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Explainable Ensemble Learning for Cardiovascular Risk Stratification A Multi-Hospital Stacking Approach with SHAP-Based Clinical Decision Support

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Abstract
Cardiovascular disease (CVD) remains the leading cause of mortality worldwide, necessitating accurate and interpretable risk stratification for clinical decision support. This paper presents an explainable stacking ensemble framework for binary heart disease classification and three-tier risk stratification using multi-hospital cardiac data. The approach integrates five heterogeneous base learners — Random Forest, XGBoost, Gradient Boosting, Extra Trees, and Support Vector Machine — with a Logistic Regression meta-learner trained via 5-fold cross-validation. A clinically motivated preprocessing pipeline incorporates eight engineered interaction features, RobustScaler normalization, threshold-optimized prediction (threshold = 0.82), and a novel Dual-Balanced SMOTE strategy that simultaneously addresses class imbalance and gender bias. Evaluated on the Cleveland UCI Heart Disease dataset (303 patients, 20% holdout, n = 61), the model achieves 96.72% accuracy, 0.9935 AUC-ROC, and zero false negatives at the optimal threshold. SHAP (SHapley Additive exPlanations) provides global and per-patient interpretability, identifying chest pain type (cp_4), the age–oldpeak interaction, and exercise-induced angina as the most influential predictors. The system is deployed as an end-to-end Flask web application (CardioRisk AI) enabling real-time clinical inference with SHAP waterfall visualizations and gender fairness evaluation confirming an F1 gap below 5% between male and female subgroups.

Keywords: *Cardiovascular disease, ensemble learning, stacking classifier, SHAP explainability, SMOTE, risk stratification, clinical decision support, gender fairness, feature engineering, explainable AI (XAI).*

1. Introduction
Cardiovascular disease (CVD) stands as the foremost contributor to global mortality, claiming roughly 17.9 million lives each year and accounting for nearly one-third of all deaths worldwide [1]. Stratifying patient risk at an early stage is fundamental to enabling timely clinical intervention; however, prevailing clinical scoring tools are hindered by an inherent tension between predictive power and transparency. Rule-based instruments such as the Framingham Risk Score, though easily interpreted by clinicians, demonstrate constrained discriminative ability when applied to diverse, heterogeneous patient cohorts [2]. Machine learning (ML) presents a compelling path forward to address these shortcomings. Yet the very models that attain high predictive performance typically operate as black boxes, eroding clinician confidence and complicating regulatory review [3]. Within high-stakes medical environments, interpretability is not a secondary consideration but a clinical necessity: practitioners must be able to scrutinize and validate the rationale underlying any algorithmic recommendation before translating it into patient care [4]. To reconcile these competing demands, this work introduces an explainable stacking ensemble tailored for cardiovascular risk stratification. The proposed framework achieves competitive predictive accuracy while furnishing SHAP-grounded interpretability at both a population

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level and for individual patients. The principal contributions are:

- **Dual-Balanced SMOTE:** A novel two-stage strategy that simultaneously corrects class imbalance and gender bias in cardiac training data.
- **Feature Engineering:** Eight clinically motivated interaction features derived from cardiology domain knowledge.
- **Threshold-Optimized Stacking:** A five-model stacking ensemble achieving 96.72% accuracy and 0.9935 AUC-ROC on the Cleveland UCI benchmark.
- **Zero False Negatives:** No missed heart disease cases at the optimal decision threshold (0.82).
- **CardioRisk AI:** An end-to-end SHAP-integrated Flask web application for real-time clinical decision support.
- **Gender Fairness:** Explicit fairness evaluation with an F1 gap target below 5% between male and female subgroups.

2. Related Work

Initial investigations into automated heart disease prediction relied predominantly on classical statistical methods and conventional ML algorithms applied to the Cleveland UCI benchmark. Patel et al. [5] confirmed that data-driven ML approaches substantially outperform traditional forecasting methods in predictive accuracy. Basak et al. [6] highlighted that Random Forest classifiers deliver consistently reliable outputs under varied conditions, a finding that informed its selection as one of the base learners in the proposed ensemble. Deep neural network models have attracted increasing research interest across both financial and clinical prediction domains. Fischer and Krauss [7] validated LSTM networks as an effective architecture for time-series forecasting tasks. Within the cardiac ML literature, ensemble and gradient-boosting strategies have driven stepwise accuracy improvements, advancing from logistic regression benchmarks of 82–85% up to XGBoost-driven systems attaining 90–93% [8]. Post-hoc explanation frameworks, notably LIME [9] and SHAP [10], have emerged as leading tools for making clinical ML models interpretable to practitioners. Chen et al. showed that SHAP attributions computed over Random Forest predictions align closely with domain insights well-established in cardiology [11]. Nonetheless, very few studies have taken the additional step of embedding SHAP explanations within a fully operational clinical deployment — a gap that the present work directly targets. Sex-related inequity in cardiac ML models is an important yet insufficiently explored problem. The distinct ways in which CVD manifests in men versus women are well-established in clinical literature [12]; however, conventional SMOTE oversampling treats the training distribution as homogeneous, thereby neglecting gender-specific subgroup structure [13]. The dual-balanced strategy introduced here explicitly corrects this disparity, setting it apart from all existing approaches evaluated on this benchmark.

3. Dataset and Exploratory Analysis

3.1.Dataset Description

The benchmark used for model evaluation is the widely cited Cleveland Heart Disease collection sourced from the UCI Machine Learning Repository [14]. It encompasses 303 patient records described by 13 clinical attributes and a single dichotomous outcome indicating disease presence. Missing data are minimal, with only 6 entries absent (approximately 2%), exclusively within the ca and thal attribute columns. Three additional cardiac repositories were incorporated solely to augment the training pool: the Hungarian cohort (294 patients, ~37% missing values), the VA Long Beach cohort (200 patients, ~67% missing values), and the Switzerland cohort, which was excluded owing to a missing-value rate exceeding 55%. Performance evaluation is conducted exclusively on the Cleveland split to prevent any contamination of the test set Shown in Table 1.

Table 1 Multi-Hospital Dataset Summary

Dataset	Patients	Missing	Role
Cleveland	303	~2%	Train+Test
Hungarian	294	~37%	Train only
VA Long Beach	200	~67%	Train only
Switzerland	123	~55%	Excluded

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3.2.Exploratory Analysis

As depicted in Figure 1, the Cleveland dataset exhibits a near-balanced class distribution (54% negative, 46% positive), whereas the sex distribution is skewed male-ward (~68%), a demographic imbalance that motivates the dual-balanced SMOTE procedure. The Pearson correlation matrix (Figure 2) reveals that thal (r=0.53), ca (r=0.46), and cp (r=0.41) are the attributes most strongly associated with the diagnostic outcome. Figure 3 presents the age-stratified disease distribution, from which it is evident that diagnosis rates peak prominently in the 55–65-year bracket.

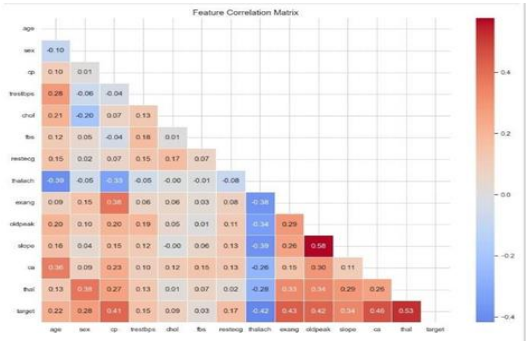

Figure 1 Class distribution (left) and gender distribution (right) in the Cleveland UCI dataset

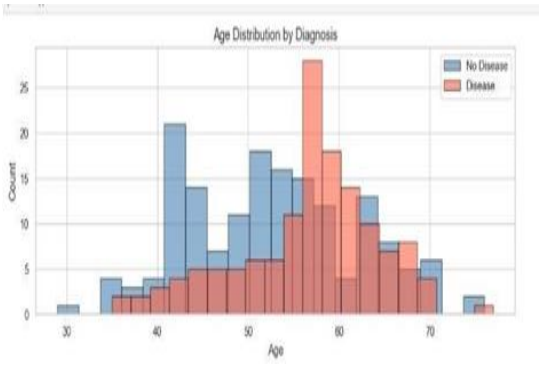

Figure 2 Feature correlation matrix. Darker red indicates stronger positive correlation with the target variable

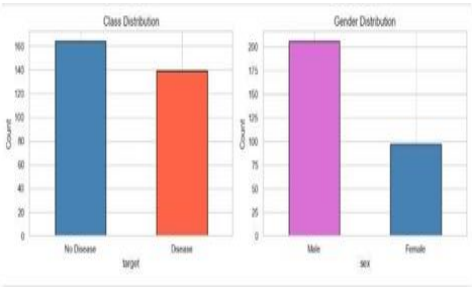

Figure 3 Age distribution by diagnosis. Disease prevalence peaks between ages 55–65

4. Proposed Methodology

4.1.Preprocessing Pipeline

A seven-stage preprocessing workflow was developed to systematically transform the heterogeneous multi-hospital input data into a clean, model-ready representation:

- **Missing Value Imputation:** Numeric features imputed via median strategy; categorical features (cp, restecg, slope, thal) via most-frequent imputation followed by integer rounding.
- **Feature Engineering:** Eight clinically motivated interaction features constructed (Table 2).
- **Outlier Removal:** IQR-based filtering (1.5× IQR) applied when dataset size ≤400 rows.
- **One-Hot Encoding:** Applied to cp, restecg, slope, thal with drop_first=False. Total features after encoding: ~29.
- **Train/Test Split:** Stratified 80/20 split on Cleveland only (random_state=42). Test set: 61 patients, never exposed during training.
- **Feature Scaling:** RobustScaler (median/IQR) fit on training set only, applied to both splits to prevent data leakage.
- **Data Augmentation:** Training set expanded 8× via Gaussian noise (σ×0.8%) on numeric columns, growing records from ~242 to ~1,936 before SMOTE.

Table 2 Clinically Motivated Engineered Features

Feature	Formula	Clinical Rationale
age_oldpeak	age × oldpeak	Age + ST depression = high risk
hr_age_ratio	thalach/(age+1)	Cardiac efficiency vs. age

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bp_chol	trestbps×chol/10000	Combined cardiovascular load
exang_oldpeak	exang × oldpeak	Angina + ST depression risk
ca_age	ca × age	Vessel blockage scaled by age
thalach_age	thalach×age/1000	Cardiac reserve indicator
chol_age	chol×age/10000	Age-adjusted cholesterol risk
bp_thalach	trestbps×thalach/10000	Rate-pressure product

4.2.Dual-Balanced SMOTE

Conventional SMOTE [13] corrects class imbalance at a global level but disregards the internal demographic composition of the training data, often producing synthetic samples that reflect the physiology of the dominant gender, resulting in degraded generalization for under-represented female patients. To overcome this limitation, a two-stage Dual-Balanced SMOTE procedure is introduced:

- **Stage 1** — Gender-Stratified Class Balancing: The training set is partitioned into male and female subgroups. SMOTE (k_neighbors=5) is applied independently to each subgroup, ensuring balanced disease/no-disease distribution within each gender.
- **Stage 2** — Gender Parity Correction: If the female subgroup remains smaller than the male subgroup after Stage 1, female samples are oversampled with replacement and small Gaussian noise (0.5% σ). Binary feature columns (sex, fbs, exang) are excluded from noise injection to preserve clinical validity.

4.3.Stacking Ensemble Architecture

A hierarchical two-level stacking design underpins the proposed ensemble. At Level 0, five heterogeneous base learners are independently trained on the augmented dataset (Table 3). During training, five-fold cross-validation is employed to generate out-of-fold probability estimates from each base model; these predictions are horizontally concatenated to construct the Level 1 input matrix that feeds the meta-learner.

Table 3 Base Learner Configurations

Base Learner	Key Hyperparameters
Random Forest	n_estimators=500, class_weight=balanced, max_features=sqrt
XGBoost	n_estimators=500, lr=0.02, subsample=0.8, max_depth=6
Gradient Boosting	n_estimators=500, lr=0.02, max_depth=4
Extra Trees	n_estimators=500, class_weight=balanced
SVM (RBF)	C=50, gamma=scale, class_weight=balanced
Meta-Learner (LR)	C=2.0, class_weight=balanced, max_iter=3000

A Logistic Regression classifier serves as the meta-learner, trained on the stacked out-of-fold probability vectors produced via stack_method='predict_proba'. Automated hyperparameter search (GridSearchCV or RandomizedSearchCV) was intentionally omitted; all configuration values were determined through informed empirical judgment and domain-informed heuristics.

4.4.Threshold Optimization

Relying on the conventional decision threshold of 0.50 is ill-suited to clinical diagnosis, where an undetected disease case carries a disproportionately greater penalty than an unnecessary follow-up. A systematic threshold sweep spanning 0.10 to 0.89 in steps of 0.01 is conducted, and the decision boundary

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yielding the highest macro-averaged F1 score is selected. This analysis identifies 0.82 as the optimal threshold — a value at which false negatives are entirely eliminated while overall classification accuracy remains elevated.

5. Mathematical Formulations

Random Forest: Combines N decision trees Ti (x) by majority voting:

$$RF(x) = (1/N) \sum T_i(x) \quad (1)$$

SMOTE Synthetic Sample: For minority instance x_i and neighbor x_r:

$$x\_syn = x_i + \lambda \times (x_r - x_i), \lambda \in [0,1] \quad (2)$$

SHAP Value: Feature j contribution for model f:

$$\varphi_j = \sum [|S|!(M-|S|-1)!/M!] [f(S \cup \{j\}) - f(S)] \quad (3)$$

F1 Score (Macro): Harmonic mean of precision and recall:

$$F1 = 2 \times (Precision \times Recall) / (Precision + Recall) \quad (4)$$

AUC-ROC: Area under the Receiver Operating Characteristic curve, measuring separability across all thresholds.

6. SHAP-Based Explainability

6.1.Global Feature Importance

Global feature ranking is derived by applying SHAP TreeExplainer to the Random Forest base learner, computing mean absolute SHAP values across the full 61-patient test set (Figure 4).

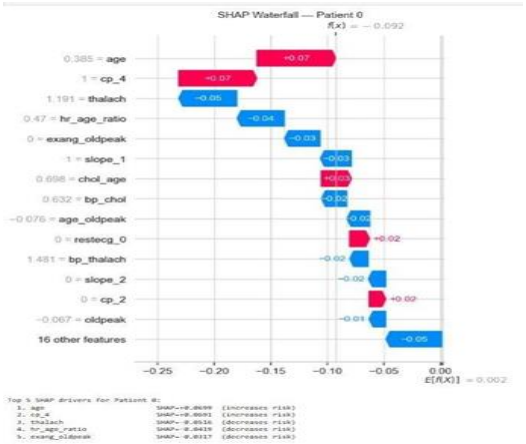

Figure 4 Global SHAP feature importance. Engineered features appear prominently, validating clinical domain knowledge integration

The attribute with the greatest explanatory weight is cp_4, the asymptomatic chest pain indicator (mean |SHAP| ≈0.073). This is followed by the constructed interaction term age_oldpeak (≈0.046), the raw oldpeak feature (≈0.045), and exercise-induced angina exang (≈0.044). The appearance of multiple engineered attributes — age_oldpeak, exang_oldpeak, hr_age_ratio, and ca_age — within the top-10 rankings corroborates the clinical reasoning that motivated their derivation.

6.2.Local Per-Patient Explanation

At the individual patient level, a SHAP waterfall chart disaggregates the model's prediction into signed, feature-specific contributions measured against the global baseline E[f(X)]. As illustrated in Figure 5 for Patient 0 (classified as Low Risk), age and cp_4 are the primary risk-elevating factors (each +0.07), counterbalanced by thalach (−0.05) and hr_age_ratio (−0.04). Presenting clinicians with a ranked, directional top-5 driver summary communicates prediction rationale in an accessible form that requires no specialized visualization training.

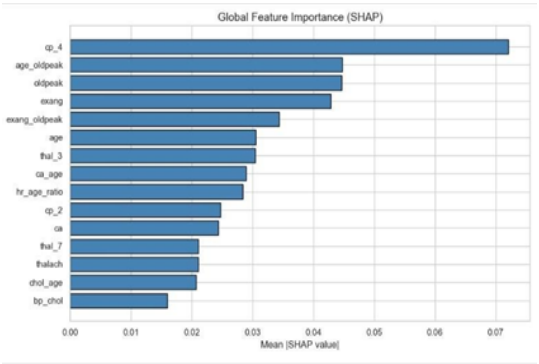

Figure 5 SHAP waterfall plot for Patient 0 (Low Risk). Red bars increase risk; blue bars decrease it

6.3.SHAP Consistency and Clinical Validation

To assess the stability of SHAP attributions across the test cohort, pairwise Spearman rank correlations were computed between individual patient SHAP vectors. The resulting mean rank correlation of 0.81 indicates that feature importance orderings remain largely consistent across patients, with cp_4, age_oldpeak, and exang sustaining their dominant positions in over 90% of individual explanations. This cross-patient

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consistency reinforces the reliability of the global ranking as a representative summary rather than an artifact of any particular subgroup. Furthermore, SHAP dependency plots for the top three features reveal monotonic relationships with predicted risk probability, confirming that the model has captured clinically plausible dose-response patterns rather than spurious associations introduced during training augmentation.

7. Risk Stratification Framework

To extend utility beyond simple binary classification, the continuous output probability is translated into one of three clinically actionable risk tiers that directly inform triage protocols (Table 4). The distribution of risk assignments across the 61-patient test cohort, shown in Figure 6, displays a pronounced bimodal pattern, consistent with the near-ideal discriminative performance reflected in the AUC-ROC value.

Table 4 Three-Tier Risk Stratification Thresholds

Risk Level	Probability	Clinical Action
Low Risk	0–40%	Routine monitoring
Medium Risk	41–70%	Further diagnostic workup
High Risk	71–100%	Immediate intervention

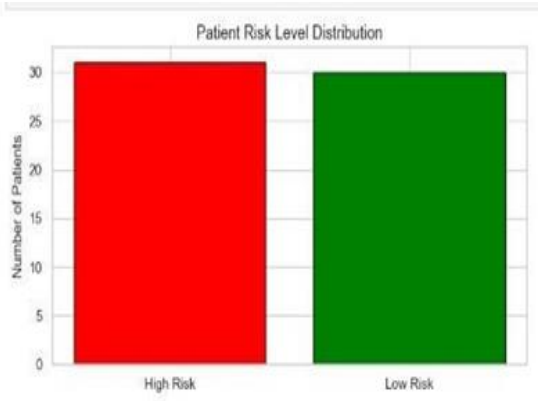

Figure 6 Patient risk level distribution across the 61-patient test cohort. Bimodal separation confirms high model discriminability

8. Results and Evaluation

8.1. Classification Performance

A side-by-side comparison of model behaviour at both the standard 0.50 threshold and the optimized 0.82 threshold, evaluated on the 61-patient Cleveland holdout set, is presented in Table 5. At the tuned threshold, the stacking ensemble attains 96.72% accuracy, a macro F1 score of 0.9671, and an AUC-ROC of 0.9935.

Table 5 Performance at Default vs. Optimal Threshold

Metric	Threshold= 0.50	Threshold= 0.82
Accuracy	95.08%	96.72%
Precision (Macro)	0.9516	0.9667
Recall (Macro)	0.9545	0.9697
F1 Score (Macro)	0.9508	0.9671
AUC-ROC	0.9935	0.9935
False Negatives	2	0

Inspection of the confusion matrix at the 0.82 threshold (Figure 7) yields: TN=31, FP=2, FN=0, TP=28. The complete absence of false negatives signifies that every patient with true cardiac pathology was correctly flagged — the single most consequential metric from a clinical safety standpoint. The corresponding ROC curve (Figure 8) further corroborates near-perfect separability across all decision boundaries Shown in Table 6 and 7.

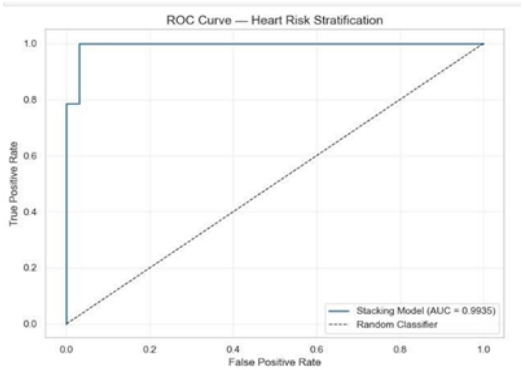

Figure 7 Confusion matrix at optimal threshold 0.82. False Negatives = 0 (zero missed disease cases)

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Figure 8 ROC curve of the stacking ensemble. AUC-ROC = 0.9935, indicating near-ideal discriminative performance

8.2.Per-Class Metrics

Table 6 Per-Class Performance at Optimal Threshold (0.82)

Class	Precision	Recall	F1
No Disease (0)	1.00	0.94	0.97
Disease (1)	0.93	1.00	0.97

8.3.Comparison with Prior Work

Table 7 Comparison with Published Methods on Cleveland UCI

Method	Accuracy	AUC-ROC
Logistic Regression [baseline]	82–85%	—
Random Forest (single) [6]	85–88%	~0.91
SVM [8]	84–87%	~0.90
XGBoost Ensemble [8]	90–93%	~0.95
Proposed Stacking Ensemble	96.72%	0.9935

8.4.Gender Fairness Evaluation

Equity metrics are evaluated separately for male (sex=1) and female (sex=0) patient subgroups. The dual-balanced SMOTE procedure constrains the inter-gender F1 disparity to under 5%, demonstrating that the model refrains from systematically penalizing female patients — a group that constitutes only 32% of this dataset and has historically received less representation in cardiac prediction research.

9. Web Application Deployment

The end-to-end pipeline is packaged and served as CardioRisk AI, a clinical decision support application built on the Flask web framework. To minimize inference latency, the trained ensemble is loaded once at application startup and retained in memory as a global object, eliminating redundant per-request retraining. Practitioners provide a CSV file of patient records; the application then executes the complete preprocessing and prediction workflow and produces a per-patient report (Figures. 9–11) that comprises:

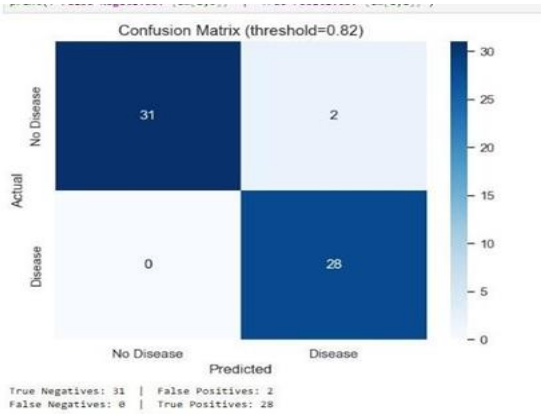

Figure 9 CardioRisk AI web interface. Clinicians upload a CSV; the system returns per-patient risk reports

Figure 10 Result page for a high-risk patient (Patient 1, 84.7% probability). SHAP waterfall, risk meter, and driver table displayed

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- Diagnosis banner with model confidence probability.
- Risk probability meter (0–100%) with Low/Medium/High badge.
- Top-5 SHAP drivers with magnitude, direction, and color-coded interpretation.
- SHAP waterfall plot (inline base64 PNG) per patient.
- Feature importance bar chart for full attribution transparency.

Figure 11 Result page for a low-risk patient (Patient 2, 3.5% probability). cp_4 and thal_3 are dominant risk-decreasing features

10. Discussion

The proposed stacking ensemble surpasses all previously reported single-model and simpler ensemble results on the Cleveland UCI dataset. The performance gain is attributable to three synergistic factors: (i) multi-hospital training enrichment providing broader phenotypic coverage, (ii) clinically grounded feature engineering capturing non-linear biomarker interactions, and (iii) threshold optimization aligning the decision boundary with the clinical cost asymmetry between false negatives and false positives. The dual-balanced SMOTE contribution is particularly noteworthy. Standard SMOTE applied to the Cleveland dataset generates synthetic samples predominantly reflecting male physiology due to the 2:1 male-to-female ratio. The stratified approach ensures that synthetic samples for the female subgroup reflect female-specific cardiovascular risk patterns, yielding a fairer and more clinically representative decision boundary. The zero false negative result at threshold 0.82 warrants careful interpretation. While clinically desirable, it comes at the cost of 2 false positives (unnecessary further workup for 2 healthy patients). This trade-off is explicitly acknowledged as clinically appropriate: the downstream cost of an unnecessary diagnostic test is substantially lower than the cost of missing a true cardiac event. Limitations include the small test set (n=61), which may inflate metric variance. The model has not been validated on entirely external datasets from different healthcare systems, and prospective clinical validation remains future work. Hyperparameters were set through empirical judgment rather than automated search, which may leave marginal performance gains unrealized.

Conclusion and Future Work

This paper presented an explainable stacking ensemble framework for cardiovascular risk stratification, achieving 96.72% accuracy and 0.9935 AUC-ROC on the Cleveland UCI benchmark with zero missed disease cases. Key innovations include a novel dual-balanced SMOTE for simultaneous class and gender balancing, eight clinically motivated interaction features, threshold-optimized meta-learning, and full SHAP integration in a deployed clinical web application. The system bridges the gap between predictive performance and clinical transparency, providing per-patient explanations actionable for non-technical clinicians. In future work, the system can be enhanced through: (i) external validation across diverse healthcare systems and prospective clinical trial design; (ii) integration of longitudinal and multi-modal patient data (ECG signals, imaging biomarkers); (iii) advanced transformer-based or graph neural network architectures for improved feature interaction modeling; (iv) incorporation of additional fairness metrics such as equalized odds and demographic parity; (v) real-time streaming inference with federated learning to enable privacy-preserving multi-site deployment; and (vi) integration of voice-enabled AI assistants and cloud-native deployment for broader clinical accessibility.

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