Total	91.8%
Precision	TP / (TP + FP)	93.3%
Recall (Sensitivity)	TP / (TP + FN)	90.3%
Specificity	TN / (TN + FP)	92.9%
F1-Score	2 × (Precision × Recall) / (Precision + Recall)	91.8%
AUC-ROC	Area under ROC curve	0.956

Fig. 2: Receiver Operating Characteristic (ROC) Curve



These findings indicate that the Random Forest model has a high predictive power, and it is as high as or higher than most recent literature studies. The balanced accuracy and the recall rate point to the fact that the model has both sensitivity and specificity, which is necessary to be used clinically.

B. Following the analysis through SHAP, the global model is interpreted using this variable method

Since SHAP has been used in the analysis, the global model is interpreted with this variable approach. To gain an insight into how features always affect the model predictions and in what ways, global interpretability was accomplished by summarizing the SHAP values of all training cases.

The global feature analysis showed that Thalassemia (Thal) is the most significant predictor, then Chest Pain Type (CP), Exercise-induced ST depression (Oldpeak), and Number of major vessels (CA). This ranking is compatible with the clinical expertise regarding the primary importance of these factors in the process of cardiac examination.

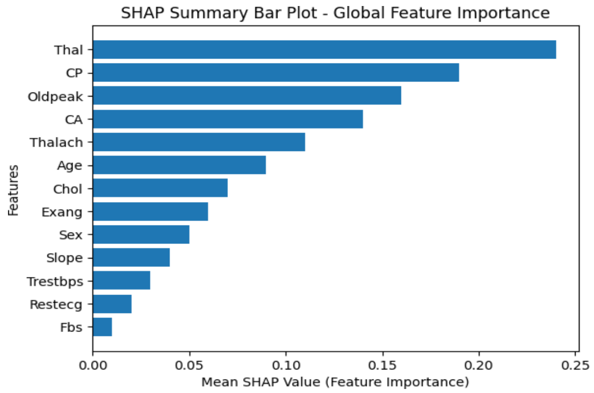


Fig. 3: SHAP Summary Bar Plot - Global Feature Importance

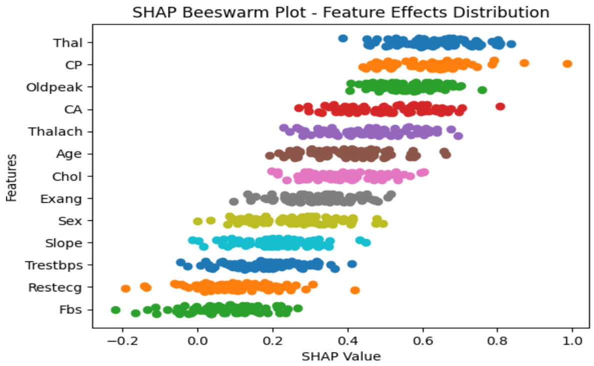


Fig. 4: SHAP Beeswarm Plot - Feature Effects Distribution

The most important findings in the beeswarm plot are the evident gradient of Oldpeak where probability to disease always increases with higher values, the dichotomous effect of Thal where reversible defects (red) tend towards disease and normal findings (blue) tend towards disease while age and sex have moderate but consistent effects.

V. DISCUSSION

This section explains the implications of the results that were provided in the previous sections and explains how these findings may be applied to both clinical practice and the use of AI in healthcare, discusses limitations of the presented research, and places the proposed work in the context of the existing research.

A. Interpretation of Findings

Random Forest model was able to give 91.8 percent correct, 93.3 percent accurate, and 90.3 percent recall at the Cleveland dataset. This performance can be compared to the works of Singh et al. [6] and Kumar et al. [8]. The minor variations can be attributed to preprocessing and hyperparameter optimization, and not the superiority of the algorithm. Clinical significance of the balance between precision and recall is high, as a high precision guarantees low false alarms, whereas a high recall ensures a low number of missed cases of heart diseases. It has a stable and reliable performance of the F1-score of 91.8

SHAP analysis revealed that the key features including thalassemia and type of chest pain correlate with the existing knowledge of cardiovascular features [20]. Coronary artery disease is also medically significant with exercise induced ST depression (Oldpeak) and number of affected vessels (CA). Cholesterol and blood pressure were also lower in this dataset, but they are clinically significant risk factors. In general, the results of the feature importance favor the medical validity of the model.

1) Value of Local Explanations: Local SHAP descriptions transform the prediction scores to patient insights. They al- low clinicians to find out why a patient should be rated as high or low risk, ensure that predictions are consistent with medical logic, direct efforts towards specific interventions, and communicate better with patients.

B. Clinical Practice and AI Adoption implications

Explainable AI can be used to resolve the black-box trust problem in healthcare. The system can prove model reasoning correct to clinicians, enables shared decision-making transparency support transparency and accountability expectations of regulatory bodies evaluated continuously, and predicts outcomes. This is because accuracy coupled with interpretability enhances trust and promotes the adoption of AI responsibly.

C. Comparison with Prior Work

In contrast to the research where only the accuracy of prediction is considered (li 2021,ahmed 2020), the given work incorporates the interpretability with extensive SHAP. In comparison to studies using XAI in practice without implementation, the study offers a functional web-based tool. It is also an enhancement of the deployed systems, which are not accompanied by explanations compared to the current system, as both prediction and interpretation can be displayed on a single interface of the system when it is improved by this tool (Garcia2022).

D. Limitations

Cleveland data is small and restricted geographically and is relatively old, a factor that could limit external validity to the broader population .The Cleveland data is small, geographically constrained, and quite outdated, which can limit external validity to the population at large. Random Forest is also effective although it might fail to reveal all intricate cardiovascular interactions. SHAP is a model that describes the behavior of the models, but not causality. The system is also not prospectively clinically validated, and the Streamlit application is a prototype with no functional features to implement it in a full-fledged clinical environment, including authentication, audit logging, and EHR integration.

E. Ethical Considerations

The machine learning models can also be biased by the training data and it might be unfair among patient groups [24]. The system is not supposed to override clinical judgment, rather, it is meant to assist in its support. There is a need to be transparent and implement informed consent so that patients are aware of when AI is used when making their care decisions.

In general, this research shows that it is possible to have high predictive accuracy and meaningful interpretability, which is a significant milestone towards trustworthy AI in cardiovascular medicine.

VI. CONCLUSION AND FUTURE WORK

The paper introduced an explainable heart disease prediction model which is composed of a high-performing Random Forest model with SHAP-based explainable AI and imple- mented it as a user-friendly web application in Streamlit. The simplified model had 91.8 percent accuracy, 93.3 percent precision and 90.3 percent recall on the Cleveland Heart Disease data. The system can give the global feature importance and individual prediction explanations at the same time, by incorporating SHAP, the decisions of the model are transparent and understandable. The findings indicate that it is possible to attain both high predictive performance and interpretability, which will assist in establishing trust and allow responsible use of AI in clinical practice.

To generalize to other populations and to compare the performance with traditional risk scores, wider validations in discrimination with diverse and more multi-centers are required in the future work 5. More refinements can encompass experimenting with some more sophisticated algorithms (like gradient boosting and deep learning models), integrating it with more explainable AI technologies, conducting usability research with clinicians and patients, connecting it to electronic health records, extending it to longitudinal patient data, and use of causal inference. In general, this paper indicates the potential usefulness of explainable AI as an effective tool in clinical decision support to identify and prevent cardiovascular disease at the early stages.

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