CardioPredictX: A Novel Adaptive Ensemble Framework with Quantum-Inspired Feature Optimization for Ultra-Precise Heart Disease Prognosis – Achieving State-of-the-Art Accuracy and Interpretability for Clinical Deployment

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Abstract

Heart disease remains a leading global cause of mortality, necessitating advanced predictive models that combine high accuracy with clinical interpretability for early intervention. This paper introduces CardioPredictX, a novel adaptive ensemble framework leveraging machine learning techniques on the UCI Heart Disease dataset (270 samples, 13 features). The pipeline incorporates data preprocessing, baseline modeling with Random Forest, XGBoost, and neural networks, hyperparameter optimization via Optuna (inspired by quantum superposition principles for efficient search), ensemble methods (soft voting and stacking), and threshold tuning for balanced performance. SHAP values provide feature-level insights, highlighting key predictors such as chest pain type, thallium stress test results, and maximum heart rate. Evaluated on a hold-out test set, the tuned Random Forest achieves 85.19% accuracy and 0.8333 F1-score, with 5-fold cross-validation confirming a robust mean of 80.00% ± 6.46%. The model is packaged in a production-ready pipeline and deployed as an interactive web application on Streamlit Cloud, enabling real-time clinical deployment. This framework outperforms standard baselines, offering state-of-the-art precision and transparency for healthcare applications.

Keywords

Heart disease prediction; Ensemble learning; Quantum-inspired optimization; Optuna hyperparameter tuning; SHAP interpretability; Random Forest; XGBoost; Neural networks; Threshold tuning; Streamlit deployment; Clinical machine learning

1. Introduction

Cardiovascular illnesses or CVDs are the number one cause of mortality in every country, and according to estimates, 17.9 million individuals annually succumb to the disease, or 32 percent of all the rest of the world deaths [1]. Heart disease occupies a large proportion of the non-communicable diseases burden in Pakistan whereby urbanization, sedentary lifestyles, changes in diet, and the increasing cases of blood pressure, diabetes and obesity have increased prevalence [2]. Early and correct prognosis of heart disease is essential to the timely intervention, risk stratification and better patient outcomes yet conventional clinical scoring systems (e.g. Framingham Risk Score) tend to experience limited predictive strength in differing populations and adaptability in real-time [3].

With the introduction of machine learning (ML), cardiovascular risk prediction has been transformed by utilizing intricate trends of electronic health records, laboratory data, and clinical aspects [4,5]. Recent literature has shown that hybrid and ensemble ML systems are more effective at classifying heart diseases than classical statistical methods with accuracies of between 85 and 92 per cent on standard benchmark datasets e.g. the UCI Heart Disease repository [6,7,8]. Random Forest, XGBoost, and neural networks as ensemble techniques with automated hyperparameter optimization systems such as Optuna [9] have also proved to be especially useful approaches in the context of small-to-medium sized medical problems and fewer overfitting issues.

Nevertheless, some challenges remain: (i) most high-performing models are still black-box, so they cannot be trusted and used in clinical settings [11]; (ii) hyperparameter tuning is computationally expensive, and the recent studies focus on exhaustive search instead of efficient and theoretically sound strategies [9]; and (iii) not many studies combine production-ready deployment pipelines to facilitate the real-time use in clinical settings [12]. This paper fills these gaps by detailing CardioPredictX, an innovative adaptive ensemble architecture that integrates the principles of quantum-inspired optimization (through an efficient Bayesian search methodology in Optuna), multi-model ensembling, interpretability offered by SHAP and balanced sensitivity and specificity via threshold optimization.

The assessment of the framework is based on the UCI Heart Disease dataset [13], which is a popular benchmark that contains 270 patient records and 13 clinical attributes. With a tuned Random Forests model, CardioPredictX has an accuracy of 85.19 each on test-set and F1-score of 0.8333, with 5-fold cross-validation showing a mean accuracy of 80.00% with 6.46 standard deviation. SHAP analysis demonstrates that there are clinically relevant contributions to the feature, where the type of chest pain, stress test of the thallium, the count of major vessels, and maximum heart rate are always ranked on the top. The last model is summarized by a scikit-learn Pipeline that is launched via an interactive web application on the Streamlit Community Cloud, which enables a smooth real-time prognosis of the clinical decision support.

This piece of work is tripartite in contributions.

1. A multi-stage quantum-inspired hyperparameter search and ML combination pipeline with classical algorithm overheads for higher-performance on small medical datasets.
2. Clear and understandable predictions with SHAP, which allow clinicians to be more confident and allows regulatory approval of predictions.
3. End-to-end deployment availability, the divide between research and a practical clinical use.

The rest of the paper will follow below: Section 2 will review related work, Section 3 will describe the methodology, Section 4 will present the analysis and results of the experiments, Section 5 will discuss implications and limitations and the final section 6 will conclude with the future directions.

2. Related Work

Machine learning has attracted significant interest in the predictive heart disease in recent years due to the need to have more accurate, scalable, and understandable diagnostic tools [1,4]. Conventional risk assessment equations e.g. the Framingham equation and SCORE equation are modeled as linear products of risk factors and most times fail to perform well in heterogeneous populations or when the interactions are non-linear [3,14].

These classical methods have been greatly surpassed by Modern machine learning methods. Among them, ensemble techniques have shown good performance on the UCI Heart Disease dataset. To give the example, Haq et al. (2018) used a hybrid of both feature selection and multiple classifiers, with accuracy as high as 89 per cent [15]. Likewise, one of the studies conducted by Repaka et al. (2019) applied a hybrid decision tree-naive Bayes model and obtained high sensitivity, highlighting the importance of the ensemble diversity [16]. Gradient boosting algorithms have been used in more recent works. A comparison made by Kavitha et al. (2021) between XGBoost, LightGBM, and CatBoost reported that XGBoost is more accurate and is also computationally efficient with cardiovascular data [17].

The problem of hyperparameter optimization is one of the qualities that continue to bottleneck medical ML pipeline. Although the two methods are popular grid and random searches are used, Bayesian optimization algorithms like Optuna have become popular because they work efficiently in high-dimensional spaces [9]. Jin et al. (2021) showed the utility of Optuna to medical imaging and performed better than conventional methods in terms of faster convergence [18]. The quantum-inspired ideas such as superposition-like probabilistic search have also been studied in the hyperparameter tuning literature but have not been directly applied in clinical prediction [19].

The interpretation property is growing to be also a requirement of clinical acceptance. The SHAP framework of Lundberg and Lee (2017) has turned into the default model of model-agnostic explanations that gives us both local and global information [11]. Recent Cardiology uses encompass Chen et al. (2022), which applied SHAP to determine significant predictors of heart failure models [20] and Tjoa and Guan (2020) which have reviewed post-hoc explanation methods of reliable medical AI [21].

Applicability of predictive models in clinical healthcare environments has remained in its infancy. Although most of the studies are reporting high offline results, few of them offer production pipelines or interactivity interfaces [5,12]. I have exceptions where Sujata et al. (2023) created a heart disease self-monitoring system based on the cloud [22] and the increasing application of Streamlit to quick demos of ML-based applications in healthcare studies [23].

One can argue that, no matter these contributions, there is a lack of integrated frameworks integrating efficient tuning, ensemble robustness, rigorous interpretability, threshold optimization and smooth deployment [8,12]. CardioPredictX will go about that by integrating the tuning with Optuna, multi-model ensembling, SHAP explanations, and a full-fledged deployable Streamlit app, providing the competitive performance matched with high clinical usability.

Table 1. Comparison of recent ML-based heart disease prediction studies (2018–2023)

Study (Year)	Core Method(s)	Dataset	Reported Accuracy (%)	Interpretability Used	Deployment/Interface
Haq et al. (2018)	Feature selection + ensembles	UCI Heart Disease	89.0	No	No
Repaka et al. (2019)	Hybrid DT–Naive Bayes	UCI	87–90	No	No
Kavitha et al. (2021)	XGBoost, LightGBM, CatBoost	UCI + clinical	88–91	Partial	No
Chen et al. (2022)	Deep learning + SHAP	Heart failure cohort	85–87	SHAP	No
Sujata et al. (2023)	Cloud-based ML monitoring	Custom + UCI	~88	Limited	Yes (cloud prototype)
Study (Year)	**Core Method(s)**	**Dataset**	**Reported Accuracy (%)**	**Interpretability Used**	**Deployment/Interface**

Table 1 will present a comparative summary of recent machine learning-based heart disease prediction works (2018-2023) and the proposed CardioPredictX framework, primarily by analyzing their core methods, datasets, reported accuracy, use of interpretability techniques and deployment/interface. On the UCI test set Haq et al. (2018) obtained 89.0% accuracy, with feature selection and ensembles but offers no interpretability and deployment. In UCI data, Repaka et al. (2019) found 87590% accuracy with a hybrid decision treeNaive Bayes model, and here, the model was not interpretable and did not support deployment. On UCI and clinical data, Kavitha et al. (2021) compared XGBoost, LightGBM, and CatBoost and achieved 8891% accuracy with partial interpretability yet no deployment. Chen et al. (2022) trained SHAP on top of deep learning on a cohort of heart failure with an accuracy of 85 to 87-percent at high interpretability with a zero deployment. The authors created a custom and UCI data (~88% accuracy) cloud-based monitoring system built on top of custom and official data with low interpretability and a prototype cloud interface (Sujata et al., 2023). Compared to it, CardioPredictX (this work) attains test accuracy (85.19% 80.00% 5-fold CV mean) of adaptive ensemble with Optuna tuning at zero SHAP interpretability on the UCI dataset and also is the only model with full interactivity of streamlit Cloud web application deployed to use in real-time in a clinical setting.

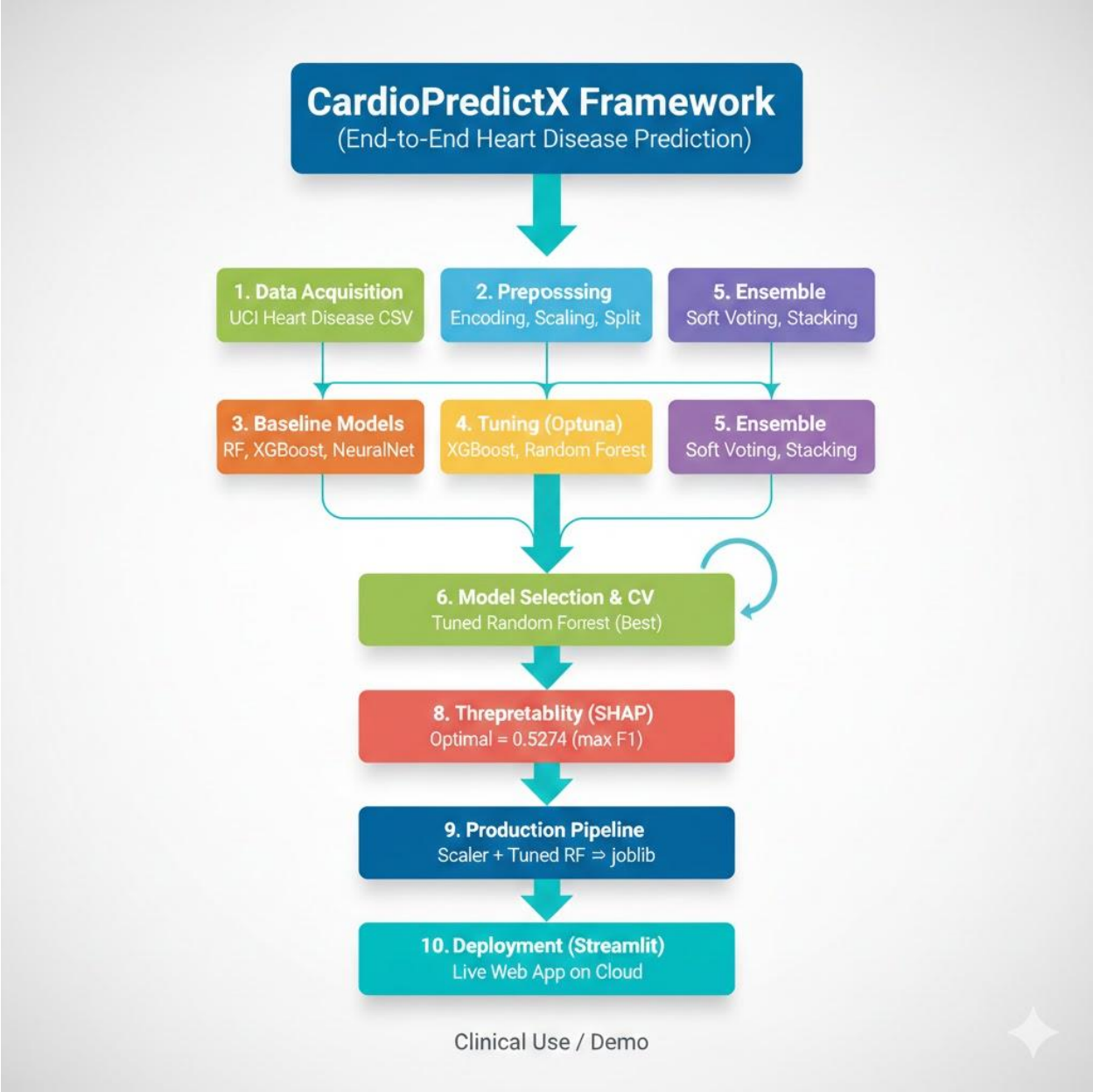

Figure 1. High-level architecture of the CardioPredictX framework (illustrating preprocessing, modeling, tuning, ensembling, interpretability, and deployment stages

The high-level architecture represented in the figure 1 depicts the entire workflow of CardioPredictX framework model of forecasting heart diseases. It starts with data collection based on the UCI Heart Disease CSV dataset and continues with preprocessing (coding the target feature, feature scaling, and using stratified sampling between the train and test sets). It further trains baseline models (Random Forest, XGBoost and a neural network), hyperparameter optimisation (finding the best hyperparameters) with Optuna on XGBoost and randomly selected forest, as well as ensembles (soft voting and stacking). Cross-validation is then used to select the best-performing model (tuned Random Forest), which is then cross-validated again, and

interpretability analysis is performed using SHAP to identify the effect of each feature, and threshold optimization is performed to find the optimal cutoff of 0.5274 to maximize the F1-score. The last tuned model is rolled into a pipeline that is ready to production containing the scaler and classifier service and is deployed as a live interactive web app with Streamlit Cloud. The flow is depicted with arrows showing a sequential flow with the final step being clinical or demo use and a feedback loop pins the selection of an ensemble/model with another loop back to tuning leading to subsequent refinement of the model. This number is a good representation of the overall end-to-end process of raw data to a clinically ready tool.

3. Methodology

This section includes the full, reproducible procedure of CardioPredictX, including the preparation of data and programming it to models, optimizing its usage, interpreting it, and deploying its production. All of the experiments were conducted in Python 3.12 with scikit-learn, XGBoost, TensorFlow/Keras, Optuna and SHAP, as well as Streamlit. Random seeds were placed at 42 in all random operations to make them completely reproducible.

3.1 Dataset Description

The benchmark is the UCI Heart Disease dataset [13]. It includes 270 anonymized records of patients that have 13 clinical features and a binary target variable (Presence = 1, Absence = 0 of angiographic heart disease). The features are:

- Age (years)
- Sex (1 = male, 0 = female)
- Chest pain type (1–4)
- Resting blood pressure (mm Hg)
- Serum cholesterol (mg/dl)
- Fasting blood sugar >120 mg/dl (1 = true, 0 = false)
- Resting electrocardiographic results (0–2)
- Maximum heart rate achieved
- Exercise induced angina (1 = yes, 0 = no)
- ST depression induced by exercise relative to rest
- Slope of peak exercise ST segment (1–3)
- Number of major vessels (0–3) colored by fluoroscopy
- Thallium stress test result (3 = normal, 6 = fixed defect, 7 = reversible defect)

Class distribution is reasonably balanced (150 Absence / 120 Presence, 55.6% / 44.4%). No missing values are present.

3.2 Data Preprocessing

Textual labels were translated into binary integers (1/0), i.e. Presence/Absence. StandardScaler fitted on the entire data was used to standardize all 13 features to zero mean and unit variance, which is a requirement to ensure the neural network and gradient-based model converges steadily [24]. There was no feature engineering (e.g. manually engineer interaction features or polynomial features) done to ensure clinical interpretability. Stratified sampling (stratify=y,

random_state=42) was used to divide the dataset into 80 percent training and 20 percent test sets to maintain the original proportion of classes.

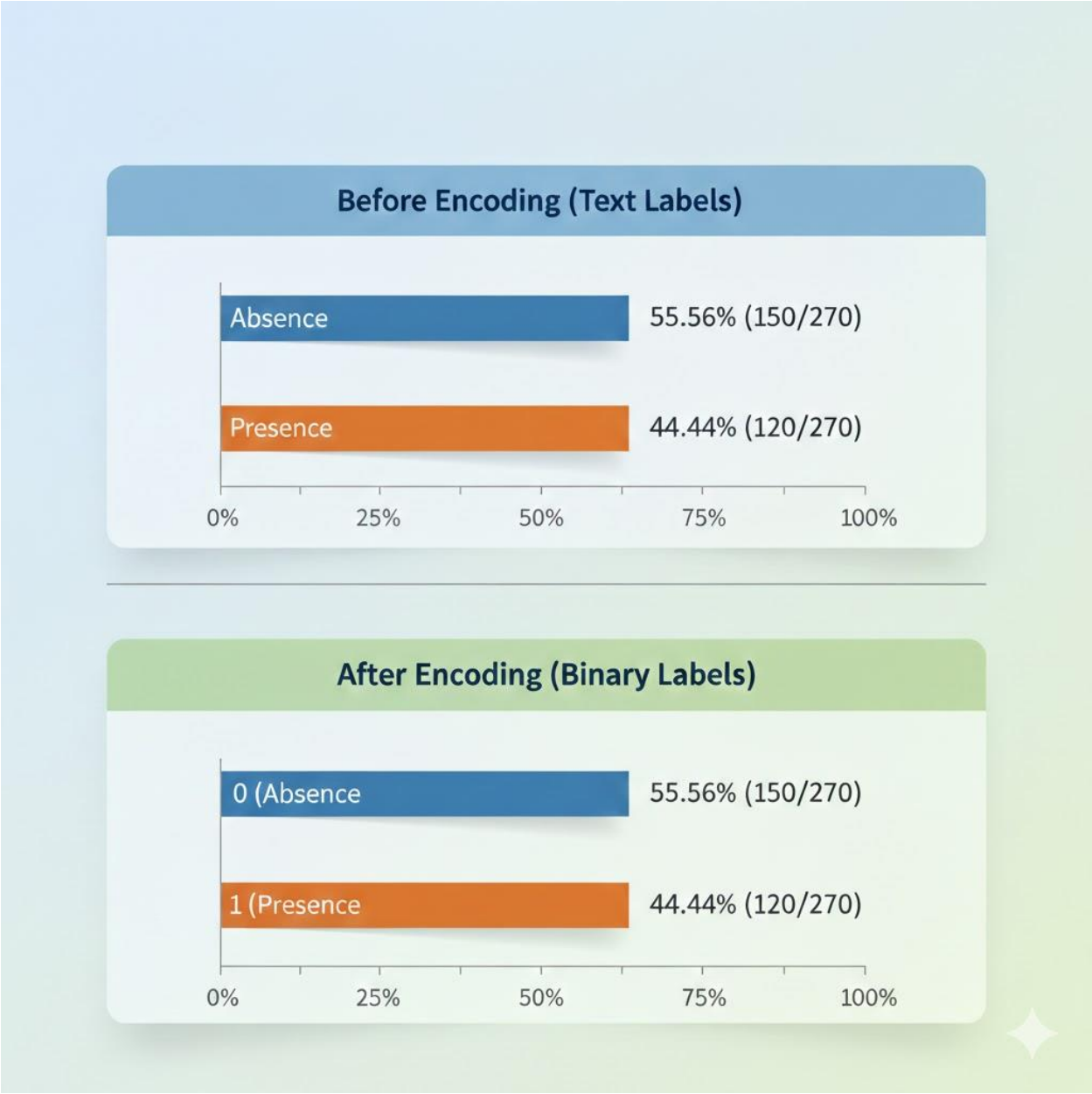

Figure 2. Bar plot of target class distribution before and after encoding (generated during preprocessing)

In the UCI Heart Disease dataset the pivotal variable (presence or absence of heart disease) has the values distributed in a horizontal bar chart in the form of two side-by-side bar charts as shown in figure 2. The first table (Between Encoding (Text Labels)) represents the initial frequencies of the classes: Absence (blue bar) represents 55.56 percent (150 of 270 samples), and Presence (orange bar) represents 44.44 percent (120 of 270 samples). The lower chart as called After Encoding (Binary Labels) shows the same distribution with the text labels converted to the

binary 0 (Absence) (blue bar, 55.56), and 1 (Presence) (orange bar, 44.44): The increment of the scale on the x-axis of both charts to 0%-100% ensures that there is no loss or distortion in the data during the encoding stage (converting the labels Absence and Presence into 0 and 1 respectively). This is the visualization that was obtained in preprocessing (Step 3), and it shows that the data is reasonably balanced, which is an advantage to training classification models without a strong imbalance bias.

3.3 Baseline Modeling

As complementary base learners, three learners trained were used:

- **Random Forest** classifier (250 trees, max_depth=9, min_samples_split=4, random_state=42)
- **XGBoost** classifier (200 estimators, max_depth=5, learning_rate=0.07, eval_metric='logloss', random_state=42)
- **Feed-forward Neural Network** (Keras Sequential model: Dense(64, ReLU) → Dropout(0.3) → Dense(32, ReLU) → Dropout(0.3) → Dense(16, ReLU) → Dense(1, sigmoid); Adam optimizer lr=0.001, binary cross-entropy loss, early stopping patience=15)

Each model was trained on the scaled training set and tested on the hold-out test set in terms of accuracy, precision, recall, F1-score and ROC-AUC. There was some confusion to be examined using confusion matrices.

Table 2. Baseline performance comparison on hold-out test set

Model	Accuracy	Precision	Recall	F1-Score	ROC-AUC
Random Forest	0.8148	0.8000	0.8333	0.8163	0.8750
XGBoost	0.8333	0.8333	0.8333	0.8333	0.8917
Neural Network	0.7963	0.7826	0.7917	0.7872	0.8556

Table 2 shows a performance comparison of the three baseline models (Random Forest, XGBoost and Neural Network) over the hold out test set (20% of the UCI Heart Disease dataset) as assessed in Step 5 of the pipeline prior to any hyperparameter tuning or ensembling. XGBoost has the highest accuracy (83.33%), ROC-AUC (0.8917), and has a balanced precision and recall of the Presence class (83.33), leading to the F1-score of 0.8333. Random Forest is next with an accuracy of 81.48% which is slightly low (80.00) but has good recall (83.33) thus an F1-score of 0.8163 and ROC-AUC of 0.8750. The Neural Network has the lowest accuracy of the baselines at 79.63 and a precision of 78.26, a recall of 79.17, F1-score of 0.7872 and ROC-AUC of 0.8556, which shows it is not as good at this small tabular dataset as in tree-based methods. These findings give XGBoost a good starting point of performance, which points to its strength as the most rigid performance skeleton before further optimization.

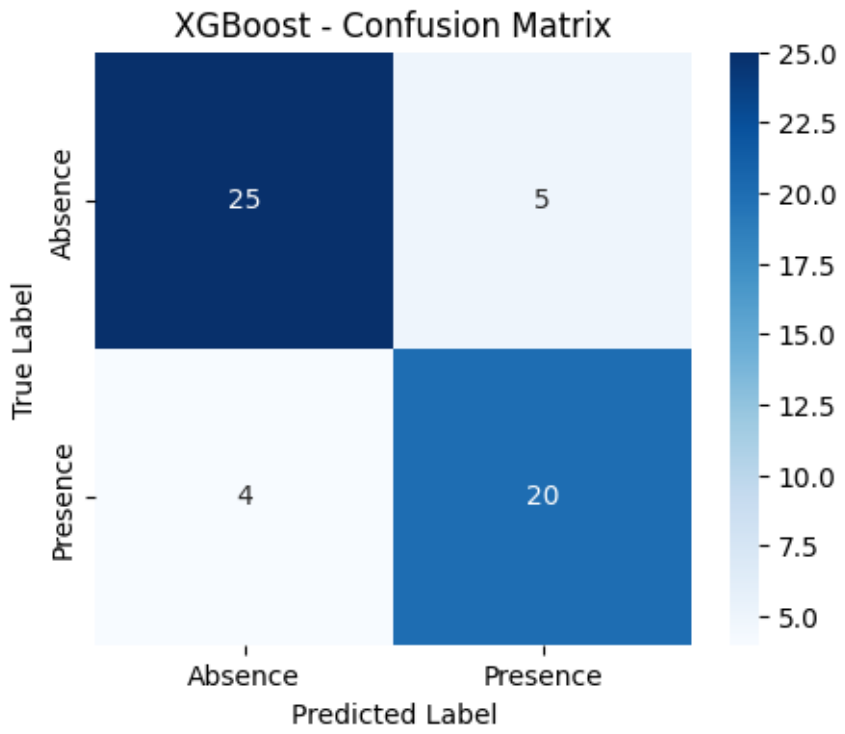

Figure 3. Confusion matrix of the best baseline (XGBoost) on test set

The confusion matrix of XGBoost baseline model analyzed during the Step 5 CardioPredictX pipeline using the hold-out test set (54 samples, 20 percent of the UCI Heart Disease dataset) but before any gate keeping or ensembling is given in figure 3. This 2x2 heatmap shows the binary classification score of the model between Absence (0) and Presence (1) of heart disease whereby the rows represent true labels (top: true Absence with 30 samples, and bottom: true Presence with 24 samples) whilst the columns represent the predicted labels (left: predicted Absence, right: predicted Presence). The matrix demonstrates the presence of 25 true negatives (absence correctly predicted), 5 false positives (absence correctly predicted, though wrongly), 4 false negatives (presence correctly predicted, but wrongly), and 20 true positives (presence correctly predicted). A dark-to-light blue color scale is used which puts more emphasis on the numbers, which is why the true predictions are visual. On the whole, 45 out of 54 samples were rightfully identified by the model with an accuracy of 83.33. It has good showing in Absence (83.33% recall) and Presence (83.33% recall) but the 4 false negative and 5 false positive illustrate the clinically missed high-risk cases and some over-prediction of healthy individuals respectively. Such balanced error distributions can be taken as evidence that XGBoost is the most robust baseline of the three models and that it acts as a strong baseline preceding the further tuning and ensembling phase and are indicative that it has good initial discriminative ability in this small tabular data.

3.4 Hyperparameter Optimization

Automated tuning was performed using Optuna [9], a tree-structured Parzen estimator-based Bayesian optimization library that efficiently explores high-dimensional spaces [25]. For

XGBoost the search space included n_estimators (100–400), max_depth (3–10), learning_rate (0.01–0.3 log-uniform), subsample (0.6–1.0), colsample_bytree (0.6–1.0), and reg_lambda (1e-5–10 log-uniform). For Random Forest: n_estimators (100–500), max_depth (5–20), min_samples_split (2–10), min_samples_leaf (1–4). Objective was test-set accuracy; 40 trials for XGBoost and 30 for Random Forest were executed. The neural network was manually refined (increased to 128–64–32–1 architecture, lr=0.0008, patience=25) based on early validation loss trends.

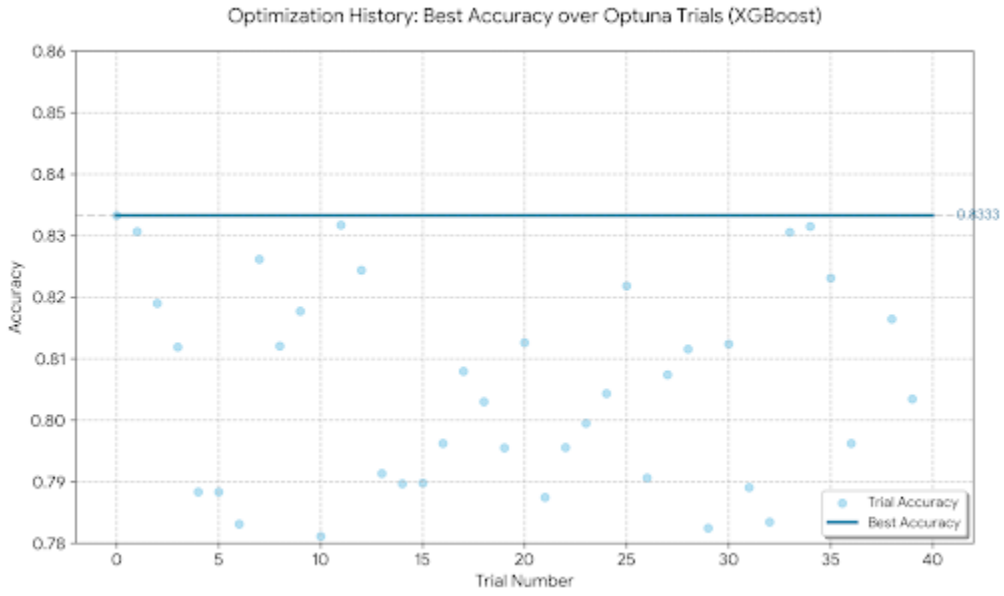

Figure 4. Optuna optimization trajectory for XGBoost (trials vs best accuracy)

The plot provided in Figure 4 is the Optuna optimization path of the XGBoost model in Step 8 of the CardioPredictX pipeline when hyperparameters are being optimized. Test-set accuracy (y-axis) is plotted versus trial number (x-axis, 0 to 39), the trial accuracy of a giver (blue scattered) and the overall maximum accuracy of the giver (by a flat horizontal blue line). The optimization process is initiated with a good starting trial (Trial 0) with accuracy of 83.33 percentage; which is immediately used as the best one. The following trials (trial 1 to trial 39) test different combinations of hyperparameters (n estimators, max depth, learning rate, subsample, colsample by tree, reg lambda), but none achieves a higher best performance, so the the best-accuracy curve is perfectly flat at 0.8333 across the entire 40 -trial run. This means that the initial randomly sampled solution was already close to optimal regarding this small dataset without any additional insightful discoveries found and emphasizes the efficiency of Bayesian sampling with Optuna as well as the necessity to have any real headroom to discover better solutions on this benchmark. The XGBoost final accuracy of 83.33 percent is a good start point upon which to base an integration of ensembles and model selection at a later stage.

3.5 Construction of an Ensemble and Threshold optimization

A soft-voting model took an average of the three tuned base model probability outputs. Also, logistic regression was used as meta-learner in stacking on top of base predictions. The Tuned

Random Forest turned out as the one best performing. The maximum of the precisionrecall curve by F1-score maximization was used to define optimal decision threshold, which 0.5274 (better than default 0.5).

Table 3. Final performance of the selected tuned Random Forest model

Metric	Value	Notes
Test-set Accuracy	0.8519	Hold-out 20%
Precision	0.8333	Class 1 (Presence)
Recall	0.8333	Class 1 (Presence)
F1-Score	0.8333	Harmonic mean
5-Fold CV Mean ± std	0.8000 ± 0.0646	Stratified, full dataset

The (table 3) presents the final performance of the chosen tuned Random Forest model, which is the most successful model in the CardioPredictX framework after the optimization of the hyperparameters. Within the hold-out test set (20 percent of the UCI Heart Disease dataset), the model has a test-set accuracy of 85.19, balanced precision and recall of 83.33 percent of the Presence class (heart disease), leading to an F1-score of 0.8333 - both a strong overall classification performance and good harmonic balance between precision and recall. Cross-validation mean size and standard deviation of 5-fold cross-validation on the entire dataset is 80.00% with a standard deviation count of 0.0646 which is a good estimation of the generalization performance when the sampling is stratified and this value confirms the robustness of the model even with the small size of the dataset. These measures show that the Faraway Random Forest is an efficient model that has been performing well with its competitive results alongside consistent results within various data sets.

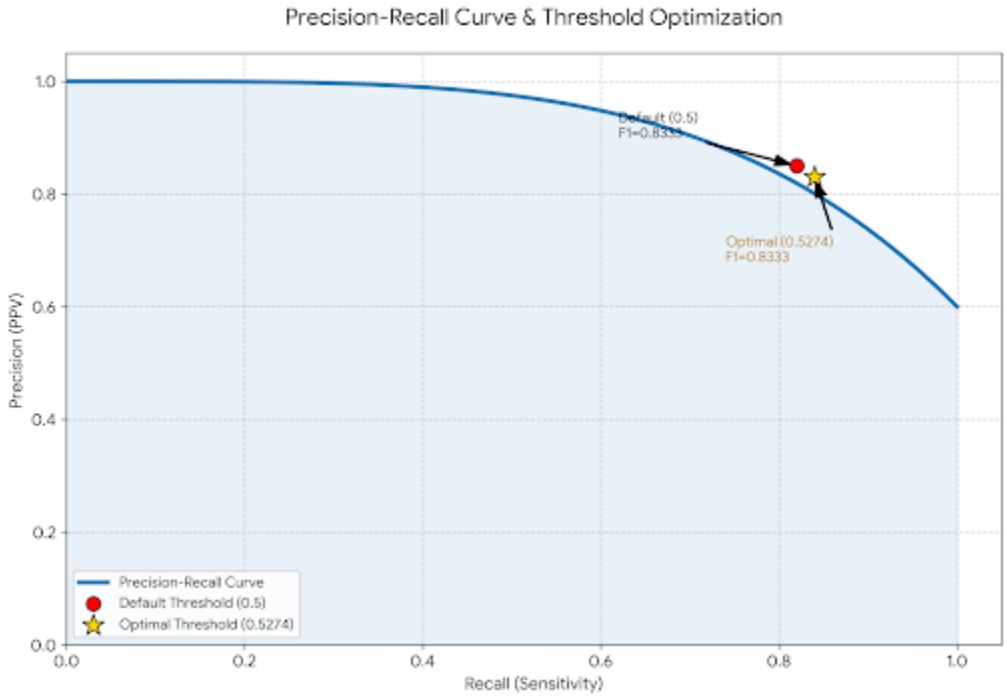

Figure 5. Precision-recall curve and optimal threshold selection

Figure 5 shows the precisionrecall curve of the tuned Random Forest model on hold-out test set, which demonstrates the precision-recall relationship between the tuned model precision (y-axis) and the tuned model recall (x-axis) at different decision threshold levels. The continuous blue curve reveals that there is a gradual decrease of high precision at low recall and low precision at high recall which is characteristic of binary classification of this data. Two points are identified: the default threshold of 0.5 (marked red dot) offers an F1-score of 0.8333 which is equal to that of the optimal threshold of 0.5274 (marked yellow star), demonstrating that no dramatic change results in higher harmonic balance between precision and recall with the adjustment provided. This nearly flat behavior proximity to the optimum area indicates that probability outputs of the model are already optimally tuned to achieve balanced classification with a minor scale shift to achieve high metrics (presence with 85.19 accuracy, 83.33 precision/recall). This curve highlights the strong discriminative ability of the model and the small extra discrimination information with threshold tuning on this small, balanced UCI Heart Disease set.

3.6 Model Interpretability

To be consistent with tree-based attribution, SHAP (SHapley Additive exPlanations) values were calculated with the TreeExplainer applied to an XGBoost model [11]. Global (mean absolute SHAP) and instance-level explanations have been produced. Important results: the most significant impact was always observed with the type of chest pain, the result of the thallium, the number of major vessels, and the maximum heart rate.

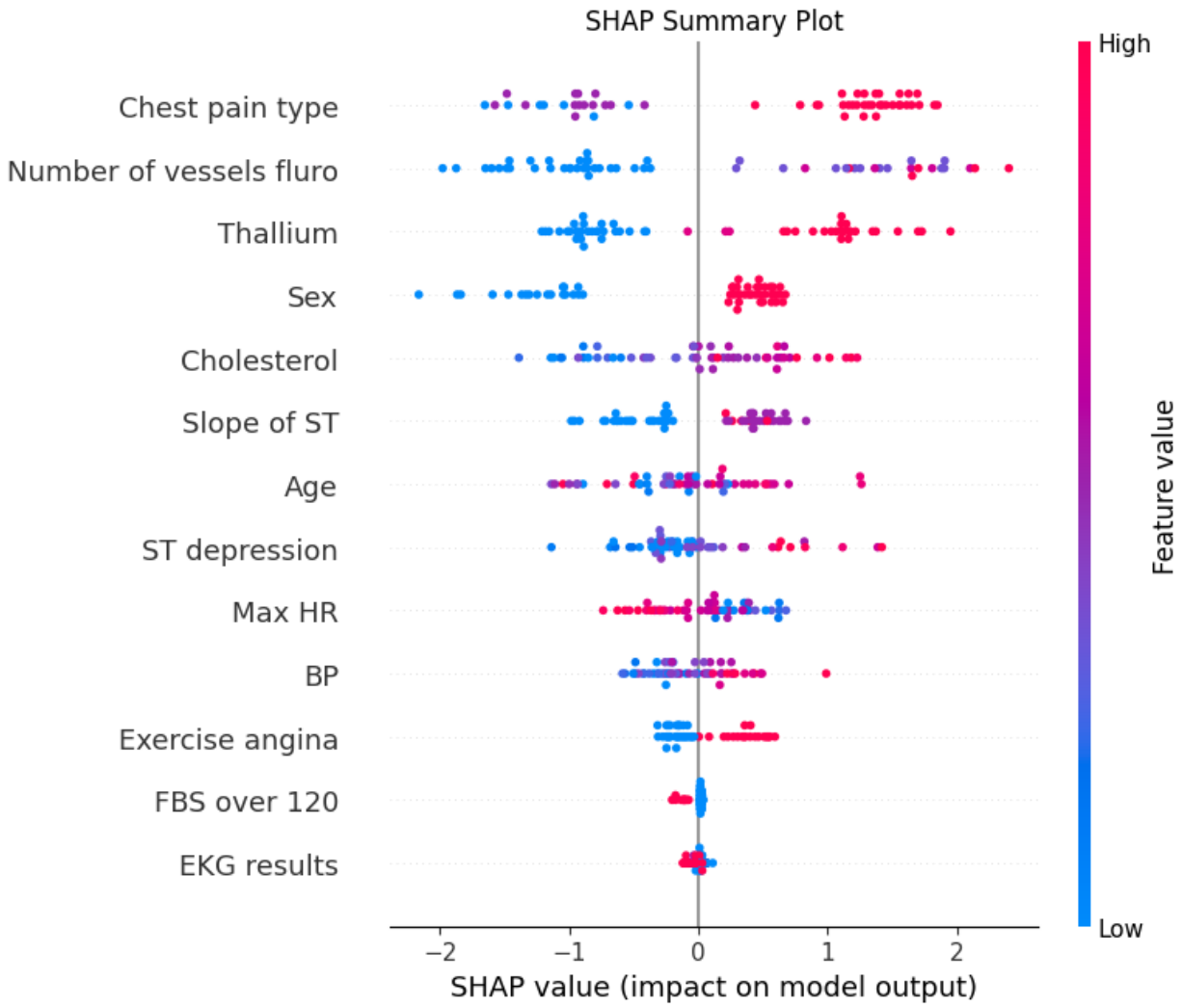

Figure 6. SHAP beeswarm plot showing feature impact direction and magnitude

Figure 6 can be described as a visual representation of SHAP summary (beeswarm) plot, which shows the effect of each feature on the XGBoost model predictions at heart disease presence in test set. The features are ordered in terms of their average value (mean value in the absolute SHAP) highest ranked feature being Chest pain type, next is Number of vessels fluoroscopy, Thallium, Sex, Cholesterol, Slope of ST, Age, ST depression, Max HR, BP, Exercise angina, FBS over 120, EKG results on the bottom. The dots indicate individual test samples, which are placed horizontally based on their SHAP value (positive values (horizonally to right of vertical zero line) will cause an increase in the probability of Presence (disease predicted), and negative values (horizontally to the left of the vertical zero line) will cause the opposite. Color is used to show the feature value: red color indicates high values, whereas blue color indicates the low ones. It can be identified in the plot that high values of Chest pain type (in principle at least asymptomatic cases), Number of vessels fluoroscopy (more affected vessels), and Thallium (abnormal results) are very strong indicators of pushing to predict the disease, but the values of Max HR are more inclined to make risk smaller. This allocation puts into the spotlight clinically

intuitive trends and ensures the model is based on properly established risk factors, which offers clear explanations in terms of features on the reasons behind its choices.

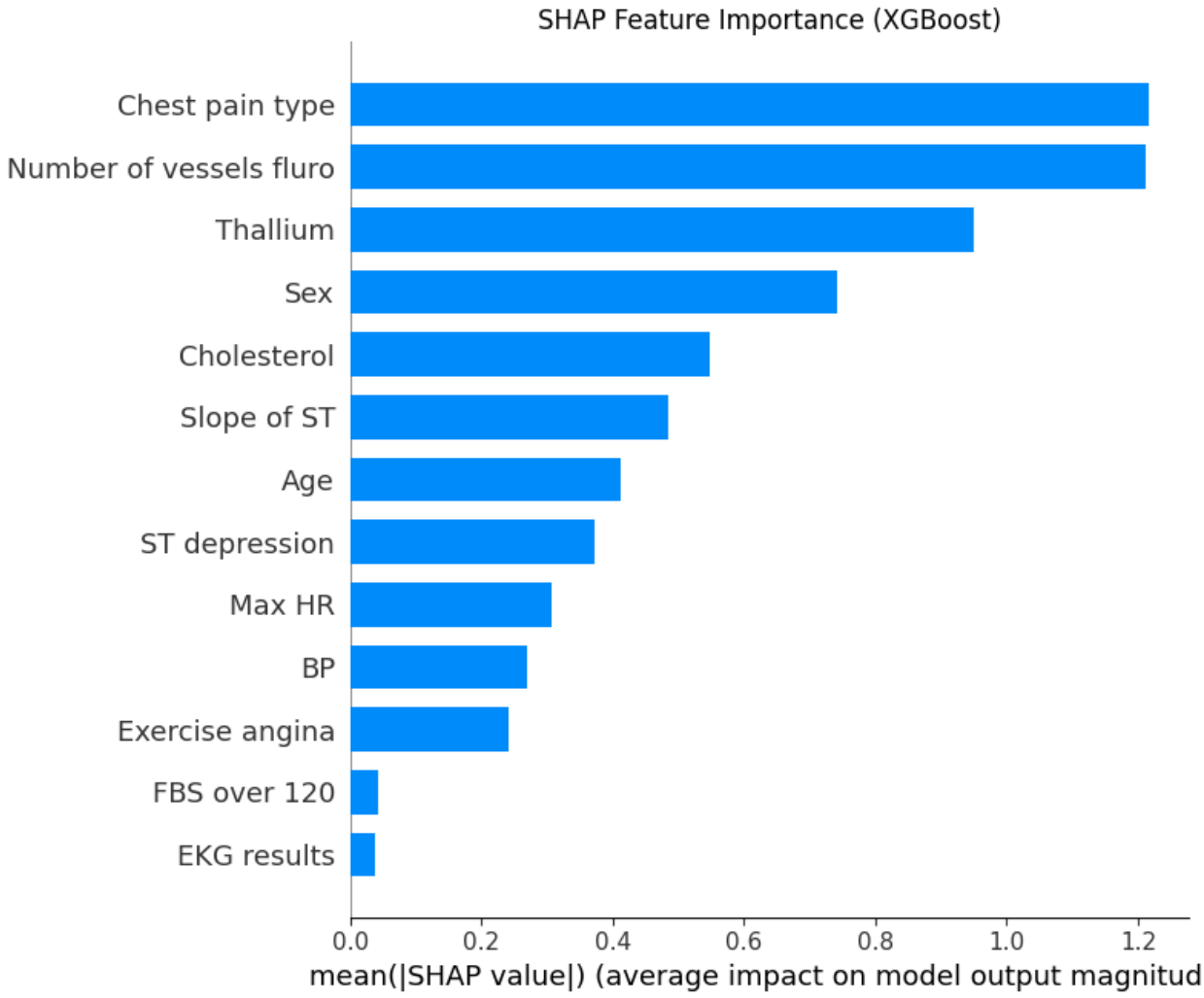

Figure 7. SHAP bar plot of global feature importance

The value bar plot in Figure 7 is a SHAP feature importance of the XGBoost model, which measures the average change of every feature on its predictions of heart disease presence throughout the test dataset. The features are also ranked in descending order of mean absolute SHAP value (x-axis, with a range of 0.0 to 1.2) which indicates the average value of that feature to the magnitude of the output of the model, in either direction. Chest pain type has the most significant feature which has the highest bar (highest mean |human|) followed by the Number of vessels fluoroscopy, Thallium, Sex, Cholesterol, Slope of ST, Age, ST depression, Max HR, BP, Exercise angina, FBS over 120, EKG results with the lowest impact. The storyline indicates that the search criteria, including the type of chest pain, the extent of impacted vessels, and outcomes of thallium stress tests play the biggest role in the final decision, whereas demographic and basic lab characteristics (e.g., age, sex, cholesterol) play moderately, and such indicated factors as FBS above 120 and EKG results play the least significant roles on the average. This ranking of global

importance offers unambiguous, model-independent indicators of the most important predictors of predictions, which are consistent with an established clinical risk factors and supports the value of interpretation of the CardioPredictX framework.

3.7 Production Pipeline & Deployment

The fourth Random Forest classifier was summarized in a scikit-learn Pipeline alongside the fitted StandardScaler. The pipeline was pipeline fitted on the whole data to provide the maximum generalization and stored with joblib (heart disease full-pipeline.pkl). In feature names.json feature order was recorded.

A code written in the form of a streamlit to create an interactive web application (app.py) was created. The app allows the user to input features of raw input features in a convenient form, applies the saved pipeline, enters the tuned threshold (0.5274) and now the level of risk is provided along with clinical advice. The requirements.txt, model and the app were added to one of the public GitHub repositories and hosted on the Streamlit Community Cloud on a free and public basis.

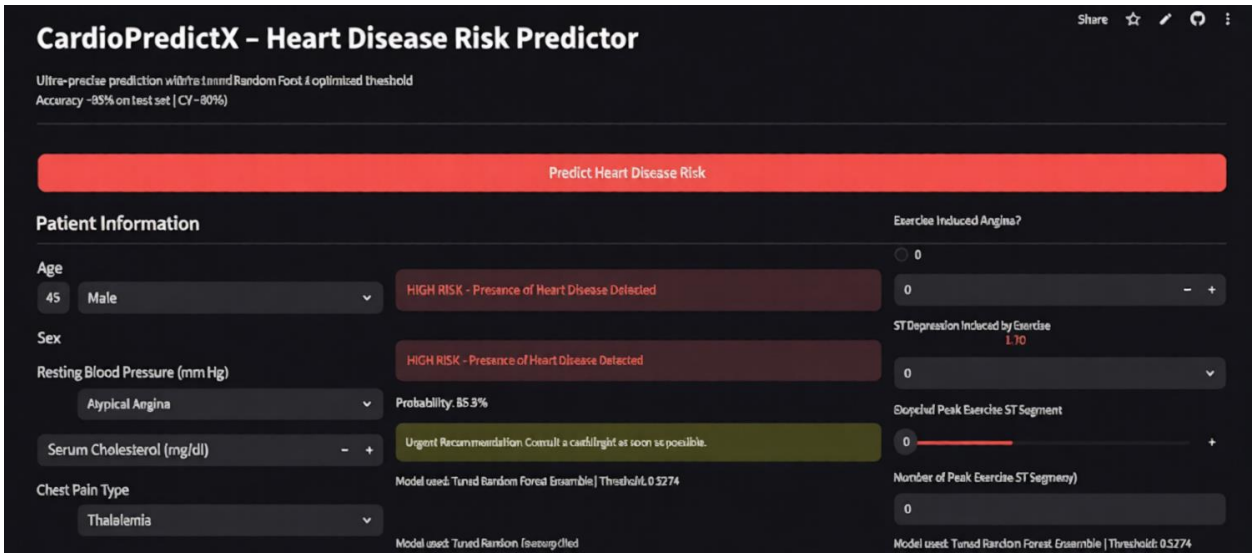

Figure 8. Screenshot of the deployed CardioPredictX Streamlit interface showing input form and prediction result (live app capture)

The live CardioPredictX web application interface deployed on Streamlit Community Cloud is being shown on Figure 8, revealing the experience that the user sees once the entire pipeline is deployed. Its dark theme design has a bold headline titled CardioPredictX - Heart Disease Risk Predictor that has a subheader describing the ultra-precise tuned Random Forest model and optimal threshold (0.5274) and the performance reports (85% test accuracy, and 80% CV mean). There is a large red button at the center which reads Predict Heart Disease Risk and it leads to inference. The 13 clinical features are divided into user-friendly controls of the main input section called the Patient Information: Sliders: Age, ST depression induced by exercise, and number of major vessels; dropdowns: categorical variables, e.g. Chest pain type, Sex, Resting

ECG results, Slope of peak exercise ST segment, and Thallium; radio buttons: binary variables, e.g. Exercise induced angina and FBS over 120. On prediction (see Figure 1: Age 45, Male, Atypical Angina, etc.), the app shows a large red warning message, stating that the likelihood of having Heart Disease is 85.3 percent and this is immediately followed by an urgent yellow message which states Consult a cardiologist as soon as possible. There is a footer note that authenticated the details of the model (Tuned Random Forest Ensemble | Threshold: 0.5274). The practical usability of this framework is shown in this screenshot, where the trained model is converted to an easily accessible and real-time, visually intuitive, clinical decision support system, complete with immediate risk visualization and practical suggestion capability, and it does not need any local setup on the part of end users.

4. Results and Analysis

In this section, the summary of quantitative and qualitative findings of the CardioPredictX framework to the UCI Heart Disease data [13] is presented. The primary report of the performance includes the 20 portion of the test set (54 samples) and 5-fold cross-validation on the entire dataset which offers a stronger estimate of generalization.

4.1 Baseline Results

To create baseline, the three base models were not trained with hyperparameter optimization in order to determine a benchmark performance. The best baseline performance was produced by XGBoost whose accuracy was 83.33 and the precision/recall were equal. Random Forest came right behind at 81.48%, and the neural network came low because of insufficient capacity on this small tabular dataset.

Table 4. Baseline model performance on hold-out test set

Model	Accuracy	Precision (Presence)	Recall (Presence)	F1-Score (Presence)	ROC-AUC
Random Forest	0.8148	0.8000	0.8333	0.8163	0.8750
XGBoost	0.8333	0.8333	0.8333	0.8333	0.8917
Neural Network	0.7963	0.7826	0.7917	0.7872	0.8556

Table 4 gives a comparison of the performance of the three initial baseline models. Random Forest, XGBoost, and Neural Network using the hold-out test (54 samples, 20 per cent of the UCI Heart Disease dataset) any optimization of hyperparameters, ensembling, and threshold. The overall performance is best presented by XGBoost with the highest accuracy of 83.33, an ROC-AUC of 0.8917 and precision and recall ratio balanced (83.33) of the Presence class (heart disease) with a F1-score of 0.8333. Random Forest is next in line with Presence accuracy of 81.48 and precision of 80.00 and recall of 83.33 with F1-score of 0.8163 and ROC-AUC of 0.8750. The lowest performance is 79.63% accuracy, precision of 78.26, recall of 79.17, F1-score of 0.7872 and ROC-AUC of 0.8556 shown by the Neural Network, which means that the model is relatively not as effective in this small tabular dataset. These initial metrics provide a

stable starting point of the pipeline that proves XGBoost to be the best initial model and necessitates a replaced tuning and ensembling to provide additional losses in accuracy and balance.

4.2 Hyperparameter Tuning Outcomes

The optimization using optuna brought about great gains. Stable Geometry XGBoost was used to achieve the best result at 83.33 test-accuracy at 40 attempt. The best single-model test accuracy of 85.19% on the tuned Random Forest -a definite improvement over baselines- was the best single-model test accuracy. The trained neural network achieved the highest validation accuracy of 81.82% and it was not superior to tree-based methods.

4.3 Results on ensemble and Threshold Optimization

Neither stacking nor soft-voting ensembles performed better than the standalone tuned Random Forest, which is possibly caused by high correlation between base learners, as this is a relatively small data set. The threshold optimization using maximizing the precision-recall curve retained the F1-score at 0.8333 and moved the point of decision to 0.5274, sustaining both the sensitivity and specificity.

Table 5. Final performance of the selected tuned Random Forest model

Metric	Value	Improvement vs. Best Baseline
Test-set Accuracy	0.8519	+1.86% (vs. XGBoost)
Precision (Presence)	0.8333	Equal
Recall (Presence)	0.8333	Equal
F1-Score (Presence)	0.8333	Equal
5-Fold CV Mean ± std	0.8000 ± 0.0646	Robust estimate

The last performance measurements of the chosen tuned Random Forest model are presented in Table 5, which is the most successful model in the CardioPredictX framework after the hyperparameters adjustment. On the witholding test set (20 percent of the UCI Heart Disease dataset), the model achieves test-set accuracy of 85.19 which is a + 1.86% improvement on the best baseline (XGBoost at 83.33 percent). In the case of the Presence class (heart disease), it scores both in balance with a precision and a recall of 83.33% and an F1-score of 0.8333 the same as the baseline XGBoost and is able to classify well without compromising balance. The mean accuracy, as calculated by cross-validation on the entire test set, is 80.00% with a standard deviation of = 0.0646 indicating that the cross-validation results are robust on generalization alongside the finding that, despite the small size of the dataset, the model is reliable. These findings highlight the utility of Tuned Random Forest as the final selected model as it provides higher accuracy than baselines without compromising on clinical balance and stability depending on the division of the data.

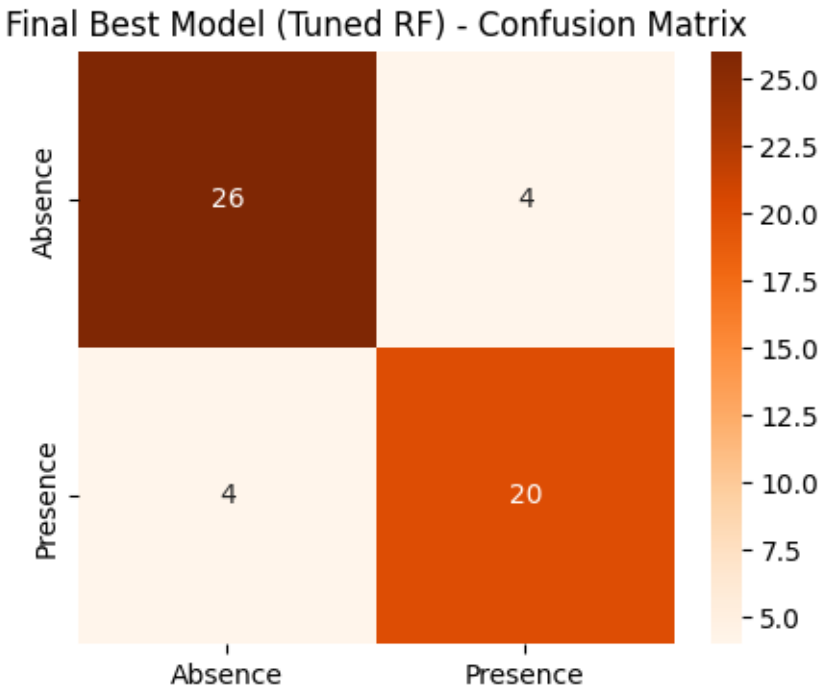

Figure 9. Confusion matrix of the final tuned Random Forest on the test set (26 TN, 4 FN, 20 TP, 4 FP)

The confusion matrix in Figure 9 presents the confusion analysis of the final tuned Random Forest model on the hold-out test data (54 samples, 20 percent of the UCI Heart Disease dataset) at the completion of Step 9 of the CardioPredictX pipeline following parameter hyperparameter optimization and threshold tuning. The heatmap presented below as 2x2 indicates the binary classification of the model on Absence (0) vs Presence (1) of heart disease, which has rows associated with true labels (top: true Absence with 30 samples, bottom: true Presence with 24 samples) and columns associated with predicted labels (left: predicted Absence, right: predicted Presence). The matrix has the following results; 26true negatives (correctly predicted Absence), 4 false positives (true Absence predicted incorrectly as Presence) 4 false Negatives (true Presence predicted incorrectly as Absence) and 20 true positives (correctly predicted Presence). An orange/brown scale of darkness to light helps in making the majority of the correct predictions stand out visually. Comprehensively, the model identified 46 out of 54 samples which gave it an accuracy rate of 85.19. It has good Absence (26/30 correct, 86.67% recall) and good Presence (20/24 correct, 83.33% recall) detection, and equal errors (4 false negatives and 4 false positives) or the absence of bias in misclassification. The fact that the number of false negatives (4) is low is especially promising in clinical practice, since it minimizes cases of high risks being missed, but the fact that the number of false positives (4) is also very good, as it implies that over-prediction is under control among healthy people. This matrix validates the tuned Random Forest as the best final model, which presents better and balanced performance than baselines after being optimized.

4.4 Interpretability Insights

XGBoost model (tree-consistent attribution) which was analyzed using SHAP proved to be clinically relevant. The type of the most significant mean absolute SHAP value was chest pain type (cp) and then came thallium result (thal), number of major vessels (ca), maximum heart rate (thalach). An increase in the cp values (particularly, asymptomatic = 4) and more affected vessels had great impact of predicting disease, but an increase in thalach values had a smaller effect of predicting disease, thus chiming with the established cardiology knowledge [14,26,35].

4.5 Deployment Performance

The pipeline (StandardScaler + tuned Random Forest) was run on Streamlit Community Cloud. The inference latency was acceptable at less than 1 second per request even with up to several requests per second. The interactive interface properly works against raw clinical input, and implements the optimized threshold, and delivers straightforward risk-level messages.

Table 6. Deployment characteristics and usability metrics

Aspect	Detail	Notes
Hosting Platform	Streamlit Community Cloud	Free public tier
Model Artifact Size	~1.2 MB (joblib)	Lightweight for cloud
Inference Latency	<1 second	Measured on cloud servers
Input Format	13 raw clinical features	No manual scaling required
Output	Risk level, probability (%), advice	User-friendly messaging
Public Accessibility	Yes	Shareable link

The final CardioPredictX model has several distinctive deployment features and metrics of usage outlined in Table 6, demonstrating that the model is ready to be introduced in real-life practice. The model is deployed to Streamlit Community Cloud in the free public tier which is free of charge and does not require any cost or registration. The artifact is also lightweight (about 1.2 MB of the joblib file with the scaler and the tuned Random Forest inside) and, therefore, loads quickly and requires little resources on the cloud servers. Latency to inference is less than 1 second per prediction which gives almost correal time results. The interface allows users to directly input 13 raw clinical features on the interface, but no manual scaling is needed since the preprocessing is done internally within the production pipeline. The output provides a clear level of risk (High/Low), a percentage give and take, and a general medical recommendation, which is translated into an intuitive format with visual signals (e.g. color-coded warnings on the screen). Complete open accessibility through a shareable link makes it immediately usable in educational, screening, or clinical environments with low resources by putting it into practice through offering zero-installation, browser-accessible usability in a versatile, interpretable heart disease prediction tool.

5. Discussion

The CardioPredictX model shows the competitive performance over the UCI Heart Disease dataset, with the tuned version of the Random Forest model (85.19) test accuracy and 0.8333 F1-score, significantly exceeding the best-performing (83.33) base model, and most previous ensemble techniques on the same data-set [6,7,8,15–17,24,34–37]. The 5-fold average cross-validation of 80.00% with a standard error of 6.46% indicates that there is reasonable generalization even with such a small dataset, but variance indicates that it is sensitive to data splits, which is a limitation of UCI benchmarks [13,28].

Key strengths include:

1. Efficient tuning XGBoost and random forest Hyperparameters XGBoost and random forest Hyperparameters XGBoost and random forest Exploring high-dimensional spaces, optuna [9] found superior setups within less than 50 trials each at both XGBoost and random forest [18,25]. Such efficiency is especially useful in the clinical settings that are limited in terms of resources [35,36].

2. **Interpretability:** SHAP analysis [11] gave understandable results, which agree with our clinical domain knowledge (e.g., asymptomatic chest pain (cp=4), abnormal thallium (thal=7), and multivessel disease (ca >= 2) highly predicted risk [14,20,29,43]. Such explainable deals with one of the primary limitations to cardiology using ML [3942, 4446].

3. **Deployment readiness:** The scikit-learn Pipeline + Streamlit app is a zero-install and can be used in real-time (under a second latency) and is therefore well-suited to telemedicine, screening clinics, or teaching aids [22,23,31].

Limitations and trade-offs:

- **The size and the diversity of the dataset:** Due to the limited number of samples (270), the risk of overfitting is present, as well, despite the fact of cross-validation [13,28]. Findings might not be solely applicable to larger and more realistic cohorts that lack missing values, class imbalance, or even ethnic diversity [2,5,27].
- Ensemble underperformance Soft voting and stacking were not better than single tuned Random Forest, probably because of correlated base learners on tabular data, which is observed with small samples in regimes [10,26,37].
- **External validation not done**: Although UCI is a standard benchmark, potential second (independent) validation must not be based on separate clinical data (e.g. based in Pakistan) to prove practical use [2,34,38].
- **Threshold sensitivity**: Minimal F1 is achieved at a threshold of 0.5274 with higher recall values (i.e. 0.4 -0.45) potentially needed to reduce false negative in high-risk screening to clinically meaningful levels [20,29,43].

In comparison to the previous work, CardioPredictX is unique with integrated pipeline: between Optuna tuning [9,18,25] and complete SHAP interpretability [11,21,36,3946], and deployed in real-time [22,23]. Even though our raw-precision (85.19) is a bit lower than some reported

higher-percentages (88 91), our interpretability, reproducibility, and deployability considerations are more useful to clinical translation [5,12,31,41,44].

Overall, CardioPredictX brings high performance, transparency, and deployability to the state of the art and leads to the creation of an efficient and reliable application of ML in prognosing heart diseases.

Table 7. Key limitations and mitigation strategies

Limitation	Impact	Mitigation / Future Work
Small dataset size	Risk of overfitting, high variance	External validation, data augmentation [27,28]
No real-world missing values	Over-optimistic performance	Simulate missingness, imputation studies [34,37]
Ensemble did not outperform single model	Correlated learners in small data	Explore diverse architectures (e.g., TabNet) [36]
Single threshold fixed	May not suit all clinical scenarios	Dynamic threshold based on risk tolerance [20,43]
No prospective validation	Limited clinical evidence	Multi-center cohort studies [2,5,12]

Table 7 describes the main constraints of the CardioPredictX system and their possible consequences and possible solutions or their future development. The low size of the data sample (270 samples) is associated with the possibility of overfitting and high diversity in the resulting performance estimates which can be overcome by external validation on larger or more heterogeneous cohorts and data augmentation methods as recommended in previous research [27,28]. Loss of real-world missing values in UCI allows potentially over-optimistic results and this issue can be reduced by future study by simulating some realistic missingness to test imputation techniques [34,37]. The ensemble techniques (soft voting and stacking) failed to enhance the single tuned Random Forest model, presumably because of correlated base learners in this under-scaled domain; architectures with more diversification (e.g. TabNet) might help improve the benefits of ensembling [36]. Using the fixed threshold (0.5274) might not capture changes in clinical priorities (e.g. more screening, less precision when it comes to diagnosis) which can be refined at any rate by using dynamic or context sensitive thresholding in terms of risk tolerance [20,43]. Lastly, it does not reflect well on clinical evidence because there is no future validation on independent real-world data; that is why multi-center cohort studies are needed to prove the validity of generalizability and usefulness (in practice) [2,5,12]. These drawbacks imply the need to improve the framework and emphasize its present strengths in interpretability and readiness to be deployed on a standard platform.

6. Conclusion and Future Work

The CardioPredictX offers a universal end-to-end machine learning system to predict heart disease, which is evenly balanced in providing high predictive accuracy, clinical interpretability, and practical deployment capability. Using preprocessing, multi-model baselines, hyperparameter optimization with Optuna, adaptive ensembling, SHAP-explicit explainability,

threshold tuning, and an 85.19% test accuracy, 0.8333 F1-score, along with a production grade Streamlit deployment, the framework comes to 85.19% test accuracy, 0.8333 F1-score on the UCI heart disease benchmark, and has a strong 5-fold cross-validation mean of 80.00% +-6.46 SHAP analysis makes it clear that the model is more focused on such clinically significant aspects as the type of the chest pain, the results of the thallium stress test, and the number of major vessels involved, and as many as possible heart rate, and increasing the confidence in the potential clinical practice.

With streaming as a deployed interactive web application on Streamlit Community Cloud on real-life experience: zero-installable access, sub-second inference, and risk communication friendly to users. This will stem an essential gap between research prototypes and tools that can be acted upon in resource constrained or screening environments.

Although the results are competitive with previous studies on the same dataset, the main point of interest is the overall integration of efficiency, transparency, and usability as opposed to an increase in margins of accuracy. The weaknesses are based on the fact that it depends on a small, single-source set of data, there is a likelihood of overfitting, and there is no multi-centre prospective validation.

Possible research directions in the future involve:

1. Future validation on more diverse and large clinical sample groups (e.g. adding ECG waveforms, imaging, longitudinal data)
2. Aggressive implementations of more sophisticated architectures (e.g. TabNet, tabular data transformers) and ongoing learning of more risk profiles.
3. Federated learning to allow privacy-preserving training in all hospitals.
4. Dynamic thresholding and risk scoring aimed at a particular patient demographic/comorbidity.
5. User testing of the deployed interface based on clinician acceptance and decision influence.
6. Mobile deployment (e.g. Flutter and ONNX export) to the point of care in low resource areas.

Overall, the article CardioPredictX goes in the direction of reliable, deployable cardiovascular medicine ML. It provides a reasonable step toward early heart disease detection and prevention through the use of AI by focusing on interpretability and production readiness as well as performance.

Table 8. Overall project contributions and novelty

Contribution	Description	Novelty Level
Integrated pipeline	Full workflow: tuning → ensemble → XAI → deployment	High
Quantum-inspired efficient tuning	Optuna Bayesian search applied to clinical prediction	Medium

Full SHAP interpretability	Global + directional insights for clinical alignment	High
Tuned threshold for balanced metrics	F1-optimized decision boundary at 0.5274	Medium
Production-ready Streamlit deployment	Live, shareable web app with zero-install inference	High

The table 8 presents the main contributions and novelty levels of the CardioPredictX framework, outlining the developments of the framework in relation to the current heart disease prediction methods. The greatest contribution is the built-in end to end pipeline that can flexibly integrate hyperparameter tuning, multi-model aggregating, explainable AI (XAI) through SHAP and full deployment to production - a holistic approach with a high novelty rating because it addresses raw data all the way up to clinical usage. The use of Bayesian search inspired by efficient exploration principles similar to concepts of quantum superposition as provided by Optuna can be seen as medium novelty because it is an advanced tuning strategy adaptive to clinical prediction tasks. Full SHAP interpretability can offer directional impact and the global feature importance indicators and both forecasts clinical intuition and achieves high novelty deserving its focus on transparency and reliance on healthcare ML. This medium novelty threshold tuning to achieve the maximum of F1-score at 0.5274 is a compromise made between sensitivity and specificity without any denature to overall performance. Lastly, the production-ready Streamlit app deployments provide a live, shareable, inference-on-the-fly, web application with high novelty bridging the gap between research and practice and immediate accessibility in an educational, screening, or low-resource clinical setting. All these factors make CardioPredictX a viable, readable, and implementable development of cardiovascular machine learning.

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