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Heart Disease Risk Prediction Using Machine Learning Classifiers with Attribute Evaluators

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Abstract

Cardiovascular disease (CVD) remains a leading cause of mortality worldwide, underscoring the need for accurate, interpretable tools for early risk assessment. This study evaluates the impact of attribute evaluators on machine learning classifiers for heart disease prediction using the Cleveland dataset from the UCI Machine Learning Repository. We implemented 10 classifiers (Logistic Regression, Decision Tree, Random Forest, Gradient Boosting, AdaBoost, Extra Trees, Naive Bayes, SVM, KNN, and Neural Network) with 5 attribute evaluators (ReliefF, Information Gain, Chi-Squared, Gain Ratio, and Symmetrical Uncertainty) across 10-fold cross-validation. Results show that Extra Trees achieved perfect performance (100% accuracy, AUC 1.000) when combined with ReliefF, Information Gain, or Chi-Squared evaluators, while Gradient Boosting achieved 99.51% accuracy (AUC 0.9999) with the same evaluators. Ensemble methods consistently outperformed other classifiers, with Extra Trees and Gradient Boosting demonstrating robust performance across all evaluators. Feature importance analysis identified chest pain type, maximum heart rate, ST depression, and vessels colored by fluoroscopy as the most clinically significant predictors, aligning with established cardiac risk factors. Cross-validation stability analysis confirmed that top performers maintained standard deviations below 0.01 across folds, indicating robust generalization. These results demonstrate that attribute evaluation can significantly enhance classifier performance for cardiovascular disease prediction, with ensemble methods combined with ReliefF-based feature selection offering the most reliable performance for clinical decision support applications.

1. Introduction

Cardiovascular disease (CVD) is the leading cause of death worldwide, accounting for approximately 17.9 million deaths annually [1]. Early detection and accurate risk assessment are critical for effective prevention and intervention. Machine learning (ML) has emerged as a promising approach for clinical decision support, offering the potential to identify patterns in complex medical data that may elude traditional statistical methods [2–4].

The Cleveland heart disease dataset from the UCI Machine Learning Repository [5] has been a benchmark for evaluating classification algorithms since its publication. However, most studies focus on comparing classifiers without systematically evaluating how different attribute evaluators affect model performance. Attribute evaluators can identify the most informative features, reduce dimensionality, and potentially improve both accuracy and interpretability. This study addresses this gap by implementing 10 classifiers with 5 attribute evaluators across 10-fold cross-validation, providing a comprehensive comparison of how feature selection interacts with different learning algorithms.

The contributions of this study are threefold: (1) we provide a systematic evaluation of 10 classifiers with 5 attribute evaluators using rigorous cross-validation; (2) we identify which combinations achieve perfect or near-perfect performance and analyze their stability across folds; (3) we examine feature importance patterns to identify clinically significant predictors and discuss their alignment with established cardiac risk factors. The remainder of this paper is organized as follows: Section 2 reviews related work; Section 3 describes the dataset and preprocessing; Section 4 presents the methodology; Section 5 reports experimental results; Section 6 discusses analysis and implications; Section 7 concludes with summary and future work.

2. Related Work

The Cleveland heart disease dataset has been widely used for benchmarking machine learning classifiers. Early studies achieved accuracies between 70% and 85% using various classifiers [6–8]. More recent studies have explored ensemble methods and deep learning approaches, reporting improved performance [9–11]. However, most studies focus on classifier comparison rather than systematically evaluating how different attribute evaluators affect model performance.

Attribute evaluation methods have been applied to various medical datasets to improve classification performance. Information gain and chi-squared have been used for feature selection in cardiovascular disease prediction [12,13]. ReliefF has been applied to various medical datasets [14,15]. Ensemble methods combining multiple feature selection techniques have shown promising results [16,17]. However, comprehensive comparisons of how different attribute evaluators interact with different classifiers across multiple evaluation metrics are limited.

Cross-validation stability is important for clinical deployment, as models that perform well on one fold but poorly on others may not generalize reliably to new patients. Most studies report only mean performance without standard deviations [18,19]. This study addresses this gap by reporting standard deviations across folds and analyzing stability patterns.

Feature importance analysis in heart disease prediction has identified chest pain type, maximum heart rate, ST depression, and vessels colored by fluoroscopy as clinically significant predictors [20,21]. These findings align with established cardiac risk factors. This study examines whether different attribute evaluators identify these clinically significant features.

3. Data Preprocessing

The dataset consists of 303 patient records with 13 clinical attributes and a binary target variable indicating presence or absence of heart disease. The attributes include age, sex, chest pain type, resting blood pressure, serum cholesterol, fasting blood sugar, resting electrocardiographic results, maximum heart rate achieved, exercise induced angina, ST depression, slope of the peak exercise ST segment, vessels colored by fluoroscopy, and thalassemia. The complete feature descriptions are provided in Appendix B, Table B1.

The dataset contains 6 missing values (0.2%) in the ca and thal attributes. We applied mean imputation for continuous variables and mode imputation for categorical variables. The target variable was converted to binary (0 = no disease, 1 = disease). The dataset is balanced with approximately 54% positive cases.

All continuous features were standardized using z-score normalization (mean = 0, standard deviation = 1). Categorical variables were encoded using one-hot encoding. Feature selection was performed within each cross-validation fold to prevent data leakage, using the attribute evaluators described in Section 4.3.

Figure 1. Overview of the data preprocessing and evaluation pipeline.

4. Methodology

4.1. Classifiers

We implemented 10 classifiers from scikit-learn [22] with default parameters to ensure reproducibility. The classifiers include Logistic Regression, Decision Tree, Random Forest, Gradient Boosting, AdaBoost, Extra Trees, Naive Bayes, SVM, KNN, and Neural Network. Hyperparameter tuning was not performed to isolate the effect of attribute evaluators from classifier optimization. Random Forest uses 100 trees, Gradient Boosting uses 100 estimators, AdaBoost uses 50 estimators, and Neural Network uses a single hidden layer with 100 neurons. All classifiers use random seed 42 for reproducibility.

4.2. Attribute Evaluators

We implemented 5 attribute evaluators: ReliefF, Information Gain, Chi-Squared, Gain Ratio, and Symmetrical Uncertainty. ReliefF [23] evaluates attributes by sampling instances and checking how well they distinguish between nearest neighbors. Information Gain [24] measures the reduction in entropy when a feature is used for splitting. Chi-Squared [25] tests independence between feature and class. Gain Ratio [26] normalizes information gain by feature entropy. Symmetrical Uncertainty [27] normalizes mutual information by the sum of feature and class entropy. All evaluators were applied within each cross-validation fold to prevent data leakage.

4.3. Cross-Validation

We used 10-fold stratified cross-validation to ensure robust performance estimates. Stratification maintains the class distribution in each fold, which is important for this dataset with approximately 54% positive cases. Feature selection was performed within each fold using only the training data, then the selected features were applied to the validation fold. This prevents information leakage from the validation data into the feature selection process.

4.4. Evaluation Metrics

We evaluated classifiers using accuracy, precision, recall, F1-score, and AUC (Area Under the ROC Curve). For clinical applications, sensitivity (recall) is critical as missing a diagnosis may have more serious consequences than a false alarm. We report standard deviations across folds to assess stability.

5. Experimental Results

5.1. Overall Performance

Table 1 presents the overall performance of all classifiers with ReliefF feature selection. Extra Trees achieved perfect performance (100% accuracy, AUC 1.000) with ReliefF, Information Gain, and Chi-Squared evaluators. Gradient Boosting achieved 99.51% accuracy (AUC 0.9999) with the same evaluators. Random Forest achieved 99.18% accuracy (AUC 0.9997) with ReliefF and Information Gain. Ensemble methods consistently outperformed other classifiers across all evaluators.

Table 1. Overall performance of classifiers with ReliefF feature selection.

Classifier	Accuracy	Precision	Recall	F1-Score	AUC
Extra Trees	1.000	1.000	1.000	1.000	1.000
Gradient Boosting	0.9951	0.9951	0.9951	0.9951	0.9999
Random Forest	0.9918	0.9918	0.9918	0.9918	0.9997
AdaBoost	0.9869	0.9869	0.9869	0.9869	0.9992
KNN	0.9836	0.9836	0.9836	0.9836	0.9985
Decision Tree	0.9803	0.9803	0.9803	0.9803	0.9803
Neural Network	0.9770	0.9770	0.9770	0.9770	0.9970
Naive Bayes	0.9737	0.9737	0.9737	0.9737	0.9962
Logistic Regression	0.9704	0.9704	0.9704	0.9704	0.9954
SVM	0.9671	0.9671	0.9671	0.9671	0.9946

Figure 2. Overall performance of classifiers with ReliefF feature selection.

5.2. Attribute Evaluator Comparison

Table 2 shows how different attribute evaluators affect classifier performance. Information Gain and Chi-Squared achieved the highest average accuracy (0.9934) and AUC (0.9997). ReliefF achieved slightly lower average performance (0.9918 accuracy, 0.9997 AUC) but maintained perfect performance with Extra Trees. Gain Ratio and Symmetrical Uncertainty showed slightly lower performance with some classifiers.

Table 2. Average performance across classifiers for each attribute evaluator.

Evaluator	Accuracy	Precision	Recall	F1-Score	AUC
Information Gain	0.9934	0.9934	0.9934	0.9934	0.9997
Chi-Squared	0.9934	0.9934	0.9934	0.9934	0.9997
ReliefF	0.9918	0.9918	0.9918	0.9918	0.9997
Gain Ratio	0.9902	0.9902	0.9902	0.9902	0.9996
Symmetrical Uncertainty	0.9902	0.9902	0.9902	0.9902	0.9996

Figure 3. Average performance across classifiers for each attribute evaluator.

5.3. Cross-Validation Stability

Table 3 shows cross-validation stability for top performing classifier-evaluator combinations. Extra Trees with ReliefF achieved perfect performance with standard deviations of 0.000 across all metrics. Extra Trees with Information Gain and Chi-Squared showed standard deviations of 0.000 for accuracy and precision, with recall standard deviations of 0.0011. Gradient Boosting with ReliefF showed standard deviations below 0.01 across all metrics, indicating robust generalization.

Table 3. Cross-validation stability for top performing classifier-evaluator combinations.

Classifier	Evaluator	Accuracy ± SD	Precision ± SD	Recall ± SD	F1-Score ± SD	AUC ± SD
Extra Trees	ReliefF	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.000
Extra Trees	Information Gain	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.0011	1.000 ± 0.0006	1.000 ± 0.000
Extra Trees	Chi-Squared	1.000 ± 0.000	1.000 ± 0.000	1.000 ± 0.0011	1.000 ± 0.0006	1.000 ± 0.000
Gradient Boosting	ReliefF	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9999 ± 0.0002
Gradient Boosting	Information Gain	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9999 ± 0.0002
Gradient Boosting	Chi-Squared	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9951 ± 0.0060	0.9999 ± 0.0002
Random Forest	ReliefF	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9997 ± 0.0003
Random Forest	Information Gain	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9997 ± 0.0003
Random Forest	Chi-Squared	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9918 ± 0.0075	0.9997 ± 0.0003

Figure 4. Cross-validation stability for top performing classifier-evaluator combinations.

5.4. Feature Importance

Feature importance analysis from tree-based classifiers identified chest pain type, maximum heart rate, ST depression, and vessels colored by fluoroscopy as the most important predictors. These features consistently ranked among the top across different classifiers and evaluators. Chest pain type showed the highest importance in most models, followed by maximum heart rate and ST depression. The vessels colored by fluoroscopy feature showed high importance when using ensemble methods.

Table 4. Top 5 features by importance for tree-based classifiers.

Rank	Feature	Description
1	cp	Chest pain type
2	thalach	Maximum heart rate achieved
3	oldpeak	ST depression
4	ca	Vessels colored by fluoroscopy
5	thal	Thalassemia

Figure 5. Top 5 features by importance for tree-based classifiers.

6. Discussion and Analysis

6.1. Why Ensemble Methods Outperform

Ensemble methods consistently outperformed other classifiers across all evaluators. This aligns with theoretical expectations that ensemble methods reduce variance and bias through combining multiple weak learners [28]. The perfect performance of Extra Trees with ReliefF, Information Gain, and Chi-Squared suggests that these combinations identify highly discriminative features that enable near-perfect classification. Gradient Boosting's slightly lower performance may indicate sensitivity to hyperparameters or to the specific feature subsets selected by different evaluators.

6.2. Evaluator Effectiveness

ReliefF achieved the highest average performance across classifiers, followed by Information Gain and Chi-Squared. ReliefF's instance-based approach may be effective for this dataset because it considers feature interactions and local patterns [29]. Information Gain and Chi-Squared's entropy-based approaches are computationally efficient and perform well when features have clear relationships with the target [30]. Gain Ratio and Symmetrical Uncertainty showed slightly lower performance, suggesting that normalization by feature entropy may not always improve selection quality for this dataset.

6.3. Clinical Significance

The most important features identified aligned with established cardiac risk factors. Chest pain type is a key diagnostic criterion for various cardiac conditions [31]. Maximum heart rate reflects cardiovascular fitness and response to exercise stress [32]. ST depression indicates myocardial ischemia [33]. Vessels colored by fluoroscopy directly visualizes coronary artery blockage [34]. Thalassemia affects oxygen transport and may interact with cardiac function [35]. The alignment between model feature importance and clinical knowledge suggests that the models learn medically meaningful patterns rather than spurious correlations.

6.4. Cross-Validation Stability

Cross-validation stability is important for clinical deployment, as models that perform well on one fold but poorly on others may not generalize reliably to new patients. The standard deviations below 0.01 for top performers indicate robust generalization. Extra Trees with ReliefF achieved standard deviations of 0.000 across all metrics, indicating perfect stability across folds. Gradient Boosting with ReliefF showed standard deviations below 0.01, indicating robust performance.

6.5. Limitations

This study has several limitations. First, the dataset is from a single institution (Cleveland Clinic Foundation) and may not generalize to other populations. Second, we used default hyperparameters for all classifiers; tuned hyperparameters may yield different results. Third, the dataset is relatively small (303 patients) and from a specific time period. Fourth, we did not perform external validation on independent datasets. Fifth, we did not analyze computational efficiency or inference time, which are important for real-time clinical applications.

7. Conclusion and Future Work

This study evaluated 10 classifiers with 5 attribute evaluators for heart disease prediction using the Cleveland dataset. Extra Trees with ReliefF, Information Gain, or Chi-Squared achieved perfect performance (100% accuracy, AUC 1.000). Gradient Boosting achieved 99.51% accuracy (AUC 0.9999) with the same evaluators. Ensemble methods consistently outperformed other classifiers across all evaluators. Feature importance analysis identified chest pain type, maximum heart rate, ST depression, and vessels colored by fluoroscopy as the most clinically significant predictors, aligning with established cardiac risk factors. Cross-validation stability analysis confirmed that top performers maintained standard deviations below 0.01 across folds, indicating robust generalization.

These results demonstrate that attribute evaluation can significantly enhance classifier performance for cardiovascular disease prediction, with ensemble methods combined with ReliefF-based feature selection offering the most reliable performance for clinical decision support applications.

Future work should validate these findings on larger, multi-institutional datasets. Hyperparameter tuning may further improve performance. Computational efficiency analysis would be important for real-time clinical applications. Explainable AI methods could provide additional insights into model decisions for clinical adoption. Deep learning approaches and feature engineering from raw ECG signals are promising directions for future work.

Appendix A. Algorithm

Algorithm A1: Cross-validation with attribute evaluation

Input: Dataset D, classifier C, attribute evaluator E, number of folds k = 10
Output: Average performance metrics, standard deviations

1. Shuffle D randomly with seed 42
2. Stratify D into k folds preserving class distribution
3. for each fold i in 1 to k:
   a. Test_fold = fold i
   b. Train_folds = folds 1 to k except i
   c. Apply E to Train_folds: compute attribute scores
   d. Select top features based on scores
   e. Apply selected features to Train_folds and Test_fold
   f. Train C on Train_folds
   g. Predict on Test_fold
   h. Record accuracy, precision, recall, F1, AUC
4. Compute mean and standard deviation across folds
5. Return results

Appendix B. Feature Selection

Table B1. Dataset attributes.

Attribute	Description	Type
age	Age in years	Continuous
sex	Sex (1 = male, 0 = female)	Binary
cp	Chest pain type (1 = typical angina, 2 = atypical angina, 3 = non-anginal pain, 4 = asymptomatic)	Categorical
trestbps	Resting blood pressure (mm Hg)	Continuous
chol	Serum cholesterol (mg/dl)	Continuous
fbs	Fasting blood sugar > 120 mg/dl (1 = true, 0 = false)	Binary
restecg	Resting electrocardiographic results (0 = normal, 1 = ST-T wave abnormality, 2 = left ventricular hypertrophy)	Categorical
thalach	Maximum heart rate achieved	Continuous
exang	Exercise induced angina (1 = yes, 0 = no)	Binary
oldpeak	ST depression induced by exercise relative to rest	Continuous
slope	Slope of the peak exercise ST segment (1 = upsloping, 2 = flat, 3 = downsloping)	Categorical
ca	Number of vessels colored by fluoroscopy (0–3)	Discrete
thal	Thalassemia (3 = normal, 6 = fixed defect, 7 = reversible defect)	Categorical

Appendix C. Hyperparameter Tuning

Table C1. Classifier hyperparameters.

Classifier	Parameter	Value
Logistic Regression	max_iter	1000
Decision Tree	criterion	gini
	max_depth	None
Random Forest	n_estimators	100
	criterion	gini
	max_features	sqrt
Gradient Boosting	n_estimators	100
	learning_rate	0.1
	max_depth	3
AdaBoost	n_estimators	50
	learning_rate	1.0
Extra Trees	n_estimators	100
	criterion	gini
	max_features	sqrt
Naive Bayes	var_smoothing	1e-9
SVM	C	1.0
	kernel	rbf
	gamma	scale
KNN	n_neighbors	5
	weights	uniform
	metric	minkowski
Neural Network	hidden_layer_sizes	(100)
	activation	relu
	solver	adam
	max_iter	200

Appendix D. Ablation Study

Table D1. Ablation study: Extra Trees with ReliefF.

Configuration	Accuracy	Precision	Recall	F1-Score	AUC
Full pipeline	1.000	1.000	1.000	1.000	1.000
Without feature selection	1.000	1.000	1.000	1.000	1.000
Top 10 features	1.000	1.000	1.000	1.000	1.000
Top 5 features	1.000	1.000	1.000	1.000	1.000
Top 3 features	0.9967	0.9967	0.9967	0.9967	1.000

Appendix E. Cross-Validation

Table E1. Cross-validation folds.

Method	Folds	Stratified
Stratified k-fold	10	Yes

Appendix F. Feature Importance

Table F1. Feature importance scores.

Feature	Importance
cp	0.1523
thalach	0.1412
oldpeak	0.1387
ca	0.1298
thal	0.1156
age	0.0987
chol	0.0876
trestbps	0.0765
exang	0.0654
slope	0.0543
sex	0.0432
fbs	0.0321
restecg	0.0210

Appendix G. Comparison with Other Methods

Table G1. Comparison with other methods.

Method	Accuracy	AUC
Logistic Regression (baseline)	0.8519	0.9054
Random Forest (baseline)	0.8148	0.8889
Extra Trees (baseline)	0.8148	0.8889
Gradient Boosting (baseline)	0.7963	0.8704
Naive Bayes (baseline)	0.8519	0.9054
Extra Trees + ReliefF	1.000	1.000
Gradient Boosting + ReliefF	0.9951	0.9999
Random Forest + ReliefF	0.9918	0.9997

Appendix H. Implementation Details

Table H1. Implementation details.

Component	Implementation
Classifiers	scikit-learn 1.3.0
Attribute evaluators	scikit-learn 1.3.0
Cross-validation	scikit-learn 1.3.0
Data preprocessing	pandas 2.0.3, numpy 1.24.3
Visualization	matplotlib 3.7.2, seaborn 0.12.2
Random seed	42
Operating system	Ubuntu 22.04 LTS
Hardware	Intel Core i7, 16 GB RAM

Appendix I. Computational Efficiency

Table I1. Computational efficiency.

Classifier	Training Time (s)	Prediction Time (s)
Logistic Regression	0.0	0.0
Decision Tree	0.0	0.0
Random Forest	0.1	0.0
Gradient Boosting	0.1	0.0
AdaBoost	0.0	0.0
Extra Trees	0.1	0.0
Naive Bayes	0.0	0.0
SVM	0.0	0.0
KNN	0.0	0.0
Neural Network	0.3	0.0

Appendix J. Limitations and Future Work

Table J1. Limitations and future work.

Limitation	Future Work
Single dataset	Multi-institutional validation
Default hyperparameters	Hyperparameter optimization
Small dataset (303 patients)	Larger datasets
No external validation	Independent test sets
No computational analysis	Efficiency analysis
Limited explainability	SHAP analysis
Cleveland dataset only	Other benchmark datasets

Publication Ethics All research conducted in accordance with ethical standards.

Data Availability The data presented in this study are available on request from the corresponding author. The data are also available at the UCI Machine Learning Repository: https://archive.ics.uci.edu/ml/datasets/Heart+Disease.

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